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Early detection of peripheral blood cell signature in children developing beta-cell autoimmunity at a young age

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Abstract

The appearance of Type 1 diabetes (T1D)-associated autoantibodies is the first and only measurable parameter to predict progression toward T1D in genetically susceptible individuals. However, autoantibodies indicate an active autoimmune reaction, wherein the immune tolerance is already broken. Therefore, there is a clear and urgent need for new biomarkers that predict the onset of the autoimmune reaction preceding autoantibody positivity or reflect progressive beta-cell destruction. Here we report the mRNA-sequencing-based analysis of 306 samples including fractionated samples of CD4+ and CD8+ T cells as well as CD4-CD8- cell~~s~~ fractions and unfractionated PBMC samples longitudinally collected from seven children that developed beta-cell autoimmunity (Cases) at a young age and their matched controls. We identified transcripts, including interleukin-32 (*IL32*) that were upregulated before T1D-associated autoantibodies appeared. Single-cell RNA-seq studies revealed that high IL32 in Case samples were contributed mainly by activated T cells and NK cells. Further, we showed that IL32 expression can be induced by a virus and cytokines in pancreatic islets and beta-cells, respectively. The results provide a basis for early detection of aberrations in the immune system function before T1D and suggest a potential role for *IL32* in the pathogenesis of T1D.

Introduction

Family and sibling studies in Type 1 diabetes (T1D) have implicated a firm genetic predisposition to a locus containing HLA class I and class II genes on chromosome 6 suggesting a role for CD4+ as well as CD8+ T cells in T1D pathogenesis (1–3). As much as 30-50% of the genetic risk is conferred by HLA class II molecules, which are crucial in antigen presentation to CD4+ T cells. Further, CD4+ cells reactive to beta-cell antigen peptides are found in peripheral blood and the pancreas, and typically secrete the cytokine IFNγ (4,5). CD4+ cells orchestrate adaptive immune responses, including that of antibody secreting B cells as well as cytotoxic CD8+ T cells. Indeed circulating autoantibodies against beta-cell antigens may appear years before the clinical onset. Further, a cytolytic CD4+ subtype might directly contribute to target cell killing (6).

Although HLA class II is associated with the development of autoantibodies, HLA class I seems to be more strongly linked to disease progression (7). Histological analysis of pancreatic sections of cadaveric donors with T1D revealed that HLA class I is highly expressed in islets (8,9). Moreover, CD8+ cells are the most abundant cell type during insulitis (10), and the islets contain CD8+ cells specific for T1D autoantigens (11). Thus, the autoimmune cascade in T1D might be initiated by self-reactive CD4+ cells that activate B cells to produce autoantibodies that target the beta-cells and unleash the cytotoxic activity of the autoreactive CD8+ cells. The environmental factors triggering and driving the autoimmunity in T1D are poorly defined, but the disease has been associated with viral infections (12), diet in early childhood (13), and reduced diversity of gut microbiota (14).

Currently, the appearance of T1D-associated autoantibodies is the first and only measurable parameter to predict progression toward T1D in genetically susceptible individuals. Although the disease progression rate varies considerably, children with genetic HLA risk expressing at least two T1D autoantibodies will very likely progress to clinical disease during the next 15 years (15). However, autoantibodies are poor prognostic markers for the timing of the clinical presentation of T1D. The appearance of autoantibodies indicates an active autoimmune reaction, wherein the immune tolerance is already broken. Therefore, there is a clear and urgent need for new biomarkers that predict the onset of the autoimmune reaction preceding autoantibody positivity or reflect progressive beta-cell destruction. Such markers would present a window for early intervention aimed at complete disease prevention. Earlier, we reported changes in whole-blood transcripts and serum proteins before the detection of diabetes-associated antibodies in children who later progressed to T1D (16,17). Therefore, we hypothesized that a comprehensive analysis of the transcriptome of longitudinal cellular samples including CD4+ and CD8+ T cells will lead to the identification of new early biomarkers.

Research Design and Methods

Study cohort

Samples were collected as part of the DIABIMMUNE study (FP7 grant no. 202063) from Finnish (n=10) and Estonian (n=4) participants (**Supplementary Table 1**). The HLA-DR-DQ genotypes were analysed as described earlier (18). 836 children with HLA-DR-DQ risk allele were monitored and sampled at 3, 6, 12, 18, 24 and 36 months of age. The study protocols were approved by the ethical committees of the participating hospitals, and the parents gave their written informed consent. Autoantibodies against insulin (IAA), glutamic acid decarboxylase (GADA), islet antigen-2 (IA-2A), and zinc transporter 8 (ZnT8A) were measured from serum with specific radiobinding assays (19). Islet cell antibodies (ICA) were analysed with immunofluorescence in autoantibody-positive subjects. The cut-off values were based on the 99th percentile in non-diabetic children, which were 2.80 relative units (RU) for IAA, 5.36 RU for GADA, 0.78 RU for IA-2A and 0.61 RU for ZnT8A. The detection limit in the ICA assay was 2.5 Juvenile Diabetes Foundation units (JDFU). A sample was considered seropositive when any of the autoantibodies exceeded the thresholds.

Sample collections

At each study visit, 8 ml of blood was drawn in sodium-heparin tubes (Vacutainer, 368480, BD). PBMCs were isolated by Ficoll-Paque centrifugation (17-1440-03 GE Healthcare), and were suspended in RPMI 1640 medium (42401-018, Gibco) supplemented with 10% DMSO (0231-500 ml, Thermo Scientific), 5% human AB serum (IPLA-SERAB-OTC, Innovative Research), 2 mM L-glutamine (G7513, Sigma-Aldrich), and 25 mM gentamicin (G-1397 Sigma-Aldrich). After overnight incubation at -80°C, samples were stored in liquid nitrogen (-180°C). For fractionation, PBMC samples were thawed quickly in a 37°C water bath, quantitated for cell numbers and viability. On an average 90% cells were viable. Magnetic antibody-coupled beads were used for sequential positive enrichment of CD4+ and CD8+ cells (11331D and 11333D Invitrogen). RNA was isolated from the samples with AllPrep kit (80224, Qiagen), and quantity and quality were determined using Qubit RNA assay (Q32852, Invitrogen) and Bioanalyzer 2100 (Agilent), respectively.

Bulk RNA-seq of PBMC and other fractions

At least 80 ng of total RNA was processed for RNA-seq with TruSeq Stranded mRNA Library Prep kit (RS-122-2101, Illumina). The sequencing was carried out with Illumina HiSeq2500 instrument using TruSeq v3; 2 x 100 bp chemistry. The average sequencing depth was around 51 million reads. Quality control was performed using FastQC (version 0.10.0). All the samples passed the quality criteria. The reads were aligned to the human reference transcriptome, GRCh37 assembly version 75 using TopHat (version 2.0.10) (20). Average mapping percentage was 93. The concordant pairs percentage was about 89. The aligned reads were counted with *htseq-count* (HTSeq 0.6.1; overlap mode of 'intersection-strict') (21). The read counts of genes were normalized using the trimmed means of the M-values (TMM implemented in the *edgeR* (22). Coding, noncoding information were taken from ensembl. Differential expression analyses were conducted separately for coding and non-coding genes, using the *edgeR* (22). The variance of the data was estimated using the trended dispersion method. Further filtering step retained only those genes as differentially expressed (DE) that had $|\text{median } \log_2 FC| > 0.5$ and had more than 65% samples across all individuals regulated in the same direction (i.e., up- or down-regulated). These filtering steps were added to discard false positives that may arise due to the heterogeneity of the samples due to normal variation, which is non-related to T1D and outliers. A flow chart of the scheme of analysis has been shown in **Supplementary Fig. 1**.

Single-cell RNA-seq (scRNA-seq)

The concentrations of the PBMC samples varied from 0.55 to 1.80 x 10^6 cells/ml. From each sample, we aimed at the recovery of 5000 single cells, loading approximately 9000 cells on the Chromium Controller using Single Cell 3′ Solution v2 reagents and following manufacturer's instructions (CG00052 Rev B, 10x Genomics). scRNA-seq sample processing was carried out in three batches on consecutive days using the same lot of reagents and chips for all samples. The cDNA was further amplified using a Veriti Thermal Cycler (Applied Biosystems/Thermo Fisher), followed by clean-up (SPRIselect kit, Beckman Coulter). Finally, enzymatic fragmentation, end repair, A-tailing, adaptor ligation and PCR were performed to produce indexed libraries, which were sequenced with Illumina HiSeq 3000 (one sample / lane) using paired end sequencing and 26 + 98 bp read-length configuration. The data were processed using the Cell Ranger pipeline version 2.0.0 yielding on average 2546 viable cells per sample, and 114,309 reads per cell.

The reads were aligned to the human reference genome (hg19) using STAR (23). The mean raw reads per cell varied 57-200 k. QC analysis and further exploration was done using Seurat (24). After filtering steps, 18,396 cells expressing 20,830 genes were retained. For details on the filtering steps please see "Supplementary Material". The data were normalized using Seurat's default. Highly variable genes (HVGs) were selected for principal component analysis (PCA). The top 20 PCs were used in the graph-based clustering. To identify marker genes for each –cluster, cells of a single cluster were compared to the cells of all other clusters combined. A gene was considered a marker of a cluster if it was expressed in at least 25% of the cells of either of the two groups and the logFC between the cluster and all other clusters was at least 0.25.

For trajectory analysis, the pooled cells were ordered in pseudotime (i.e., placed along a trajectory corresponding to a type of biological transition, such as differentiation) using Monocle 2 (25). The analysis was performed on cells specifically from CD4+ and CD8+ T-cell clusters. For the details on the trajectory analyses, please see "Supplementary Material".

RT-PCR analysis

For PBMC samples, 50 ng of total RNA was treated with DNaseI (Invitrogen), and cDNA was synthesized with Transcriptor First Strand cDNA Synthesis Kit (Roche). For isoform-specific (*IL32α*, *β*, and γ) assay, qPCR analysis was performed in triplicate runs using SYBR Select master mix (Applied Biosystems). ΔCt values were calculated relative to *EF1α*. For CD4+ T cells and pancreatic islets, RNA was isolated using the RNeasy Mini Kit (74106, Qiagen) and RNeasy Plus Mini Kit (74134, Qiagen), respectively. Purified RNA was treated with DNaseI and cDNA was synthesized with SuperScript II Reverse Transcriptase (18064014, Invitrogen). For the detection of global *IL32*, qPCR reactions were run using a custom TaqMan Gene Expression Assay reagent (#AJ5IQA9, Thermo Scientific) in duplicate and in two separate runs. ΔCt values were calculated relative to *GAPDH*. The amplification was monitored with QuantStudio 12K Flex Real-Time PCR System, under the following PCR conditions: 10 minutes at 95 °C, followed by 40 cycles of 15" at 95 °C and 60" at 60 °C and analysed with QuantStudio Software on Thermo Cloud.

For EndoC-βH1 cells data, cDNA was synthesized using the Maxima first-strand cDNA synthesis kit as per manufacturer's recommendations (Thermo Fisher Scientific). All reactions were performed in duplicates on at least three biological replicates. *Cyclophilin-A* was used as an endogenous control. Primer sequences are presented in **Supplementary Table 2**.

ELISA

To measure secreted IL-32 levels we used IL-32 duoset ELISA kit (R&D Systems, (DY3040-05 and DY008) following manufacturer's instructions.

Intracellular staining and flow cytometry

The cells were fixed for 10 minutes in Fix buffer I (BD, 557870), followed by 45 minutes permeabilization using ice-cold permeabilization buffer III (BD, 558050). The cells were stained using APC-conjugated IL-32α antibody (R&D, IC30402A) and FITC-conjugated IFNγ antibody (Invitrogen, MHCIFG01) in PBS containing 0.5% FCS. The data were acquired in BD Fortessa and analysed using FlowJo (version 10.4.2).

EndoC-βH1 cell culture

The EndoC-βH1 human beta-cell line was obtained from Univercell Biosolution S.A.S., France. The cells were cultured as described (26). EndoC-βH1 cells were stimulated with either IL-32γ alone (100 ng/ml, R&D Systems) or in combination with a cocktail of IL-1β (5 ng/ml, R&D Systems) and IFN-γ (50 ng/ml, R&D Systems) for 24 h. RNA samples were collected at the end of each treatment and analysed by RT-qPCR.

Human CD4 T-cell isolation and culturing

CD4+ T cells were isolated from cord-blood collected from neonates born in Turku University Hospital and were cultured in IMDM containing 1%AB serum in absence (Th0) or presence (Th1) of 2.5ng/ml if IL-12 (R&D). Cells were activated with plate bound CD3 (0.5 µg/well of a

24 well-plate) and soluble CD28 (0.5 µg/ml), both from Immunotech, with or without 50 ng/ml rIL-32-γ (R&D). 12 ng/ml IL-2 was added at 48h. For IFNγ neutralization, anti-IFNγ antibody (10 µg/ml, R&D: MAB285) was used. For reactivation, cells were treated with 5ng/ml PMA (Calbiochem) and 0.5pg/ml Ionomycin (Sigma) for 5h.

Human pancreatic islets, their infection with Coxsackie B Virus

Human islets were isolated from pancreases obtained from brain dead organ donors and purified by handpicking to a purity of > 90%. Islet culturing and virus infection with Coxsackie B virus-1 (CBV-1-7-10796 (CBV-1-7) was performed as described (27). Islets were collected at the day 4 timepoint, and RNA was extracted using the RNeasy Plus Mini Kit or the AllPrep DNA/RNA Mini Kit (Qiagen). For RNA-seq, 100 ng of total RNA from three donors was used for library preparation according to Illumina TruSeq RNA Sample Preparation v2 Guide (part # 15026495). The high quality of the libraries was confirmed with Agilent Bioanalyzer 2100 and Qubit Fluorometric Quantitation (Life Technologies). The libraries were pooled in two pools and run in 2 lanes on the Illumina HiSeq 2500 instrument using 2 x 100 bp.

Results

Fractionation of PBMC sample into CD4+, CD8+ and CD4-CD8- cellular subsets reveals distinct and overlapping gene expression signatures

We performed RNA-seq of 306 longitudinal samples including unfractionated PBMCs, as well as CD4 enriched (CD4+), CD8 enriched (CD8+), and CD4 and CD8 cell depleted (CD4-CD8-) cell fractions from seven Case-Control pairs (**Table 1**). The seven Case children who developed T1D-related autoantibodies (Aab+) were selected from the DIABIMMUNE Birth Cohort (18), where HLA-susceptible children are sampled at 3–36 months of age (**Fig. 1A**). All seven children developed T1D-associated autoantibodies by the age of 2 years (**Table 1**) and four of them developed clinical T1D between the ages of 2.4 and 3.7 years. For each Case, an autoantibody-negative Control child was matched for gender, date and place of birth, and HLA-conferred risk category.

The samples clustered according to the cell fraction (**Fig. 1B**) and the clustering was not affected by Case-Control status or sampling age, indicating that cell fraction–specific differences dominated over variation derived from other factors (**Supplementary Fig. 2A and 2B**). When CD4+, CD8+ and CD4-CD8- samples from Controls were compared to the unfractionated PBMC samples (also referred to as a fraction henceforth), 889, 399, and 1002 genes were DE specifically in CD4+ (e.g., *CD28*, *CTLA4*), CD8+ (e.g., *CD8A*, *CD8B*, *KLRK1*), and CD4-CD8- (e.g., *IL1A*, *IL1B*, *IL6)* fractions, respectively (**Fig. 1C** and **Supplementary Table 3**). CD4+ and CD8+ fractions shared 1815 DE genes, of which 1803 genes (99%) were concordant (either up or down in both fractions) (**Supplementary Fig. 2C, Supplementary Table 3**). In summary, fractionation of the PBMC population based on the T-cell phenotype allowed improved detection of DE genes and enabled identification of cell subset–specific gene expression signatures.

RNA-seq analysis identifies transcriptomic changes associated with beta-cell autoimmunity

Comparison of Case samples to their respective Controls identified 51, 69, 143 and 85 genes as DE (FDR<0.05) in CD4+, CD8+, CD4-CD8- and PBMC fractions, respectively (**Supplementary**

Table 4); with a total of 278 unique DE genes in one or more fractions (**Fig. 2A**). Six genes *AMICA1*, *BTN3A2*, *IL32*, *RPSAP15*, *RPSAP58* and *WASH7P* were upregulated in the Cases in all four fractions (**Fig. 2A**). Only 16% of the DE genes have previously been reported as DE in genetically susceptible prediabetic children using microarrays (16,28,29) or RT-PCR (30–32), confirming dysregulation of these genes in children progressing to T1D. Besides protein-coding genes, 54 non-coding genes, including three antisense, two sense intronic, seven enhancer and 18 promoter-associated lncRNAs, were DE. To our knowledge, none of these lncRNAs has been linked to the aetiology of T1D (16,28–32).

Hierarchical clustering identifies co-regulated gene expression clusters associated with T1D autoimmunity

Gene- and sample-wise hierarchical clustering for each cell fraction, including PBMCs, identified a cluster, upregulated in the Case samples in all four fractions (**Fig. 2B and Supplementary Fig. 3A-D**). Interestingly, this cluster consistently contained *IL32* and *BTN3A2*, along with other fraction-specific genes (**Fig. 2C**). In the CD8+ fraction, expression of a distinct cluster, including *IFNG,* was lower in most of the Case samples than Control samples (**Supplementary Fig. 3B**). Surprisingly, in the PBMC fraction, we detected Case-specific upregulation of a cluster, including insulin (*INS*), glucagon (*CGC*) and regulin 1 alpha (*REG1A*) transcripts (**Supplementary Fig. 3D**), which are predominantly expressed in the pancreas.

To explicitly define coregulated genes in these clusters, we calculated Euclidean distances for *IL32* (in each fraction), *IFNG* (in CD8+ fraction), and *INS* (in PBMC fraction) and considered the genes with a median Euclidean distance < 2.5 across all Case-Control pairs to be co-clustering with the gene of interest (**Supplementary Table 5A**). In three of the four fractions, the *IL32* cluster included *BTN3A2*, *AMICA1*, *LARS* and *RSU1* (**Fig. 2C**). *IL32*, *AMICA1* and *BNT3A2* show concerted gene expression profiles in CD4+ samples (**Fig. 2D**). In at least two of four fractions, this cluster also comprised *TRBV4-1*, *TMEM14C*, *UROS*, *WASH7P*, *BTN3A3*, *CARD8*, *CCDC167* and *LINC01184*. The profile of these and other interesting genes are shown in **Supplementary Fig. 4A-AB.** Upon examining the overrepresented transcription factor binding sites (TFBS) on the promoters of *IL32* cluster genes, the V$IK_Q5_01 motif bound by Ikaros (IKZF1) was revealed to be among the enriched TFBS shared in both the CD4+ and PBMC fractions (**Supplementary Table 5B**). IKZF1 has been genetically associated with T1D (33). The T1D-associated risk allele rs10272724 (T) increases IKZF1 transcript level (34).

IFNG cluster of the CD8+ cells included *TBX21* (codes for TBET), *BHLHE40*, and *ZEB2*, transcription factors expressed in CD8+ T cells (35), as well as *NKG7*, *OASL*, and *KLRD1* (**Supplementary Table 5A**). ZEB2 has been reported to drive terminal effector CD8+ cell differentiation together with T-bet (36). In the PBMC fraction, *GCG* and *REG1A* were coregulated with *INS* (**Supplementary Table 4A, Supplementary Fig. 5**).

Transcriptional changes preceding the appearance of T1D-related autoantibodies are enriched in the CD8+ T-cell fraction

To identify changes that occur immediately before the first detection of T1D-related autoantibodies (i.e., seroconversion), we performed a separate differential expression analysis for the samples drawn at most 12 months before seroconversion. Altogether 121 coding and non-coding genes were DE in Cases, as compared to their matched Controls

(**Supplementary Table 4** and **Supplementary Fig. 6**). Notably, more than half of these (58%) were detected only in the CD8+ fraction. Besides *IL32*, only two other genes were common to all fractions *RPSAP58*, and *RPSAP15*, both being the pseudogenes with unknown functions with very similar expression profiles **(Supplementary Fig. 4M-T)**.

Higher *IL32* expression in Cases was validated using qRT-PCR. Interestingly, all three major isoforms (*IL32α*, *IL-32β* and *IL32γ*) were upregulated in PBMC samples in all the Case children at each of the time points including 3 months (**Fig. 3A** and **Supplementary Fig. 7**). Among these isoforms, *IL-32γ* was expressed at the highest level, followed by *IL-32β* and *IL-32α*.

Single-cell RNA sequencing (scRNA-seq) identifies T and NK cells as the *IL32* high population

To specify the cell populations responsible for the *IL32* and *INS* signatures, we performed scRNA-seq on four selected Case and their nearest matched Control PBMC samples where the expression of *IL32* or *INS* was high (or low) based on the bulk RNA-seq data (**Supplementary Table 6**). Unsupervised clustering of 18,396 single cells from all eight PBMC scRNA-seq runs identified 13 clusters (**Fig. 3B and Supplementary Fig. 8**). The two largest clusters expressing high *CCR7* were merged as one cluster of naive T cells reducing the number of clusters to 12. Clusters named as *RGCC+ T cells*, *CD62L+ T cells*, and *Activated Th cells* expressed lower levels of *CCR7*. *Activated CD8+ T cells* cluster expressed high levels of *CD8A* and *CD8B* as well as *NKG7* and two separate clusters of CD8+ T cells expressing either granulysin or granzyme A were observed (*Activated GNLY+ CD8+ T cells* and *Activated GZMA+ CD8+ T cells*, respectively). A subcluster of Activated GZMA+ CD8+ cells had higher expression of cell-cycle genes (e.g., *STMN1*, *TUBA1B*) and was named Activated proliferating GZMA+ CD8+ T cells. An

NK cell cluster was positive for expression of *CD56*, *NKG7*, and *GNLY* and negative for *CD8A* and *CD3E*. A B-cell cluster was identified by the expression of *MS4A1*, *CD79A* and *CD79B*, whereas the Monocyte/DCs cluster was composed of cells expressing *CD14* or *FCGR3A, LYZ and TYROBP*. Interestingly, the expression of many HLA class II molecules was as high in B cells as in monocytes, suggesting high antigen-presentation potential.

The contribution of different Case or Control samples to the cells in a given cellular population (cluster) varied from cluster to cluster (**Supplementary Fig. 9** and **10A-B**). The naive T cells cluster was dominated by the cells from the Control samples ($p<0.05$) whereas the *Monocyte/DC* cluster had more cells from Cases ($p<0.005$, **Supplementary Fig. 10B**). Case 9, with the highest *IL32* expression levels in the bulk RNA-seq data, dominated the *CD62L+ T-cell* cluster, *Activated NK cells*, and most clearly, *Activated and proliferating GZMA+ CD8+ T cell* clusters (**Supplementary Fig. 10B**). Conversely, Control children 5 and 9 seemed to dominate the cluster of *Developing T cells* expressing pre-T-cell receptor *PTCRA* suggesting the presence of immature T cells in those samples.

Insulin, glucagon, or *REG1A* expression were not detected even in the *INS*-high samples of Cases 5 and 9, leaving the origin of these transcripts in bulk RNA-seq as an open question. In contrast, *IL32* expression was clear, and as expected, it was explicitly over-expressed in the Case samples (**Supplementary Fig. 11**). *IL32* was expressed at a very low level in Monocyte/DC, B cells, and *Developing T cell* clusters, however, it was expressed at higher levels by both the T cells and the NK cells **(Fig. 3C)**.

To further define the relationship of *IL32* expression and T-cell activation status, we performed separate trajectory analyses for the CD4+ and CD8+ T cells. The less activated precursor populations (naive and RGCC+ T cells), which detect CD4 and CD8 transcripts in low abundances, were used as starting point for the trajectory analyses. The results revealed three major cellular branches (I-III) in the data both in CD4+ as well as CD8+ T cells (**Fig. 3D-I**). The branch I consisted mainly of naive T cells, among which cells from the Control samples were enriched (**Fig. 3E and H, Supplementary Fig. 12**). In contrast, the highest levels of *IL32* were expressed by cells close to the end points of branches II and III, corresponding to more advanced stages of differentiation (**Fig. 3F** and **I, Supplementary Fig. 12**).

IL-32 and IFNγ are co-expressed by Th1 cells

To further study IL-32 expression, we measured intracellular IL-32 expression at protein level in CD4+ T cells isolated from human umbilical cord blood. Cells were either activated through CD3/CD28 in the absence of cytokine (Th0) or were differentiated towards a Th1 cell lineage for 72h. IL-32 was induced upon activation and, unlike IFNγ, was expressed both in Th0 as well as Th1 cells **(Fig. 4A)**. Interestingly in Th1 cells, most IFNγ-producing cells were also positive for IL-32 (**Fig. 4A; Supplementary Fig. 13A**) and the proportions of IL-32-positive cells and the per cell IL-32 levels were higher in IFNγ-producing Th1 cells than in Th0 cells (**Fig. 4B-C**). Furthermore, neutralization of IFNγ significantly reduced IL-32 secretion by Th1 cells (**Fig. 4D**) confirming that IFNγ positively regulates *IL32* expression. IL-32 expression was also induced by IL-32 itself in Th1 cells, both at the RNA level (**Fig. 4E**) as well as in the culture supernatant upon 48 h re-stimulation after seven days of polarization in Th1 condition (**Fig. 4F**).

Pancreatic beta-cells can express IL32 in response to cytokine stimulation and viral infection

To study how the elevated *IL32* expression may influence beta-cell function, we treated human EndoC-βH1 beta-cell line for 24 h with either recombinant IL-32γ alone or in combination with the pro-inflammatory cytokines IL-1β and IFNγ. In agreement with earlier published data on pancreatic ductal cancer cell lines (37), IL-1β and IFNγ significantly induced *IL32* expression in human EndoC-βH1 cells **(Fig. 4G)** However, addition of IL-32γ did not further enhance i) the IL-1β- and IFNγ-induced *IL32* expression, ii) the expression of inflammatory cytokines *TNFA, IL6* and *IL8* (**Fig. 4G**), iii) the expression of ER stress marker genes (ATF3, ATF4, ATF6, HSPA5, CHOP, sXBP1) (**Supplementary Fig. 13B**) in EndoC-βH1 cells. Furthermore, the IL-32γ treatment did not affect the expression of beta-cell–specific genes, such as *INS*, *MAFA* or *PDX1* (**Supplementary Fig. 13C**). These results suggest that, while IL-32 does not appear to directly affect the survival or the differentiation status of the beta-cells, beta-cells actively contribute to inflammation in the islets by secreting IL-32 upon stimulation by cytokines.

Coxsackie B viruses are beta-cell trophic viruses that have been linked to the development of T1D (38–43). To study the possible trigger of *IL32* expression in beta-cells, we infected purified human pancreatic islets of three cadaveric donors with Coxsackie B virus CBV1-7 strain. Infection by the virus led to the induction of *IL32* expression in the islets (**Fig. 4H**). We further validated this finding in the three islet samples used for RNA-seq as well as one additional islet sample using qRT-PCR assays and found a consistent increase in the IL32 expression upon CBV1-7 infection (**Fig. 4I**). Taken together these results suggest that upon a viral infection **(Fig. 4H-I)** or a cytokine rush **(Fig. 4H)**, beta-cells may upregulate IL-32 secretion contributing to inflammation.

Discussion

We identified a panel of novel molecular players detected early in children who developed T1D-associated autoantibodies or even the clinical disease at a young age. Since the immunological changes related to T1D are known to be strongest among the T1D cases diagnosed at an early age (44), focusing on this age group should enhance the possibility to detect aberrations in the immune system predisposing to the disease. In this study, unbiased RNA-seq of CD4+ and CD8+ cells revealed many T1D-associated DE transcripts not previously reported. Analysis of the PBMC population offers an excellent overview of stable gene expression patterns but, at the same time, appears to mask some of the subtle fraction-specific changes. Such changes included upregulation of *CD52* detected only in the CD4+ cell fraction and downregulation of the *IFNG* and associated transcription factors ZEB2, TBX21 and ZNF683 detected specifically in the CD8+ cells. Further studies are needed to understand whether at-risk children have defects in formulating effector CD8+ response, or their effector CD8+ cells have homed to the sites of inflammation in the pancreas.

We selected *IL32* as our candidate for functional studies because it has not been linked to seroconversion before, it is easy to measure with available assays from clinical samples, and as a secreted molecule it can potentially affect the function of several cell types in paracrine and systemic fashion. Increased expression of IL32 in Cases across many cell types before seroconversion suggest that *IL32* is a critical member of the immunological signature characteristic for children developing beta-cell autoimmunity.

IL-32 is expressed by many immune and epithelial cells and has been described to be proinflammatory (45). However, to our knowledge, it has not been associated with human beta-cell autoimmunity. In contrast, *IL32* is downregulated in CD4+ T cells from recently diagnosed adult T1D patients (46) which along with our findings suggests a dynamic changes in immune cell signalling during the pathogenesis of the disease. On the other hand, IL-32 overexpression was observed in synovial biopsies of patients with rheumatoid arthritis (47), in inflamed mucosa of inflammatory bowel disease patients (48), and in the serum of myasthenia gravis patients (49) indicating a connection between IL32 and autoimmunity in general. In T cells, IL-32 is induced by T-cell activation, and it modulates human CD4+ T-cell effector function by promoting Th1 and Th17 responses (50). Both Th1 and Th17 cells have been linked to the T1D pathogenesis in both human and mouse(50). The *IL32* gene has been identified only in higher mammals, excluding rodents. Nonetheless, human IL-32γ transgenic mice exhibit impaired glucose tolerance, increased levels of IFNγ and other proinflammatory cytokines in the pancreas, as well as accelerated streptozotocin-induced experimental T1D (51). No specific cell-surface receptor for IL-32 has been identified, but it may act through cell-surface integrins or proteinase-3 (52).

Our results showed that *IL32* was often co-regulated with genes previously linked to autoimmunity. For example, the BTN3 gene cluster reside in the extended MHC Class I locus. Further, BTN3 genes have been associated with T1D in a genetic screen, especially in the case of BTN3A2 (53). AMICA1, is a plasma membrane protein involved in lymphocyte migration through its interaction with Coxsackie-adenovirus receptor (CAR) expressed in epithelial cells and has been associated with multiple sclerosis (54). An analogous scenario could be envisaged for T1D: CAR is expressed by the pancreatic islet cells, including beta-cells (42), and its expression is elevated in autoantibody-positive individuals and T1D patients (55) suggesting that it might help recruit T cells to the islets. Interestingly, the findings point to human-specific phenomena not detectable in mouse models as IL-32 and the BTN3 protein family are not encoded by the mouse genome.

The strength of our study is that the children studied here comprise a homogeneous population with the early appearance of T1D-associated autoantibodies. Increasing evidence suggests that T1D can be subdivided to different phenotypes, e.g. characterized by age-dependent B-cell infiltration in the pancreas (56), defect in Coxsackievirus-induced antibody response in children with early insulin autoimmunity (57), or rapid versus slow progression to clinical disease (58). Thus, our results may not apply to “late progressors”, adolescents, and adults. Although the analysis of the global transcriptome of T-cell subsets of prediabetic children over the period of seroconversion is unique, a limitation of the current study is the analysis of only seven Aab+ children. The results of this study need to be validated and expanded on a larger cohort of prediabetic children but serve as a starting point for better understanding of immunological changes preceding the clinical onset of the disease. In the future, we are interested in addressing if our findings on cellular level are reflected also in IL-32 levels in plasma as well as to study if IL-32 alone or in combination of other identified molecules would have sufficient sensitivity and specificity as early indicators for T1D.

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Author Contributions

JS conducted bioinformatic analyses. HK, ST and UU led biological interpretation of the results. HK, ST, JS and UU drafted the manuscript. HK, JS and UU prepared the figures. HK was responsible for supervising EK. TH, HS, JH, AP and VT were responsible for sample collection, sample storage, and further clinical information of the children. RLu was responsible for study design, cell fractionation, sample analysis and data production. TL provided expertise in scRNA-seq study design, sample and data analysis, and interpretation of the results. RA, EK and OR were responsible for the isoform-specific *IL32* RT-PCR assay and the intracellular IL-32 staining in T cells and interpretation of the results. VC and TO carried out the experiments and interpreted the results of the studies in pancreatic beta-cells. MKA and GF were responsible for experiments on virus-infected pancreatic islets. HL was responsible for computational data analysis, interpretation of the results, editing the manuscript and supervising JS. MK was responsible for the DIABIMMUNE study design, sample collection, sample storage, clinical information of the children, directing of the clinical study, interpreting the results and editing the manuscript. RL was responsible for study design, sample and data analysis, interpretation of the results, writing the manuscript and supervision of the study. All authors contributed to the final version of the manuscript.

Guarantor Statement

RL and HL are the guarantors of this work, and had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

Prior Presentation Information

The results described in this study have not be presented in any conference/proceedings elsewhere.

Conflict of Interests

The authors declare that they have no conflict of interest.

Data and Resource Availability

All the raw data will be deposited to European genome-phenome archive (EGA) for access. The study does not involve any non-commercial reagents and tools.

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FIGURE LEGENDS

Figure 1. **Fractionation of PBMC sample into CD4+, CD8+ and CD4-CD8- cellular subsets reveals distinct and overlapping gene expression signatures. A)** Outline of the sample collection and cell fractionation. **B)** tSNE (t-Distributed Stochastic Neighbor Embedding) visualization of the log2-transformed expression data (without any filtering steps) coloured according to cell fraction information. **C)** Number of DE genes, when CD4+, CD8+ and CD4-CD8- fractionated samples were compared to their original PBMC aliquots. The functionally important fraction-specific upregulated genes are highlighted in red. Analysis was restricted to healthy Controls only. For the gene lists, see **Supplementary Table 3**.

Figure 2. **RNA-seq analysis identifies transcriptomic changes associated with beta cell autoimmunity. A)** Number and overlap of DE genes between Cases and Controls identified in cell fractions analysed. Genes shared between all four fractions are highlighted. **B)** Heatmap of the genes DE in CD4+ T cells between the Cases and Controls. Values are presented as $\log_2$FC (truncated between [-2, 2]) between each Case-Control pair at each timepoint (3–36 months) and standardized to the mean of each gene. Genes co-regulated with *IL32* (< 2.5 Euclidean distance) are marked with red box and text. Additional information about the samples is marked on top of the heatmap. 'Before/After SC' informs whether the Case-sample was collected before (Before SC) or after seroconversion (After SC). 'Pair Info' provides the case-control pair information. The 'SC / T1D' annotation indicates whether the Case has progressed to clinical T1D diagnosis (T1D) or not (SC). **C)**

Number and overlap of *IL32* co-clustered genes in indicated cell fractions. Genes regulated at least in two fractions are highlighted. **D)** Profiles of *IL32*, *AMICA1* and *BNT3A2* in CD4+ samples, presented in $\log_2$ RPKM scale. For individual profiles, see **Supplementary Fig. 4**. The Case-Control pairs are grouped according to the diagnosis of the Cases. T1D= Case has been diagnosed with clinical T1D, SC=Case has seroconverted to autoantibody positivity.

Figure 3. scRNA-seq of PBMCs identifies T and NK cells as *IL32* high populations

A) Expression of *IL32γ* isoform in longitudinal PBMC samples of Cases and their Controls (n=7+7), assayed by qRT-PCR. For alpha and beta isoforms, please see **Supplementary Fig. 7. B)** tSNE clusters from the pooled data from all scRNA-seq samples (4 Cases and 4 Controls, in total 18 396 cells). Clusters are named according to the expression of classical marker genes, such as *CD8A* (for details and marker gene list, please see **Supplementary Fig. 8**; for contribution of each sample per cluster, please refer to **Supplementary Fig. 9** and **10**. **C)** Expression of *IL32* in the 12 cell clusters (natural logarithm transformation with addition of 1). For Case-Control comparison, please see **Supplementary Fig. 11**. **D-F)** trajectories emerging when using the data from CD4+ cells and the precursor cells, as well as **G-I)** from CD8+ and the precursor cells. Here, precursor cells refer to cells from the naive and RGCC+ T cell clusters. For the trajectory analysis of all the cells from all clusters as well as the breakdown of each individual cluster, please see **Supplementary Fig. 12**. In **D)** and **G)**, cells are coloured based on the contributions from different tSNE clusters. In **E)** and **H),** cells are coloured by the Case (orange) or Control (grey) status. In **F)** and **I),** cells are coloured by the intensity of IL32 expression ($\log_{10}$ transformation with addition of 0.1).

Figure 4. Virus- and cytokine induce *IL32* expression by pancreatic beta cells

A) Representative FACS dot plots showing IFN-γ and IL-32 double staining in Th0 and Th1 polarized CD4+ cells. Staining controls and two other replicates are shown in **Supplementary Fig. 13A.** Percent IL-32 positive cells as well as Median Fluorescence Intensity (MFI) data (mean+/- SD) from all the three replicates are shown in **B) and C),** respectively. Statistical significance was determined by paired two tailed t-test. **D)** IL-32 secretion in culture supernatant as measured by ELISA. Cells were cultured in Th0/1 condition for 72 h in the presence (+) or absence (-) of anti-IFNγ. The expression plotted is relative to Th0 (-). Statistical significance was determined by paired two tailed t-test. **E)** *IL32* expression in non-polarized Th0 cells and cells differentiated to Th1 for 72h in the presence (+) or absence (-) of IL-32γ as measured by the Taqman assay. The expression is calculated relative to *EEF1A*. Statistical significance was determined by unpaired two tailed t-test. **F)** IL-32 secretion in culture supernatant as measured by ELISA. Cells were cultured in Th0/1 condition for 7 days in the presence (+) or absence (-) of IL-32γ, followed by washing and re-stimulation by PMA and ionomycin for 48 h. The expression plotted is relative to Th0 (-). Statistical significance was determined by paired two tailed t-test. **G)** Expression of the *TNFA* and *IL6* or *IL8* and *IL32* genes when the EndoC-βH1 cells were stimulated with IL32γ alone or in combination with other inflammatory cytokines for 24 h. The fold-change is calculated compared to non-treated (NT) cells. The results shown here are from four independent biological replicates (mean +/- SD). Statistical significance was determined by paired two tailed t-test. **H)** *IL32* expression as measured in an RNA-seq experiment where pancreatic islets were infected with CBV1-7.

Statistical significance was determined by EdgeR. **I)** *IL32* expression in virus infected pancreatic islets as measured by RT-qPCR Taqman assay. The expression is calculated as 2^-(dCt). The statistical significance is determined by paired two-tailed t-test. *= p-value <0.05, ** = p-value <0.01, and *** = FDR<0.001.

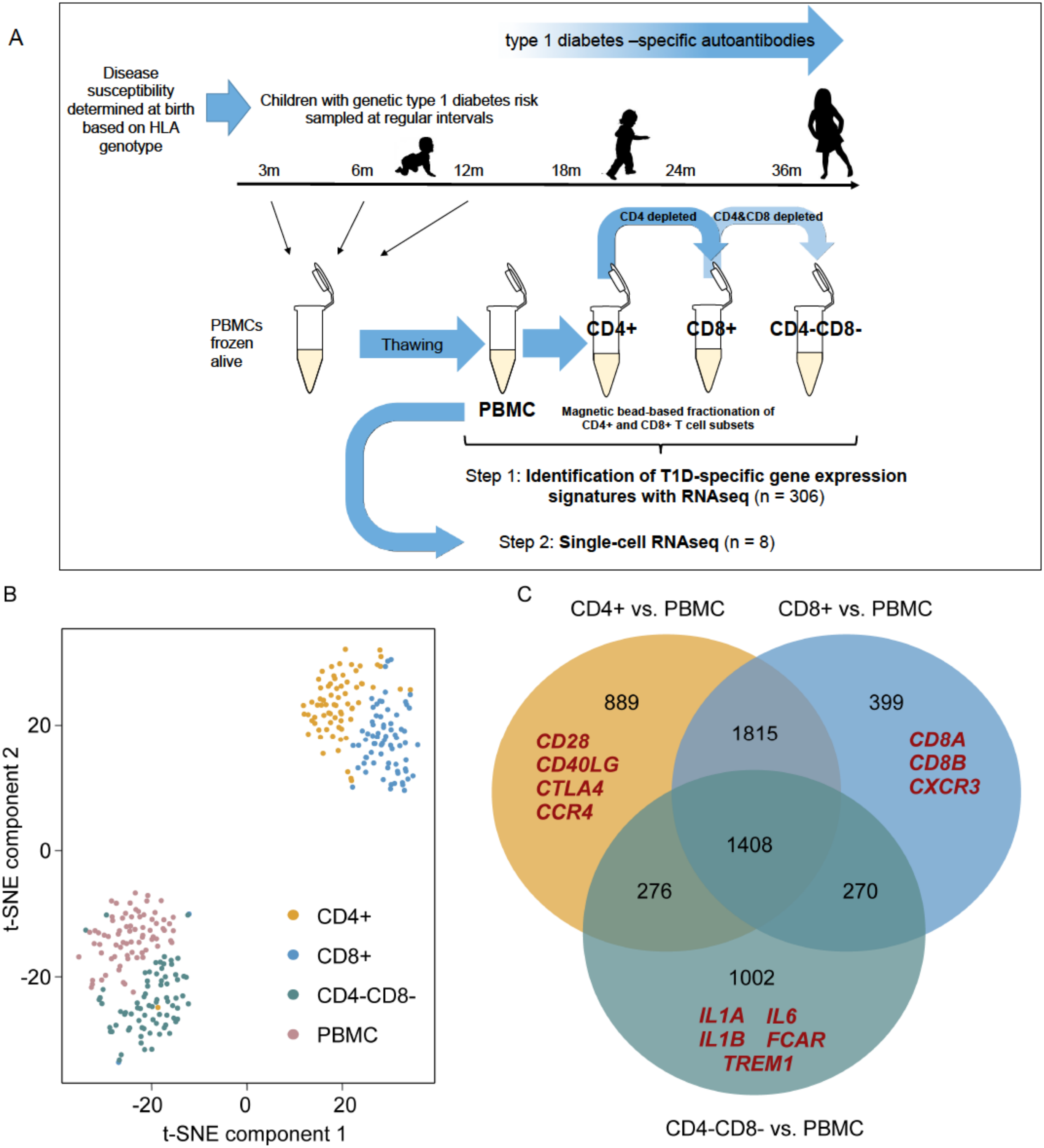
TABLES

Table 1. Summary of the Case and Control children sampled at the age of 3–36 months.

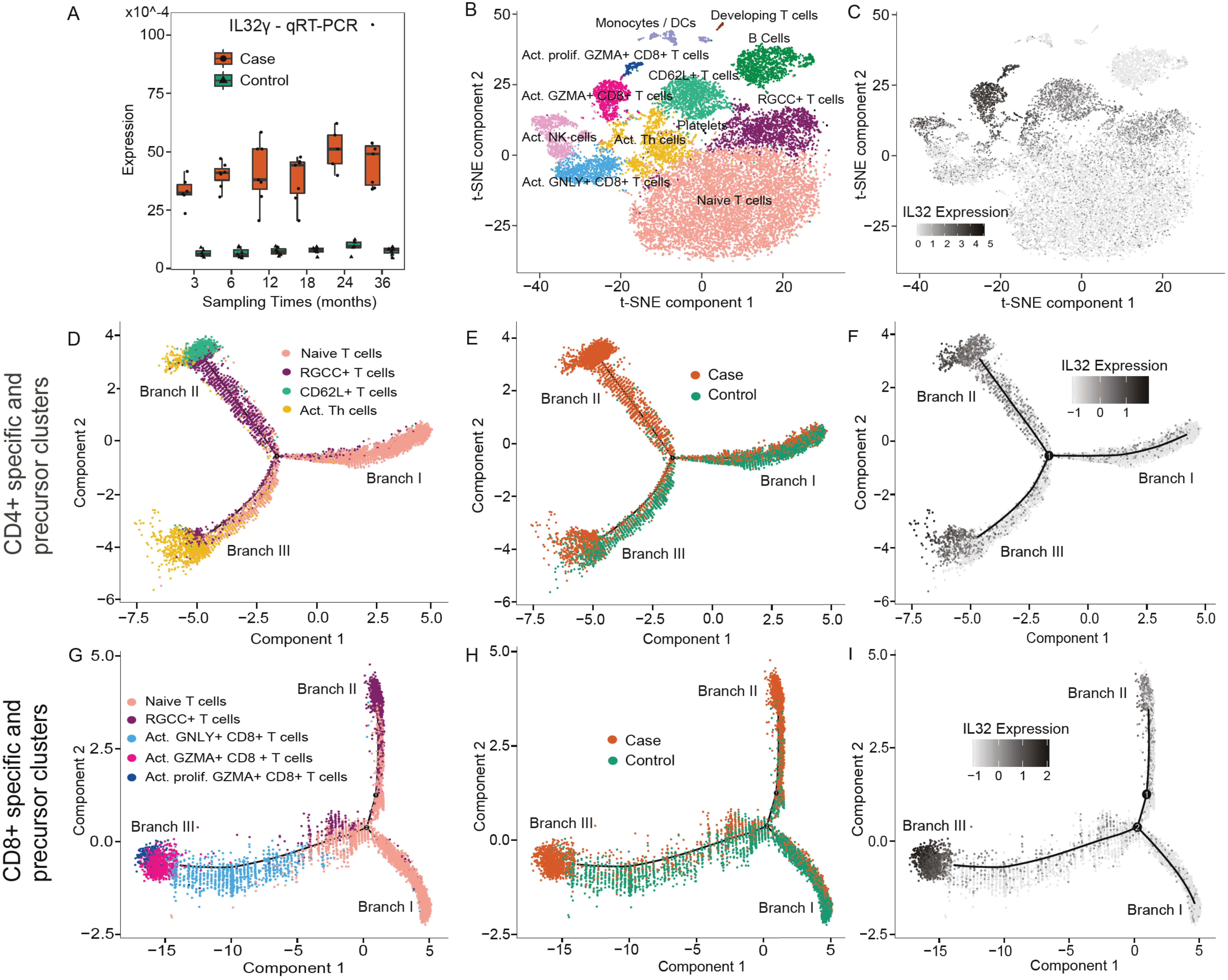
Case #	Gender	Seroconversion* age	First autoantibodies	Age at T1D diagnosis	Matched control #
Case 1	Female	12 mo	IAA, GADA	3.2 y	Control 1
Case 2	Male	12 mo	IAA	-	Control 2
Case 3	Male	18 mo	IAA, ICA	3.7 y	Control 3
Case 5	Female	24 mo	IAA, IA-2A, ZnT8A, ICA	2.6 y	Control 5
Case 9	Male	18 mo	IAA, GADA, ICA	-	Control 9
Case 10	Male	12 mo	IAA, GADA	-	Control 10.1 Control 10.2
Case 11	Female	18 mo	GADA	2.4 y	Control 11

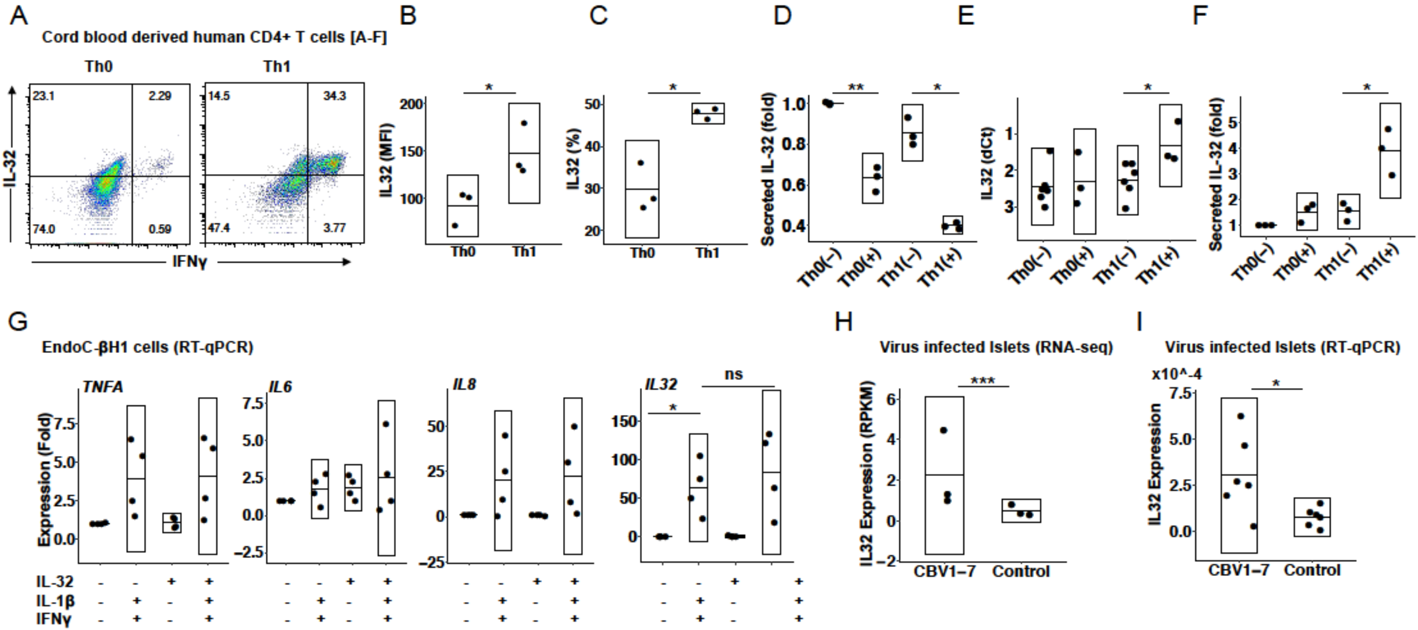
*First detection of T1D-associated autoantibodies.

For further details, see **Supplementary Table 1**.


A
type 1 diabetes –specific autoantibodies
Disease susceptibility determined at birth based on HLA genotype
Children with genetic type 1 diabetes risk sampled at regular intervals
3m
6m
12m
18m
24m
36m
CD4 depleted
CD4&CD8 depleted
PBMCs frozen alive
Thawing
CD4+
CD8+
CD4-CD8-
PBMC
Magnetic bead-based fractionation of CD4+ and CD8+ T cell subsets
Step 1: Identification of T1D-specific gene expression signatures with RNAseq (n = 306)
Step 2: Single-cell RNAseq (n = 8)
B
t-SNE component 2
t-SNE component 1
20
0
-20
-20
0
20
CD4+
CD8+
CD4-CD8-
PBMC
C
CD4+ vs. PBMC
CD8+ vs. PBMC
CD4-CD8- vs. PBMC
889
399
1815
1408
276
270
1002
CD28
CD40LG
CTLA4
CCR4
CD8A
CD8B
CXCR3
IL1A
IL6
IL1B
FCAR
TREM1

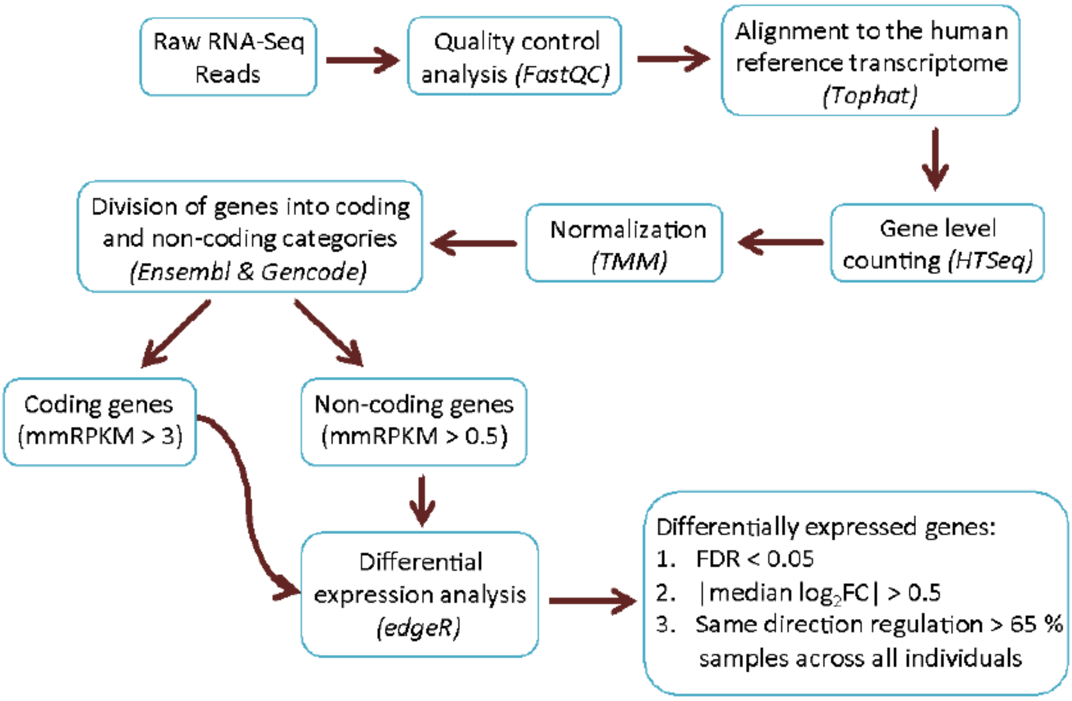

A
CD4+
CD8+
CD4-CD8-
PBMC
48
109
26
5
0
19
46
2
2
6
3
3
2
3
4
AMICA1
BTN3A2
IL32
RPSAP15
RPSAP58
WASH7P
C
CD4+
CD8+
CD4-CD8-
PBMC
1
45
7
0
0
4
39
0
1
2
2
0
1
1
2
IL32
BTN3A2
UROS
WASH7P
AMICA1
TRBV4-1
TMEM14C
LARS
RSU1
BTN3A3
CARD8
CCDC167
LINC01184
D
CD4+ cells: IL32 + AMICA1 + BTN3A2
T1D - Pair 1
T1D - Pair 3
T1D - Pair 5
T1D - Pair 11
SC - Pair 2
SC - Pair 9
SC - Pair 10
log2 (RPKM Values)
6
4
2
-12
0
12
24
Seroconversion-Centered Times (months)
Gene Name
IL32
AMICA1
BTN3A2
Group
Case
Control
B
Sampling w.r.t. SC
Pair Info
SC / T1D
FHL1
CTD−3092A11.1
RP11−632K20.2
XXyac−YRM2039.2
ENSG00000215513
LINC00665
SH2D3C
CTA−29F11.1
NAPRT1
DIP2A−IT1
SNX25
GDPD5
ABCA1
LZTS3
ABCG1
HES4
RP11−589C21.6
GADD45G
SPRY1
THBS1
TYMP
APOBEC3A
FAM26F
RPSAP58
RPSAP15
WASH7P
AP006222.2
TMEM8A
RP11−706O15.3
RP11−747H7.3
PRKXP1
AC092580.4
PDPR
CPT1A
GZMA
IL32
TRBV4−1
LINC01259
H1F0
CTA−445C9.15
SH3BP1
ENSG00000269996
LARS
RGS14
C17orf62
BTN3A2
TMEM14C
CD52
AMICA1
DGKQ
UROS
Pair3_18months
Pair 2_36months
Pair1_6months
Pair9_12months
Pair5_24months
Pair5_36months
Pair10_12months
Pair3_36months
Pair9_3months
Pair9_24months
Pair9_6months
Pair9_18months
Pair2_3months
Pair2_6months
Pair2_12months
Pair2_18months
Pair2_24months
Pair3_3months
Pair3_6months
Pair3_12months
Pair11_3months
Pair9_36months
Pair11_24months
Pair11_36months
Pair10_36months
Pair10_6months
Pair10_18months
Pair1_18months
Pair1_24months
Pair1_36months
Pair1_3months
Pair1_12months
Pair5_3months
Pair5_6months
Pair5_12months
Pair5_18months
2
1
0
−1
−2
Sampling w.r.t. SC
Before SC
After SC
Pair Info
Pair 1
Pair 2
Pair 3
Pair 5
Pair 9
Pair 10
Pair 11
SC / T1D
SC
T1D


A
x10^-4
IL32γ - qRT-PCR
Case
Control
Expression
100
75
50
25
0
3
6
12
18
24
36
Sampling Times (months)
B
Monocytes / DCs
Developing T cells
B Cells
Act. prolif. GZMA+ CD8+ T cells
CD62L+ T cells
Act. GZMA+ CD8+ T cells
RGCC+ T cells
Platelets
Act. NK cells
Act. Th cells
Act. GNLY+ CD8+ T cells
Naive T cells
t-SNE component 2
t-SNE component 1
50
25
0
−25
−40
−20
0
20
C
IL32 Expression
0 1 2 3 4 5
t-SNE component 2
t-SNE component 1
CD4+ specific and precursor clusters
D
Naive T cells
RGCC+ T cells
CD62L+ T cells
Act. Th cells
Branch II
Branch I
Branch III
Component 2
Component 1
4
2
0
−2
−4
−6
−7.5
−5.0
−2.5
0.0
2.5
5.0
E
Case
Control
Branch II
Branch I
Branch III
Component 2
Component 1
F
IL32 Expression
−1 0 1
Branch II
Branch I
Branch III
Component 2
Component 1
CD8+ specific and precursor clusters
G
Naive T cells
RGCC+ T cells
Act. GNLY+ CD8+ T cells
Act. GZMA+ CD8 + T cells
Act. prolif. GZMA+ CD8+ T cells
Branch II
Branch III
Branch I
Component 2
Component 1
5.0
2.5
0.0
−2.5
−15
−10
−5
0
5
H
Case
Control
Branch II
Branch III
Branch I
Component 2
Component 1
I
IL32 Expression
−1 0 1 2
Branch II
Branch III
Branch I
1
2
Component 2
Component 1


A
Cord blood derived human CD4+ T cells [A-F]
Th0
Th1
IL-32
IFNγ
23.1
2.29
74.0
0.59
14.5
34.3
47.4
3.77
B
IL32 (MFI)
200
150
100
Th0
Th1
*
C
IL32 (%)
50
40
30
20
Th0
Th1
*
D
Secreted IL-32 (fold)
1.0
0.8
0.6
0.4
Th0(–)
Th0(+)
Th1(–)
Th1(+)
**
*
E
IL32 (dCt)
1
2
3
Th0(–)
Th0(+)
Th1(–)
Th1(+)
*
F
Secreted IL-32 (fold)
5
4
3
2
1
Th0(–)
Th0(+)
Th1(–)
Th1(+)
*
G
EndoC-βH1 cells (RT-qPCR)
TNFA
Expression (Fold)
7.5
5.0
2.5
0.0
IL6
7.5
5.0
2.5
0.0
–2.5
IL8
50
25
0
–25
IL32
150
100
50
0
*
ns
IL-32
IL-1β
IFNγ
- - + +
- + - +
- + - +
- - + +
- + - +
- + - +
- - + +
- + - +
- + - +
- - + +
- + - +
- + - +
H
Virus infected Islets (RNA-seq)
IL32 Expression (RPKM)
6
4
2
0
–2
CBV1–7
Control
***
I
Virus infected Islets (RT-qPCR)
x10^-4
IL32 Expression
7.5
5.0
2.5
0.0
CBV1–7
Control
*

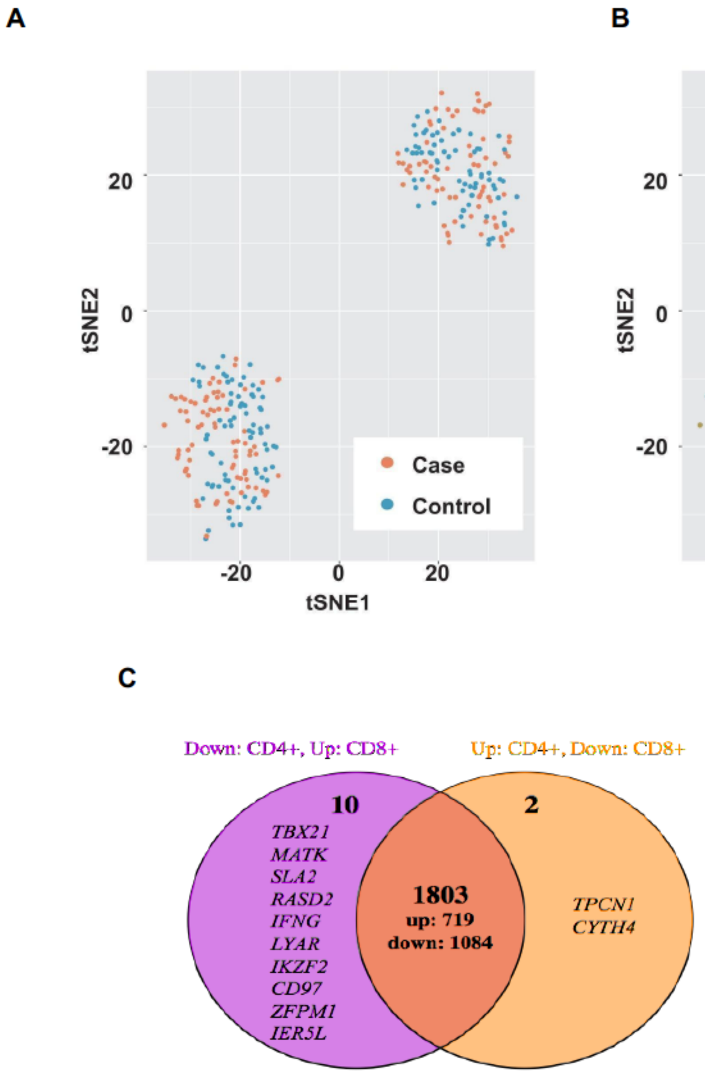
Supplementary Figures

Early detection of peripheral blood cell signature in children developing beta cell autoimmunity at a young age



Supplementary Figure 1. Related to Figure 2.

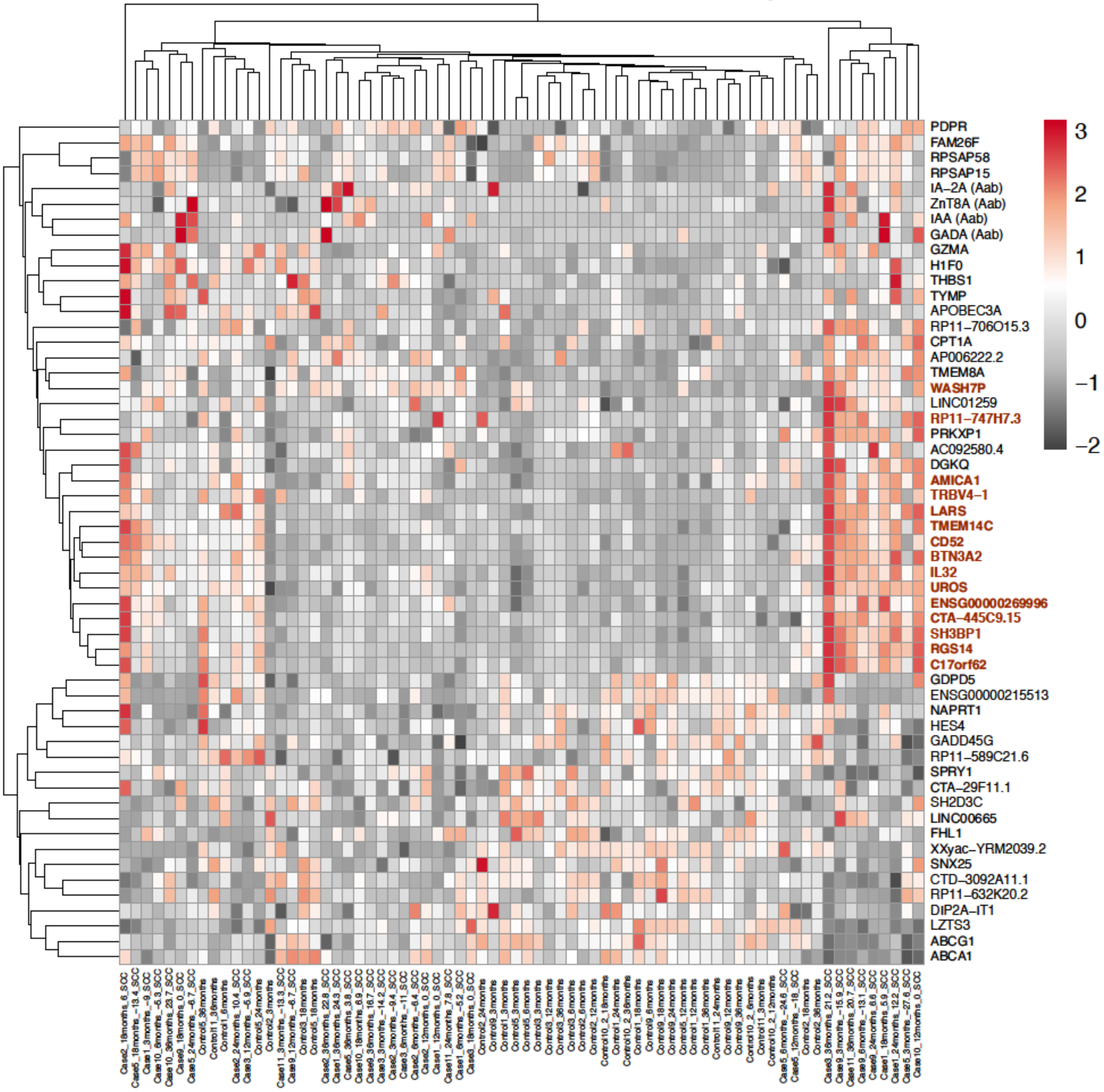
Flow chart depicting the steps taken in the differential expression analyses of the RNA-seq data in this study.



Supplementary Figure 2. Related to Figure 1.

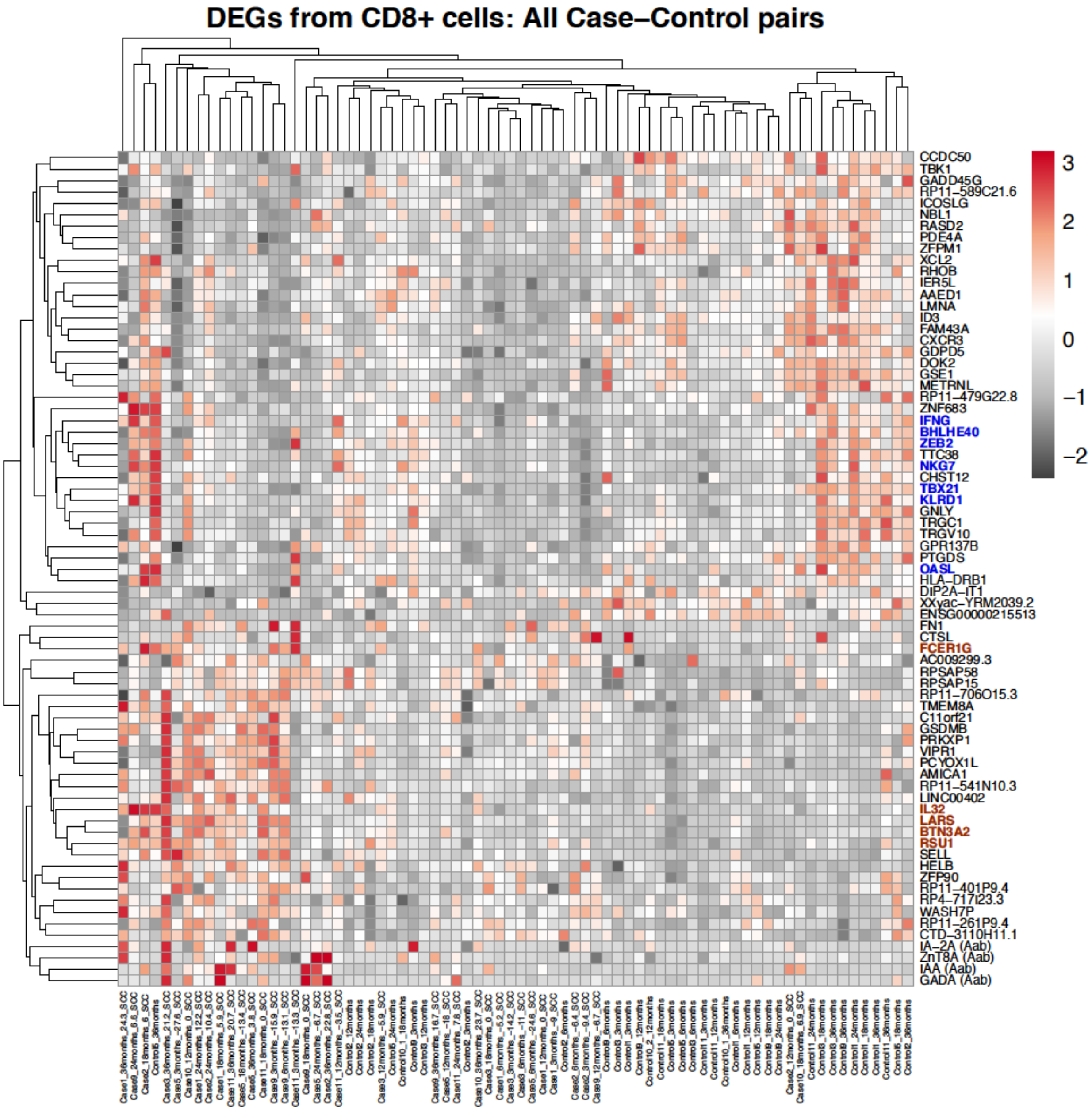
A-B) tSNE (t-Distributed Stochastic Neighbor Embedding) visualization of the log2-transformed expression data from all cell fractions and all genes. **Figure 1** was colored according to cell fractions, and here the colouring of the samples is done according to **A)** Case and Control status and **B)** age at sample collection. For further sample information, see **Table 1** and **Supplementary Table 1**. **C)** Venn diagram expanding on the 1815 genes found DE in both CD4+ vs PBMC and CD8+ vs PBMC analyses (**Figure 1C**). Here, the intersection represents the genes regulated in the same direction. For full lists of genes, see **Supplementary Table 2.**

DEGs from CD4+ cells: All Case−Control pairs



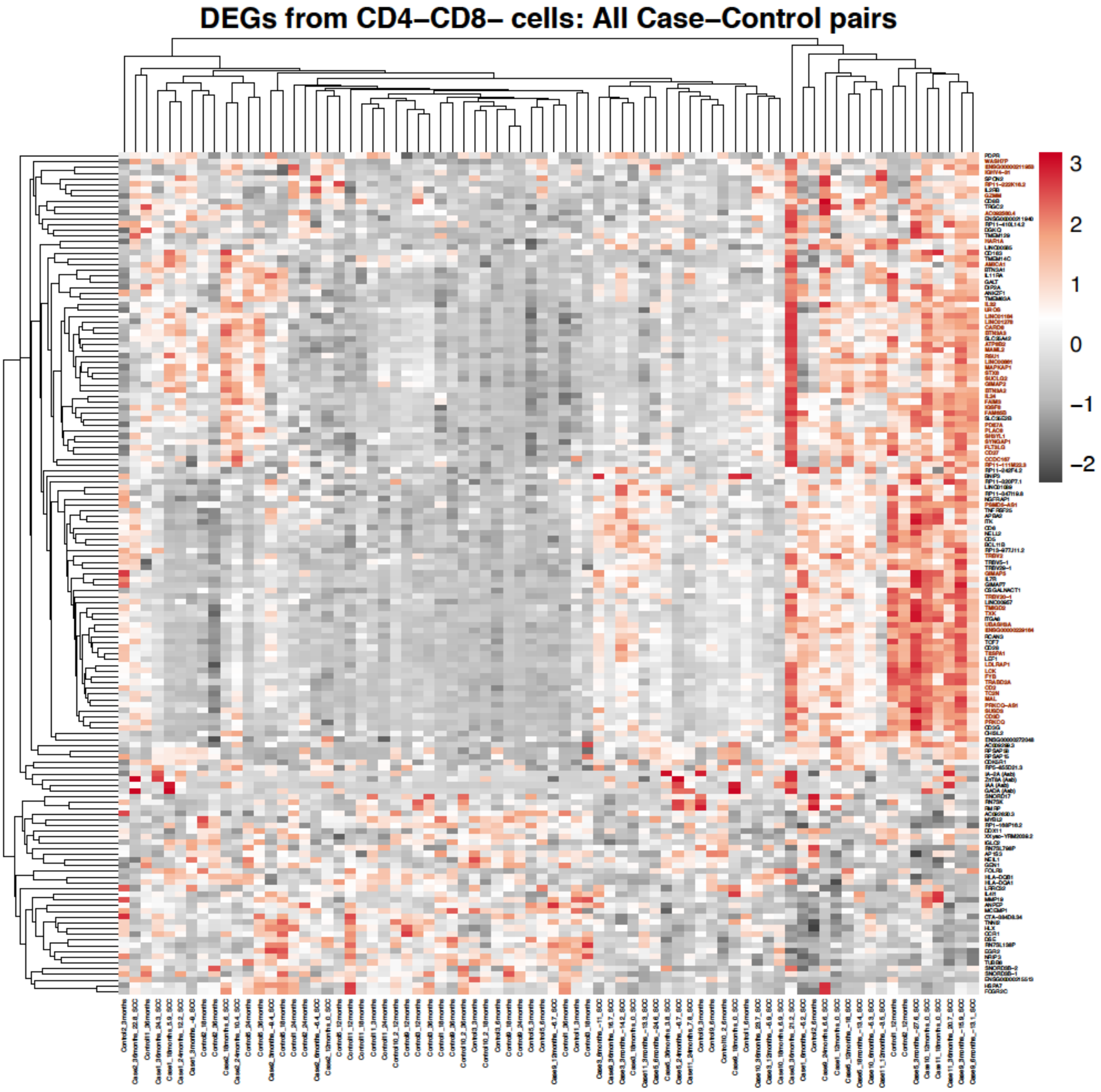
Supplementary Figure 3A. Related to Figure 2.

Hierarchical clustering of the levels of standardized autoantibodies (IAA, IA-2A, ZnT8A, and GADA) and the 51 differentially expressed (DE) genes between the Cases and Controls detected in the CD4+ fraction. Each gene's expression was standardized across samples from each case-control pair individually. Genes with an Euclidean distance (ED)< 2.5 to IL-32 (co-clustering results from k-means clustering) are marked with red text (Supplementary table 4). The samples labels along the x-axis include the sample number, case/control indicator, age of sampling in months, and months to (negative no. of months) or from (positive no. of months) seroconversion time. Here, SCC stands for seroconversion-centered, which is why the months to/from seroconversion are negative or positive.



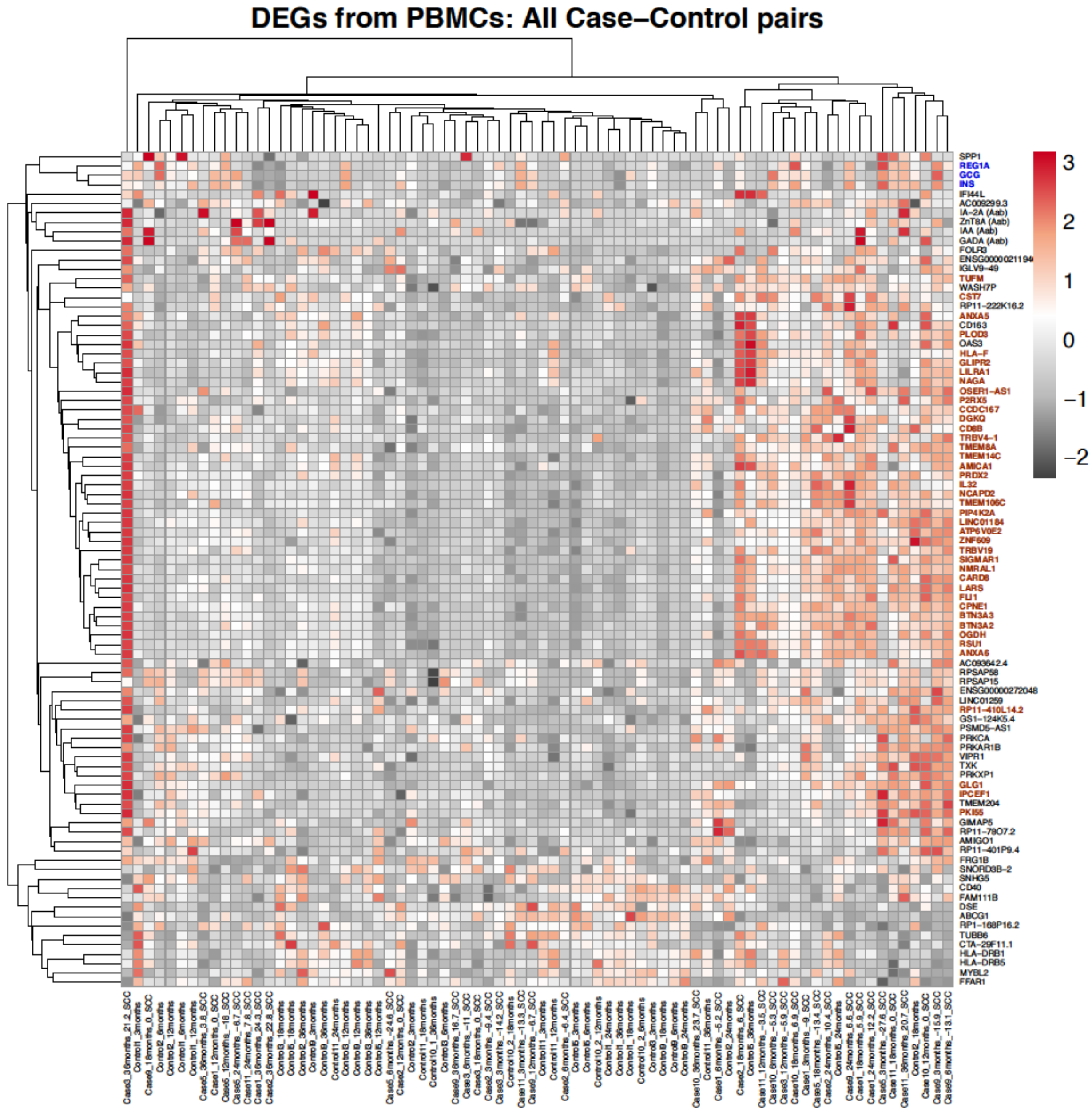
Supplementary Figure 3B. Related to Figure 2.

Hierarchical clustering of the levels of standardized autoantibodies (IAA, IA-2A, ZnT8A, and GADA) and the 69 DE genes between the Cases and Controls detected in the CD8+ fraction. Each gene's expression was standardized across samples from each case-control pair individually. Genes with an Euclidean distance (ED) < 2.5 to IL-32 (co-clustering results from k-means clustering) are marked with red text and those with ED < 2.5 to IFNG are marked with blue text (Supplementary table 4). The samples labels along the x-axis include the sample number, case/control indicator, age of sampling in months, and months to (negative no. of months) or from (positive no. of months) seroconversion time. Here, SCC stands for seroconversion-centered, which is why the months to/from seroconversion are negative or positive.



Supplementary Figure 3C. Related to Figure 2.

Hierarchical clustering of the levels of standardized autoantibodies (IAA, IA-2A, ZnT8A, and GADA) and the 143 DE genes between the Cases and Controls detected in the CD4-CD8- fraction. The expression of each gene was standardized across samples from each case-control pair individually. Genes with an Euclidean distance (ED) < 2.5 to IL-32 (co-clustering results from k-means clustering) are marked with red text (Supplementary table 4). The samples labels along the x-axis include the sample number, case/control indicator, age of sampling in months, and months to (negative no. of months) or from (positive no. of months) seroconversion time. Here, SCC stands for seroconversion-centered, which is why the months to/from seroconversion are negative or positive.

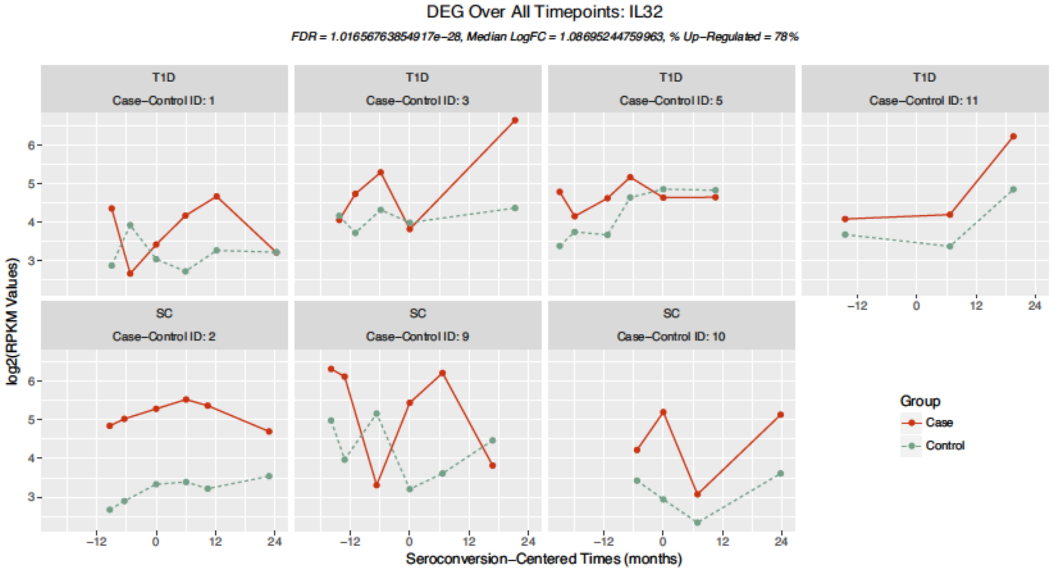


Supplementary Figure 3D. Related to Figure 2.

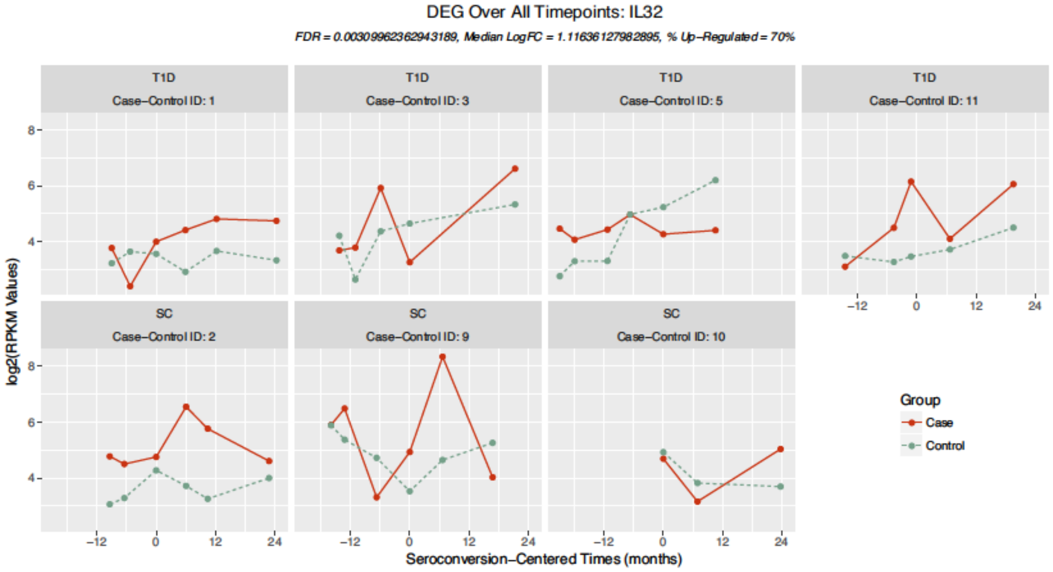
Hierarchical clustering of the levels of standardized autoantibodies (IAA, IA-2A, ZnT8A, and GADA) and the 85 DE genes between the Cases and Controls detected in the PBMC population. Each gene's expression was standardized across samples from each case-control pair individually. Genes with an Euclidean distance (ED) < 2.5 to IL-32 (co-clustering results from k-means clustering) are marked with red text and those with ED < 2.5 to INS are marked with blue text (Supplementary table 4). The samples labels along the x-axis include the sample number, case/control indicator, age of sampling in months, and months to (negative no. of months) or from (positive no. of months) seroconversion time. Here, SCC stands for seroconversion-centered, which is why the months to/from seroconversion are negative or positive.

Supplementary Figure 4A-W. Related to Figure 2.

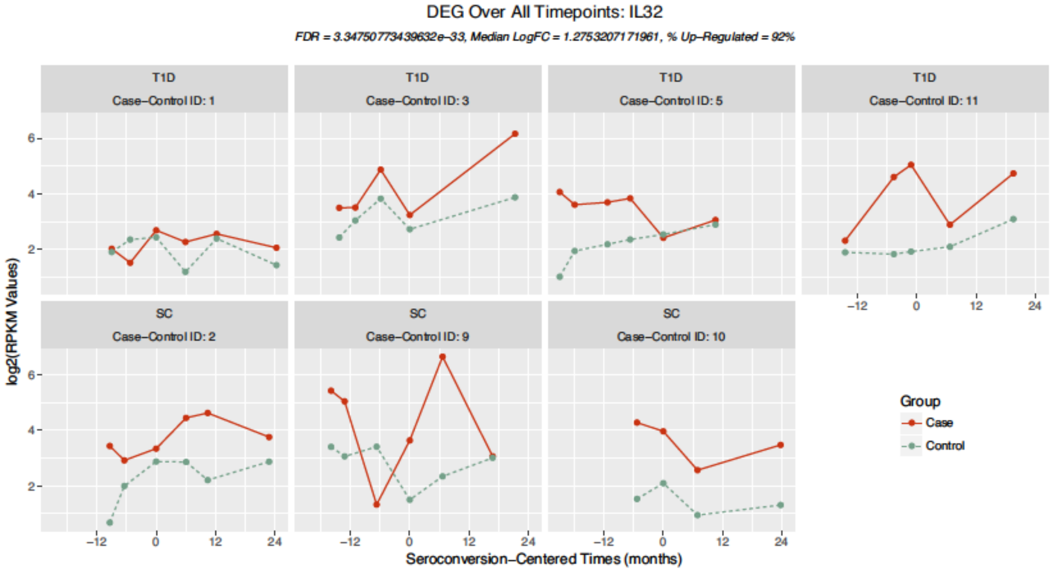
Expression profile plots of genes highlighted in the manuscript:



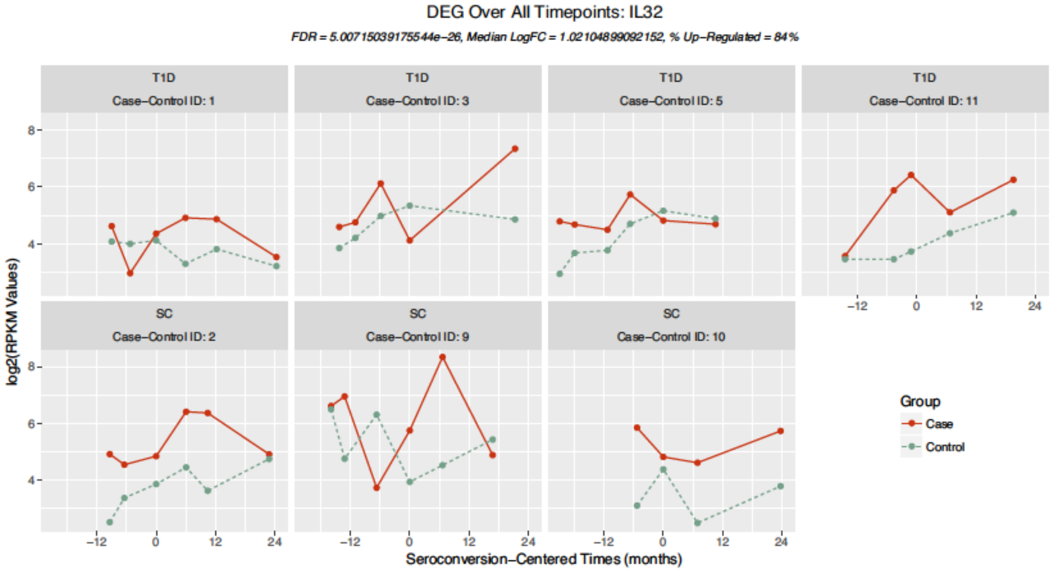
A) Expression levels of IL-32 gene in CD4+ cells.



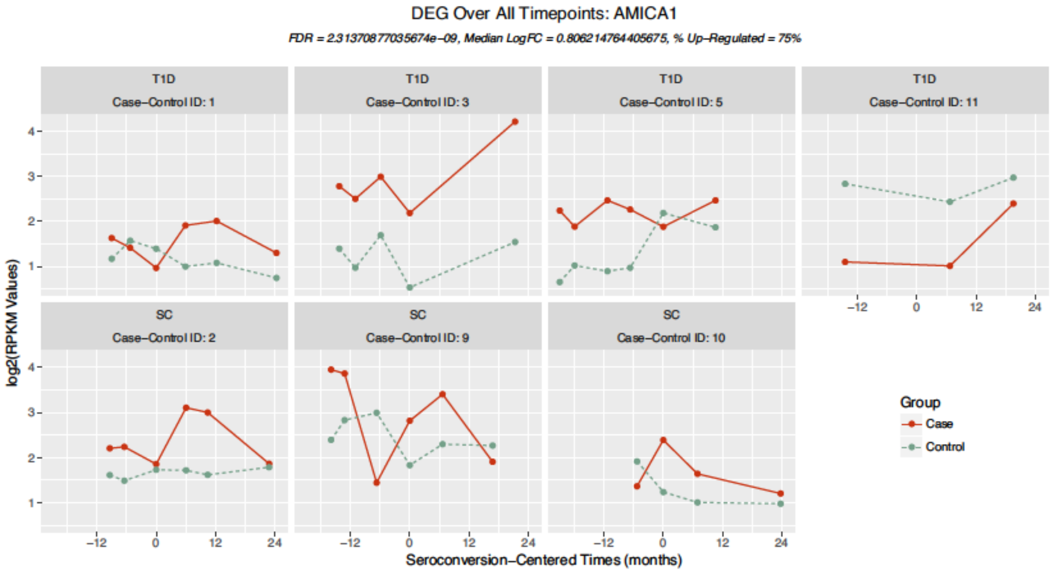
B) Expression levels of IL-32 gene in CD8+ cells.



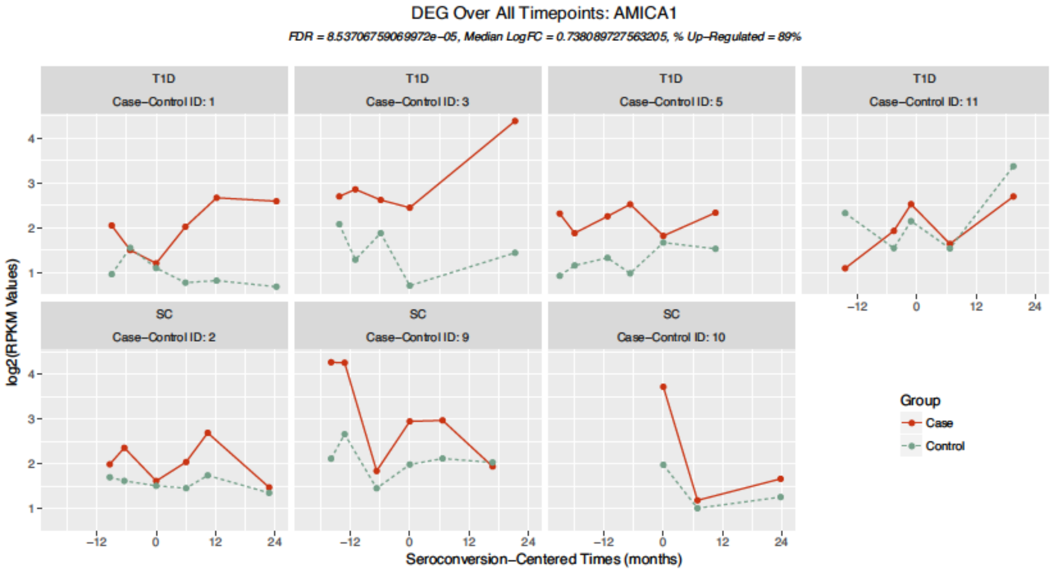
C) Expression levels of IL-32 gene in CD4-CD8- cells.



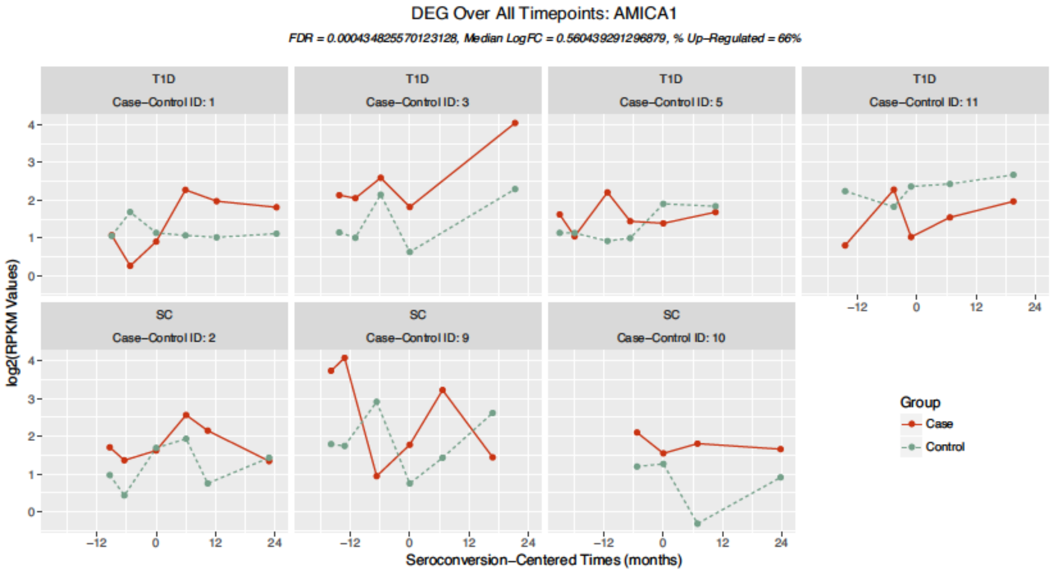
D) Expression levels of IL-32 gene in PBMCs.



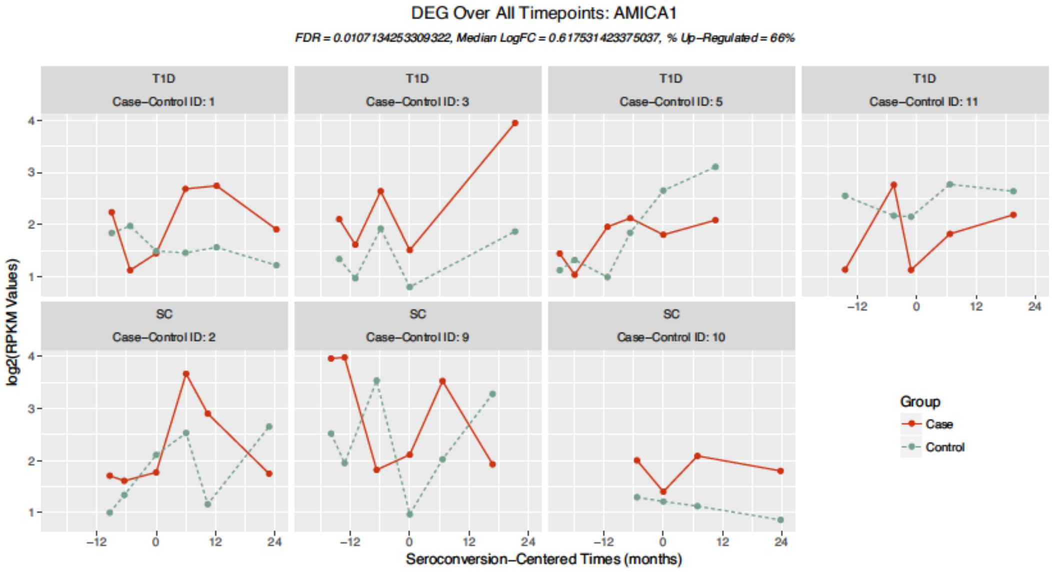
E) Expression levels of AMICA1 gene in CD4+ cells.



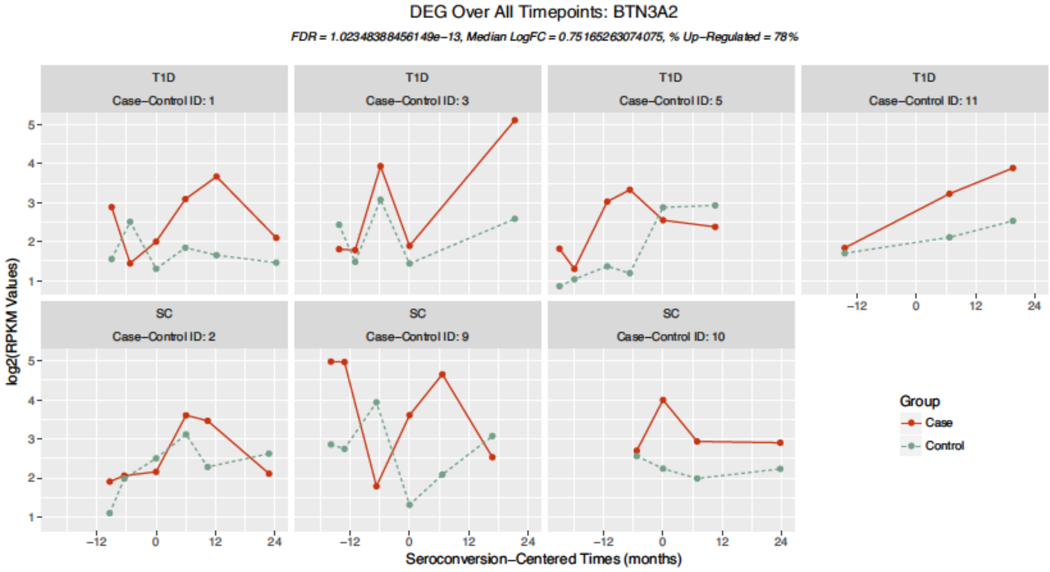
F) Expression levels of AMICA1 gene in CD8+ cells.



G) Expression levels of AMICA1 gene in CD4-CD8- cells.

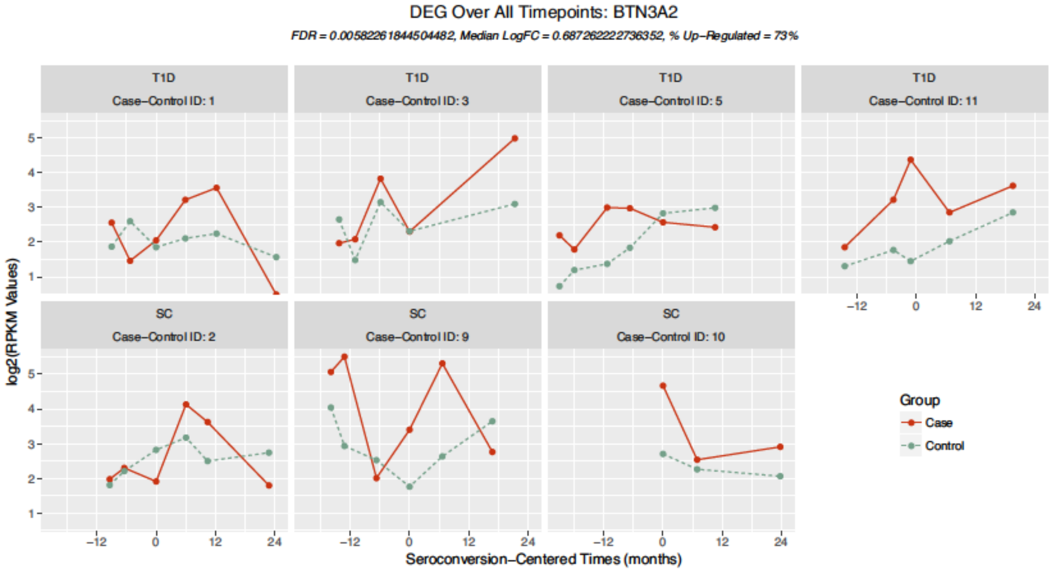


H) Expression levels of AMICA1 gene in PBMCs.


DEG Over All Timepoints: BTN3A2

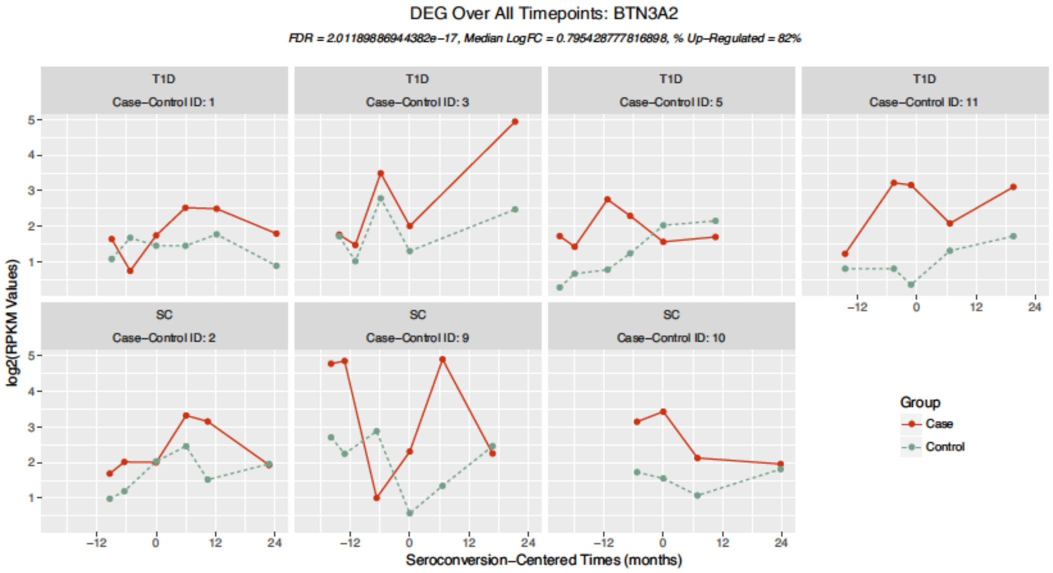
FDR = 1.02348388456149e−13, Median LogFC = 0.75165263074075, % Up−Regulated = 78%

I) Expression levels of BTN3A2 gene in CD4+ cells.

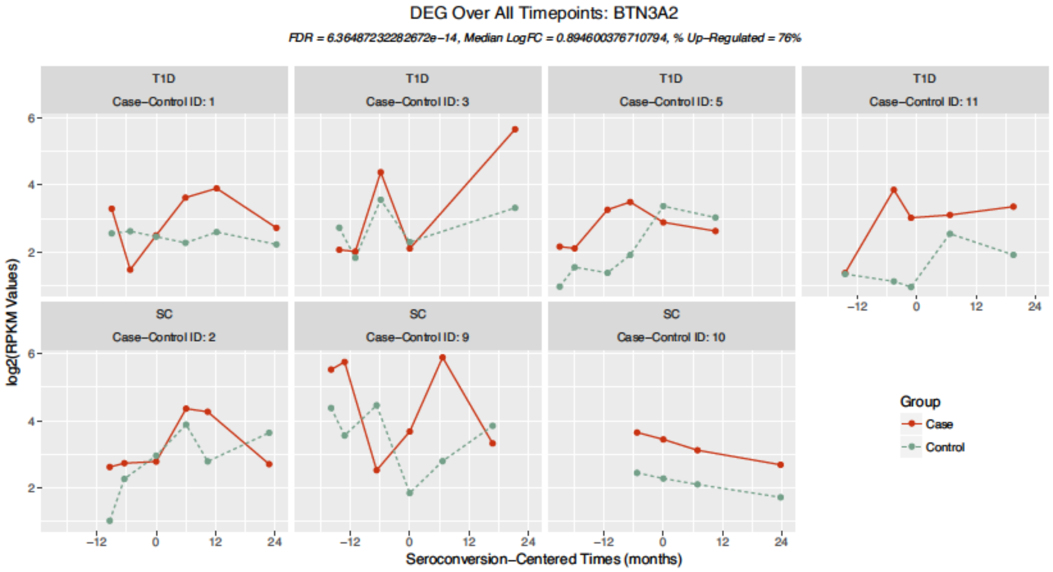

DEG Over All Timepoints: BTN3A2

FDR = 0.00582261844504482, Median LogFC = 0.687262222736352, % Up−Regulated = 73%

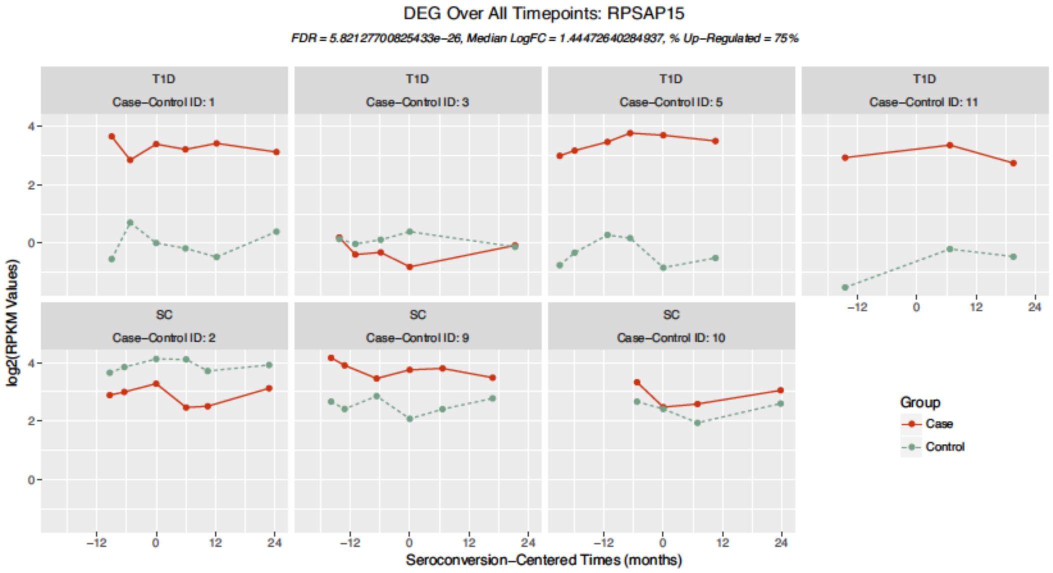
J) Expression levels of BTN3A2 gene in CD8+ cells.



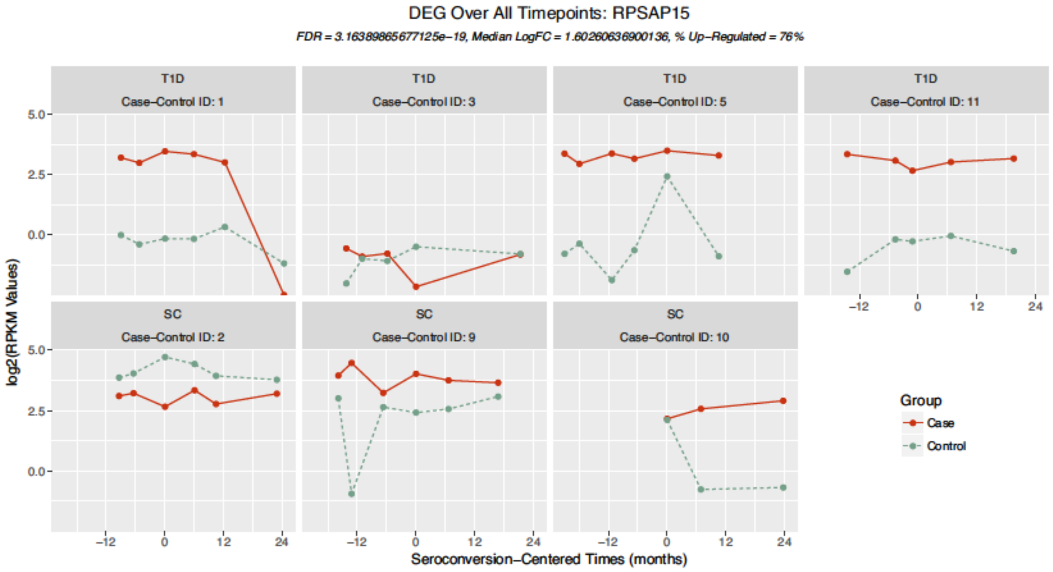
K) Expression levels of BTN3A2 gene in CD4-CD8- cells.



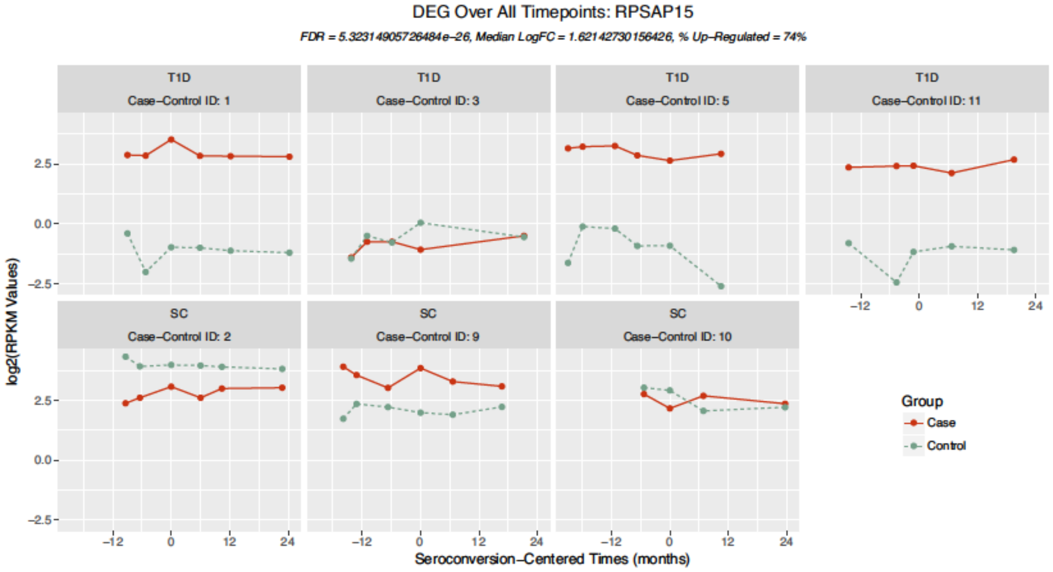
L) Expression levels of BTN3A2 gene in PBMCs.



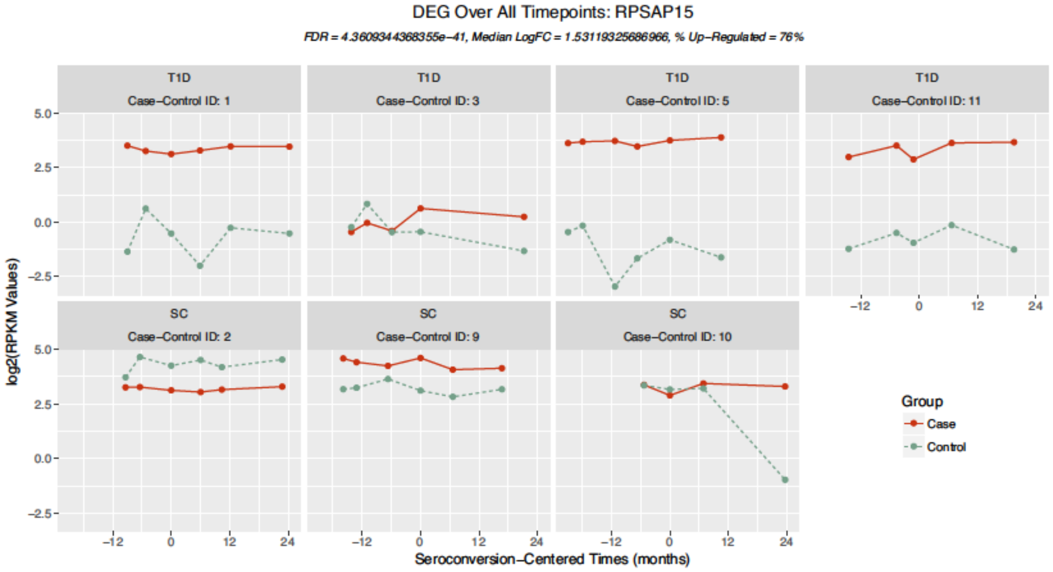
M) Expression levels of RPSAP15 gene in CD4+ cells.



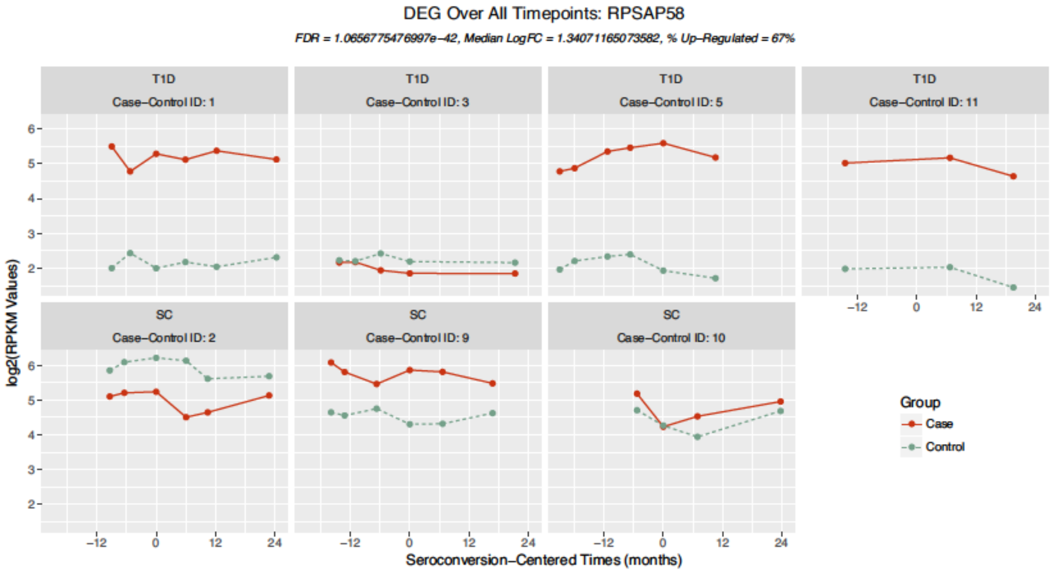
N) Expression levels of RPSAP15 gene in CD8+ cells.



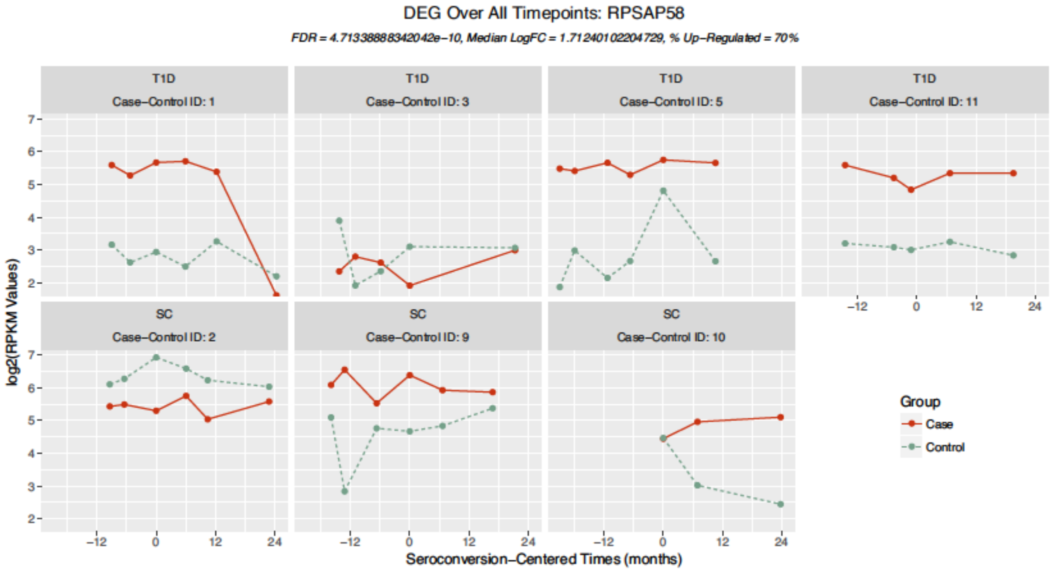
O) Expression levels of RPSAP15 gene in CD4-CD8- cells.



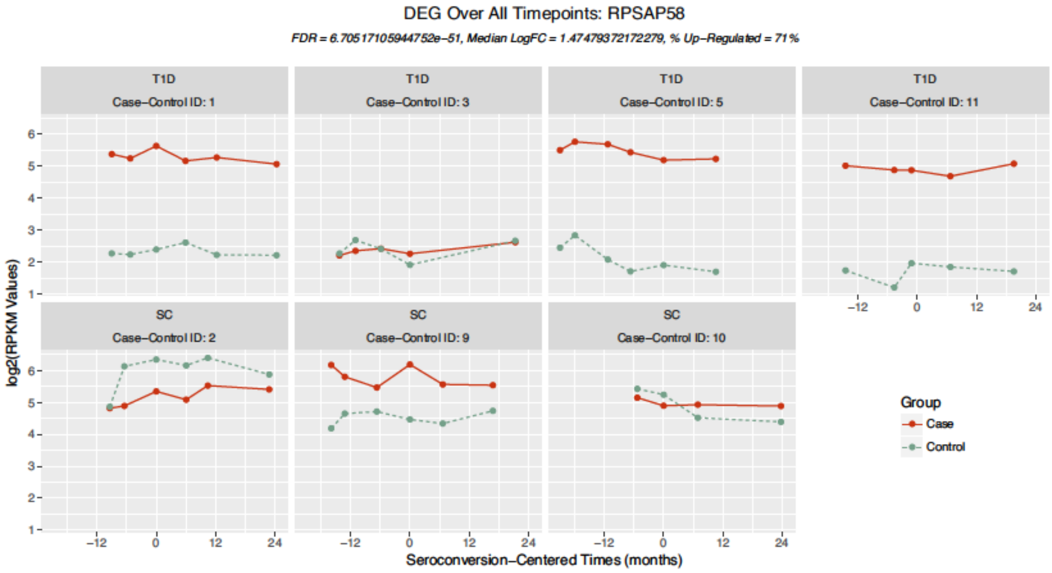
P) Expression levels of RPSAP15 gene in PBMCs.



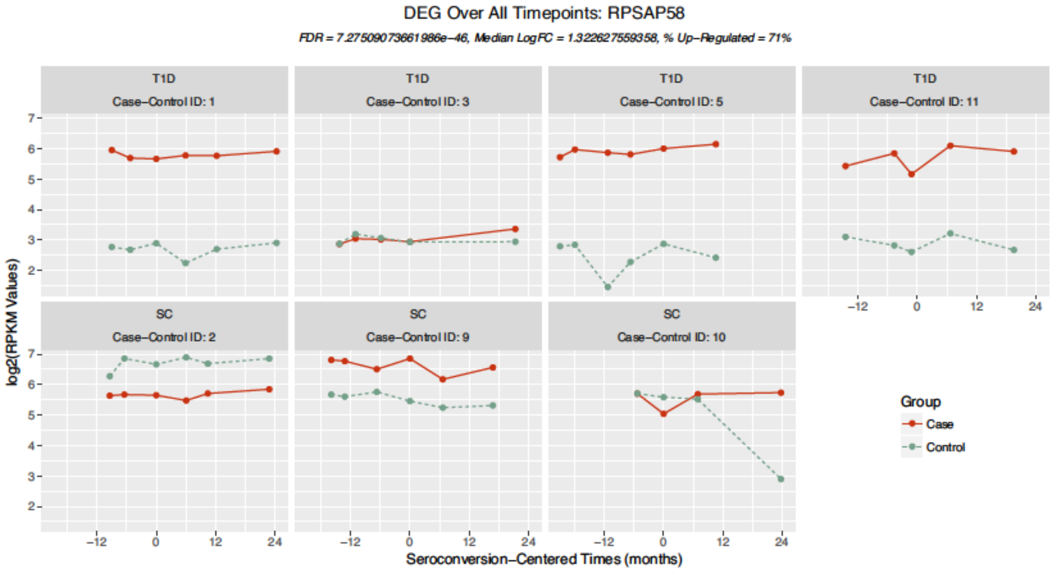
Q) Expression levels of RPSAP58 gene in CD4+ cells.



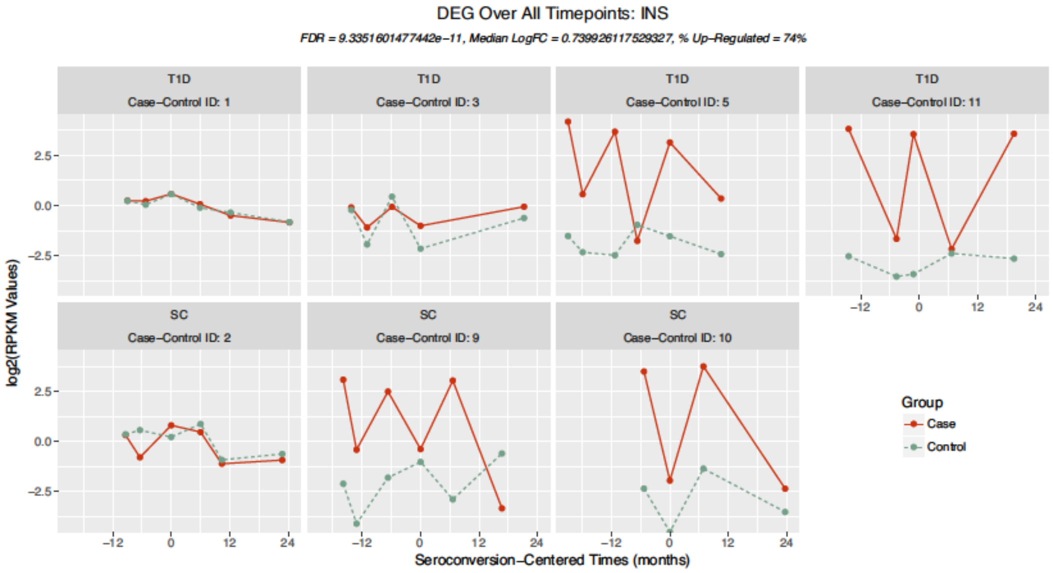
R) Expression levels of RPSAP58 gene in CD8+ cells.



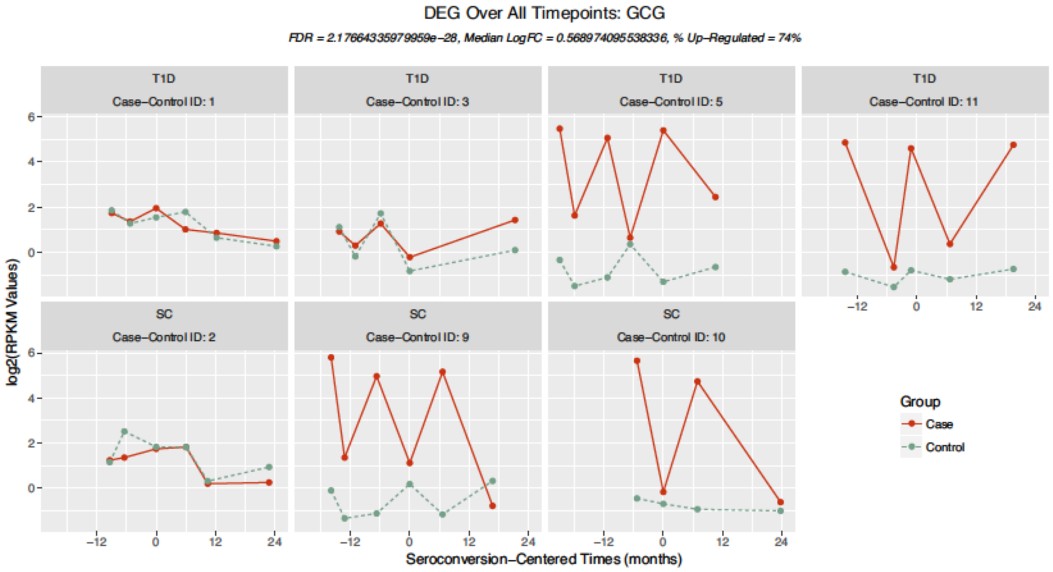
S) Expression levels of RPSAP58 gene in CD4-CD8- cells.



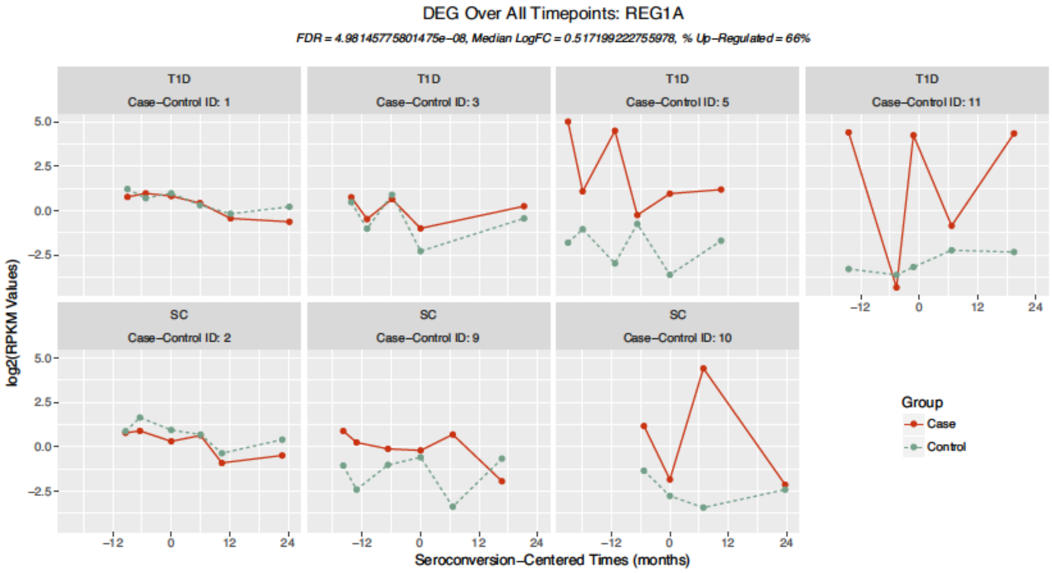
T) Expression levels of RPSAP58 gene in PBMCs.



U) Expression levels of INS gene in PBMCs.

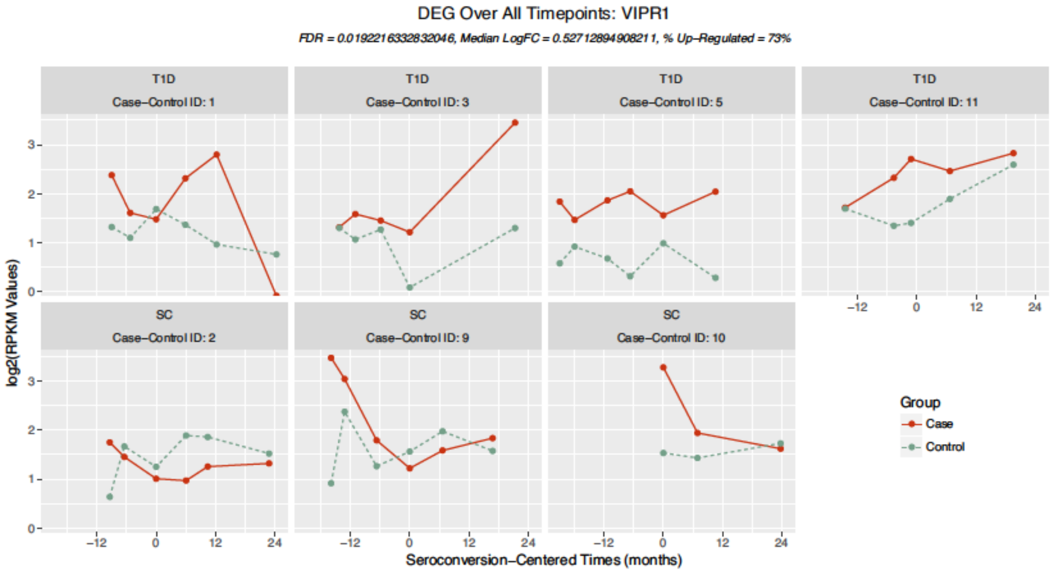


V) Expression levels of GCG gene in PBMCs.

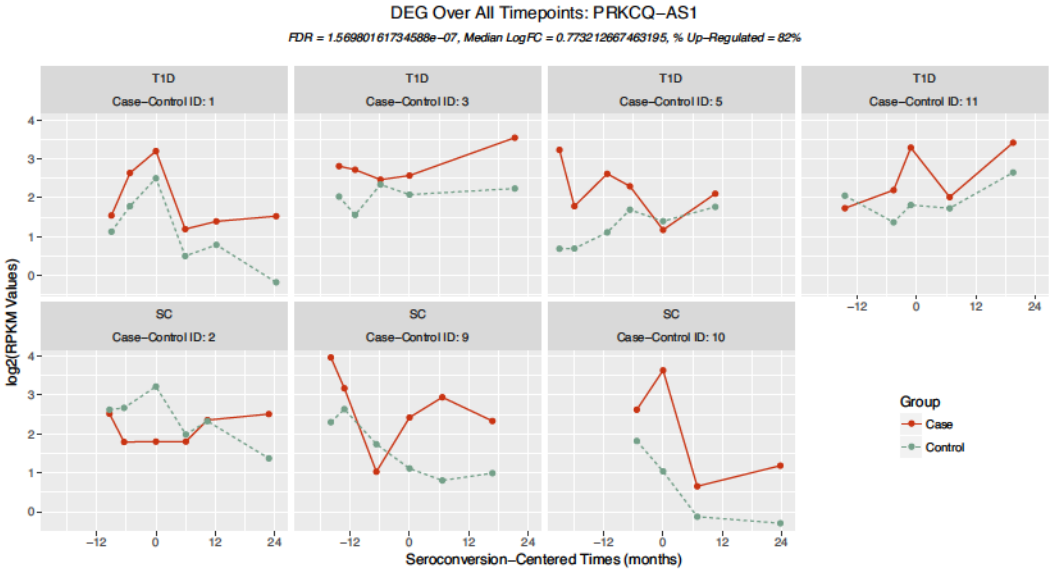


W) Expression levels of REG1A gene in PBMCs.

X) Expression levels of TRBV4-1 gene in CD4+ cells.

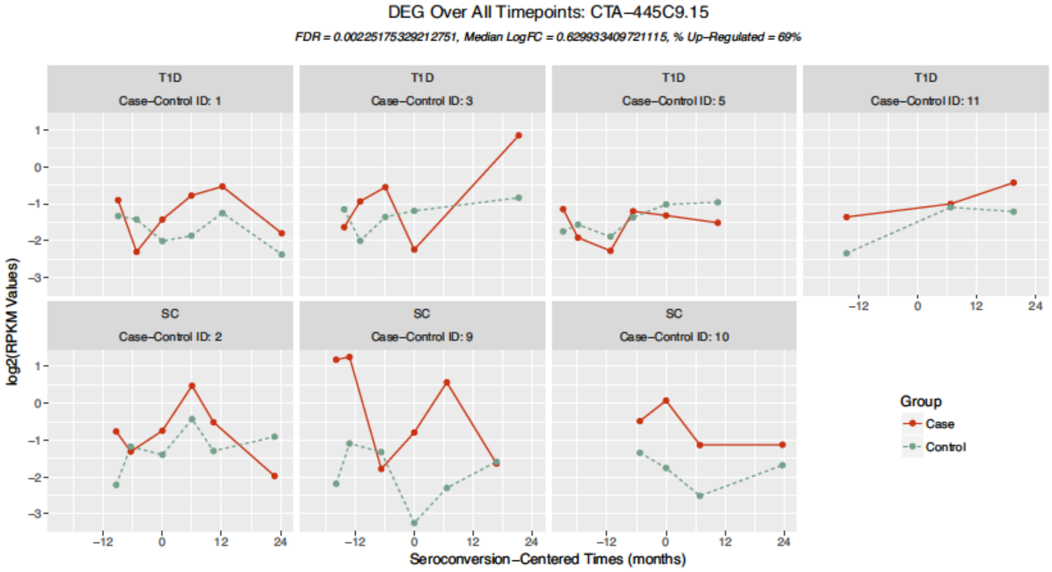


Y) Expression levels of VIPR1 gene in CD8+ cells.

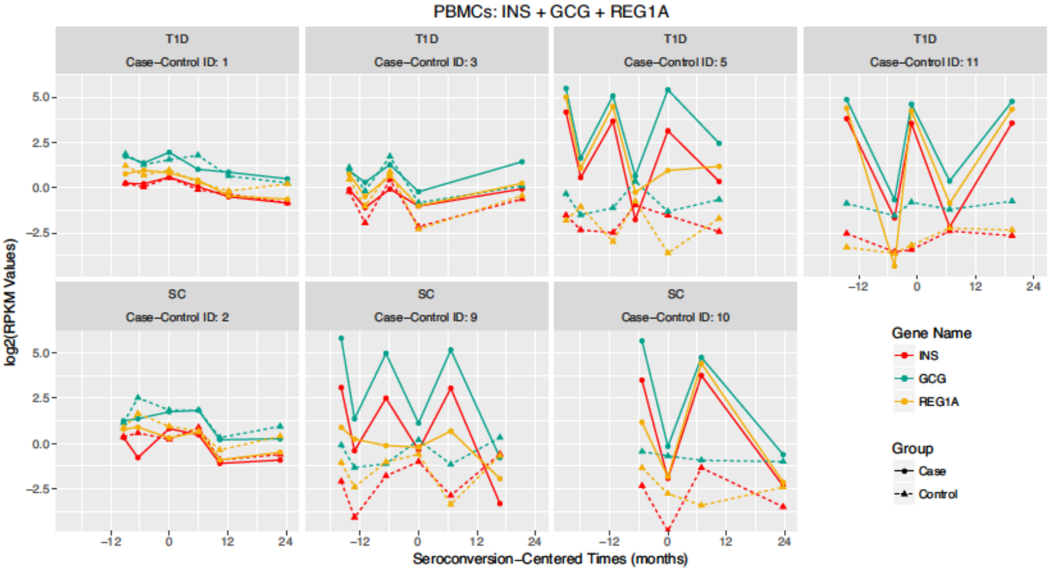


Z) Expression levels of PRKCQ-AS1 gene in CD4-CD8- cells.

AA) Expression levels of RP11-747H7.3 gene in CD4+ cells.

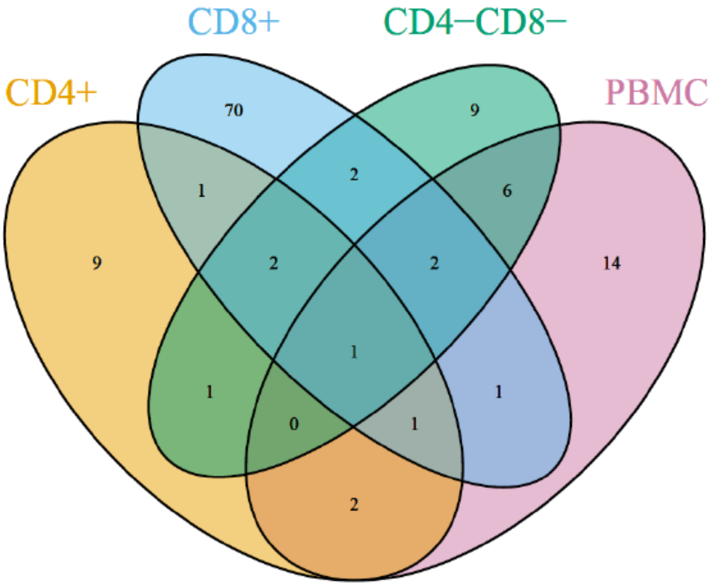


AB) Expression levels of CTA-445C9.15 gene in CD4+ cells.



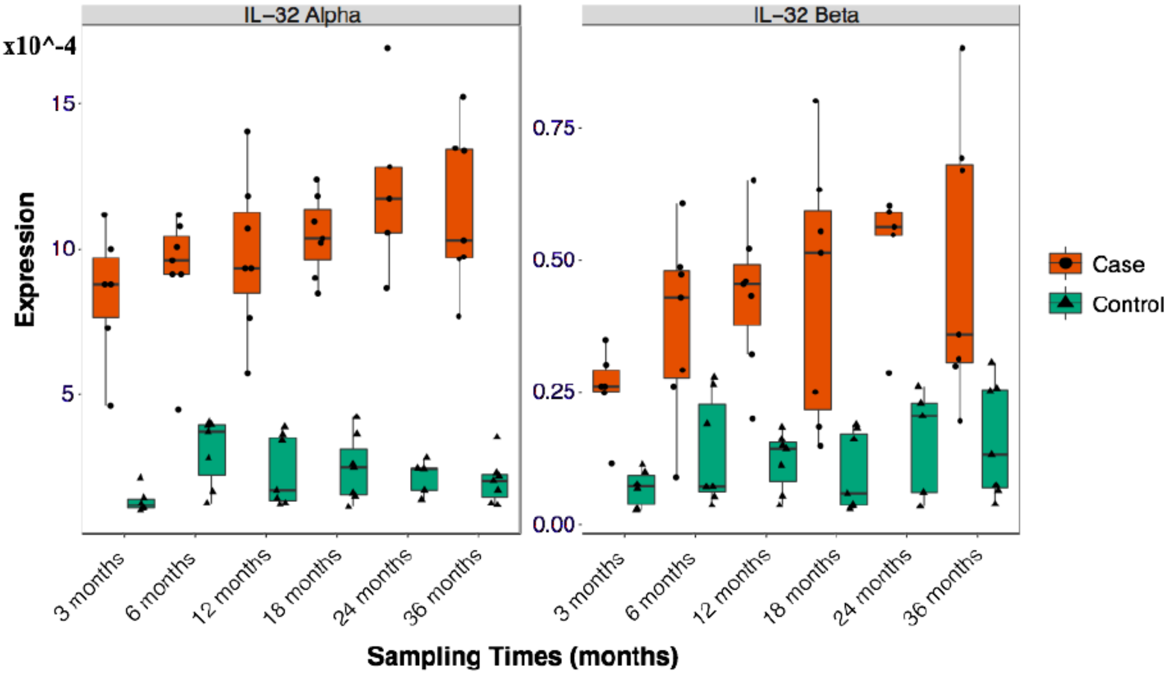
Supplementary Figure 5. Related to Figure 2.

PBMC-specific co-regulation of pancreatic transcripts Insulin (INS), Glucagon (CGC) and Regulin 1 alpha (REG1A). Profiles of *INS*, *CGC* and *REG1A* show concerted gene expression profiles. For individual profiles, see Supplementary Figure 4.



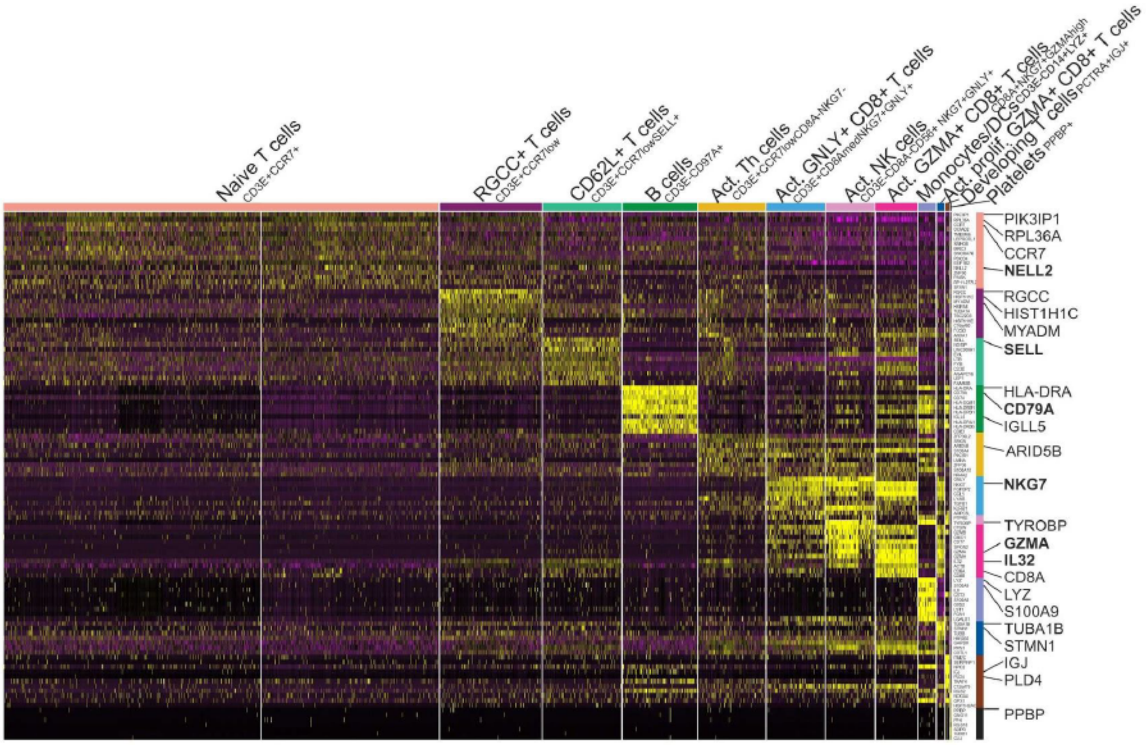
Supplementary Figure 6. Related to Figure 2.

Number of DE genes between the Cases and Controls in the time-window of 12 months before seroconversion (RPKM > 3 for coding genes and RPKM < 0.5 for non-coding genes, Up- or downregulated in ≥ 65% of the Cases). For complete listing, see Supplementary Table 3 columns “12 mo before SC”.



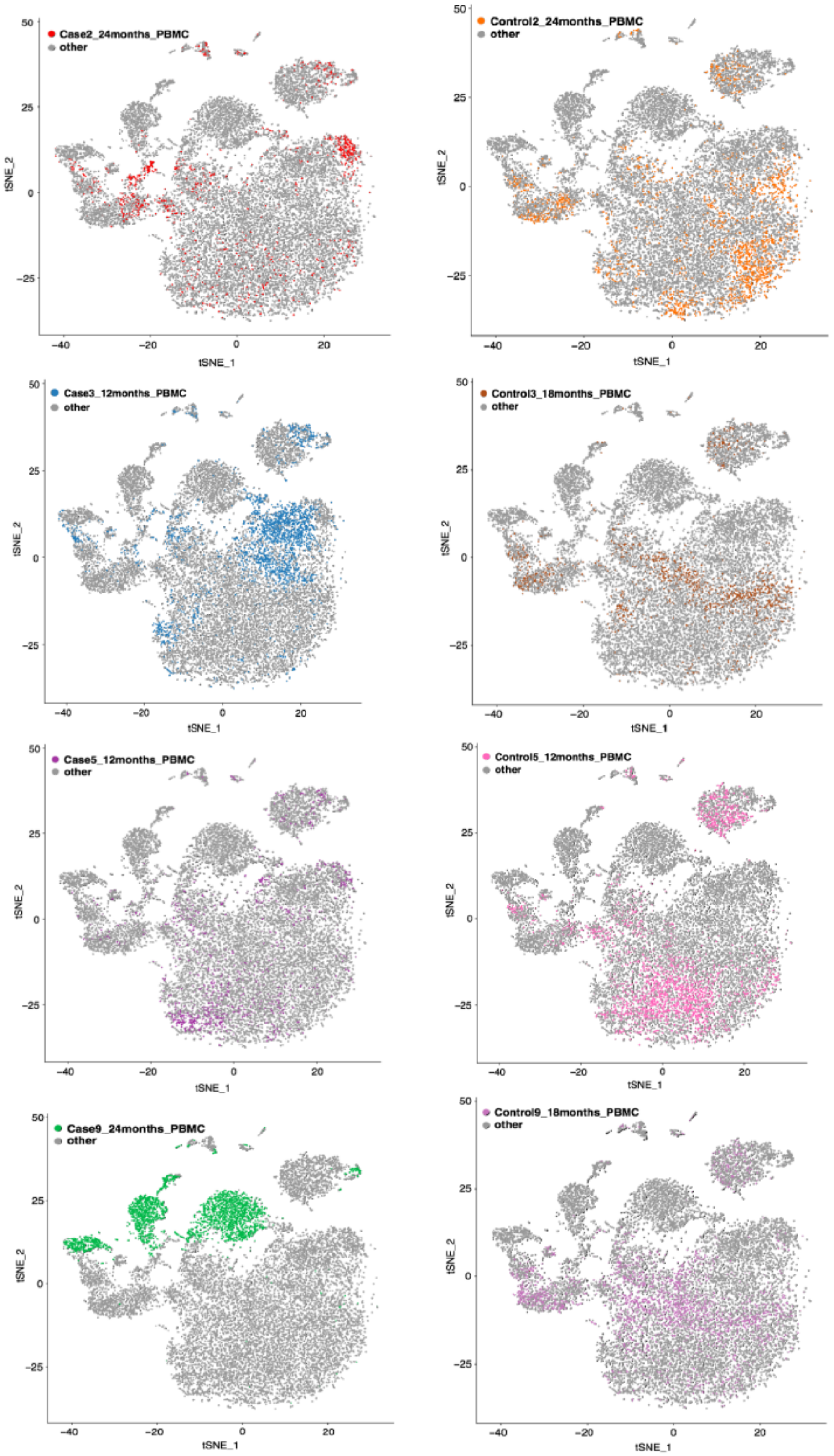
Supplementary Figure 7. Related to Figure 3A.

mRNA expression of IL32 isoforms analysed in PBMC samples of Cases (n=7) and their matched Controls (n=7) by qRT-PCR. For expression level plot of IL32γ isoform, please refer to **Figure 3A.**



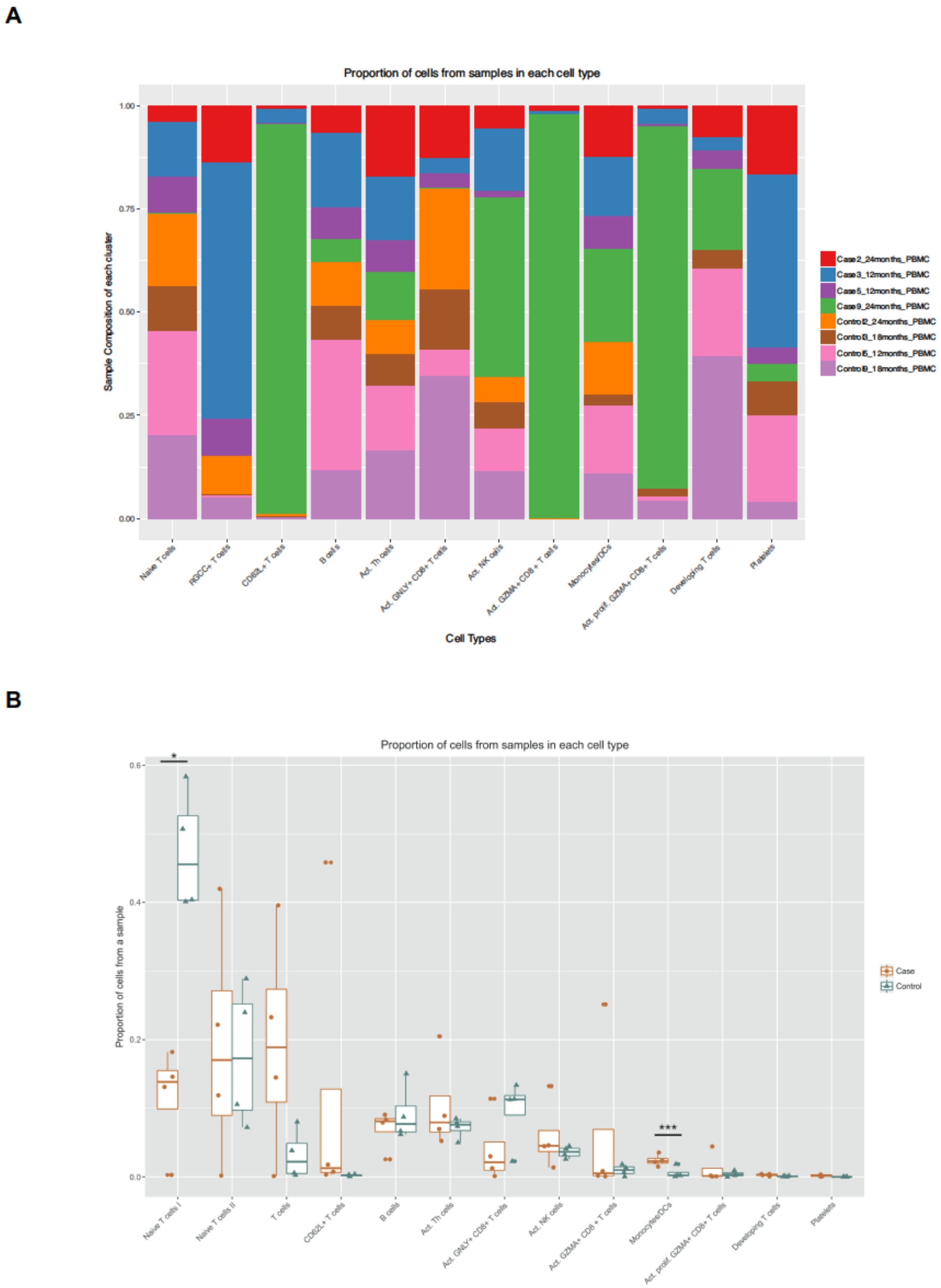
Supplementary Figure 8. Related to Figure 3.

Heatmap of the top 10 most highly expressed genes in the 13 clusters identified after Seurat clustering analysis of the pooled single-cell RNA-Seq data (4 Cases + 4 Controls) represented as a tSNE plot in **Figure 3B**. As the two biggest clusters were similar in their gene expression profiles, they were merged to form the Naive T cell cluster, leaving in total 12 cell clusters. Genes used in the annotation of the cell clusters are marked on the right column, where bolded genes are those that were also found to be DE between Cases and Controls in the bulk RNA-seq data analysis (**Supplementary Table 3**).



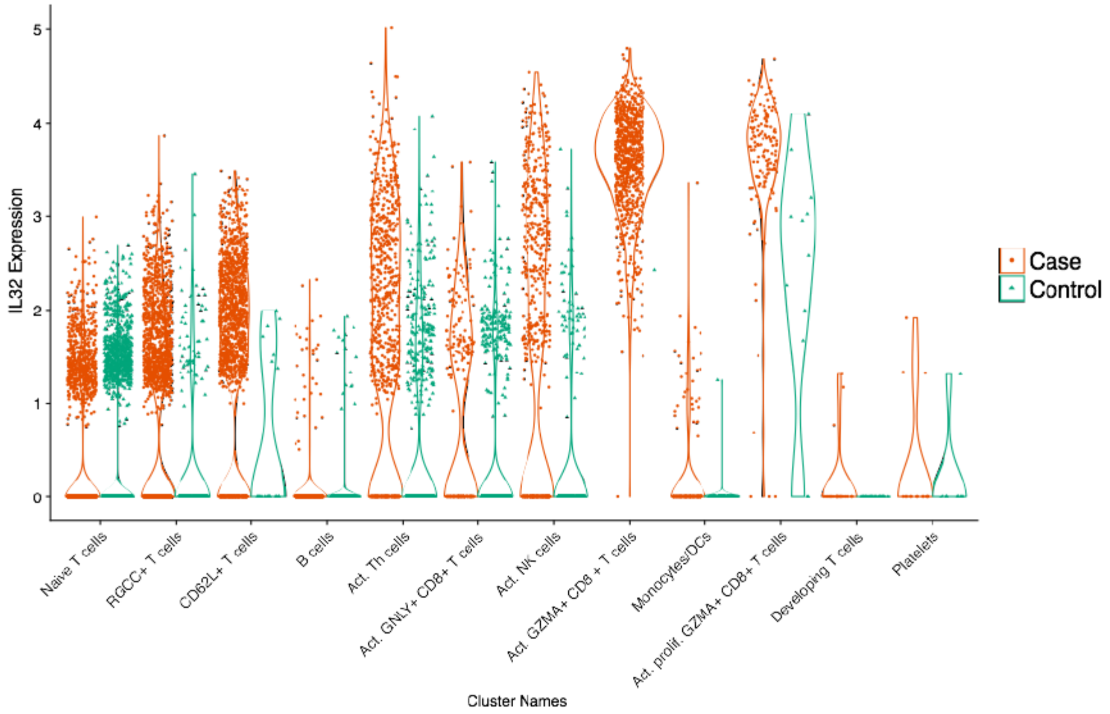
Supplementary Figure 9. Related to Figure 3.

Contribution of individual samples in the t-SNE visualization of pooled single-cell RNA-Seq data, presented in **Figure 3B** and **C**.



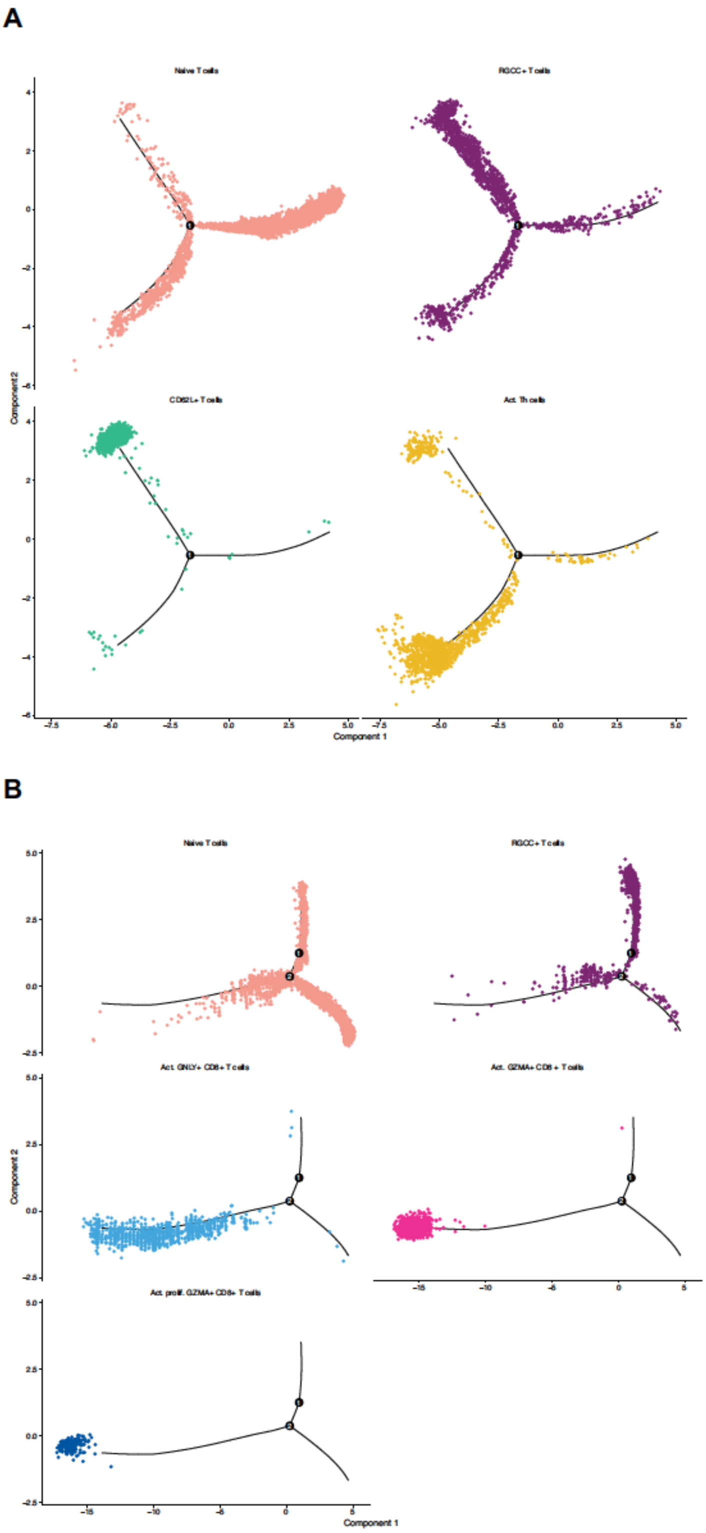
Supplementary Figure 10. Related to Figure 3.

A) Proportion of cells coming from individual samples per cluster (cluster-wise proportioning) **B)** Box-plot highlighting the proportions of cells per cluster in Case (orange) and Control (green) samples. * $p < 0.05$, *** $p < 0.005$ according to paired t-test of the sample-wise proportions of cells per cluster.



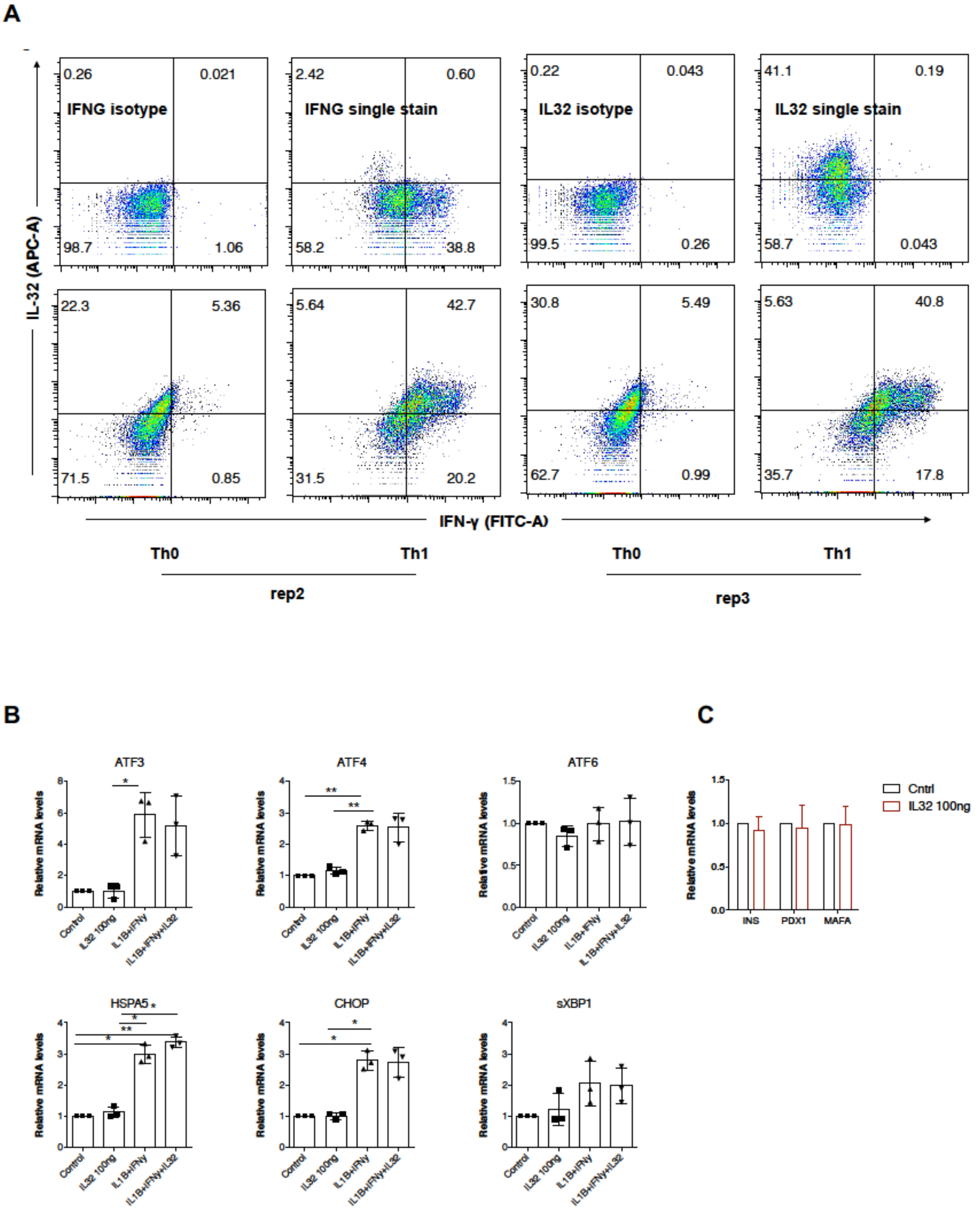
Supplementary Figure 11. Related to Figure 3.

Violin plot showing the expression of *IL32* in the 12 cell clusters identified from the single-cell RNA-Seq data, displayed separately for Cases (orange) and Controls (green).



Supplementary Figure 12. Related to Figure 3.

A) Trajectory in pseudotime of CD4+ specific and **B)** CD8+ specific cells along with the precursor cells plotted individually.



Supplementary Figure 13. Related to Figure 4.

A) Two additional replicates of the Th0/Th1 intracellular staining data shown in **Figure 4C**. **B)** EndoC-βH1 cells were treated for 24 h with recombinant IL-32*γ* in presence and absence of IL-1β and IFNγ, and the expression of ER stress markers *ATF3*, *ATF4*, *ATF6*, *CHOP*, *HSPA5* and *sXBP1* was measured by RT-qPCR assay. **C)** Expression of endocrine marker genes *INS*, *PDX1* and *MAFA* was measured after treatment of EndoC-βH1 cells with 100 ng of IL-32γ for 24h. In **B-C** fold change is calculated as compared to non-treated (control) cells. Statistical significance was determined by Tukey's multiple comparisons test. * =p-value <0.05 while ** =p-value <0.01.

Supplementary Material

Bulk RNA-seq data analysis

RNA-seq data processing and analysis

Of the 306 RNA-seq samples (**Supplementary Table 1**), 298 were used for the differential expression analysis because some Case samples had more than one corresponding control samples. The average sequencing depth of the samples in this study was around 51 million paired-end reads. Quality control checks were performed on the raw RNA-seq data using FastQC (version 0.10.0, http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). The reads were aligned to the human reference transcriptome, Human GRCh37 assembly version 75 (http://feb2014.archive.ensembl.org/index.html), using TopHat (version 2.0.10), where the default parameters of the software were retained. On average, approximately 93% of the reads from each sample in each fraction were mapped (average overall read mapping of samples in each cell type was CD4+: 93%, CD8+: 92.6%, CD4-CD8-: 93.4%, PBMC: 93.5%). This resulted in about 89% of concordant pair alignments (CD4+: 88.9%, CD8+: 88.93%, CD4-CD8-: 89.89%, PBMC: 89.89%). The aligned reads, with a mapping quality > 10, were counted at the gene level availing the *htseq-count* function from the HTSeq package and using the overlap resolution mode of 'intersection-strict' (htseq-count version 0.6.1). The read counts of genes were normalized using the trimmed means of the M-values (TMM) method, implemented in the software package *edgeR*, which adjusts for varying sequencing depths as well as normalizes for the RNA composition. Using the biotype information, the genes were divided into coding and non-coding categories. The biotype data for each gene were retrieved from the Ensemble database , and the descriptions of biotypes were taken from Gencode (http://www.gencodegenes.org/gencode_biotypes.html).

Filtering genes using RPKM values

First, the RPKM values were calculated for each gene in each sample of the analysis, where the length of the gene was taken to be the sum of the lengths of all its known exons. Second, a max-of-means RPKM value (mmRPKM) was computed for each gene to assess the overall expression of the gene in all the samples of the analysis. As the differential expression analyses in this study usually involved two groups (e.g., cases and controls, CD4+ and PBMCs), the max-of-means of RPKM value refers to: maximum(mean("RPKM values in Group 1"), mean("RPKM values in Group 2")). Subsequently, coding genes with mmRPKM > 3 and non-coding genes with mmRPKM > 0.5 were retained. These filtering criteria usually retained about 7000–7500 coding genes and 600–700 non-coding genes.

Differential expression analysis

Differential expression analyses were conducted separately for coding and non-coding genes, using the *edgeR* package. The variance of the data was estimated using the trended dispersion method.

Post-differential analysis filtering steps (only for paired sample analyses)

The *edgeR* output of differentially expressed (DE) genes with FDR < 0.05 from the paired sample analyses were further subjected to median $\log_2$FC filtering, where DE genes with a |median $\log_2$FC| > 0.5 were retained for downstream filtering step. The final filtering step retained only those genes as DE that had more than 65% samples across all individuals regulated in the same direction (i.e., up- or down-regulated). These filtering steps were added to discard false positives that may arise due to the heterogeneity of the samples due to normal variation, which is non-related to T1D and outliers. A visual depiction of the RNA-seq data processing and analysis pipeline has been shown in **Supplementary Figure 2**.

Analysis 1: Cell fraction vs PBMC

In this analysis, the expressions of genes from each cell fraction (i.e., CD4+, CD8+ and CD4-CD8-) were compared to those of the (paired) original PBMC population of Control children. Samples collected at all ages were included but were required to have expression data from both the fraction under analysis as well as PBMCs.

Analysis 2: Cases versus Controls – over all timepoints

The aim of this analysis was to identify genes that are differentially expressed in children who have seroconverted to autoantibody positivity (Cases) in comparison to those who have not (Controls). Each Case child was matched to a Control child, according to date of birth, HLA-risk class, gender and country. Case samples were compared to the samples from their matched Controls that were collected at the same age. In these analyses, other than for pairing purposes, the sampling ages were not utilized.

Differential expression analysis of Cases and Controls were compared with another method. The RNA-seq data of the filtered coding and non-coding genes were modelled using generalized linear mixed effects models (GLMMs) using *glmer()* function from *lme4* package (23). A random effect is added in this model for each child's samples. GLMM with the negative binomial likelihood was fit to the data using the *MASS* package, where the dispersion values per gene were obtained from the *edgeR*. For the filtered coding and non-coding genes from all fractions, the Spearman rank correlation coefficients of the results from the two methods ranged between 0.91 and 0.96 with an average of 0.936, indicating similar ranking of the genes after FDR correction in both the methods. Further details of RNA-seq data analysis can be found in the "Supplementary Material".

Analysis 3: Cases versus Controls – 12 months before the seroconversion window

This analysis is similar to **Analysis 2** in terms of the Case versus Control analysis set-up. However, to understand gene expression changes that take place in Cases right before seroconversion, this analysis compared only those Case samples that were taken at most 12 months before seroconversion with their matched Control samples.

For comparison, the RNA-Seq data of the filtered coding and non-coding genes were also modelled using generalized linear mixed effects models (GLMMs) using the same design as explained in **Analysis 2**. A random effect is added in this model for each child's samples. The *glmer()* function from *lme4* package was used here for modelling. GLMM with the negative binomial likelihood was fit to the data using the *MASS* package, where the dispersion values per gene were obtained from the *edgeR* **Analysis 2**. For the filtered coding and non-coding genes from all fractions, the Spearman rank correlation coefficients of the results from the two methods ranged between 0.91 and 0.96 with an average of 0.936, indicating similar ranking of the genes after FDR correction in both the methods.

Differential gene clustering

To find the genes and autoantibodies (together referred to as 'features' in this section) co-regulated/co-clustering with *IL32* in each cell-fraction, *k*-means clustering, followed with Euclidean distance based co-clustering selection criteria, was performed on the expression levels of coding and non-coding differentially expressed genes (**Analysis 2**) as well as on the autoantibodies. Due to the heterogeneity of the data and the disease, the clustering was done individually on each case and its matched control. Before clustering, the RPKM expression values of each gene and expression level of each autoantibody were $\log_2$ transformed to ensure approximately normal distribution of the values, and gene-wise standardized to make the features comparable.

For each possible number of clusters (i.e., from 2 to total number of features - 1), the features were clustered using the *k*-means clustering algorithm (*kmeans* function implemented in R *stats* package). Subsequently, using the resulting classification of features into clusters along with the Euclidean distance measures between the features, a silhouette score was calculated. The optimum number of clusters was chosen to be the one with the largest silhouette score. The features were then clustered into the "optimum number of clusters" using *k*-means clustering with 20 random sets of initialization values and sufficient iterations for convergence, where the configuration with minimum loss score was reported as the best clustering. Once clustered, the cluster containing *IL32* was considered the *IL32*-cluster with its co-regulated features.

To summarize over the *IL32*-clusters from the seven case-control pairs, a feature co-clustering with *IL32* in at least one case-control pair was considered to co-cluster with *IL32* if the median of its Euclidean distances to *IL32* across all pairs was below 2.5. This selection criteria, based on median Euclidean distance to *IL32,* ensured that only those features were considered to co-cluster with *IL32* that co-clustered with it in at least 5–6 case-control pairs (**Supplementary Table 4**).

As *IFNG*-cluster in CD8+ cells and *INS*-cluster in PBMCs were of specific interest also, the Euclidean distance-based summarization over the seven case-control pairs was repeated for these genes as well (**Supplementary Table 4**).

Transcription factor binding site analysis

Overrepresented transcription factor binding motifs on the promoters of *IL32* and its co-regulated genes were analysed with updated (2018) TRANSFAC database, using the Fmatch tool with default parameters (best supported promoter, -10,000 to +1000 bp around transcription start site) and a randomly selected gene set as a background. Afterwards the *p*-values were corrected for multiple testing using the Benjamini-Hochberg method. Results with FDR < 0.05 are presented in **Supplementary Table 4**.

Single-cell RNA-seq data processing and analysis

The Chromium single-cell 3' RNA-Seq data from four Case and four Control samples (**Supplementary Table 5**) was individually preprocessed using the Cell Ranger Single-Cell Software Suite. The reads were aligned to the human reference genome (hg19) using STAR and the data from non-cellular barcodes were filtered out. Across samples, the mean raw reads per cell varied between ~57 k to ~200 k (**Supplementary Table 5**). To identify rare cell types, the cells from different samples were pooled together using Cell Ranger's multi-library aggregation algorithm where the samples were normalized using subsampling normalization. The downsampling (subsampling normalization) of sample reads after pooling retained on average ~31 k confidently mapped reads per cell (from ~59 k raw reads per cell on average). These mapped to the median of 801 genes per cell. After the pooling, expression of 32,738 genes from 20,370 cells was obtained.

For QC analysis and further exploration of the single-cell RNA-Seq data the Seurat R package was used. Firstly, all the genes expressed in less than one cell and all the cells expressing less than 200 genes or more than 4000 genes were filtered out. Furthermore, any cells containing more than 5% of mitochondrial genes or a UMI count higher than 5000 but a gene count less than 500, were also filtered out. The latter filtering steps involved filtering of cells with high UMI count but low gene count on the basis of the gene count and UMI count relationship plots following the recommendations of Seurat tool. After these quality control filtering steps, 18,396 cells expressing 20,830 genes were retained for downstream analyses.

The filtered data were normalized using Seurat's default global-scaling normalization method, 'LogNormalize', and variation from uninteresting sources (i.e., the number of molecules detected and percentage of mitochondrial genes expressed per cell) was regressed out. To capture the heterogeneity of the single-cell data and cluster the cells, a set of highly variable genes (HVGs) was selected, whose average expression was above 0.0125, and dispersion above 0.5 resulting in ~1200 HVGs in pooled cell library. Principal component analysis (PCA) was then performed on the HVGs, and the resulting top 20 PCs were used in the graph-based clustering employed by Seurat, keeping other parameters as default.

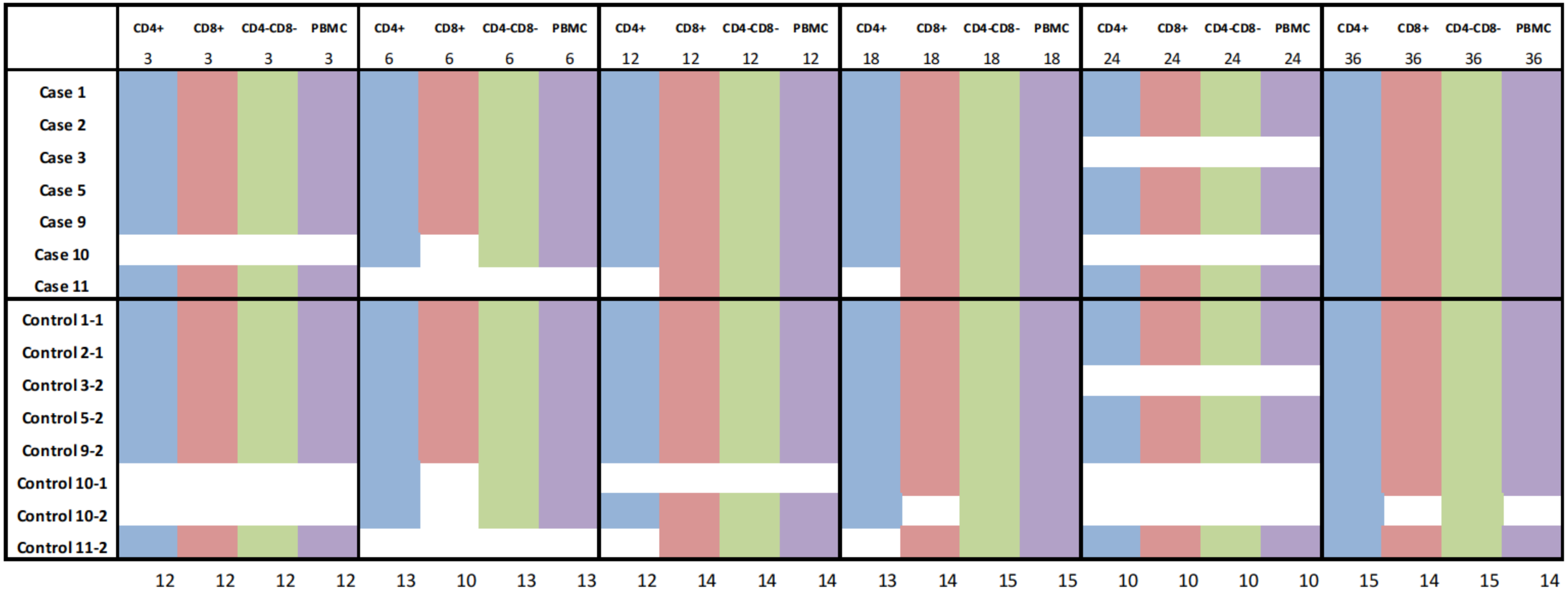
To determine the cell type represented in each cluster, markers defining the clusters were determined via differential expression algorithm implemented in Seurat, where cells of a single cluster were compared to the cells of all other clusters combined. A gene was considered a marker of a cluster if it was expressed in at least 25% of the cells of either of the two clusters and the log fold change between the cluster and all other clusters was at least 0.25. On average, one to five genes were used as markers for each cluster (**Supplementary Figure 8**). On the basis of these cluster-specific markers, no biological difference was found in two of the 13 clusters, which both represented cells from naive T cells. Therefore, they were merged into a single cluster and were labeled as naive T cells, resulting in a total of 12 different clusters.

Single-cell RNA-seq trajectory analysis

The QC filtered pooled cells from the Seurat analysis were ordered in pseudotime (i.e., placed along a trajectory corresponding to a type of biological transition, such as differentiation) using Monocle 2. The trajectory analysis was performed on cells specifically from CD4+ (CD62L+ T cells and Act. Th cells) and CD8+ (Act. GNLY+ CD8+ T cells, Act. GZMA+ CD8+ T cells and Act. prolif. GZMA+ CD8+ T cells) T-cell clusters, using the cell typing information from the Seurat analysis. In both CD8+ and CD4+ specific cell ordering, cells identified as naive T cells or T cells were also included. The trajectory analysis in Monocle 2 has three major steps.

In the first step, all genes expressed in at least 1% of the cells were used in a principal component analysis, whose resulting top PCs (six in the case of CD8+ and 11 in the case of CD4+ specific single-cell trajectory analyses) were used to initialize the t-SNE ordination of the cells. Then, the *dpFeature* function was used to cluster the cells defined in the 2-D t-SNE space. Finally, the differential gene expression test of all genes expressed in more than 10 cells was performed between the clusters defined in the previous step as a way to extract the genes that distinguish them from each other. The top 1000 significant genes were then selected for subsequent steps of the analysis. The second step reduced the dimensionality of the data using the feature genes from the previous step and availing technique called reverse graph embedding (RGE) implemented in DDRTree algorithm. In the final step, cells were ordered along the trajectory by performing manifold learning on the tree from the second step.

Supplementary Table 1A: Description of time-points where samples from each Case and Control was available for the analysis



	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC
	3	3	3	3	6	6	6	6	12	12	12	12	18	18	18	18	24	24	24	24	36	36	36	36
Case 1	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Case 2	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Case 3	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪					🟦	🟥	🟩	🟪
Case 5	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Case 9	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Case 10					🟦		🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪					🟦	🟥	🟩	🟪
Case 11	🟦	🟥	🟩	🟪						🟥	🟩	🟪		🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Control 1-1	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Control 2-1	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Control 3-2	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪					🟦	🟥	🟩	🟪
Control 5-2	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Control 9-2	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
Control 10-1					🟦		🟩	🟪					🟦	🟥	🟩	🟪					🟦	🟥	🟩	🟪
Control 10-2					🟦		🟩	🟪	🟦	🟥	🟩	🟪	🟦		🟩	🟪					🟦		🟩	
Control 11-2	🟦	🟥	🟩	🟪						🟥	🟩	🟪		🟥	🟩	🟪	🟦	🟥	🟩	🟪	🟦	🟥	🟩	🟪
	12	12	12	12	13	10	13	13	12	14	14	14	13	14	15	15	10	10	10	10	15	14	15	14

Total Number of Samples = 306

Coloured = Sampled

Empty = Not Sampled

Supplementary Table 1B: Description of Cases and Control samples including seropositivity

Case/Control #	Study site	Gender	T1D diagnosis	T1D diagnosis age	HLA risk category	Family T1D diagnosis history	PARTICIPANT	SAMPLE MONTH	IAA (>2.80 RU)	GADA (>5.36 RU)	IA-2A (>0.77 RU)	ZnT8A (>0.61 RU)	ICA (>2 JDFU)
Case 1	FINLAND	Female	Yes	3.2	Moderately increased	Father age 9	E003251	0	0.32	0.18	0.06	0.07	3
								3	0.01	0	0.08	0.06	0
								6	0.45	0	0.16	0.08	0
								12	14.08	21.75	0.08	0.3	0
								18	53.07	1933.3	88.23	6.37	374
								24	14.44	305.98	510.62	12.89	747
								36	2.3	119.94	678.3	22.46	512
Case 2	FINLAND	Male	No		Moderately increased	Father age 27	E003989	0	0	0	0.13	0.05	0
								3	0	0	0.14	0.06	0
								6	0	0	0.15	0.06	0
								12	13.46	0	0.15	0.02	0
								18	12.75	3.46	0.07	0.1	6
								24	7.28	22.16	0.11	0.15	0
								36	5.96	173.27	0.15	7.53	512
Case 3	FINLAND	Male	Yes	3.67	Moderately increased	Maternal uncle age 12	E006574	0	0	0	0.07	0.12	0
								3	0	0	0.09	0.04	0
								6	0.42	0	0.08	0.03	
								12	0.7	0.07	0.1	0.05	
								18	8.93	0.71	0.08	0.14	6
								24	30.08	195.49	1013.95	13.67	1024
								36	11.9	64.38	894.54	36.06	2048
Case 5	FINLAND	Female	Yes	2.63	High	Maternal grandmother age 15	E010937	0	0.06	0	0.04	0.05	0
								3	0	0	0.05	0.06	0
								6	0.22	0	0.07	0.06	0
								12	0.09	1.1	0.1	0.03	0
								18	2.42	0	0.17	0.07	0
								24	6.49	2.64	19.82	3.58	47
								36	3.97	0.32	74.61	0.5	256
Case 9	FINLAND	Male	o, transient abs		Moderately increased		E026079	0	0	0	0.14	0.06	0
								3	0	0	0.08	0.13	0
								6	1.36	0	0.07	0.07	0
								12	0.39	1.43	0.08	0.06	0
								18	12.28	11.57	0.11	0.1	4
								24	1.55	0.99	0.16	0.1	0
								36	4.7	0	0.09	0.13	0
Case 10	ESTONIA	Female	lo, transient abs		Slightly increased		T013815	0	0	0	0.13	0.15	0
								6	0.04	0	0.05	0.05	0
								12	21.78	18.46	0.07	0.09	0
								18	34.01	1.94	0.08	0.12	0
								36	8.09	0	0.14	0.1	0
Case 11	ESTONIA	Female	Yes	2.41	Moderately increased	Father age 5	T025418	0	0.53	0	0.09	0.04	0
								3	0.05	0	0.08	0.03	0
								12	0.98	3.95	0.09	0.11	0
								18	0.54	131.68	0.19	0.17	0
								24	8.59	189.7	0.39	0.13	512
								36	32.98	26.36	3.48	0.15	16
Control 1	FINLAND	Female	No		Moderately increased		E003061	0	0.19	0.26	0.08	0.06	
								3	0	0	0.06	0.04	

							6	0	0	0.08	0.06
							12	0.28	0.07	0.09	0.07
							18	0	0	0.07	0.07
							24	0.28	1.56	0.09	0.13
							36	0.92	0.71	0.11	0.09
Control 2	FINLAND	Male	No	Moderately increased		E001463	0	0.31	0	0.02	0.18
							3	0.14	0	0.02	0.1
							6	0.63	0	0	0.07
							12	0.2	0	0.06	0.06
							18	0	0	0.16	0.1
							24	0	0.93	0.1	0.05
							36	0.14	0	0.1	0.09
Control 3	FINLAND	Male	No	Moderately increased		E006646	0	0.62	0	0.09	0.02
							3	0	0	0.13	0.03
							6	0.53	0	0.11	0.03
							12	0	0	0.12	0.05
							18	0	0	0.09	0.07
							36	0.23	0	0.14	0.11
Control 5	FINLAND	Female	No	High	Father age 6	E013487	3	0.36	0	0.1	0.09
							6	0.34	0	0.07	0.07
							12	0.02	1.62	0.08	0.07
							18	0.46	1.57	0.07	0.15
							24	0.86	0.39	0.07	0.11
							36	0	0	0.07	0.07
Control 9	FINLAND	Male	No	Moderately increased		E026325	0	0	0	0.12	0.07
							3	0.77	0	0.32	0.1
							6	1.03	0	0.09	0.08
							12	1.41	0.21	0.06	0.1
							18	0.28	0.72	0.11	0.09
							24	0.38	0	0.11	0.09
							36	0	0	0.07	0.1
Control 10.1	ESTONIA	Female	No	Slightly increased		T012808	0	0	0.24	0.08	0.05
							18	0.49	1.14	0.1	0.14
							36	0.68	0	0.12	0.1
Control 10.2	ESTONIA	Female	No	Slightly increased		T014292	0	0	0	0.15	0.08
							6	0.17	0.09	0.08	0.09
							12	0.56	0.21	0.13	0.07
							18	0.39	0	0.08	0.12
							36	0.62	0	0.09	0.09
Control 11	ESTONIA	Female	No	Moderately increased		T026177	0	0.7	0	0.12	0.03
							3	0.35	0	0.06	0.05
							12	0.95	0.05	0.11	0.1
							18	0.12	0	0.13	0.08
							24	0.75	0	0.12	0.1
							36	0.53	0	0.13	0.11

Supplementary Table 2: Primers and probes used in this study

Primers/probes used for T cells

	Target cDNA	Sequence of 5'-primer (F)	Sequence of 3'-primer (R)	Probe (if applicable)
	IL32α	5´-GCTGGAGGACGACTTCAAAGA-3´	5´-GGGCTCCGTAGGACTTGTCA-3´	
	IL32β	5´-TCTGTCTCTCTCGGGCCTTG-3´	5´-GGCTCCGTAGGACTGGAAAG-3´;	
	IL32γ	5´-AGGCCCGAATGGTAATGCT-3´	5´-GGCCACAGTGTCCTCAGTGTCACA-3´	
	EF1α	5´- AGCAAAAACGACCCACCA-3'	5´-GCCTGGATGGTTCAGGATAA-3´	
	GAPDH	3'-CCGGCTTTCTTCGCAGTAG-5'	5'-CACGGACGCCTGGAAGA-3'	5'-FAM-ACCAGGCGCCCAATACGACCAA-TAMRA-3'

Primers used for EndoC-βH1 cells

	Target cDNA	Sequence of 5'-primer (F)	Sequence of 3'-primer (R)
	Cyclophilin A	ATGGCAAATGCTGGACCCAACA	ACATGCTTGCCATCCAACCACT
*	IL32	GAGCTCTTCATGTCCTCTTTCC	GGCAAAGGTGGTGTCAGTAT
*	IL8	AAATCTGGCAACCCTAGTCTG	GTGAGGTAAGATGGTGGCTAAT
*	IL6	CCAGAGCTGTGCAGATGAGT	GGGTCAGGGGTGGTTATTGC
*	TNFa	GATCCCTGACATCTGGAATCTG	GAAACATCTGGAGAGAGGAAGG
*	BAD	ATCATGGAGGCGCTG	CTTAAAGGAGTCCACAAACTC
*	BAX	AACTGGACAGTAACATGGAG	TTGCTGGCAAAGTAGAAAAG
	HSPA5 (BIP)	TGGCTGGAAAGCCACCAAGATGCT	GGGGGAGGGCCTGCACTTCCAT
	DDIT3 (CHOP)	GCACCTCCCAGAGCCCTCACTC	CCCGGGCTGGGGAATGACCA
	sXBP1	CTGCTGAGTCCGCAGCAGGTGCA	GGTCCAAGTTGTCCAGAATGC
	ATF4	AAGGCGGGCTCCTCCGAATGG	CAATCTGTCCCGGAGAAGGCATCC
	ATF6	ACCTGCTGTTACCAGCTACCACCCA	GCATCATCACTTCGTAGTCCTGCCC
	ATF3	AGAAAGAGTCGGAGAAGC	TGAAGGTTGAGCATGTATATC
	INS	TGTCCTTCTGCCATGGCCCT	TTCACAAAGGCTGCGGCTGG
	PDX1	AAGTCTACCAAAGCTCACGCG	GTGCGCGTCCGCTTGTTCT
	MAFA	GCCAGGTGGAGCAGCTGAA	CTTCTCGTATTTCTCCTTGTAC

*** KiCqStart® SYBR® Green Primers**
Predesigned primers for gene expression analysis

Supplementary Table 3A. Differentially expressed coding genes in CD4+, CD8+ and CD4-CD8- fraction compared to the original PBMC fraction (using samples from healthy control children only).

							Median LogFC			FDR			Percent Up			Percent Down		
Ensembl Gene IDs	Gene Names	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)	CD4+ vs PBMC	CD8+ vs PBMC	CD4-CD8- vs. PBMC	CD4+ vs PBMC	CD8+ vs PBMC	CD4-CD8- vs. PBMC	CD4+ vs PBMC	CD8+ vs PBMC	CD4-CD8- vs. PBMC	CD4+ vs PBMC	CD8+ vs PBMC	CD4-CD8- vs. PBMC

ZNF683	ZNF683	zinc finger protein 683	Other	other	
DIRAS1	DIRAS1	DIRAS family GTPase 1	Plasma Membrane	enzyme	
B3GNT5	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltra	Cytoplasm	enzyme	
BASP1	BASP1	brain abundant membrane attached signal protein 1	Nucleus	transcription regulator	
METRNL	METRNL	meteorin like, glial cell differentiation regulator	Cytoplasm	other	
CD19	CD19	CD19 molecule	Plasma Membrane	transmembrane receptor	blinatumomab, MEDI-5
FAM20C	FAM20C	FAM20C, golgi associated secretory pathway kinase	Extracellular Space	enzyme	
ALS2CL	ALS2CL	ALS2 C-terminal like	Cytoplasm	other	
THBD	THBD	thrombomodulin	Plasma Membrane	transmembrane receptor	
CD300LB	CD300LB	CD300 molecule like family member b	Plasma Membrane	other	
HLA-DQB1	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	Plasma Membrane	other	
CIITA	CIITA	class II major histocompatibility complex transactivator	Nucleus	transcription regulator	
PRF1	PRF1	perforin 1	Cytoplasm	transporter	
S1PR5	S1PR5	sphingosine-1-phosphate receptor 5	Plasma Membrane	G-protein coupled receptor	fingolimod phosphate, fing
RAP2B	RAP2B	RAP2B, member of RAS oncogene family	Plasma Membrane	enzyme	
ANXA3	ANXA3	annexin A3	Plasma Membrane	other	
ZNF703	ZNF703	zinc finger protein 703	Nucleus	other	
ADAP2	ADAP2	ArfGAP with dual PH domains 2	Cytoplasm	other	
SEMA4B	SEMA4B	semaphorin 4B	Plasma Membrane	other	
ANO9	ANO9	anoctamin 9	Plasma Membrane	ion channel	
TNFAIP2	TNFAIP2	TNF alpha induced protein 2	Extracellular Space	other	
TCN2	TCN2	transcobalamin 2	Extracellular Space	transporter	
METTL7A	METTL7A	methyltransferase like 7A	Cytoplasm	other	
CD300LF	CD300LF	CD300 molecule like family member f	Plasma Membrane	other	
CD300E	CD300E	CD300e molecule	Plasma Membrane	other	
FCAR	FCAR	Fc fragment of IgA receptor	Plasma Membrane	other	
LILRB4	LILRB4	leukocyte immunoglobulin like receptor B4	Plasma Membrane	other	
LILRA5	LILRA5	leukocyte immunoglobulin like receptor A5	Plasma Membrane	other	
HBA2	HBA1/HBA2	hemoglobin subunit alpha 2	Extracellular Space	transporter	[illegible]
FAM111B	FAM111B	family with sequence similarity 111 member B	Other	other	
H1F0	H1F0	H1 histone family member 0	Nucleus	other	
PAX5	PAX5	paired box 5	Nucleus	transcription regulator	
HLA-DRB1	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	Plasma Membrane	transmembrane receptor	apolizumab
S100A4	S100A4	S100 calcium binding protein A4	Cytoplasm	other	
SULF2	SULF2	sulfatase 2	Plasma Membrane	enzyme	
PLXNB2	PLXNB2	plexin B2	Plasma Membrane	transmembrane receptor	
TCF4	TCF4	transcription factor 4	Nucleus	transcription regulator	
HLA-DQA1	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	Plasma Membrane	transmembrane receptor	
GM2A	GM2A	GM2 ganglioside activator	Cytoplasm	enzyme	
TLE1	TLE1	transducin like enhancer of split 1	Nucleus	transcription regulator	
SERPINA1	SERPINA1	serpin family A member 1	Extracellular Space	other	
C5AR1	C5AR1	complement C5a receptor 1	Plasma Membrane	G-protein coupled receptor	
MPEG1	MPEG1	macrophage expressed 1	Cytoplasm	other	
PSAP	PSAP	prosaposin	Extracellular Space	other	
CFD	CFD	complement factor D	Extracellular Space	peptidase	
FAM49A	FAM49A	family with sequence similarity 49 member A	Other	other	
PLCG2	PLCG2	phospholipase C gamma 2	Cytoplasm	enzyme	
SIRPA	SIRPA	signal regulatory protein alpha	Plasma Membrane	phosphatase	
HLA-DRB5	HLA-DRB5	major histocompatibility complex, class II, DR beta 5	Plasma Membrane	transmembrane receptor	
SH2D1B	SH2D1B	SH2 domain containing 1B	Cytoplasm	other	
CBR1	CBR1	carbonyl reductase 1	Cytoplasm	enzyme	
FCGR3A	FCGR3A/FCGR3B	Fc fragment of IgG receptor IIIa	Plasma Membrane	transmembrane receptor	IgG
MAFB	MAFB	MAF bZIP transcription factor B	Nucleus	transcription regulator	
HLA-DOA	HLA-DOA	major histocompatibility complex, class II, DO alpha	Plasma Membrane	transmembrane receptor	
HLA-DMA	HLA-DMA	major histocompatibility complex, class II, DM alpha	Plasma Membrane	transmembrane receptor	
HLA-DRA	HLA-DRA	major histocompatibility complex, class II, DR alpha	Plasma Membrane	transmembrane receptor	
LST1	LST1	leukocyte specific transcript 1	Plasma Membrane	other	
GPR56	ADGRG1	adhesion G protein-coupled receptor G1	Plasma Membrane	G-protein coupled receptor	
IGKC	IGKC	immunoglobulin kappa constant	Extracellular Space	other	
IGKV4-1	IGKV4-1	immunoglobulin kappa variable 4-1	Extracellular Space	peptidase	
IGLV4-69	IGLV4-69	immunoglobulin lambda variable 4-69	Other	other	
IGLV6-57	IGLV6-57	immunoglobulin lambda variable 6-57	Extracellular Space	other	
IGLV1-51	IGLV1-51	immunoglobulin lambda variable 1-51	Extracellular Space	other	
IGLV1-47	IGLV1-47	immunoglobulin lambda variable 1-47	Extracellular Space	other	
IGLV7-46	IGLV7-46	immunoglobulin lambda variable 7-46 (gene/pseudoge	Other	other	
IGLV1-44	IGLV1-44	immunoglobulin lambda variable 1-44	Other	other	
IGLV1-40	IGLV1-40	immunoglobulin lambda variable 1-40	Other	other	
IGLV3-25	IGLV3-25	immunoglobulin lambda variable 3-25	Extracellular Space	other	
IGLV2-23	IGLV2-23	immunoglobulin lambda variable 2-23	Other	other	
IGLV3-21	IGLV3-21	immunoglobulin lambda variable 3-21	Extracellular Space	other	
IGLV3-19	IGLV3-19	immunoglobulin lambda variable 3-19	Extracellular Space	other	
IGLV2-14	IGLV2-14	immunoglobulin lambda variable 2-14	Extracellular Space	other	
IGLV2-11	IGLV2-11	immunoglobulin lambda variable 2-11	Extracellular Space	other	
NA					
IGLV3-1	IGLV3-1	immunoglobulin lambda variable 3-1	Other	other	
IGLC2	IGLC2	immunoglobulin lambda constant 2	Extracellular Space	other	
IGLC3	IGLC3	immunoglobulin lambda constant 3 (Kern-Oz+ marker)	Extracellular Space	other	
IGHA2	IGHA2	immunoglobulin heavy constant alpha 2 (A2m marker)	Extracellular Space	other	
IGHG2	IGHG2	immunoglobulin heavy constant gamma 2 (G2m marke	Plasma Membrane	peptidase	
IGHA1	IGHA1	immunoglobulin heavy constant alpha 1	Extracellular Space	other	
IGHG1	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marke	Extracellular Space	peptidase	
IGHG3	IGHG3	immunoglobulin heavy constant gamma 3 (G3m marke	Extracellular Space	other	
IGHD	IGHD	immunoglobulin heavy constant delta	Extracellular Space	other	
IGHM	IGHM	immunoglobulin heavy constant mu	Plasma Membrane	transmembrane receptor	
IGHV6-1	IGHV6-1	immunoglobulin heavy variable 6-1	Other	other	
IGHV1-2	IGHV1-2	immunoglobulin heavy variable 1-2	Other	other	
IGHV2-5	IGHV2-5	immunoglobulin heavy variable 2-5	Other	other	
IGHV3-7	IGHV3-7	immunoglobulin heavy variable 3-7	Extracellular Space	other	
NA					
IGHV3-11	IGHV3-11	immunoglobulin heavy variable 3-11 (gene/pseudogene	Other	other	
IGHV3-15	IGHV3-15	immunoglobulin heavy variable 3-15	Other	other	
IGHV1-18	IGHV1-18	immunoglobulin heavy variable 1-18	Other	other	
IGHV3-21	IGHV3-21	immunoglobulin heavy variable 3-21	Other	other	
IGHV3-23	IGHV3-23	immunoglobulin heavy variable 3-23	Extracellular Space	other	
NA					
IGHV3-33	IGHV3-33	immunoglobulin heavy variable 3-33	Extracellular Space	other	
IGHV4-34	IGHV4-34	immunoglobulin heavy variable 4-34	Other	other	
IGHV4-39	IGHV4-39	immunoglobulin heavy variable 4-39	Other	other	
IGHV1-46	IGHV1-46	immunoglobulin heavy variable 1-46	Other	other	
IGHV3-48	IGHV3-48	immunoglobulin heavy variable 3-48	Other	other	
IGHV3-49	IGHV3-49	immunoglobulin heavy variable 3-49	Other	other	
IGHV5-51	IGHV5-51	immunoglobulin heavy variable 5-51	Other	other	
IGHV3-53	IGHV3-53	immunoglobulin heavy variable 3-53	Other	other	
IGHV1-69	IGHV1-69	immunoglobulin heavy variable 1-69	Other	other	
CLIC1	CLIC1	chloride intracellular channel 1	Nucleus	ion channel	
C19orf38	C19orf38	chromosome 19 open reading frame 38	Other	other	
GOLGA8A	GOLGA8A/GOLGA8B	golgin A8 family member A	Cytoplasm	other	
CEBPD	CEBPD	CCAAT/enhancer binding protein delta	Nucleus	transcription regulator	
HLA-DPB1	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	Plasma Membrane	transmembrane receptor	
IGHV4-59	IGHV4-59	immunoglobulin heavy variable 4-59	Extracellular Space	other	
IGHV3-74	IGHV3-74	immunoglobulin heavy variable 3-74	Other	other	
HLA-DRB6	HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (p	Other	other	
HLA-DPA1	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	Plasma Membrane	transmembrane receptor	
IGHV4-61	IGHV4-61	immunoglobulin heavy variable 4-61	Other	other	
NA					
HLA-DQB2	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	Plasma Membrane	transmembrane receptor	
GPX1	GPX1	glutathione peroxidase 1	Cytoplasm	enzyme	
NFAM1	NFAM1	NFAT activating protein with ITAM motif 1	Plasma Membrane	transmembrane receptor	
HLA-DQA2	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	Plasma Membrane	transmembrane receptor	
IGKV3-20	IGKV3-20	immunoglobulin kappa variable 3-20	Extracellular Space	peptidase	
LILRA2	LILRA2	leukocyte immunoglobulin like receptor A2	Plasma Membrane	other	
IGKV1-17	IGKV1-17	immunoglobulin kappa variable 1-17	Extracellular Space	other	
IGKV1-8	IGKV1-8	immunoglobulin kappa variable 1-8	Other	other	
IGKV1-16	IGKV1-16	immunoglobulin kappa variable 1-16	Extracellular Space	other	
IGKV2-24	IGKV2-24	immunoglobulin kappa variable 2-24	Other	other	
IGKV3-11	IGKV3-11	immunoglobulin kappa variable 3-11	Other	other	
PLEKHO1	PLEKHO1	pleckstrin homology domain containing O1	Cytoplasm	other	
HLA-DMB	HLA-DMB	major histocompatibility complex, class II, DM beta	Plasma Membrane	transmembrane receptor	
IGKV2-40	IGKV2-40	immunoglobulin kappa variable 2-40	Extracellular Space	other	
IGKV1-12	IGKV1-12	immunoglobulin kappa variable 1-12	Other	other	
IGKV1-5	IGKV1-5	immunoglobulin kappa variable 1-5	Extracellular Space	other	
IGKV3-15	IGKV3-15	immunoglobulin kappa variable 3-15	Other	other	
IGKV1-27	IGKV1-27	immunoglobulin kappa variable 1-27	Other	other	
HBB	HBB	hemoglobin subunit beta	Cytoplasm	transporter	[illegible]
LYN	LYN	LYN proto-oncogene, Src family tyrosine kinase	Cytoplasm	kinase	[illegible]
IGLL5	IGLL1/IGLL5	immunoglobulin lambda like polypeptide 1	Plasma Membrane	other	
RP11-[illegible]					
SLC1A4	SLC1A4	solute carrier family 1 member 4	Plasma Membrane	transporter	riluzole
KYNU	KYNU	kynureninase	Cytoplasm	enzyme	
PRKCE	PRKCE	protein kinase C epsilon	Cytoplasm	kinase	[illegible]
OGFRL1	OGFRL1	opioid growth factor receptor like 1	Other	other	
RNASE6	RNASE6	ribonuclease A family member k6	Extracellular Space	enzyme	
GNS	GNS	glucosamine (N-acetyl)-6-sulfatase	Cytoplasm	enzyme	
SIGLEC14	SIGLEC14	sialic acid binding Ig like lectin 14	Plasma Membrane	other	
P2RX1	P2RX1	purinergic receptor P2X 1	Plasma Membrane	ion channel	
IGLV10-54	IGLV10-54	immunoglobulin lambda variable 10-54	Other	other	
CEBPB	CEBPB	CCAAT/enhancer binding protein beta	Nucleus	transcription regulator	
SCIMP	SCIMP	SLP adaptor and CSK interacting membrane protein	Plasma Membrane	other	
PID1	PID1	phosphotyrosine interaction domain containing 1	Cytoplasm	other	
XCL2	XCL2	X-C motif chemokine ligand 2	Extracellular Space	cytokine	
ADAM19	ADAM19	ADAM metallopeptidase domain 19	Plasma Membrane	peptidase	
[illegible]	[illegible]	[illegible] centriolin binding protein	Cytoplasm	other	
[illegible]					
SRC	SRC	SRC proto-oncogene, non-receptor tyrosine kinase	Cytoplasm	kinase	[illegible]
RHPN1	RHPN1	rhophilin Rho GTPase binding protein 1	Cytoplasm	other	
HCAR3	HCAR3	hydroxycarboxylic acid receptor 3	Plasma Membrane	other	[illegible]
CD300A	CD300A	CD300a molecule	Plasma Membrane	transmembrane receptor	
YWHAH	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygena	Cytoplasm	transcription regulator	
TNFRSF1A	TNFRSF1A	TNF receptor superfamily member 1A	Plasma Membrane	transmembrane receptor	[illegible]
TBK1	TBK1	TANK binding kinase 1	Cytoplasm	kinase	
HBA1	HBA1/HBA2	hemoglobin subunit alpha 2	Extracellular Space	transporter	[illegible]
NA					
NIPAL4	NIPAL4	NIPA like domain containing 4	Other	other	
KLF4	KLF4	Kruppel like factor 4	Nucleus	transcription regulator	
FAM53B	FAM53B	family with sequence similarity 53 member B	Other	other	
ITGAX	ITGAX	integrin subunit alpha X	Plasma Membrane	transmembrane receptor	
MID1IP1	MID1IP1	MID1 interacting protein 1	Cytoplasm	other	
TMEM170B	TMEM170B	transmembrane protein 170B	Other	other	
IGFBP7	IGFBP7	insulin like growth factor binding protein 7	Extracellular Space	transporter	
IGKV1-6	IGKV1-6	immunoglobulin kappa variable 1-6	Other	other	
N4BP3	N4BP3	NEDD4 binding protein 3	Cytoplasm	other	
ELF4	ELF4	E74 like ETS transcription factor 4	Nucleus	transcription regulator	
NAGA	NAGA	alpha-N-acetylgalactosaminidase	Cytoplasm	enzyme	
GNA15	GNA15	G protein subunit alpha 15	Plasma Membrane	enzyme	
DDAH2	DDAH2	dimethylarginine dimethylaminohydrolase 2	Cytoplasm	enzyme	
GLIPR2	GLIPR2	GLI pathogenesis related 2	Cytoplasm	other	
CHP1	CHP1	calcineurin like EF-hand protein 1	Cytoplasm	transporter	
S100A6	S100A6	S100 calcium binding protein A6	Cytoplasm	transporter	
QPCT	QPCT	glutaminyl-peptide cyclotransferase	Cytoplasm	enzyme	
RNF135	RNF135	ring finger protein 135	Cytoplasm	enzyme	
CD300C	CD300C	CD300c molecule	Plasma Membrane	transmembrane receptor	
LYL1	LYL1	LYL1, basic helix-loop-helix family member	Nucleus	transcription regulator	
CSF2RB	CSF2RB	colony stimulating factor 2 receptor beta common subu	Plasma Membrane	transmembrane receptor	[illegible]
BID	BID	BH3 interacting domain death agonist	Cytoplasm	other	
IGHV[illegible]	IGHV[illegible]	immunoglobulin heavy variable [illegible]	Other	other	
MZB1	MZB1	marginal zone B and B1 cell specific protein	Extracellular Space	other	
MARCO	MARCO	macrophage receptor with collagenous structure	Plasma Membrane	transmembrane receptor	
IGHV[illegible]					
IER3	IER3	immediate early response 3	Cytoplasm	other	
NA					
CLEC12A	CLEC12A	C-type lectin domain family 12 member A	Plasma Membrane	other	
THEMIS2	THEMIS2	thymocyte selection associated family member 2	Other	other	
MBOAT7	MBOAT7	membrane bound O-acyltransferase domain containing	Plasma Membrane	enzyme	
CD1C	CD1C	CD1c molecule	Plasma Membrane	other	
ST6GAL1	ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1	Cytoplasm	enzyme	
IGHV1-24	IGHV1-24	immunoglobulin heavy variable 1-24	Other	other	
GRINA	GRINA	glutamate ionotropic receptor NMDA type subunit asso	Other	ion channel	
CDC42EP3	CDC42EP3	CDC42 effector protein 3	Cytoplasm	other	
FAM43A	FAM43A	family with sequence similarity 43 member A	Other	other	
ASGR2	ASGR2	asialoglycoprotein receptor 2	Plasma Membrane	transmembrane receptor	
B4GALT5	B4GALT5	beta-1,4-galactosyltransferase 5	Cytoplasm	enzyme	
C15orf39	C15orf39	chromosome 15 open reading frame 39	Cytoplasm	other	
SEMA6B	SEMA6B	semaphorin 6B	Plasma Membrane	other	
IGLV5-45	IGLV5-45	immunoglobulin lambda variable 5-45	Other	other	
FABP5	FABP5	fatty acid binding protein 5	Cytoplasm	transporter	
CXCL8	CXCL8	C-X-C motif chemokine ligand 8	Extracellular Space	cytokine	
SLC43A2	SLC43A2	solute carrier family 43 member 2	Plasma Membrane	transporter	
CHST2	CHST2	carbohydrate sulfotransferase 2	Cytoplasm	enzyme	
ADAMTS10	ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 m	Extracellular Space	peptidase	
ALOX5	ALOX5	arachidonate 5-lipoxygenase	Cytoplasm	enzyme	[illegible]
HES1	HES1	hes family bHLH transcription factor 1	Nucleus	transcription regulator	
SPOPL	SPOPL	speckle type BTB/POZ protein like	Other	other	
PLXDC1	PLXDC1	plexin domain containing 1	Plasma Membrane	other	
GNA12	GNA12	G protein subunit alpha 12	Plasma Membrane	enzyme	
TP53I11	TP53I11	tumor protein p53 inducible protein 11	Other	other	
SPRY2	SPRY2	sprouty RTK signaling antagonist 2	Plasma Membrane	other	
IGHV3-73	IGHV3-73	immunoglobulin heavy variable 3-73	Other	other	
RHOC	RHOC	ras homolog family member C	Plasma Membrane	enzyme	
NUAK2	NUAK2	NUAK family kinase 2	Other	kinase	
RSRP1	RSRP1	arginine and serine rich protein 1	Other	other	
SMPDL3A	SMPDL3A	sphingomyelin phosphodiesterase acid like 3A	Extracellular Space	enzyme	
PDIA6	PDIA6	protein disulfide isomerase family A member 6	Cytoplasm	enzyme	
ASAH1	ASAH1	N-acylsphingosine amidohydrolase 1	Cytoplasm	enzyme	
ANXA5	ANXA5	annexin A5	Plasma Membrane	transporter	
PPAP2B	PLPP3	phospholipid phosphatase 3	Plasma Membrane	phosphatase	

[illegible]	MESDC1	MESDC1	mesoderm development candidate 1	Other	other	
[illegible]	TBXAS1	TBXAS1	thromboxane A synthase 1	Plasma Membrane	enzyme	[illegible]
[illegible]	IGHV3-38	IGHV3-38	immunoglobulin heavy variable 3-38	Other	other	
[illegible]	CHST15	CHST15	carbohydrate sulfotransferase 15	Plasma Membrane	enzyme	
[illegible]	VAV3	VAV3	vav guanine nucleotide exchange factor 3	Cytoplasm	transcription regulator	
[illegible]	SDC2	SDC2	syndecan 2	Plasma Membrane	other	
[illegible]	GAB2	GAB2	GRB2 associated binding protein 2	Cytoplasm	other	
[illegible]	PARVB	PARVB	parvin beta	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	PPP1R18	PPP1R18	protein phosphatase 1 regulatory subunit 18	Other	other	
[illegible]	EGR2	EGR2	early growth response 2	Nucleus	transcription regulator	
[illegible]	BACH1					
[illegible]	GZMA	GZMA	granzyme A	Cytoplasm	peptidase	
[illegible]	EREG	EREG	epiregulin	Extracellular Space	growth factor	
[illegible]	SNX30	SNX30	sorting nexin family member 30	Other	other	
[illegible]	IGKV2D-29	IGKV2D-29	immunoglobulin kappa variable 2D-29	Other	other	
[illegible]	FOXP4	FOXP4	forkhead box P4	Nucleus	transcription regulator	
[illegible]	BHLHE40	BHLHE40	basic helix-loop-helix family member e40	Nucleus	transcription regulator	
[illegible]	RHOQ	RHOQ	ras homolog family member Q	Plasma Membrane	enzyme	
[illegible]	EVI2B	EVI2B	ecotropic viral integration site 2B	Plasma Membrane	other	
[illegible]	ADRBK2	GRK3	G protein-coupled receptor kinase 3	Cytoplasm	kinase	
[illegible]	TAF1C	TAF1C	TATA-box binding protein associated factor, RNA polym	Nucleus	transcription regulator	
[illegible]	HAS1	HAS1	hyaluronan synthase 1	Plasma Membrane	enzyme	
[illegible]	HK2	HK2	hexokinase 2	Cytoplasm	kinase	
[illegible]	ZMIZ1	ZMIZ1	zinc finger MIZ-type containing 1	Nucleus	other	
[illegible]	KBTBD8	KBTBD8	kelch repeat and BTB domain containing 8	Other	other	
[illegible]	PNKD	PNKD	paroxysmal nonkinesigenic dyskinesia	Nucleus	other	
[illegible]	APOBR	APOBR	apolipoprotein B receptor	Plasma Membrane	transmembrane receptor	
[illegible]	IFI6	IFI6	interferon alpha inducible protein 6	Cytoplasm	other	
[illegible]	TREML1	TREML1	triggering receptor expressed on myeloid cells like 1	Plasma Membrane	other	
[illegible]	FTL	FTL	ferritin light chain	Cytoplasm	enzyme	
[illegible]	LRRC32	LRRC32	leucine rich repeat containing 32	Plasma Membrane	other	
[illegible]	ODF3B	ODF3B	outer dense fiber of sperm tails 3B	Other	enzyme	
[illegible]	CHSY1	CHSY1	chondroitin sulfate synthase 1	Cytoplasm	enzyme	
[illegible]	CXCL2	CXCL2	C-X-C motif chemokine ligand 2	Extracellular Space	cytokine	
[illegible]	HIC1	HIC1	HIC ZBTB transcriptional repressor 1	Nucleus	transcription regulator	
[illegible]	EGR3	EGR3	early growth response 3	Nucleus	transcription regulator	
[illegible]	RXRA	RXRA	retinoid X receptor alpha	Nucleus	ligand-dependent nuclear receptor	[illegible]
[illegible]	CDKN1A	CDKN1A	cyclin dependent kinase inhibitor 1A	Nucleus	kinase	
[illegible]	HAVCR2	HAVCR2	hepatitis A virus cellular receptor 2	Plasma Membrane	other	
[illegible]	EDC4	EDC4	enhancer of mRNA decapping 4	Cytoplasm	other	
[illegible]	TPI1	TPI1	triosephosphate isomerase 1	Cytoplasm	enzyme	
[illegible]	MOB3A	MOB3A	MOB kinase activator 3A	Other	other	
[illegible]	IGLV8-61	IGLV8-61	immunoglobulin lambda variable 8-61	Other	other	
[illegible]	GPRASP1	GPRASP1	G protein-coupled receptor associated sorting protein 1	Cytoplasm	transporter	
[illegible]	TSPAN13	TSPAN13	tetraspanin 13	Plasma Membrane	other	
[illegible]	GSTO1	GSTO1	glutathione S-transferase omega 1	Cytoplasm	enzyme	
[illegible]	FCGRT	FCGRT	Fc fragment of IgG receptor and transporter	Plasma Membrane	transmembrane receptor	
[illegible]	CREG1	CREG1	cellular repressor of E1A stimulated genes 1	Nucleus	transcription regulator	
[illegible]	ARPC1B	ARPC1B	actin related protein 2/3 complex subunit 1B	Cytoplasm	other	
[illegible]	SCML1	SCML1	sex comb on midleg-like 1 (Drosophila)	Nucleus	transcription regulator	
[illegible]	NFKBID	NFKBID	NFKB inhibitor delta	Nucleus	transcription regulator	
[illegible]	CCDC71L	CCDC71L	coiled-coil domain containing 71 like	Other	other	
[illegible]	CSAD	CSAD	cysteine sulfinic acid decarboxylase	Cytoplasm	enzyme	
[illegible]	IGKV1D-8	IGKV1D-8	immunoglobulin kappa variable 1D-8	Other	other	
[illegible]	ANKZF1	ANKZF1	ankyrin repeat and zinc finger domain containing 1	Nucleus	transcription regulator	
[illegible]	B4GALT1	B4GALT1	beta-1,4-galactosyltransferase 1	Cytoplasm	enzyme	
[illegible]	PRKAR2B	PRKAR2B	protein kinase cAMP-dependent type II regulatory subu	Cytoplasm	kinase	
[illegible]	USP28	USP28	ubiquitin specific peptidase 28	Cytoplasm	peptidase	
[illegible]	WARS	WARS	tryptophanyl-tRNA synthetase	Cytoplasm	enzyme	
[illegible]	IL6	IL6	interleukin 6	Extracellular Space	cytokine	[illegible]
[illegible]	CLCF1	CLCF1	cardiotrophin like cytokine factor 1	Extracellular Space	cytokine	
[illegible]	LGALS9	LGALS9	galectin 9	Plasma Membrane	other	
[illegible]	SNX18	SNX18	sorting nexin 18	Cytoplasm	transporter	
[illegible]	CLEC4A	CLEC4A	C-type lectin domain family 4 member A	Plasma Membrane	transmembrane receptor	
[illegible]	TPST2	TPST2	tyrosylprotein sulfotransferase 2	Cytoplasm	enzyme	
[illegible]	CD9	CD9	CD9 molecule	Plasma Membrane	other	
[illegible]	TBX21	TBX21	T-box 21	Nucleus	transcription regulator	
[illegible]	CENPT	CENPT	centromere protein T	Cytoplasm	other	
[illegible]	TMEM209	TMEM209	transmembrane protein 209	Cytoplasm	other	
[illegible]	FAM26F	FAM26F	family with sequence similarity 26 member F	Other	other	
[illegible]	RNF144B	RNF144B	ring finger protein 144B	Cytoplasm	enzyme	
[illegible]	RGS19	RGS19	regulator of G-protein signaling 19	Cytoplasm	other	
[illegible]	GLUL	GLUL	glutamate-ammonia ligase	Cytoplasm	enzyme	
[illegible]	TRAF3IP3	TRAF3IP3	TRAF3 interacting protein 3	Other	other	
[illegible]	CCL7	CCL7	C-C motif chemokine ligand 7	Extracellular Space	cytokine	[illegible]
[illegible]	MAPKAPK3	MAPKAPK3	mitogen-activated protein kinase-activated protein kina	Nucleus	kinase	
[illegible]	SH3BP2	SH3BP2	SH3 domain binding protein 2	Cytoplasm	other	
[illegible]	PGD	PGD	phosphogluconate dehydrogenase	Cytoplasm	enzyme	
[illegible]	PLCG1	PLCG1	phospholipase C gamma 1	Cytoplasm	enzyme	
[illegible]	AOAH	AOAH	acyloxyacyl hydrolase	Extracellular Space	enzyme	
[illegible]	MATK	MATK	megakaryocyte-associated tyrosine kinase	Cytoplasm	kinase	
[illegible]	PLCD1	PLCD1	phospholipase C delta 1	Cytoplasm	enzyme	
[illegible]	CPPED1	CPPED1	calcineurin like phosphoesterase domain containing 1	Cytoplasm	enzyme	
[illegible]	CTSL	CTSL	cathepsin L	Cytoplasm	peptidase	[illegible]
[illegible]	WDR55	WDR55	WD repeat domain 55	Nucleus	other	
[illegible]	AP1S2	AP1S2	adaptor related protein complex 1 sigma 2 subunit	Cytoplasm	transporter	
[illegible]	CAPNS1	CAPNS1	calpain small subunit 1	Cytoplasm	peptidase	
[illegible]	PPWD1	PPWD1	peptidylprolyl isomerase domain and WD repeat contai	Nucleus	enzyme	
[illegible]	HOTAIRM1	HOTAIRM1	HOXA transcript antisense RNA, myeloid-specific 1	Other	other	
[illegible]	03-Sep	03-Sep	septin 3	Cytoplasm	enzyme	
[illegible]	EIF4EBP1	EIF4EBP1	eukaryotic translation initiation factor 4E binding prote	Cytoplasm	translation regulator	
[illegible]	MTR	MTR	5-methyltetrahydrofolate-homocysteine methyltransfer	Cytoplasm	enzyme	[illegible]
[illegible]	ETS2	ETS2	ETS proto-oncogene 2, transcription factor	Nucleus	transcription regulator	
[illegible]	VASP	VASP	vasodilator-stimulated phosphoprotein	Plasma Membrane	other	
[illegible]	GPX1P1	GPX1P1	glutathione peroxidase pseudogene 1	Other	other	
[illegible]	SCO2	SCO2	SCO2, cytochrome c oxidase assembly protein	Cytoplasm	other	
[illegible]	LSP1					
[illegible]	TRDC	TRDC	T cell receptor delta constant	Other	other	
[illegible]	AIF1	AIF1	allograft inflammatory factor 1	Nucleus	other	
[illegible]	ADAM15	ADAM15	ADAM metallopeptidase domain 15	Plasma Membrane	peptidase	
[illegible]	LENG8	LENG8	leukocyte receptor cluster member 8	Other	other	
[illegible]	IGLV1-36	IGLV1-36	immunoglobulin lambda variable 1-36	Other	other	
[illegible]	EXOSC10	EXOSC10	exosome component 10	Nucleus	kinase	
[illegible]	TPP1	TPP1	tripeptidyl peptidase 1	Cytoplasm	peptidase	
[illegible]	IGKV5-2	IGKV5-2	immunoglobulin kappa variable 5-2	Other	other	
[illegible]	EGR1	EGR1	early growth response 1	Nucleus	transcription regulator	
[illegible]	BST1	BST1	bone marrow stromal cell antigen 1	Plasma Membrane	enzyme	
[illegible]	S100A10	S100A10	S100 calcium binding protein A10	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	SGSM2	SGSM2	small G protein signaling modulator 2	Cytoplasm	other	
[illegible]	PDLIM7	PDLIM7	PDZ and LIM domain 7	Cytoplasm	other	
[illegible]	RP2	RP2	retinitis pigmentosa 2 (X-linked recessive)	Cytoplasm	enzyme	
[illegible]	PTPN12	PTPN12	protein tyrosine phosphatase, non-receptor type 12	Cytoplasm	phosphatase	
[illegible]	SH3BGRL3	SH3BGRL3	SH3 domain binding glutamate rich protein like 3	Nucleus	other	
[illegible]	[illegible]	CCDC18-AS1	CCDC18 antisense RNA 1	Other	other	
[illegible]	RETN	RETN	resistin	Extracellular Space	other	
[illegible]	IFITM10	IFITM10	interferon induced transmembrane protein 10	Other	other	
[illegible]	MCEMP1	MCEMP1	mast cell expressed membrane protein 1	Cytoplasm	other	
[illegible]	HSPH1	HSPH1	heat shock protein family H (Hsp110) member 1	Cytoplasm	other	
[illegible]	PTX3	PTX3	pentraxin 3	Extracellular Space	other	
[illegible]	LCP1	LCP1	lymphocyte cytosolic protein 1	Cytoplasm	other	
[illegible]	VSTM1	VSTM1	V-set and transmembrane domain containing 1	Other	other	
[illegible]	CHST10	CHST10	carbohydrate sulfotransferase 10	Cytoplasm	enzyme	
[illegible]	PILRA	PILRA	paired immunoglobin like type 2 receptor alpha	Plasma Membrane	other	
[illegible]	ZYX	ZYX	zyxin	Plasma Membrane	other	
[illegible]	IGLV3-9	IGLV3-9	immunoglobulin lambda variable 3-9 (gene/pseudogene)	Other	other	
[illegible]	PRDM1	PRDM1	PR/SET domain 1	Nucleus	transcription regulator	
[illegible]	CRTAP	CRTAP	cartilage associated protein	Extracellular Space	other	
[illegible]	FOSL1	FOSL1	FOS like 1, AP-1 transcription factor subunit	Nucleus	transcription regulator	
[illegible]	DUSP5	DUSP5	dual specificity phosphatase 5	Nucleus	phosphatase	
[illegible]	CTSB	CTSB	cathepsin B	Cytoplasm	peptidase	
[illegible]	ENTPD4	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	Cytoplasm	enzyme	
[illegible]	GPX3	GPX3	glutathione peroxidase 3	Extracellular Space	enzyme	
[illegible]	CDK5RAP3	CDK5RAP3	CDK5 regulatory subunit associated protein 3	Nucleus	other	
[illegible]	KLRB1	KLRB1	killer cell lectin like receptor B1	Plasma Membrane	transmembrane receptor	
[illegible]	OASL	OASL	2'-5'-oligoadenylate synthetase like	Cytoplasm	enzyme	
[illegible]	MAFF	MAFF	MAF bZIP transcription factor F	Nucleus	transcription regulator	
[illegible]	IGHV1-8	IGHV1-8	immunoglobulin heavy variable 1-8	Other	other	
[illegible]	JAK3	JAK3	Janus kinase 3	Cytoplasm	kinase	[illegible]
[illegible]	GPC2	GPC2	glypican 2	Plasma Membrane	other	
[illegible]	GADD45G	GADD45G	growth arrest and DNA damage inducible gamma	Nucleus	other	
[illegible]	CHRM3-AS2	CHRM3-AS2	CHRM3 antisense RNA 2	Other	other	
[illegible]	FES	FES	FES proto-oncogene, tyrosine kinase	Cytoplasm	kinase	
[illegible]	TIMP2	TIMP2	TIMP metallopeptidase inhibitor 2	Extracellular Space	other	
[illegible]	MSL3	MSL3	male-specific lethal 3 homolog (Drosophila)	Nucleus	transcription regulator	
[illegible]	KLF11	KLF11	Kruppel like factor 11	Nucleus	transcription regulator	
[illegible]	KLHL3	KLHL3	kelch like family member 3	Cytoplasm	other	
[illegible]	SLC11A1	SLC11A1	solute carrier family 11 member 1	Plasma Membrane	transporter	
[illegible]	NCF1	NCF1	neutrophil cytosolic factor 1	Cytoplasm	enzyme	
[illegible]	AGPAT2	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2	Cytoplasm	enzyme	
[illegible]	NPEPL1	NPEPL1	aminopeptidase-like 1	Nucleus	peptidase	
[illegible]	VDR	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	Nucleus	[illegible]	[illegible]
[illegible]	IFNGR2	IFNGR2	interferon gamma receptor 2	Plasma Membrane	transmembrane receptor	interferon gamma-1b
[illegible]	LAPTM5	LAPTM5	lysosomal protein transmembrane 5	Plasma Membrane	other	
[illegible]	TLR1	TLR1	toll like receptor 1	Plasma Membrane	transmembrane receptor	
[illegible]	VOPP1	VOPP1	vesicular, overexpressed in cancer, prosurvival protein	Nucleus	other	
[illegible]	[illegible]	[illegible]	[illegible] transcription factor 1	Nucleus	transcription regulator	
[illegible]	TYK2	TYK2	tyrosine kinase 2	Plasma Membrane	kinase	[illegible]
[illegible]	MTSS1	MTSS1	MTSS1, I-BAR domain containing	Cytoplasm	other	
[illegible]	[illegible]	[illegible]	[illegible] family member 3	Nucleus	other	
[illegible]	GALNT2	GALNT2	polypeptide N-acetylgalactosaminyltransferase 2	Cytoplasm	enzyme	
[illegible]	CD58	CD58	CD58 molecule	Plasma Membrane	transmembrane receptor	
[illegible]	TESC	TESC	tescalcin	Cytoplasm	other	
[illegible]	PHLDA1	PHLDA1	pleckstrin homology like domain family A member 1	Cytoplasm	other	
[illegible]	FOSL2	FOSL2	FOS like 2, AP-1 transcription factor subunit	Nucleus	transcription regulator	
[illegible]	SUGP2	SUGP2	SURP and G-patch domain containing 2	Nucleus	other	
[illegible]	SNRNP70	SNRNP70	small nuclear ribonucleoprotein U1 subunit 70	Nucleus	other	
[illegible]	GPR84	GPR84	G protein-coupled receptor 84	Plasma Membrane	G-protein coupled receptor	
[illegible]	GSTM2	GSTM2	glutathione S-transferase mu 2	Cytoplasm	enzyme	
[illegible]	LY6E	LY6E	lymphocyte antigen 6 family member E	Plasma Membrane	other	[illegible]
[illegible]	RNASE2	RNASE2	ribonuclease A family member 2	Cytoplasm	enzyme	
[illegible]	TUBGCP6	TUBGCP6	tubulin gamma complex associated protein 6	Cytoplasm	other	
[illegible]	NOD2	NOD2	nucleotide binding oligomerization domain containing :	Cytoplasm	other	
[illegible]	IGHV3-43	IGHV3-43	immunoglobulin heavy variable 3-43	Other	other	
[illegible]	NCF4	NCF4	neutrophil cytosolic factor 4	Cytoplasm	enzyme	
[illegible]	HIST1H2AC	HIST1H2AC	histone cluster 1 H2A family member c	Nucleus	other	
[illegible]	LMBR1L	LMBR1L	limb development membrane protein 1 like	Plasma Membrane	other	
[illegible]	ZNF317	ZNF317	zinc finger protein 317	Other	other	
[illegible]	FOLR3	FOLR3	folate receptor 3	Extracellular Space	other	
[illegible]	APOBEC3C	APOBEC3C	apolipoprotein B mRNA editing enzyme catalytic subunit	Other	enzyme	
[illegible]	GAL3ST4	GAL3ST4	galactose-3-O-sulfotransferase 4	Cytoplasm	enzyme	
[illegible]	LIPA	LIPA	lipase A, lysosomal acid type	Cytoplasm	enzyme	
[illegible]	HECTD3	HECTD3	HECT domain E3 ubiquitin protein ligase 3	Cytoplasm	enzyme	
[illegible]	NUP85	NUP85	nucleoporin 85	Cytoplasm	other	
[illegible]	GNG5	GNG5	G protein subunit gamma 5	Plasma Membrane	other	
[illegible]	IRF4	IRF4	interferon regulatory factor 4	Nucleus	transcription regulator	
[illegible]	ZNF467	ZNF467	zinc finger protein 467	Nucleus	transcription regulator	
[illegible]	ENGASE	ENGASE	endo-beta-N-acetylglucosaminidase	Cytoplasm	enzyme	
[illegible]	ITGB2	ITGB2	integrin subunit beta 2	Plasma Membrane	transmembrane receptor	
[illegible]	USP21	USP21	ubiquitin specific peptidase 21	Cytoplasm	peptidase	
[illegible]	SH3BGRL	SH3BGRL	SH3 domain binding glutamate rich protein like	Cytoplasm	other	
[illegible]	GAPDH	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	Cytoplasm	enzyme	
[illegible]	PRNP	PRNP	prion protein	Plasma Membrane	other	
[illegible]	CEP95	CEP95	centrosomal protein 95	Cytoplasm	other	
[illegible]	ENG	ENG	endoglin	Plasma Membrane	transmembrane receptor	
[illegible]	WDR75	WDR75	WD repeat domain 75	Nucleus	other	
[illegible]	GSE1	GSE1	Gse1 coiled-coil protein	Extracellular Space	other	
[illegible]	NAMPT	NAMPT	nicotinamide phosphoribosyltransferase	Extracellular Space	cytokine	[illegible]
[illegible]	SLC16A6	SLC16A6	solute carrier family 16 member 6	Plasma Membrane	transporter	
[illegible]	TBC1D1	TBC1D1	TBC1 domain family member 1	Nucleus	other	
[illegible]	KLC4	KLC4	kinesin light chain 4	Other	other	
[illegible]	USP6NL	USP6NL	USP6 N-terminal like	Plasma Membrane	other	
[illegible]	WASH4P					
[illegible]	NA					
[illegible]	ASPHD2	ASPHD2	aspartate beta-hydroxylase domain containing 2	Other	enzyme	
[illegible]	FAM118B	FAM118B	family with sequence similarity 118 member B	Nucleus	other	
[illegible]	AMT	AMT	aminomethyltransferase	Cytoplasm	enzyme	
[illegible]	ADAP1	ADAP1	ArfGAP with dual PH domains 1	Nucleus	other	
[illegible]	SOCS6	SOCS6	suppressor of cytokine signaling 6	Cytoplasm	other	
[illegible]	MAN1A1	MAN1A1	mannosidase alpha class 1A member 1	Cytoplasm	enzyme	
[illegible]	AGTRAP	AGTRAP	angiotensin II receptor associated protein	Plasma Membrane	G-protein coupled receptor	
[illegible]	LIMS1	LIMS1	LIM zinc finger domain containing 1	Plasma Membrane	other	
[illegible]	HNRNPH1	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1	Nucleus	other	
[illegible]	RHOG	RHOG	ras homolog family member G	Cytoplasm	enzyme	
[illegible]	GZMK	GZMK	granzyme K	Cytoplasm	peptidase	
[illegible]	TTC38	TTC38	tetratricopeptide repeat domain 38	Cytoplasm	other	
[illegible]	SRSF11	SRSF11	serine and arginine rich splicing factor 11	Nucleus	other	
[illegible]	GPR65	GPR65	G protein-coupled receptor 65	Plasma Membrane	G-protein coupled receptor	
[illegible]	TMEM86A	TMEM86A	transmembrane protein 86A	Cytoplasm	other	
[illegible]	CLIC3	CLIC3	chloride intracellular channel 3	Nucleus	ion channel	
[illegible]	SENP7	SENP7	SUMO1/sentrin specific peptidase 7	Nucleus	peptidase	
[illegible]	PPT1	PPT1	palmitoyl-protein thioesterase 1	Cytoplasm	enzyme	
[illegible]	C7orf50	C7orf50	chromosome 7 open reading frame 50	Other	other	
[illegible]	BTAF1	BTAF1	B-TFIID TATA-box binding protein associated factor 1	Nucleus	transcription regulator	

[illegible]	TENM1	TENM1	teneurin transmembrane protein 1	Plasma Membrane	peptidase	
[illegible]	ARF6	ARF6	ADP ribosylation factor 6	Plasma Membrane	transporter	
[illegible]	NCR3	NCR3	natural cytotoxicity triggering receptor 3	Plasma Membrane	transmembrane receptor	
[illegible]	MAP3K7CL	MAP3K7CL	MAP3K7 C-terminal like	Other	other	
[illegible]	UBE2E1	UBE2E1	ubiquitin conjugating enzyme E2 E1	Cytoplasm	enzyme	
[illegible]	SLC7A5	SLC7A5	solute carrier family 7 member 5	Plasma Membrane	transporter	
[illegible]	GABARAP	GABARAP	GABA type A receptor-associated protein	Cytoplasm	transporter	
[illegible]	PRAM1	PRAM1	PML-RARA regulated adaptor molecule 1	Other	other	
[illegible]	NFKB2	NFKB2	nuclear factor kappa B subunit 2	Nucleus	transcription regulator	
[illegible]	DHX38	DHX38	DEAH-box helicase 38	Nucleus	enzyme	
[illegible]	CXCR3	CXCR3	C-X-C motif chemokine receptor 3	Plasma Membrane	G-protein coupled receptor	
[illegible]	ACTN4	ACTN4	actinin alpha 4	Cytoplasm	transcription regulator	
[illegible]	EMP3	EMP3	epithelial membrane protein 3	Plasma Membrane	other	
[illegible]	CD151	CD151	CD151 molecule (Raph blood group)	Plasma Membrane	other	
[illegible]	IGLV9-49	IGLV9-49	immunoglobulin lambda variable 9-49	Other	other	
[illegible]	KCTD12	KCTD12	potassium channel tetramerization domain containing 1	Plasma Membrane	ion channel	
[illegible]	SPON2	SPON2	spondin 2	Extracellular Space	other	
[illegible]	SPPL2B	SPPL2B	signal peptide peptidase like 2B	Plasma Membrane	peptidase	
[illegible]	VPS52	VPS52	VPS52, GARP complex subunit	Cytoplasm	other	
[illegible]	CXXC1	CXXC1	CXXC finger protein 1	Nucleus	transcription regulator	
[illegible]	WDR81	WDR81	WD repeat domain 81	Other	other	
[illegible]	ATP6V1F	ATP6V1F	ATPase H+ transporting V1 subunit F	Cytoplasm	enzyme	
[illegible]	ENO1	ENO1	enolase 1	Cytoplasm	enzyme	
[illegible]	TRMU	TRMU	tRNA 5-methylaminomethyl-2-thiouridylate methyltrans	Cytoplasm	enzyme	
[illegible]	AP3M2	AP3M2	adaptor related protein complex 3 mu 2 subunit	Cytoplasm	transporter	
[illegible]	PYCARD	PYCARD	PYD and CARD domain containing	Cytoplasm	transcription regulator	
[illegible]	C18orf58	C18orf58	chromosome 18 open reading frame 58	Other	other	
[illegible]	SRGN	SRGN	serglycin	Cytoplasm	other	
[illegible]	THOC1	THOC1	THO complex 1	Nucleus	transcription regulator	
[illegible]	SH3BP5	SH3BP5	SH3 domain binding protein 5	Cytoplasm	other	
[illegible]	ZBTB7B	ZBTB7B	zinc finger and BTB domain containing 7B	Nucleus	transcription regulator	
[illegible]	[illegible]	[illegible]	uncharacterized [illegible]	Other	other	
[illegible]	MPP1	MPP1	membrane palmitoylated protein 1	Plasma Membrane	kinase	
[illegible]	AP1B1	AP1B1	adaptor related protein complex 1 beta 1 subunit	Cytoplasm	other	
[illegible]	LTBP4	LTBP4	latent transforming growth factor beta binding protein	Extracellular Space	other	
[illegible]	SPHK1	SPHK1	sphingosine kinase 1	Cytoplasm	kinase	
[illegible]	DBH-AS1	DBH-AS1	DBH antisense RNA 1	Other	other	
[illegible]	CDK11A	CDK11A	cyclin dependent kinase 11A	Nucleus	kinase	
[illegible]	KIAA0907	KIAA0907	KIAA0907	Nucleus	other	
[illegible]	CSF1	CSF1	colony stimulating factor 1	Extracellular Space	cytokine	
[illegible]	MXRA7	MXRA7	matrix remodeling associated 7	Other	other	
[illegible]	TNNI2	TNNI2	troponin I2, fast skeletal type	Cytoplasm	enzyme	
[illegible]	[illegible]	MTCO1P12	mitochondrially encoded cytochrome c oxidase I pseudo	Other	other	
[illegible]	GMEB1	GMEB1	glucocorticoid modulatory element binding protein 1	Nucleus	transcription regulator	
[illegible]	JAZF1	JAZF1	JAZF zinc finger 1	Nucleus	transcription regulator	
[illegible]	CHST12					
[illegible]	TALDO1	TALDO1	transaldolase 1	Cytoplasm	enzyme	
[illegible]	ATG2B	ATG2B	autophagy related 2B	Other	other	
[illegible]	NLRP1	NLRP1	NLR family pyrin domain containing 1	Cytoplasm	other	
[illegible]	ANAPC2	ANAPC2	anaphase promoting complex subunit 2	Nucleus	other	
[illegible]	MOV10	MOV10	Mov10 RISC complex RNA helicase	Nucleus	enzyme	
[illegible]	NPRL2	NPRL2	NPR2-like, GATOR1 complex subunit	Cytoplasm	kinase	
[illegible]	POMT1	POMT1	protein O-mannosyltransferase 1	Cytoplasm	enzyme	
[illegible]	IDUA	IDUA	iduronidase, alpha-L-	Cytoplasm	enzyme	
[illegible]	IFITM2	IFITM2	interferon induced transmembrane protein 2	Cytoplasm	other	
[illegible]	EMP1	EMP1	epithelial membrane protein 1	Plasma Membrane	other	
[illegible]	GSTP1	GSTP1	glutathione S-transferase pi 1	Cytoplasm	enzyme	
[illegible]	ARHGAP25	ARHGAP25	Rho GTPase activating protein 25	Cytoplasm	other	
[illegible]	CDKN1C	CDKN1C	cyclin dependent kinase inhibitor 1C	Nucleus	other	
[illegible]	SPG7	SPG7	SPG7, paraplegin matrix AAA peptidase subunit	Cytoplasm	peptidase	
[illegible]	CCDC84	CCDC84	coiled-coil domain containing 84	Other	other	
[illegible]	WDR6	WDR6	WD repeat domain 6	Cytoplasm	other	
[illegible]	LPGAT1	LPGAT1	lysophosphatidylglycerol acyltransferase 1	Cytoplasm	enzyme	
[illegible]	RARA-AS1	RARA-AS1	RARA antisense RNA 1	Other	other	
[illegible]	CMIP	CMIP	c-Maf inducing protein	Cytoplasm	other	
[illegible]	MINK1	MINK1	misshapen like kinase 1	Cytoplasm	kinase	
[illegible]	QSOX1	QSOX1	quiescin sulfhydryl oxidase 1	Cytoplasm	enzyme	
[illegible]	TBKBP1	TBKBP1	TBK1 binding protein 1	Other	other	
[illegible]	RRN3P1	RRN3P1	RRN3 homolog, RNA polymerase I transcription factor p	Other	other	
[illegible]	TPP2	TPP2	tripeptidyl peptidase 2	Cytoplasm	peptidase	
[illegible]	TNFSF13B	TNFSF13B	tumor necrosis factor superfamily member 13b	Extracellular Space	cytokine	belimumab
[illegible]	CFL1	CFL1	cofilin 1	Nucleus	other	
[illegible]	PMAIP1	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	Cytoplasm	other	
[illegible]	C19orf48	C19orf48	chromosome 19 open reading frame 48	Other	other	
[illegible]	SERTAD3	SERTAD3	SERTA domain containing 3	Nucleus	transcription regulator	
[illegible]	FUCA2	FUCA2	fucosidase, alpha-L- 2, plasma	Extracellular Space	enzyme	
[illegible]	ITPK1	ITPK1	inositol-tetrakisphosphate 1-kinase	Cytoplasm	kinase	
[illegible]	DYNC1LI2	DYNC1LI2	dynein cytoplasmic 1 light intermediate chain 2	Cytoplasm	other	
[illegible]	VAT1	VAT1	vesicle amine transport 1	Plasma Membrane	transporter	
[illegible]	MAP2K3	MAP2K3	mitogen-activated protein kinase kinase 3	Cytoplasm	kinase	
[illegible]	MT-CO2	MT-CO2	cytochrome c oxidase subunit II	Cytoplasm	enzyme	
[illegible]	BLVRB	BLVRB	biliverdin reductase B	Cytoplasm	enzyme	
[illegible]	SLC30A1	SLC30A1	solute carrier family 30 member 1	Plasma Membrane	transporter	
[illegible]	NA					
[illegible]	SH2B3	SH2B3	SH2B adaptor protein 3	Plasma Membrane	other	
[illegible]	RAB44	RAB44	RAB44, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	FHL3	FHL3	four and a half LIM domains 3	Plasma Membrane	other	
[illegible]	PPP1R9B	PPP1R9B	protein phosphatase 1 regulatory subunit 9B	Cytoplasm	enzyme	
[illegible]	TNFSF9	TNFSF9	tumor necrosis factor superfamily member 9	Plasma Membrane	cytokine	
[illegible]	MAPK8IP1	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein	Cytoplasm	other	
[illegible]	SERPINB2	SERPINB2	serpin family B member 2	Extracellular Space	other	
[illegible]	CHST11	CHST11	carbohydrate sulfotransferase 11	Cytoplasm	enzyme	
[illegible]	PAN2	PAN2	PAN2 poly(A) specific ribonuclease subunit	Cytoplasm	peptidase	
[illegible]	AP3S1	AP3S1	adaptor related protein complex 3 sigma 1 subunit	Cytoplasm	transporter	
[illegible]	NAA16	NAA16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	Nucleus	enzyme	
[illegible]	CCNL2	CCNL2	cyclin L2	Nucleus	other	
[illegible]	SNHG12	SNHG12	small nucleolar RNA host gene 12	Other	other	
[illegible]	OLR1	OLR1	oxidized low density lipoprotein receptor 1	Plasma Membrane	transmembrane receptor	
[illegible]	LAMP2	LAMP2	lysosomal associated membrane protein 2	Plasma Membrane	enzyme	
[illegible]	TARBP1	TARBP1	TAR (HIV-1) RNA binding protein 1	Nucleus	transcription regulator	
[illegible]	EFHD2	EFHD2	EF-hand domain family member D2	Other	other	
[illegible]	TRIO	TRIO	trio Rho guanine nucleotide exchange factor	Cytoplasm	kinase	
[illegible]	SIPA1L3	SIPA1L3	signal induced proliferation associated 1 like 3	Extracellular Space	other	
[illegible]	TMCO3	TMCO3	transmembrane and coiled-coil domains 3	Other	transporter	
[illegible]	BCL7A	BCL7A	BCL tumor suppressor 7A	Nucleus	other	
[illegible]	IGSF6	IGSF6	immunoglobulin superfamily member 6	Plasma Membrane	transmembrane receptor	
[illegible]	LUC7L3	LUC7L3	LUC7 like 3 pre-mRNA splicing factor	Nucleus	other	
[illegible]	PLSCR1	PLSCR1	phospholipid scramblase 1	Plasma Membrane	enzyme	
[illegible]	OGT	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	Cytoplasm	enzyme	
[illegible]	KLHDC3	KLHDC3	kelch domain containing 3	Cytoplasm	other	
[illegible]	SNHG1	SNHG1	small nucleolar RNA host gene 1	Other	other	
[illegible]	BSG	BSG	basigin (Ok blood group)	Plasma Membrane	transporter	
[illegible]	AKIRIN2	AKIRIN2	akirin 2	Nucleus	other	
[illegible]	BCAP31	BCAP31	B-cell receptor-associated protein 31	Cytoplasm	transporter	
[illegible]	CD82	CD82	CD82 molecule	Plasma Membrane	other	
[illegible]	MED28	MED28	mediator complex subunit 28	Nucleus	transcription regulator	
[illegible]	CXorf21	CXorf21	chromosome X open reading frame 21	Other	enzyme	
[illegible]	IGHV3OR15-7	IGHV3OR15-7	immunoglobulin heavy variable 3/OR15-7 (non-functior	Other	other	
[illegible]	PTPN18	PTPN18	protein tyrosine phosphatase, non-receptor type 18	Nucleus	phosphatase	
[illegible]	SERPINB8	SERPINB8	serpin family B member 8	Cytoplasm	other	
[illegible]	MAPK7	MAPK7	mitogen-activated protein kinase 7	Cytoplasm	kinase	
[illegible]	PEX1	PEX1	peroxisomal biogenesis factor 1	Cytoplasm	enzyme	
[illegible]	NA					
[illegible]	PPP1R14B	PPP1R14B	protein phosphatase 1 regulatory inhibitor subunit 14B	Cytoplasm	phosphatase	
[illegible]	PCSK7	PCSK7	proprotein convertase subtilisin/kexin type 7	Cytoplasm	peptidase	
[illegible]	CDC42EP4	CDC42EP4	CDC42 effector protein 4	Cytoplasm	other	
[illegible]	DPH1	DPH1	diphthamide biosynthesis 1	Cytoplasm	other	
[illegible]	[illegible]	[illegible]	[illegible] domain containing 1	Nucleus	other	
[illegible]	ST6GALNAC4	ST6GALNAC4	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferas	Cytoplasm	enzyme	
[illegible]	GIGYF1	GIGYF1	GRB10 interacting GYF protein 1	Extracellular Space	other	
[illegible]	RARS	RARS	arginyl-tRNA synthetase	Cytoplasm	enzyme	
[illegible]	CASP8	CASP8	caspase 8	Nucleus	peptidase	
[illegible]	SBNO2	SBNO2	strawberry notch homolog 2	Other	transcription regulator	
[illegible]	TRAK1	TRAK1	trafficking kinesin protein 1	Nucleus	other	
[illegible]	RAB11FIP1	RAB11FIP1	RAB11 family interacting protein 1	Cytoplasm	other	
[illegible]	CKAP4	CKAP4	cytoskeleton associated protein 4	Cytoplasm	other	
[illegible]	PLBD2	PLBD2	phospholipase B domain containing 2	Extracellular Space	other	
[illegible]	TTC39B	TTC39B	tetratricopeptide repeat domain 39B	Other	other	
[illegible]	TGFBR1	TGFBR1	transforming growth factor beta receptor 1	Plasma Membrane	kinase	galunisertib, TEW-719
[illegible]	BTN3A1	BTN3A1	butyrophilin subfamily 3 member A1	Extracellular Space	other	
[illegible]	DHRS7	DHRS7	dehydrogenase/reductase 7	Other	enzyme	
[illegible]	DNMBP	DNMBP	dynamin binding protein	Cytoplasm	other	
[illegible]	TKT	TKT	transketolase	Cytoplasm	enzyme	
[illegible]	NFKBIE	NFKBIE	NFKB inhibitor epsilon	Nucleus	transcription regulator	
[illegible]	DDX11	DDX11	DEAD/H-box helicase 11	Cytoplasm	enzyme	
[illegible]	GGA2	GGA2	golgi associated, gamma adaptin ear containing, ARF b	Cytoplasm	transporter	
[illegible]	CD164	CD164	CD164 molecule	Plasma Membrane	transmembrane receptor	
[illegible]	PPP1CA	PPP1CA	protein phosphatase 1 catalytic subunit alpha	Cytoplasm	phosphatase	
[illegible]	C20orf27	C20orf27	chromosome 20 open reading frame 27	Other	other	
[illegible]	BRI3	BRI3	brain protein I3	Cytoplasm	other	
[illegible]	CXorf65	CXorf65	chromosome X open reading frame 65	Other	other	
[illegible]	MMS19	MMS19	MMS19 homolog, cytosolic iron-sulfur assembly compo	Nucleus	transcription regulator	
[illegible]	ATF3	ATF3	activating transcription factor 3	Nucleus	transcription regulator	
[illegible]	APBA3	APBA3	amyloid beta precursor protein binding family A memb	Cytoplasm	transporter	
[illegible]	RLTPR	CARMIL2	capping protein regulator and myosin 1 linker 2	Plasma Membrane	other	
[illegible]	PRELID1	PRELID1	PRELI domain containing 1	Cytoplasm	other	
[illegible]	YTHDC2	YTHDC2	YTH domain containing 2	Cytoplasm	enzyme	
[illegible]	MARS					
[illegible]	DDX51	DDX51	DEAD-box helicase 51	Other	enzyme	
[illegible]	METTL17	METTL17	methyltransferase like 17	Nucleus	other	
[illegible]	PGAM1	PGAM1	phosphoglycerate mutase 1	Cytoplasm	phosphatase	
[illegible]	PHLDB3	PHLDB3	pleckstrin homology like domain family B member 3	Other	other	
[illegible]	NRARP	NRARP	NOTCH-regulated ankyrin repeat protein	Nucleus	transcription regulator	
[illegible]	MAPK14	MAPK14	mitogen-activated protein kinase 14	Cytoplasm	kinase	[illegible], ralimetinib, [illegible]
[illegible]	CLK2	CLK2	CDC like kinase 2	Nucleus	kinase	
[illegible]	PTCD3	PTCD3	pentatricopeptide repeat domain 3	Cytoplasm	other	
[illegible]	AHSA2	AHSA2	activator of HSP90 ATPase homolog 2	Other	other	
[illegible]	NA					
[illegible]	DCPS	DCPS	decapping enzyme, scavenger	Nucleus	enzyme	
[illegible]	SLA2	SLA2	Src like adaptor 2	Plasma Membrane	other	
[illegible]	DDX56	DDX56	DEAD-box helicase 56	Nucleus	enzyme	
[illegible]	UBXN4	UBXN4	UBX domain protein 4	Extracellular Space	other	
[illegible]	RHOA	RHOA	ras homolog family member A	Cytoplasm	enzyme	
[illegible]	PLD3	PLD3	phospholipase D family member 3	Cytoplasm	enzyme	
[illegible]	NCF1B	NCF1B	neutrophil cytosolic factor 1B pseudogene	Other	other	
[illegible]	SLC25A24	SLC25A24	solute carrier family 25 member 24	Cytoplasm	transporter	
[illegible]	DNAJA4	DNAJA4	DnaJ heat shock protein family (Hsp40) member A4	Nucleus	other	
[illegible]	[illegible]	SLC25A25-AS1	SLC25A25 antisense RNA 1	Other	other	
[illegible]	MAGED2	MAGED2	MAGE family member D2	Plasma Membrane	other	
[illegible]	C16orf80	CFAP20	cilia and flagella associated protein 20	Cytoplasm	other	
[illegible]	GALT	GALT	galactose-1-phosphate uridylyltransferase	Cytoplasm	enzyme	
[illegible]	E2F6	E2F6	E2F transcription factor 6	Nucleus	transcription regulator	
[illegible]	RBKS	RBKS	ribokinase	Cytoplasm	kinase	
[illegible]	[illegible]					
[illegible]	PRKCB	PRKCB	protein kinase C beta	Cytoplasm	kinase	[illegible], ruboxistaurin,
[illegible]	FHIT	FHIT	fragile histidine triad	Cytoplasm	enzyme	
[illegible]	GOLGA2P5	GOLGA2P5	golgin A2 pseudogene 5	Other	other	
[illegible]	CCNL1	CCNL1	cyclin L1	Nucleus	other	
[illegible]	MAP1LC3B	MAP1LC3B	microtubule associated protein 1 light chain 3 beta	Cytoplasm	other	
[illegible]	C2CD5	C2CD5	C2 calcium dependent domain containing 5	Cytoplasm	other	
[illegible]	CD37	CD37	CD37 molecule	Plasma Membrane	other	[illegible]
[illegible]	APBB3					
[illegible]	APBA2	APBA2	amyloid beta precursor protein binding family A memb	Cytoplasm	transporter	
[illegible]	IRF3	IRF3	interferon regulatory factor 3	Nucleus	transcription regulator	
[illegible]	IGFBP4	IGFBP4	insulin like growth factor binding protein 4	Extracellular Space	other	
[illegible]	NARS	NARS	asparaginyl-tRNA synthetase	Cytoplasm	enzyme	
[illegible]	ALDOA	ALDOA	aldolase, fructose-bisphosphate A	Cytoplasm	enzyme	
[illegible]	RHBDF2	RHBDF2	rhomboid 5 homolog 2	Cytoplasm	other	
[illegible]	SNRNP200	SNRNP200	small nuclear ribonucleoprotein U5 subunit 200	Nucleus	enzyme	
[illegible]	AGER	AGER	advanced glycosylation end-product specific receptor	Plasma Membrane	transmembrane receptor	2,3-O-desulfated hepa
[illegible]	PPIF	PPIF	peptidylprolyl isomerase F	Cytoplasm	enzyme	
[illegible]	DMAP1	DMAP1	DNA methyltransferase 1 associated protein 1	Nucleus	transcription regulator	
[illegible]	MGEA5	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	Cytoplasm	enzyme	
[illegible]	LY6G5B	LY6G5B	lymphocyte antigen 6 family member G5B	Other	other	
[illegible]	CCDC130	CCDC130	coiled-coil domain containing 130	Other	other	
[illegible]	RALGPS2	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	Other	other	
[illegible]	WIPI1	WIPI1	WD repeat domain, phosphoinositide interacting 1	Cytoplasm	other	
[illegible]	RFX7	RFX7	regulatory factor X7	Other	other	
[illegible]	ATP13A1	ATP13A1	ATPase 13A1	Extracellular Space	transporter	
[illegible]	[illegible]					
[illegible]	FLYWCH1	FLYWCH1	FLYWCH-type zinc finger 1	Other	other	
[illegible]	SIRPB1	SIRPB1	signal regulatory protein beta 1	Plasma Membrane	other	
[illegible]	STOM	STOM	stomatin	Plasma Membrane	other	
[illegible]	CA2	CA2	carbonic anhydrase 2	Cytoplasm	enzyme	chlorthalidone, diclo
[illegible]	RUNX3	RUNX3	runt related transcription factor 3	Nucleus	transcription regulator	
[illegible]	DDX39B	DDX39B	DExD-box helicase 39B	Nucleus	enzyme	
[illegible]	IL2RB	IL2RB	interleukin 2 receptor subunit beta	Plasma Membrane	transmembrane receptor	[illegible]
[illegible]	ADRB2	ADRB2	adrenoceptor beta 2	Plasma Membrane	G-protein coupled receptor	[illegible]
[illegible]	ENO2	ENO2	enolase 2	Cytoplasm	enzyme	
[illegible]	DDX39A	DDX39A	DExD-box helicase 39A	Nucleus	enzyme	
[illegible]	HIVEP1	HIVEP1	human immunodeficiency virus type I enhancer binding	Nucleus	transcription regulator	
[illegible]	TNFRSF12A	TNFRSF12A	TNF receptor superfamily member 12A	Plasma Membrane	transmembrane receptor	
[illegible]	MKNK2	MKNK2	MAP kinase interacting serine/threonine kinase 2	Cytoplasm	kinase	eFT508
[illegible]	SKIV2L	SKIV2L	Ski2 like RNA helicase	Nucleus	enzyme	
[illegible]	APBB1	APBB1	amyloid beta precursor protein binding family B memb	Cytoplasm	transcription regulator	

[illegible]	P2RX5	P2RX5	purinergic receptor P2X 5	Plasma Membrane	ion channel	
[illegible]	FBXO38	FBXO38	F-box protein 38	Other	other	
[illegible]	EML3	EML3	echinoderm microtubule associated protein like 3	Other	other	
[illegible]	BCL2L11	BCL2L11	BCL2 like 11	Cytoplasm	other	
[illegible]	C1orf35	C1orf35	chromosome 1 open reading frame 35	Other	other	
[illegible]	MAP1S	MAP1S	microtubule associated protein 1S	Cytoplasm	enzyme	
[illegible]	AP1G2	AP1G2	adaptor related protein complex 1 gamma 2 subunit	Cytoplasm	transporter	
[illegible]	RP11-[illegible]					
[illegible]	TMEM41B	TMEM41B	transmembrane protein 41B	Other	other	
[illegible]	MAPKBP1	MAPKBP1	mitogen-activated protein kinase binding protein 1	Other	other	
[illegible]	TPD52L2	TPD52L2	tumor protein D52 like 2	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	IL10RA	IL10RA	interleukin 10 receptor subunit alpha	Plasma Membrane	transmembrane recepto	
[illegible]	TFEB	TFEB	transcription factor EB	Nucleus	transcription regulator	
[illegible]	PLIN2	PLIN2	perilipin 2	Plasma Membrane	other	
[illegible]	CALHM2	CALHM2	calcium homeostasis modulator 2	Other	other	
[illegible]	GLYR1	GLYR1	glyoxylate reductase 1 homolog	Nucleus	other	
[illegible]	TLE3	TLE3	transducin like enhancer of split 3	Nucleus	other	
[illegible]	IFT122	IFT122	intraflagellar transport 122	Nucleus	other	
[illegible]	WRN	WRN	Werner syndrome RecQ like helicase	Nucleus	enzyme	
[illegible]	IARS	IARS	isoleucyl-tRNA synthetase	Cytoplasm	enzyme	
[illegible]	SMAD3	SMAD3	SMAD family member 3	Nucleus	transcription regulator	
[illegible]	CLK1	CLK1	CDC like kinase 1	Nucleus	kinase	
[illegible]	CYB561A3	CYB561A3	cytochrome b561 family member A3	Cytoplasm	other	
[illegible]	OAF	OAF	out at first homolog	Cytoplasm	other	
[illegible]	PRMT7	PRMT7	protein arginine methyltransferase 7	Cytoplasm	enzyme	
[illegible]	MT-ND1	MT-ND1	NADH dehydrogenase, subunit 1 (complex I)	Cytoplasm	enzyme	
[illegible]	SPINT2	SPINT2	serine peptidase inhibitor, Kunitz type 2	Extracellular Space	other	
[illegible]	GNG7	GNG7	G protein subunit gamma 7	Plasma Membrane	enzyme	
[illegible]	NUP205	NUP205	nucleoporin 205	Nucleus	other	
[illegible]	CUL9	CUL9	cullin 9	Cytoplasm	other	
[illegible]	NAA25	NAA25	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	Cytoplasm	other	
[illegible]	SASH3	SASH3	SAM and SH3 domain containing 3	Cytoplasm	other	
[illegible]	[illegible]	[illegible]	[illegible] domain family member 8	Other	other	
[illegible]	PRKACA	PRKACA	protein kinase cAMP-activated catalytic subunit alpha	Cytoplasm	kinase	
[illegible]	LASP1	LASP1	LIM and SH3 protein 1	Cytoplasm	transporter	
[illegible]	UBA7					
[illegible]	SUV420H2	KMT5C	lysine methyltransferase 5C	Nucleus	enzyme	
[illegible]	CPQ	CPQ	carboxypeptidase Q	Extracellular Space	peptidase	
[illegible]	NA					
[illegible]	SDR39U1	SDR39U1	short chain dehydrogenase/reductase family 39U mem	Nucleus	other	
[illegible]	SARDH	SARDH	sarcosine dehydrogenase	Cytoplasm	enzyme	
[illegible]	SEMA4C	SEMA4C	semaphorin 4C	Plasma Membrane	other	
[illegible]	ZRANB2	ZRANB2	zinc finger RANBP2-type containing 2	Nucleus	transcription regulator	
[illegible]	EIF2B5	EIF2B5	eukaryotic translation initiation factor 2B subunit epsilo	Cytoplasm	other	
[illegible]	SSR1	SSR1	signal sequence receptor subunit 1	Cytoplasm	other	
[illegible]	RIT1	RIT1	Ras like without CAAX 1	Plasma Membrane	enzyme	
[illegible]	GRIPAP1	GRIPAP1	GRIP1 associated protein 1	Plasma Membrane	other	
[illegible]	NCAPH2	NCAPH2	non-SMC condensin II complex subunit H2	Nucleus	other	
[illegible]	[illegible]					
[illegible]	AGPAT9	GPAT3	glycerol-3-phosphate acyltransferase 3	Cytoplasm	enzyme	
[illegible]	CHST7	CHST7	carbohydrate sulfotransferase 7	Cytoplasm	enzyme	
[illegible]	OTUD1	OTUD1	OTU deubiquitinase 1	Other	peptidase	
[illegible]	RBM25	RBM25	RNA binding motif protein 25	Nucleus	other	
[illegible]	ZFP36L1	ZFP36L1	ZFP36 ring finger protein like 1	Nucleus	transcription regulator	
[illegible]	LMF2	LMF2	lipase maturation factor 2	Other	other	
[illegible]	SLC11A2	SLC11A2	solute carrier family 11 member 2	Plasma Membrane	transporter	
[illegible]	NPHP3	NPHP3	nephrocystin 3	Extracellular Space	other	
[illegible]	LAT	LAT	linker for activation of T-cells	Plasma Membrane	kinase	
[illegible]	TBC1D4	TBC1D4	TBC1 domain family member 4	Cytoplasm	other	
[illegible]	DENND3	DENND3	DENN domain containing 3	Cytoplasm	other	
[illegible]	PGAP3	PGAP3	post-GPI attachment to proteins 3	Cytoplasm	enzyme	
[illegible]	COL18A1	COL18A1	collagen type XVIII alpha 1 chain	Extracellular Space	other	[illegible]
[illegible]	TRAF1	TRAF1	TNF receptor associated factor 1	Cytoplasm	other	
[illegible]	FUS	FUS	FUS RNA binding protein	Nucleus	transcription regulator	
[illegible]	LIMK1	LIMK1	LIM domain kinase 1	Cytoplasm	kinase	[illegible]
[illegible]	NAP1L4	NAP1L4	nucleosome assembly protein 1 like 4	Cytoplasm	other	
[illegible]	CMTR1	CMTR1	cap methyltransferase 1	Nucleus	enzyme	
[illegible]	ZNF512B	ZNF512B	zinc finger protein 512B	Nucleus	other	
[illegible]	MAN1B1	MAN1B1	mannosidase alpha class 1B member 1	Cytoplasm	enzyme	
[illegible]	CSTF2	CSTF2	cleavage stimulation factor subunit 2	Nucleus	other	
[illegible]	IFIT2	IFIT2	interferon induced protein with tetratricopeptide repea	Cytoplasm	other	
[illegible]	CCDC64	BICDL1	BICD family like cargo adaptor 1	Cytoplasm	other	
[illegible]	DCAF8	DCAF8	DDB1 and CUL4 associated factor 8	Other	other	
[illegible]	[illegible]					
[illegible]	P4HTM	P4HTM	prolyl 4-hydroxylase, transmembrane	Cytoplasm	enzyme	
[illegible]	ZC3H12D	ZC3H12D	zinc finger CCCH-type containing 12D	Cytoplasm	other	
[illegible]	REPIN1	REPIN1	replication initiator 1	Nucleus	other	
[illegible]	PI4K2A	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	Cytoplasm	kinase	
[illegible]	BMF	BMF	Bcl2 modifying factor	Cytoplasm	other	
[illegible]	ATM	ATM	ATM serine/threonine kinase	Nucleus	kinase	[illegible]
[illegible]	CAPS	CAPS	calcyphosine	Cytoplasm	other	
[illegible]	NRIP1	NRIP1	nuclear receptor interacting protein 1	Nucleus	transcription regulator	
[illegible]	POLR3B	POLR3B	RNA polymerase III subunit B	Nucleus	transcription regulator	
[illegible]	GYG1	GYG1	glycogenin 1	Cytoplasm	enzyme	
[illegible]	TRPC4AP	TRPC4AP	transient receptor potential cation channel subfamily C	Cytoplasm	transporter	
[illegible]	DDX26B	INTS6L	integrator complex subunit 6 like	Nucleus	other	
[illegible]	PRPF39	PRPF39	pre-mRNA processing factor 39	Nucleus	other	
[illegible]	RHOT2	RHOT2	ras homolog family member T2	Cytoplasm	enzyme	
[illegible]	NEURL4	NEURL4	neuralized E3 ubiquitin protein ligase 4	Other	other	
[illegible]	TNIK	TNIK	TRAF2 and NCK interacting kinase	Plasma Membrane	kinase	
[illegible]	ENTHD2	TEPSIN	TEPSIN, adaptor related protein complex 4 accessory p	Nucleus	other	
[illegible]	RNF187	RNF187	ring finger protein 187	Nucleus	enzyme	
[illegible]	ARRDC4	ARRDC4	arrestin domain containing 4	Other	other	
[illegible]	NA					
[illegible]	PLIN3	PLIN3	perilipin 3	Cytoplasm	other	
[illegible]	SAV1	SAV1	salvador family WW domain containing protein 1	Cytoplasm	other	
[illegible]	GCN1L1	GCN1	GCN1, eIF2 alpha kinase activator homolog	Cytoplasm	translation regulator	
[illegible]	DDX17	DDX17	DEAD-box helicase 17	Nucleus	enzyme	
[illegible]	PBX4	PBX4	PBX homeobox 4	Nucleus	transcription regulator	
[illegible]	RP11-[illegible]					
[illegible]	KBTBD6	KBTBD6	kelch repeat and BTB domain containing 6	Other	other	
[illegible]	ASMTL-AS1	ASMTL-AS1	ASMTL antisense RNA 1	Other	other	
[illegible]	SH3BP1	SH3BP1	SH3 domain binding protein 1	Other	other	
[illegible]	MTCH1	MTCH1	mitochondrial carrier 1	Cytoplasm	other	
[illegible]	USP36	USP36	ubiquitin specific peptidase 36	Nucleus	peptidase	
[illegible]	ERVK3-1	ERVK3-1		Other	other	
[illegible]	LGMN	LGMN	legumain	Cytoplasm	peptidase	
[illegible]	TRMT11	TRMT11	tRNA methyltransferase 11 homolog	Other	enzyme	
[illegible]	LRCH4	LRCH4	leucine rich repeats and calponin homology domain co	Cytoplasm	transcription regulator	
[illegible]	TMEM127	TMEM127	transmembrane protein 127	Other	other	
[illegible]	OSGEP	OSGEP	O-sialoglycoprotein endopeptidase	Nucleus	peptidase	
[illegible]	TESPA1	TESPA1	thymocyte expressed, positive selection associated 1	Cytoplasm	other	
[illegible]	SNX11	SNX11	sorting nexin 11	Cytoplasm	transporter	
[illegible]	CTD-[illegible]					
[illegible]	CHMP4B	CHMP4B	charged multivesicular body protein 4B	Cytoplasm	other	
[illegible]	ELOVL1					
[illegible]	TBC1D10C	TBC1D10C	TBC1 domain family member 10C	Nucleus	other	
[illegible]	ZDHHC7	ZDHHC7	zinc finger DHHC-type containing 7	Cytoplasm	enzyme	
[illegible]	BZW1	BZW1	basic leucine zipper and W2 domains 1	Cytoplasm	translation regulator	
[illegible]	USP20	USP20	ubiquitin specific peptidase 20	Cytoplasm	peptidase	
[illegible]	DDB2	DDB2	damage specific DNA binding protein 2	Nucleus	other	
[illegible]	CTD-[illegible]					
[illegible]	RNF11	RNF11	ring finger protein 11	Cytoplasm	enzyme	
[illegible]	SLC6A6	SLC6A6	solute carrier family 6 member 6	Plasma Membrane	transporter	
[illegible]	ST3GAL2	ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	Cytoplasm	enzyme	
[illegible]	ARPC3	ARPC3	actin related protein 2/3 complex subunit 3	Cytoplasm	other	
[illegible]	CLIP2	CLIP2	CAP-Gly domain containing linker protein 2	Cytoplasm	transcription regulator	
[illegible]	STAT2	STAT2	signal transducer and activator of transcription 2	Nucleus	transcription regulator	
[illegible]	TNPO2	TNPO2	transportin 2	Nucleus	transporter	
[illegible]	ERCC5	ERCC5	ERCC excision repair 5, endonuclease	Nucleus	enzyme	
[illegible]	EIF4A1	EIF4A1	eukaryotic translation initiation factor 4A1	Cytoplasm	translation regulator	
[illegible]	USP8	USP8	ubiquitin specific peptidase 8	Cytoplasm	peptidase	
[illegible]	FARP2	FARP2	FERM, ARH/RhoGEF and pleckstrin domain protein 2	Cytoplasm	other	
[illegible]	CCDC88	CCDC88	coiled-coil domain containing 88	Other	other	
[illegible]	SLC25A45	SLC25A45	solute carrier family 25 member 45	Cytoplasm	transporter	
[illegible]	KIF22	KIF22	kinesin family member 22	Nucleus	other	
[illegible]	ELAC2	ELAC2	elaC ribonuclease Z 2	Nucleus	enzyme	
[illegible]	HERPUD1	HERPUD1	homocysteine inducible ER protein with ubiquitin like d	Cytoplasm	other	
[illegible]	CNPY3	CNPY3	canopy FGF signaling regulator 3	Cytoplasm	other	
[illegible]	NDUFAF6	NDUFAF6	NADH:ubiquinone oxidoreductase complex assembly fa	Cytoplasm	other	
[illegible]	ARL8A	ARL8A	ADP ribosylation factor like GTPase 8A	Cytoplasm	enzyme	
[illegible]	EIF2B4	EIF2B4	eukaryotic translation initiation factor 2B subunit delta	Cytoplasm	other	
[illegible]	AXIN2	AXIN2	axin 2	Cytoplasm	other	
[illegible]	SUN1	SUN1	Sad1 and UNC84 domain containing 1	Nucleus	other	
[illegible]	NRM	NRM	nurim (nuclear envelope membrane protein)	Nucleus	other	
[illegible]	NOL9	NOL9	nucleolar protein 9	Nucleus	kinase	
[illegible]	NA					
[illegible]	ATP6V0B	ATP6V0B	ATPase H+ transporting V0 subunit b	Cytoplasm	transporter	
[illegible]	MT-ND5	MT-ND5	NADH dehydrogenase, subunit 5 (complex I)	Cytoplasm	enzyme	
[illegible]	LITAF	LITAF	lipopolysaccharide induced TNF factor	Nucleus	transcription regulator	
[illegible]	DIP2A	DIP2A	disco interacting protein 2 homolog A	Nucleus	transcription regulator	
[illegible]	ITGA6	ITGA6	integrin subunit alpha 6	Plasma Membrane	transmembrane recepto	
[illegible]	ARRB1	ARRB1	arrestin beta 1	Cytoplasm	other	
[illegible]	PLEKHF2	PLEKHF2	pleckstrin homology and FYVE domain containing 2	Cytoplasm	other	
[illegible]	HCST	HCST	hematopoietic cell signal transducer	Plasma Membrane	transmembrane recepto	
[illegible]	PDE4B	PDE4B	phosphodiesterase 4B	Cytoplasm	enzyme	[illegible]
[illegible]	GRB2	GRB2	growth factor receptor bound protein 2	Cytoplasm	kinase	[illegible]
[illegible]	EZH1	EZH1	enhancer of zeste 1 polycomb repressive complex 2 sub	Nucleus	enzyme	
[illegible]	CHD1	CHD1	chromodomain helicase DNA binding protein 1	Nucleus	enzyme	[illegible]
[illegible]	MT-ND4L	MT-ND4L	NADH dehydrogenase, subunit 4L (complex I)	Cytoplasm	enzyme	
[illegible]	SAT1	SAT1	spermidine/spermine N1-acetyltransferase 1	Cytoplasm	enzyme	
[illegible]	LPIN1	LPIN1	lipin 1	Nucleus	phosphatase	
[illegible]	ZFP90	ZFP90	ZFP90 zinc finger protein	Nucleus	transcription regulator	
[illegible]	STAP1	STAP1	signal transducing adaptor family member 1	Cytoplasm	other	
[illegible]	C12orf49	C12orf49	chromosome 12 open reading frame 49	Other	other	
[illegible]	HDAC6	HDAC6	histone deacetylase 6	Nucleus	transcription regulator	[illegible]
[illegible]	TMC8	TMC8	transmembrane channel like 8	Cytoplasm	other	
[illegible]	PIDD1	PIDD1	p53-induced death domain protein 1	Cytoplasm	other	
[illegible]	SLC8B1	SLC8B1	solute carrier family 8 member B1	Plasma Membrane	transporter	
[illegible]	HIP1R	HIP1R	huntingtin interacting protein 1 related	Cytoplasm	other	
[illegible]	GNA13	GNA13	G protein subunit alpha 13	Plasma Membrane	enzyme	
[illegible]	CCDC57	CCDC57	coiled-coil domain containing 57	Other	other	
[illegible]	EHD1	EHD1	EH domain containing 1	Cytoplasm	other	
[illegible]	D2HGDH	D2HGDH	D-2-hydroxyglutarate dehydrogenase	Cytoplasm	enzyme	
[illegible]	FAM73B	MIGA2	mitoguardin 2	Other	other	
[illegible]	PNISR	PNISR	PNN interacting serine and arginine rich protein	Nucleus	other	
[illegible]	PCBP1	PCBP1	poly(rC) binding protein 1	Nucleus	translation regulator	
[illegible]	COPA	COPA	coatomer protein complex subunit alpha	Cytoplasm	transporter	
[illegible]	MTPN	MTPN	myotrophin	Nucleus	transcription regulator	
[illegible]	SREK1	SREK1	splicing regulatory glutamic acid and lysine rich protein	Nucleus	other	
[illegible]	YWHAQ	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	Cytoplasm	other	
[illegible]	PI4KAP2	PI4KAP2	phosphatidylinositol 4-kinase alpha pseudogene 2	Other	other	
[illegible]	LTA4H	LTA4H	leukotriene A4 hydrolase	Cytoplasm	enzyme	
[illegible]	KDM1A	KDM1A	lysine demethylase 1A	Nucleus	enzyme	[illegible]
[illegible]	ENTPD6	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (put	Cytoplasm	enzyme	
[illegible]	GLG1	GLG1	golgi glycoprotein 1	Cytoplasm	other	
[illegible]	POLE	POLE	DNA polymerase epsilon, catalytic subunit	Nucleus	enzyme	[illegible]
[illegible]	SH3BP5-AS1	SH3BP5-AS1	SH3BP5 antisense RNA 1	Other	other	
[illegible]	GPR183	GPR183	G protein-coupled receptor 183	Plasma Membrane	-protein coupled recepto	
[illegible]	NARFL	NARFL	nuclear prelamin A recognition factor like	Cytoplasm	other	
[illegible]	ECE1	ECE1	endothelin converting enzyme 1	Plasma Membrane	peptidase	
[illegible]	TPD52	TPD52	tumor protein D52	Cytoplasm	other	
[illegible]	APOBEC3G	APOBEC3G	apolipoprotein B mRNA editing enzyme catalytic subunit	Nucleus	enzyme	
[illegible]	RARA	RARA	retinoic acid receptor alpha	Nucleus	[illegible]dependent nuclear rec	[illegible]
[illegible]	ATAD2	ATAD2	ATPase family, AAA domain containing 2	Nucleus	enzyme	
[illegible]	RANGAP1	RANGAP1	Ran GTPase activating protein 1	Nucleus	other	
[illegible]	CYB5R4	CYB5R4	cytochrome b5 reductase 4	Cytoplasm	enzyme	
[illegible]	NFRKB	NFRKB	nuclear factor related to kappaB binding protein	Nucleus	transcription regulator	
[illegible]	HABP4	HABP4	hyaluronan binding protein 4	Cytoplasm	other	
[illegible]	SEC24C	SEC24C	SEC24 homolog C, COPII coat complex component	Cytoplasm	transporter	
[illegible]	FUK	FUK	fucokinase	Cytoplasm	kinase	
[illegible]	SYT11	SYT11	synaptotagmin 11	Cytoplasm	transporter	
[illegible]	BCKDK	BCKDK	branched chain ketoacid dehydrogenase kinase	Cytoplasm	kinase	
[illegible]	SLC35F2	SLC35F2	solute carrier family 35 member F2	Other	other	
[illegible]	ILKAP	ILKAP	ILK associated serine/threonine phosphatase	Cytoplasm	phosphatase	
[illegible]	CMTM3	CMTM3	CKLF like MARVEL transmembrane domain containing 3	Extracellular Space	cytokine	
[illegible]	TNFAIP8	TNFAIP8	TNF alpha induced protein 8	Nucleus	enzyme	
[illegible]	RRM2B	RRM2B	ribonucleotide reductase regulatory TP53 inducible sub	Nucleus	enzyme	[illegible]
[illegible]	DDX41	DDX41	DEAD-box helicase 41	Nucleus	enzyme	
[illegible]	TMC6	TMC6	transmembrane channel like 6	Cytoplasm	transporter	
[illegible]	LZTR1	LZTR1	leucine zipper like transcription regulator 1	Cytoplasm	transcription regulator	
[illegible]	DHX36	DHX36	DEAH-box helicase 36	Cytoplasm	enzyme	
[illegible]	ITM2C	ITM2C	integral membrane protein 2C	Cytoplasm	other	
[illegible]	AARSD1	AARSD1	alanyl-tRNA synthetase domain containing 1	Nucleus	enzyme	
[illegible]	PLK3	PLK3	polo like kinase 3	Nucleus	kinase	
[illegible]	NAA50	NAA50	N(alpha)-acetyltransferase 50, NatE catalytic subunit	Cytoplasm	enzyme	
[illegible]	CD99	CD99	CD99 molecule	Plasma Membrane	other	
[illegible]	PSMC6	PSMC6	proteasome 26S subunit, ATPase 6	Nucleus	peptidase	
[illegible]	FGFRL1	FGFRL1	fibroblast growth factor receptor like 1	Plasma Membrane	transmembrane recepto	
[illegible]	EPN1	EPN1	epsin 1	Plasma Membrane	other	
[illegible]	CD2	CD2	CD2 molecule	Plasma Membrane	other	[illegible]
[illegible]	SLC7A6	SLC7A6	solute carrier family 7 member 6	Plasma Membrane	transporter	
[illegible]	LAPTM4A	LAPTM4A	lysosomal protein transmembrane 4 alpha	Cytoplasm	other	
[illegible]	DNAH1	DNAH1	dynein axonemal heavy chain 1	Extracellular Space	other	

[illegible]	RBM5	RBM5	RNA binding motif protein 5	Nucleus	other	
[illegible]	IRAK2	IRAK2	interleukin 1 receptor associated kinase 2	Plasma Membrane	kinase	
[illegible]	RPAIN	RPAIN	RPA interacting protein	Nucleus	other	
[illegible]	GGA3	GGA3	golgi associated, gamma adaptin ear containing, ARF b	Cytoplasm	transporter	
[illegible]	SEPSECS	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA	Cytoplasm	enzyme	
[illegible]	CMTM6	CMTM6	CKLF like MARVEL transmembrane domain containing 6	Extracellular Space	cytokine	
[illegible]	VAV3	VAV3	vav guanine nucleotide exchange factor 3	Extracellular Space	cytokine	
[illegible]	SRSF7	SRSF7	serine and arginine rich splicing factor 7	Nucleus	other	
[illegible]	H1FX	H1FX	H1 histone family member X	Nucleus	other	
[illegible]	ARF3	ARF3	ADP ribosylation factor 3	Cytoplasm	enzyme	
[illegible]	XPC	XPC	XPC complex subunit, DNA damage recognition and rep	Nucleus	other	
[illegible]	CDK11B	CDK11B	cyclin dependent kinase 11B	Nucleus	kinase	
[illegible]	SP140L	SP140L	SP140 nuclear body protein like	Other	other	
[illegible]	TRAP1	TRAP1	TNF receptor associated protein 1	Cytoplasm	enzyme	
[illegible]	MRPL38	MRPL38	mitochondrial ribosomal protein L38	Cytoplasm	other	
[illegible]	BRAT1	BRAT1	BRCA1 associated ATM activator 1	Nucleus	other	
[illegible]	SGSM3	SGSM3	small G protein signaling modulator 3	Plasma Membrane	other	
[illegible]	PRKCI	PRKCI	protein kinase C iota	Cytoplasm	kinase	ingenol mebutate
[illegible]	SLC1A4	SLC1A4	solute carrier family 1 member 4	Cytoplasm	transporter	
[illegible]	POLR1C	POLR1C	RNA polymerase I subunit C	Nucleus	enzyme	
[illegible]	NOL11	NOL11	nucleolar protein 11	Nucleus	other	
[illegible]	CDK2AP1	CDK2AP1	cyclin dependent kinase 2 associated protein 1	Nucleus	other	
[illegible]	NUP188	NUP188	nucleoporin 188	Nucleus	transporter	
[illegible]	DAP	DAP	death associated protein	Cytoplasm	transcription regulator	
[illegible]	SCAP	SCAP	SREBF chaperone	Cytoplasm	other	
[illegible]	RAB37	RAB37	RAB37, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	ARNTL	ARNTL	aryl hydrocarbon receptor nuclear translocator like	Nucleus	transcription regulator	
[illegible]	SLA	SLA	Src like adaptor	Plasma Membrane	other	
[illegible]	ANAPC4	ANAPC4	anaphase promoting complex subunit 4	Nucleus	enzyme	
[illegible]	SLC35A2	SLC35A2	solute carrier family 35 member A2	Cytoplasm	enzyme	
[illegible]	TRMT1	TRMT1	tRNA methyltransferase 1	Extracellular Space	enzyme	
[illegible]	OVGP1	OVGP1	oviductal glycoprotein 1	Extracellular Space	enzyme	
[illegible]	ABCD4	ABCD4	ATP binding cassette subfamily D member 4	Cytoplasm	transporter	
[illegible]	PIK3CB	PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic	Cytoplasm	kinase	dactolisib, pictilisib, b
[illegible]	TMEM86A	TMEM86A	transmembrane protein 86	Cytoplasm	other	
[illegible]	PRKRIR	THAP12	THAP domain containing 12	Nucleus	other	
[illegible]	ZC3H8	ZC3H8	zinc finger CCCH-type containing 8	Nucleus	transcription regulator	
[illegible]	PASK	PASK	PAS domain containing serine/threonine kinase	Cytoplasm	kinase	
[illegible]	MYO1G	MYO1G	myosin IG	Cytoplasm	other	
[illegible]	DNMT1	DNMT1	DNA methyltransferase 1	Nucleus	enzyme	[illegible], decitab
[illegible]	SERTAD3	SERTAD3	SERTA domain containing 3	Cytoplasm	transcription regulator	
[illegible]	MT-ND6	MTND6	NADH dehydrogenase, subunit 6 (complex I)	Cytoplasm	enzyme	
[illegible]	PKIG	PKIG	cAMP-dependent protein kinase inhibitor gamma	Other	other	
[illegible]	C1orf162	C1orf162	chromosome 1 open reading frame 162	Other	transporter	
[illegible]	BRK1	BRK1	BRICK1, SCAR/WAVE actin nucleating complex subunit	Cytoplasm	other	
[illegible]	ZNF706	ZNF706	zinc finger protein 706	Other	other	
[illegible]	GAA	GAA	glucosidase alpha, acid	Cytoplasm	enzyme	miglitol, acarbose
[illegible]	PDK1	PDK1	pyruvate dehydrogenase kinase 1	Cytoplasm	kinase	dichloroacetic acid
[illegible]	LTBP4	LTBP4	latent transforming growth factor beta binding protein	Extracellular Space	growth factor	
[illegible]	ITK	ITK	IL2 inducible T-cell kinase	Cytoplasm	kinase	pazopanib
[illegible]	DMTF1	DMTF1	cyclin D binding myb like transcription factor 1	Nucleus	transcription regulator	
[illegible]	TIAL1	TIAL1	TIA1 cytotoxic granule associated RNA binding protein l	Nucleus	transcription regulator	
[illegible]	TXNRD1	TXNRD1	thioredoxin reductase 1	Cytoplasm	enzyme	[illegible]
[illegible]	UBE2D1	UBE2D1	ubiquitin conjugating enzyme E2 D1	Cytoplasm	enzyme	
[illegible]	CORO7	CORO7/CORO7-PAM16	coronin 7	Cytoplasm	other	
[illegible]	GLTP	GLTP	glycolipid transfer protein	Cytoplasm	transporter	
[illegible]	DNAJC2	DNAJC2	DnaJ heat shock protein family (Hsp40) member C2	Nucleus	other	
[illegible]	PTGDS	PTGDS	prostaglandin D2 synthase	Cytoplasm	enzyme	
[illegible]	GORAB	GORAB	golgin, RAB6 interacting	Cytoplasm	other	
[illegible]	PRCP	PRCP	prolylcarboxypeptidase	Cytoplasm	peptidase	
[illegible]	[illegible]					
[illegible]	TTLL3	TTLL3	tubulin tyrosine ligase like 3	Extracellular Space	enzyme	
[illegible]	WRAP73	WRAP73	WD repeat containing, antisense to TP73	Nucleus	other	
[illegible]	SH3D19	SH3D19	SH3 domain containing 19	Cytoplasm	other	
[illegible]	PKM	PKM	pyruvate kinase, muscle	Cytoplasm	kinase	CAP-232
[illegible]	PSMD6-AS2	PSMD6-AS2	PSMD6 antisense RNA 2	Other	other	
[illegible]	TMED5	TMED5	transmembrane p24 trafficking protein 5	Cytoplasm	other	
[illegible]	FAM102A	FAM102A	family with sequence similarity 102 member A	Other	other	
[illegible]	NA					
[illegible]	DHX30	DHX30	DExH-box helicase 30	Nucleus	enzyme	
[illegible]	[illegible]	[illegible]	sphingomyelin phosphodiesterase 4, neutral membrane	Other	other	
[illegible]	PHLDA2	PHLDA2	pleckstrin homology like domain family A member 2	Cytoplasm	other	
[illegible]	STAT6	STAT6	signal transducer and activator of transcription 6	Nucleus	transcription regulator	
[illegible]	TCAP	TCAP	titin-cap	Cytoplasm	other	
[illegible]	MT-ND4	MTND4	NADH dehydrogenase, subunit 4 (complex I)	Cytoplasm	enzyme	
[illegible]	OAZ1	OAZ1	ornithine decarboxylase antizyme 1	Cytoplasm	enzyme	
[illegible]	TRBV20-1	TRBV20-1	T cell receptor beta variable 20-1 (non-functional)	Other	other	
[illegible]	IL3RA	IL3RA	interleukin 3 receptor subunit alpha	Plasma Membrane	transmembrane receptor	[illegible]
[illegible]	[illegible]	[illegible]	[illegible], guanine nucleotide exchange factor	Extracellular Space	other	
[illegible]	QTRT1	QTRT1	queuine tRNA-ribosyltransferase catalytic subunit 1	Cytoplasm	enzyme	
[illegible]	HVCN1	HVCN1	hydrogen voltage gated channel 1	Plasma Membrane	ion channel	
[illegible]	XAB2	XAB2	XPA binding protein 2	Nucleus	other	
[illegible]	ZNF835	ZNF835	zinc finger protein 835	Nucleus	other	
[illegible]	PHF1	PHF1	PHD finger protein 1	Nucleus	transcription regulator	
[illegible]	CAPN3	CAPN3	calpain 3	Cytoplasm	peptidase	
[illegible]	VARS2	VARS2	valyl-tRNA synthetase 2, mitochondrial	Cytoplasm	enzyme	
[illegible]	UHRF2	UHRF2	ubiquitin like with PHD and ring finger domains 2	Nucleus	enzyme	
[illegible]	ANKFY1	ANKFY1	ankyrin repeat and FYVE domain containing 1	Cytoplasm	transcription regulator	
[illegible]	NAB2	NAB2	NGFI-A binding protein 2	Nucleus	transcription regulator	
[illegible]	CROCCP2	CROCCP2	ciliary rootlet coiled-coil, rootletin pseudogene 2	Other	other	
[illegible]	EIF6	EIF6	eukaryotic translation initiation factor 6	Cytoplasm	translation regulator	
[illegible]	CD6	CD6	CD6 molecule	Plasma Membrane	transmembrane receptor	
[illegible]	NAMPTL	NAMPTP1	nicotinamide phosphoribosyltransferase pseudogene 1	Other	other	
[illegible]	SCRN1	SCRN1	secernin 1	Cytoplasm	other	
[illegible]	PRPF3	PRPF3	pre-mRNA processing factor 3	Nucleus	other	
[illegible]	VIM	VIM	vimentin	Cytoplasm	other	
[illegible]	MVB12B	MVB12B	multivesicular body subunit 12B	Cytoplasm	other	
[illegible]	CASP7	CASP7	caspase 7	Cytoplasm	peptidase	
[illegible]	PCGF3	PCGF3	polycomb group ring finger 3	Nucleus	other	
[illegible]	CDK5R1	CDK5R1	cyclin dependent kinase 5 regulatory subunit 1	Nucleus	kinase	
[illegible]	ZBTB34	ZBTB34	zinc finger and BTB domain containing 34	Nucleus	other	
[illegible]	MCM3AP	MCM3AP	minichromosome maintenance complex component 3 a	Nucleus	other	
[illegible]	TOR2A	TOR2A	torsin family 2 member A	Extracellular Space	other	
[illegible]	BRD9	BRD9	bromodomain containing 9	Other	other	
[illegible]	CTC1	CTC1	CST telomere replication complex component 1	Nucleus	other	
[illegible]	AAED1	AAED1	AhpC/TSA antioxidant enzyme domain containing 1	Other	other	
[illegible]	SNX3	SNX3	sorting nexin 3	Cytoplasm	transporter	
[illegible]	MSTO1	MSTO1	misato 1, mitochondrial distribution and morphology re	Cytoplasm	other	
[illegible]	DDX56	DDX56	DEAD-box helicase 56	Nucleus	enzyme	
[illegible]	AFF3	AFF3	AF4/FMR2 family member 3	Nucleus	transcription regulator	
[illegible]	[illegible]	[illegible]	[illegible] homolog	Nucleus	other	
[illegible]	MAN2B1	MAN2B1	mannosidase alpha class 2B member 1	Cytoplasm	enzyme	
[illegible]	CBX7	CBX7	chromobox 7	Nucleus	other	
[illegible]	ECHDC2	ECHDC2	enoyl-CoA hydratase domain containing 2	Other	other	
[illegible]	SIN3B	SIN3B	SIN3 transcription regulator family member B	Nucleus	transcription regulator	
[illegible]	RNF216	RNF216	ring finger protein 216	Cytoplasm	enzyme	
[illegible]	[illegible]	[illegible]	uncharacterized [illegible]	Other	other	
[illegible]	SVIL	SVIL	supervillin	Plasma Membrane	other	
[illegible]	TRAT1	TRAT1	T cell receptor associated transmembrane adaptor 1	Plasma Membrane	kinase	
[illegible]	NUP107	NUP107	nucleoporin 107	Nucleus	transporter	
[illegible]	UBASH3A	UBASH3A	ubiquitin associated and SH3 domain containing A	Cytoplasm	enzyme	
[illegible]	TICAM1	TICAM1	toll like receptor adaptor molecule 1	Nucleus	other	
[illegible]	RASGRP2	RASGRP2	RAS guanyl releasing protein 2	Cytoplasm	other	
[illegible]	EML4	EML4	echinoderm microtubule associated protein like 4	Cytoplasm	other	
[illegible]	ABTB1	ABTB1	ankyrin repeat and BTB domain containing 1	Cytoplasm	translation regulator	
[illegible]	CREB3L2	CREB3L2	cAMP responsive element binding protein 3 like 2	Nucleus	transcription regulator	
[illegible]	HOOK1	HOOK1	hook microtubule tethering protein 1	Cytoplasm	other	
[illegible]	HERC1	HERC1	HECT and RLD domain containing E3 ubiquitin protein l	Cytoplasm	other	
[illegible]	USP35	USP35	ubiquitin specific peptidase 35	Extracellular Space	peptidase	
[illegible]	STK38	STK38	serine/threonine kinase 38	Nucleus	kinase	
[illegible]	KIFC3	KIFC3	kinesin family member C3	Cytoplasm	other	
[illegible]	NCBP1	NCBP1	nuclear cap binding protein subunit 1	Nucleus	other	
[illegible]	ABI3	ABI3	ABI family member 3	Plasma Membrane	other	
[illegible]	KIAA0247	SUSD6	sushi domain containing 6	Other	other	
[illegible]	CCAR2	CCAR2	cell cycle and apoptosis regulator 2	Cytoplasm	peptidase	
[illegible]	PTP4A2	PTP4A2	protein tyrosine phosphatase type IVA, member 2	Cytoplasm	phosphatase	
[illegible]	RGS1	RGS1	regulator of G-protein signaling 1	Plasma Membrane	other	
[illegible]	FBXO6	FBXO6	F-box protein 6	Cytoplasm	enzyme	
[illegible]	ULK3	ULK3	unc-51 like kinase 3	Cytoplasm	kinase	
[illegible]	WBP1	WBP1	WW domain binding protein 1	Cytoplasm	other	
[illegible]	CDK5RAP1	CDK5RAP1	CDK5 regulatory subunit associated protein 1	Extracellular Space	enzyme	
[illegible]	SUSD1	SUSD1	sushi domain containing 1	Other	other	
[illegible]	PLEKHA2	PLEKHA2	pleckstrin homology domain containing A2	Cytoplasm	other	
[illegible]	CANX	CANX	calnexin	Cytoplasm	other	
[illegible]	MTATP6P1	MTATP6P1	mitochondrially encoded ATP synthase 6 pseudogene 1	Other	other	
[illegible]	FAM127A	FAM127A	family with sequence similarity 127 member A	Plasma Membrane	other	
[illegible]	CROCC	CROCC	ciliary rootlet coiled-coil, rootletin	Plasma Membrane	other	
[illegible]	MEGF6	MEGF6	multiple EGF like domains 6	Cytoplasm	other	
[illegible]	RINT1	RINT1	RAD50 interactor 1	Nucleus	other	
[illegible]	IKBKAP	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B	Cytoplasm	other	
[illegible]	PPIB	PPIB	peptidylprolyl isomerase B	Nucleus	enzyme	
[illegible]	ALOX5AP	ALOX5AP	arachidonate 5-lipoxygenase activating protein	Plasma Membrane	other	
[illegible]	RCSD1	RCSD1	RCSD domain containing 1	Other	other	
[illegible]	ERP27	ERP27	endoplasmic reticulum protein 27	Other	other	
[illegible]	[illegible]					
[illegible]	ITGB1	ITGB1	integrin subunit beta 1	Plasma Membrane	transmembrane receptor	
[illegible]	STMN3	STMN3	stathmin 3	Nucleus	other	
[illegible]	ZNF83	ZNF83	zinc finger protein 83	Nucleus	transcription regulator	
[illegible]	DTX3	DTX3	deltex E3 ubiquitin ligase 3	Cytoplasm	other	
[illegible]	BST2	BST2	bone marrow stromal cell antigen 2	Plasma Membrane	other	
[illegible]	CYBA	CYBA	cytochrome b-245 alpha chain	Cytoplasm	enzyme	
[illegible]	[illegible]	[illegible]	[illegible] like	Cytoplasm	other	
[illegible]	HMHA1	ARHGAP45	Rho GTPase activating protein 45	Cytoplasm	transporter	
[illegible]	ZNF274	ZNF274	zinc finger protein 274	Nucleus	transcription regulator	
[illegible]	DOCK10	DOCK10	dedicator of cytokinesis 10	Cytoplasm	other	
[illegible]	P2RY11	P2RY11	purinergic receptor P2Y11	Plasma Membrane	G-protein coupled recepto	
[illegible]	DUSP1	DUSP1	dual specificity phosphatase 1	Nucleus	phosphatase	
[illegible]	RRAGC	RRAGC	Ras related GTP binding C	Cytoplasm	enzyme	
[illegible]	TMCO6	TMCO6	transmembrane and coiled-coil domains 6	Other	other	
[illegible]	MAPK6	MAPK6	mitogen-activated protein kinase 6	Cytoplasm	kinase	
[illegible]	LIMD2	LIMD2	LIM domain containing 2	Nucleus	other	
[illegible]	APMAP	APMAP	adipocyte plasma membrane associated protein	Plasma Membrane	enzyme	
[illegible]	CCR4	CCR4	C-C motif chemokine receptor 4	Plasma Membrane	G-protein coupled recepto	mogamulizumab
[illegible]	ATP1B3	ATP1B3	ATPase Na+/K+ transporting subunit beta 3	Plasma Membrane	transporter	
[illegible]	THOC2	THOC2	THO complex 2	Nucleus	other	
[illegible]	PPP4R1	PPP4R1	protein phosphatase 4 regulatory subunit 1	Other	phosphatase	
[illegible]	TLN1					
[illegible]	TNNT3	TNNT3	troponin T3, fast skeletal type	Cytoplasm	other	
[illegible]	ICOS	ICOS	inducible T-cell costimulator	Plasma Membrane	transmembrane receptor	
[illegible]	MT-CYB	MT-CYB	cytochrome b	Cytoplasm	enzyme	[illegible]
[illegible]	ERMARD	ERMARD	ER membrane associated RNA degradation	Other	other	
[illegible]	IMPDH1	IMPDH1	inosine monophosphate dehydrogenase 1	Cytoplasm	enzyme	[illegible]
[illegible]	TUBA1C	TUBA1C	tubulin alpha 1c	Cytoplasm	other	[illegible]
[illegible]	EDAR	EDAR	ectodysplasin A receptor	Plasma Membrane	transmembrane receptor	
[illegible]	BDH2	BDH2	3-hydroxybutyrate dehydrogenase 2	Cytoplasm	enzyme	
[illegible]	MRPL32	MRPL32	mitochondrial ribosomal protein L32	Cytoplasm	translation regulator	
[illegible]	COG1	COG1	component of oligomeric golgi complex 1	Cytoplasm	transporter	
[illegible]	PCID2	PCID2	PCI domain containing 2	Nucleus	transcription regulator	
[illegible]	ABHD4	ABHD4	abhydrolase domain containing 4	Cytoplasm	peptidase	
[illegible]	C10orf32					
[illegible]	TSPYL2	TSPYL2	TSPY like 2	Nucleus	other	
[illegible]	TTC17	TTC17	tetratricopeptide repeat domain 17	Cytoplasm	other	
[illegible]	POLRMT	POLRMT	RNA polymerase mitochondrial	Cytoplasm	enzyme	
[illegible]	EHMT2	EHMT2	euchromatic histone lysine methyltransferase 2	Nucleus	transcription regulator	
[illegible]	TMED4	TMED4	transmembrane p24 trafficking protein 4	Cytoplasm	transporter	
[illegible]	YBX3	YBX3	Y-box binding protein 3	Nucleus	transcription regulator	
[illegible]	CABIN1	CABIN1	calcineurin binding protein 1	Nucleus	other	
[illegible]	ELP2	ELP2	elongator acetyltransferase complex subunit 2	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	FASTK	FASTK	Fas activated serine/threonine kinase	Cytoplasm	kinase	
[illegible]	NA					
[illegible]	HGS	HGS	hepatocyte growth factor-regulated tyrosine kinase sub	Cytoplasm	other	
[illegible]	WASH4P	WASH4P	WAS protein family homolog 4 pseudogene	Other	other	
[illegible]	[illegible]					
[illegible]	SNAPC4	SNAPC4	small nuclear RNA activating complex polypeptide 4	Nucleus	transcription regulator	
[illegible]	RAC1	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family,	Plasma Membrane	enzyme	
[illegible]	AKAP9	AKAP9	A-kinase anchoring protein 9	Cytoplasm	other	
[illegible]	UBAP2L	UBAP2L	ubiquitin associated protein 2 like	Nucleus	other	
[illegible]	EHD4	EHD4	EH domain containing 4	Plasma Membrane	enzyme	
[illegible]	ARFGAP1	ARFGAP1	ADP ribosylation factor GTPase activating protein 1	Cytoplasm	transporter	
[illegible]	KIF21B	KIF21B	kinesin family member 21B	Cytoplasm	other	
[illegible]	GPS2	GPS2	G protein pathway suppressor 2	Nucleus	transcription regulator	
[illegible]	DUS1L	DUS1L	dihydrouridine synthase 1 like	Other	other	
[illegible]	CUX1	CUX1	cut like homeobox 1	Nucleus	transcription regulator	
[illegible]	TJAP1	TJAP1	tight junction associated protein 1	Plasma Membrane	other	
[illegible]	LIG1	LIG1	DNA ligase 1	Nucleus	enzyme	
[illegible]	[illegible]					
[illegible]	NCSTN	NCSTN	nicastrin	Plasma Membrane	other	[illegible]
[illegible]	ABL1	ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase	Nucleus	kinase	[illegible]
[illegible]	HSBP1	HSBP1	heat shock factor binding protein 1	Nucleus	other	
[illegible]	C12orf75	C12orf75	chromosome 12 open reading frame 75	Other	other	
[illegible]	GDI2	GDI2	GDP dissociation inhibitor 2	Cytoplasm	other	
[illegible]	GGT7	GGT7	gamma-glutamyltransferase 7	Plasma Membrane	enzyme	
[illegible]	ARPC5	ARPC5	actin related protein 2/3 complex subunit 5	Cytoplasm	other	
[illegible]	UBR1	UBR1	ubiquitin protein ligase E3 component n-recognin 1	Cytoplasm	enzyme	

[illegible]	ATG2A	ATG2A	autophagy related 2A	Plasma Membrane	other	1.25	1.23	1.11	0.00	0.00	0.00	97	100	100	3	0	0
[illegible]	ZBED1	ZBED1	zinc finger BED-type containing 1	Nucleus	enzyme	-1.11	-1.56	-0.86	0.00	0.00	0.00	0	0	5	100	100	95
[illegible]	PTMS	PTMS	parathymosin	Nucleus	other	-1.90	-1.66	-0.41	0.00	0.00	0.00	0	8	24	100	92	76
[illegible]	SARM1	SARM1	sterile alpha and TIR motif containing 1	Plasma Membrane	transmembrane receptor	1.29	0.85	-0.20	0.00	0.00	0.00	100	100	79	0	0	21
[illegible]	TOP2B	TOP2B	topoisomerase (DNA) II beta	Nucleus	enzyme	1.29	1.12	0.97	0.00	0.00	0.00	100	100	95	0	0	5
[illegible]	ABCF3	ABCF3	ATP binding cassette subfamily F member 3	Other	transporter	1.21	1.20	0.76	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	02-Mar	02-Mar	membrane associated ring-CH-type finger 2	Cytoplasm	enzyme	-1.32	-1.58	-0.67	0.00	0.00	0.00	0	0	11	100	100	89
[illegible]	ABHD13A	ABHD13A	abhydrolase domain containing 13A	Other	enzyme	1.21	1.48	0.38	0.00	0.00	0.00	100	100	78	0	0	22
[illegible]	ZNF672	ZNF672	zinc finger protein 672	Nucleus	other	-1.40	-1.30	0.18	0.00	0.00	0.01	0	0	73	100	100	27
[illegible]	ADCK3	COQ8A	coenzyme Q8A	Cytoplasm	kinase	1.35	0.92	0.02	0.00	0.00	0.77	100	100	54	0	0	46
[illegible]	TBRG1	TBRG1	transforming growth factor beta regulator 1	Nucleus	other	1.31	1.32	0.79	0.00	0.00	0.00	100	100	97	0	0	3
[illegible]	HAPLN3	HAPLN3	hyaluronan and proteoglycan link protein 3	Extracellular Space	other	1.39	0.81	-0.81	0.00	0.00	0.00	100	95	8	0	5	92
[illegible]	FTH1	FTH1	ferritin heavy chain 1	Cytoplasm	enzyme	-1.10	-0.96	0.12	0.00	0.00	0.01	0	3	68	100	97	32
[illegible]	DDB1	DDB1	damage specific DNA binding protein 1	Nucleus	other	1.25	1.25	0.66	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	EZR	EZR	ezrin	Plasma Membrane	other	-1.10	-0.28	0.40	0.00	0.00	0.00	0	19	95	100	81	5
[illegible]	TBC1D2B	TBC1D2B	TBC1 domain family member 2B	Other	other	1.17	1.03	0.25	0.00	0.00	0.55	100	97	54	0	3	46
[illegible]	C3orf60A	C3orf60A/C3orf60B	chromosome 3 open reading frame 60A	Other	other	1.41	1.54	1.36	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	VPS11	VPS11	VPS11, CORVET/HOPS core subunit	Cytoplasm	transporter	1.39	1.31	0.75	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	NDOR1	NDOR1	NADPH dependent diflavin oxidoreductase 1	Cytoplasm	enzyme	1.36	1.30	1.17	0.00	0.00	0.00	100	100	97	0	0	3
[illegible]	FAM160B2	FAM160B2	family with sequence similarity 160 member B2	Other	other	1.30	0.88	0.47	0.00	0.00	0.00	100	100	86	0	0	14
[illegible]	OSTF1	OSTF1	osteoclast stimulating factor 1	Nucleus	transcription regulator	-1.48	-1.09	-0.82	0.00	0.00	0.00	0	0	30	100	100	70
[illegible]	SGK1	SGK1	serum/glucocorticoid regulated kinase 1	Cytoplasm	kinase	-0.99	-1.79	0.40	0.00	0.00	0.00	0	0	61	100	100	39
[illegible]	C17orf49	C17orf49	chromosome 17 open reading frame 49	Nucleus	other	1.60			0.00			100			0		
[illegible]	GTPBP8	GTPBP8	GTP binding protein 8 (mitochondrial)	Cytoplasm	enzyme	1.50	1.17		0.00	0.00		100	100		0	0	
[illegible]	GOLGA1	GOLGA1	golgin A1	Cytoplasm	other	1.57			0.00			100			0		
[illegible]	TC2N	TC2N	tandem C2 domains, nuclear	Nucleus	transporter	1.25	0.00	-1.10	0.00	0.69	0.00	100	50	0	0	50	100
[illegible]	PIGL	PIGL	phosphatidylinositol glycan anchor biosynthesis class L	Cytoplasm	enzyme	1.70	1.38	0.60	0.00	0.00	0.00	100	100	92	0	0	8
[illegible]	PRDX4	PRDX4	peroxiredoxin 4	Cytoplasm	enzyme	-1.66	-1.87	-0.18	0.00	0.00	0.05	0	0	41	100	100	59

[illegible]	CARKD	NAXD	NAD(P)HX dehydratase	Cytoplasm	enzyme	
[illegible]	ANAPC1	ANAPC1	anaphase promoting complex subunit 1	Nucleus	other	
[illegible]	SH3GL1P1	SH3GL1P1	SH3 domain containing GRB2 like 1, endophilin A2 pseu	Other	other	
[illegible]	ROGDI	ROGDI	rogdi homolog	Nucleus	other	
[illegible]	NAT10	NAT10	N-acetyltransferase 10	Nucleus	enzyme	
[illegible]	LYRM1	LYRM1	LYR motif containing 1	Cytoplasm	other	
[illegible]	INPP4B	INPP4B	inositol polyphosphate-4-phosphatase type II B	Cytoplasm	phosphatase	
[illegible]	GDE1	GDE1	glycerophosphodiester phosphodiesterase 1	Plasma Membrane	enzyme	
[illegible]	NA					
[illegible]	FAM83G	FAM83G	family with sequence similarity 83 member G	Other	other	
[illegible]	POMGNT1	POMGNT1	protein O-linked mannose N-acetylglucosaminyltransfe	Cytoplasm	enzyme	
[illegible]	MUTYH	MUTYH	mutY DNA glycosylase	Nucleus	enzyme	
[illegible]	TACC3	TACC3	transforming acidic coiled-coil containing protein 3	Nucleus	other	
[illegible]	STARD3NL	STARD3NL	STARD3 N-terminal like	Cytoplasm	other	
[illegible]	[illegible]	EIF4A2	eukaryotic translation initiation factor 4A2	Cytoplasm	translation regulator	
[illegible]	OSGIN2	OSGIN2	oxidative stress induced growth inhibitor family membe	Other	other	
[illegible]	CD28	CD28	CD28 molecule	Plasma Membrane	transmembrane recepto	
[illegible]	INPP5B	INPP5B	inositol polyphosphate-5-phosphatase B	Plasma Membrane	phosphatase	
[illegible]	HSD17B11	HSD17B11	hydroxysteroid 17-beta dehydrogenase 11	Cytoplasm	enzyme	
[illegible]	ACAD8	ACAD8	acyl-CoA dehydrogenase family member 8	Cytoplasm	enzyme	
[illegible]	IFNG	IFNG	interferon gamma	Extracellular Space	cytokine	
[illegible]	TTC37	TTC37	tetratricopeptide repeat domain 37	Nucleus	other	
[illegible]	HAUS5	HAUS5	HAUS augmin like complex subunit 5	Cytoplasm	other	
[illegible]	TMEM38B	TMEM38B	transmembrane protein 38B	Nucleus	ion channel	
[illegible]	SIPA1L1	SIPA1L1	signal induced proliferation associated 1 like 1	Cytoplasm	other	
[illegible]	ECI2	ECI2	enoyl-CoA delta isomerase 2	Cytoplasm	enzyme	
[illegible]	LDB1	LDB1	LIM domain binding 1	Nucleus	transcription regulator	
[illegible]	INPP5B	INPP5B	inositol polyphosphate-5-phosphatase B	Cytoplasm	phosphatase	
[illegible]	02-Sep	02-Sep	septin 2	Cytoplasm	enzyme	
[illegible]	CCDC88A	CCDC88A	coiled-coil domain containing 88A	Cytoplasm	other	
[illegible]	KLC2	KLC2	kinesin light chain 2	Cytoplasm	other	
[illegible]	COQ10A	COQ10A	coenzyme Q10A	Cytoplasm	other	
[illegible]	RAB3GAP2	RAB3GAP2	RAB3 GTPase activating non-catalytic protein subunit 2	Cytoplasm	enzyme	
[illegible]	TMEM50B	TMEM50B	transmembrane protein 50B	Plasma Membrane	other	
[illegible]	SIPA1	SIPA1	signal-induced proliferation-associated 1	Cytoplasm	other	
[illegible]	DNAJC3	DNAJC3	DnaJ heat shock protein family (Hsp40) member C3	Cytoplasm	other	
[illegible]	KAT2A	KAT2A	lysine acetyltransferase 2A	Cytoplasm	enzyme	
[illegible]	LIMD2	LIMD2	LIM domain containing 2	Other	other	
[illegible]	CHMP7	CHMP7	charged multivesicular body protein 7	Cytoplasm	transporter	
[illegible]	NINJ1	NINJ1	ninjurin 1	Plasma Membrane	other	
[illegible]	ZNF276	ZNF276	zinc finger protein 276	Nucleus	other	
[illegible]	WDR74	WDR74	WD repeat domain 74	Nucleus	other	
[illegible]	SYTL2	SYTL2	synaptotagmin like 2	Cytoplasm	other	
[illegible]	SMC4	SMC4	structural maintenance of chromosomes 4	Nucleus	transporter	
[illegible]	IFI27L2	IFI27L2	interferon alpha inducible protein 27 like 2	Other	other	
[illegible]	[illegible]					
[illegible]	GPR160	GPR160	G protein-coupled receptor 160	Plasma Membrane	G-protein coupled recepto	
[illegible]	ADTRP	ADTRP	androgen dependent TFPI regulating protein	Plasma Membrane	other	
[illegible]	PRMT9	PRMT9	protein arginine methyltransferase 9	Other	other	
[illegible]	LPCAT1	LPCAT1	lysophosphatidylcholine acyltransferase 1	Cytoplasm	enzyme	
[illegible]	FERMT3	FERMT3	fermitin family member 3	Cytoplasm	enzyme	
[illegible]	CDV3	CDV3	CDV3 homolog	Cytoplasm	other	
[illegible]	P4HB	P4HB	prolyl 4-hydroxylase subunit beta	Cytoplasm	enzyme	
[illegible]	SLC1A5	SLC1A5	solute carrier family 1 member 5	Plasma Membrane	transporter	
[illegible]	[illegible]					
[illegible]	RAPGEF6	RAPGEF6	Rap guanine nucleotide exchange factor 6	Plasma Membrane	other	
[illegible]	SPG21	SPG21	spastic paraplegia 21 (autosomal recessive, Mast syndr	Plasma Membrane	enzyme	
[illegible]	SEC14L2	SEC14L2	SEC14 like lipid binding 2	Cytoplasm	transporter	
[illegible]	UTP15	UTP15	UTP15, small subunit processome component	Nucleus	other	
[illegible]	ATAD3B	ATAD3B	ATPase family, AAA domain containing 3B	Nucleus	other	
[illegible]	PPP1R3B	PPP1R3B	protein phosphatase 1 regulatory subunit 3B	Cytoplasm	other	
[illegible]	SACM1L	SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	Cytoplasm	phosphatase	
[illegible]	EFR3A	EFR3A	EFR3 homolog A	Plasma Membrane	other	
[illegible]	NR4A1	NR4A1	nuclear receptor subfamily 4 group A member 1	Nucleus	ligand-dependent nuclear rec	
[illegible]	C4orf3	C4orf3	chromosome 4 open reading frame 3	Other	other	
[illegible]	ZBED6CL	ZBED6CL	ZBED6 C-terminal like	Other	other	
[illegible]	PXYLP1	PXYLP1	2-phosphoxylose phosphatase 1	Cytoplasm	phosphatase	
[illegible]	PDZD8	PDZD8	PDZ domain containing 8	Extracellular Space	other	
[illegible]	SSH1	SSH1	slingshot protein phosphatase 1	Cytoplasm	phosphatase	
[illegible]	TGFBR3	TGFBR3	transforming growth factor beta receptor 3	Plasma Membrane	kinase	
[illegible]	NOP2	NOP2	NOP2 nucleolar protein	Nucleus	other	
[illegible]	LONP1	LONP1	lon peptidase 1, mitochondrial	Cytoplasm	peptidase	
[illegible]	IFT20	IFT20	intraflagellar transport 20	Cytoplasm	other	
[illegible]	INPP4A	INPP4A	inositol polyphosphate-4-phosphatase type I A	Cytoplasm	phosphatase	
[illegible]	PELP1	PELP1	proline, glutamate and leucine rich protein 1	Nucleus	other	
[illegible]	VPS4A	VPS4A	vacuolar protein sorting 4 homolog A	Cytoplasm	enzyme	
[illegible]	TMEM184C	TMEM184C	transmembrane protein 184C	Other	other	
[illegible]	DTX1	DTX1	deltex E3 ubiquitin ligase 1	Nucleus	transcription regulator	
[illegible]	SORL1	SORL1	sortilin related receptor 1	Cytoplasm	transporter	
[illegible]	PQLC1	PQLC1	PQ loop repeat containing 1	Other	other	
[illegible]	QRICH1	QRICH1	glutamine rich 1	Nucleus	other	
[illegible]	UBR2	UBR2	ubiquitin protein ligase E3 component n-recognin 2	Nucleus	enzyme	
[illegible]	PCM1	PCM1	pericentriolar material 1	Cytoplasm	other	
[illegible]	MARK4	MARK4	microtubule affinity regulating kinase 4	Cytoplasm	kinase	
[illegible]	NA					
[illegible]	DGCR14	DGCR14	DiGeorge syndrome critical region gene 14	Nucleus	other	
[illegible]	VPS8	VPS8	VPS8, CORVET complex subunit	Cytoplasm	other	
[illegible]	VCL	VCL	vinculin	Plasma Membrane	enzyme	
[illegible]	TOR3A	TOR3A	torsin family 3 member A	Cytoplasm	enzyme	
[illegible]	PMEPA1	PMEPA1	prostate transmembrane protein, androgen induced 1	Plasma Membrane	other	
[illegible]	JARID2	JARID2	jumonji and AT-rich interaction domain containing 2	Nucleus	transcription regulator	
[illegible]	ZC3H7B	ZC3H7B	zinc finger CCCH-type containing 7B	Nucleus	other	
[illegible]	SERF2	SERF2	small EDRK-rich factor 2	Other	other	
[illegible]	MSRB1	MSRB1	methionine sulfoxide reductase B1	Nucleus	enzyme	
[illegible]	[illegible]					
[illegible]	TAGAP	TAGAP	T-cell activation RhoGTPase activating protein	Cytoplasm	other	
[illegible]	NGDN	NGDN	neuroguidin	Nucleus	other	
[illegible]	IFRD1	IFRD1	interferon related developmental regulator 1	Nucleus	other	
[illegible]	APPL2	APPL2	adaptor protein, phosphotyrosine interacting with PH d	Cytoplasm	other	
[illegible]	FYB	FYB	FYN binding protein	Nucleus	other	
[illegible]	APPL1	APPL1	adaptor protein, phosphotyrosine interacting with PH d	Cytoplasm	other	
[illegible]	DUS3L	DUS3L	dihydrouridine synthase 3 like	Other	other	
[illegible]	PICK1	PICK1	protein interacting with PRKCA 1	Cytoplasm	enzyme	
[illegible]	TP53I13	TP53I13	tumor protein p53 inducible protein 13	Other	other	
[illegible]	ERGIC1	ERGIC1	endoplasmic reticulum-golgi intermediate compartmen	Cytoplasm	other	
[illegible]	SMIM15	SMIM15	small integral membrane protein 15	Other	other	
[illegible]	STRBP	STRBP	spermatid perinuclear RNA binding protein	Cytoplasm	other	
[illegible]	SPIDR	SPIDR	scaffolding protein involved in DNA repair	Nucleus	other	
[illegible]	S100B	S100B	S100 calcium binding protein B	Cytoplasm	other	
[illegible]	PFN1	PFN1	profilin 1	Cytoplasm	other	
[illegible]	NFX1	NFX1	nuclear transcription factor, X-box binding 1	Nucleus	transcription regulator	
[illegible]	SLTM	SLTM	SAFB like transcription modulator	Nucleus	other	
[illegible]	PTOV1	PTOV1	prostate tumor overexpressed 1	Nucleus	other	
[illegible]	[illegible]					
[illegible]	LCK	LCK	LCK proto-oncogene, Src family tyrosine kinase	Cytoplasm	kinase	dasatinib, AP-23[illegible]
[illegible]	MAN2A2	MAN2A2	mannosidase alpha class 2A member 2	Cytoplasm	enzyme	
[illegible]	ACTG1	ACTG1	actin gamma 1	Cytoplasm	other	
[illegible]	UBA3	UBA3	ubiquitin like modifier activating enzyme 3	Cytoplasm	enzyme	
[illegible]	CXorf40B	CXorf40A/CXorf40B	chromosome X open reading frame 40A	Other	other	
[illegible]	DNAJA3	DNAJA3	DnaJ heat shock protein family (Hsp40) member A3	Cytoplasm	other	
[illegible]	MFGE8	MFGE8	milk fat globule-EGF factor 8 protein	Extracellular Space	other	
[illegible]	ZPR1	ZPR1	ZPR1 zinc finger protein	Nucleus	transcription regulator	
[illegible]	HIST1H1C	HIST1H1C	histone cluster 1 H1 family member c	Nucleus	other	
[illegible]	PKN2	PKN2	protein kinase N2	Cytoplasm	kinase	
[illegible]	[illegible]					
[illegible]	TRAPPC11	TRAPPC11	trafficking protein particle complex 11	Cytoplasm	other	
[illegible]	HSF2	HSF2	heat shock transcription factor 2	Nucleus	transcription regulator	
[illegible]	TMX4	TMX4	thioredoxin related transmembrane protein 4	Cytoplasm	enzyme	
[illegible]	CLK4	CLK4	CDC like kinase 4	Nucleus	kinase	
[illegible]	DIS3L2	DIS3L2	DIS3 like 3'-5' exoribonuclease 2	Cytoplasm	enzyme	
[illegible]	CDC25B	CDC25B	cell division cycle 25B	Nucleus	phosphatase	
[illegible]	SURF4	SURF4	surfeit 4	Cytoplasm	other	
[illegible]	ZFC3H1	ZFC3H1	zinc finger C3H1-type containing	Extracellular Space	other	
[illegible]	CNPY4	CNPY4	canopy FGF signaling regulator 4	Other	other	
[illegible]	[illegible]					
[illegible]	NUP188	NUP188	nucleoporin 188	Nucleus	other	
[illegible]	SLC30A7	SLC30A7	solute carrier family 30 member 7	Cytoplasm	transporter	
[illegible]	C1orf27	C1orf27	chromosome 1 open reading frame 27	Other	other	
[illegible]	RMND5A	RMND5A	required for meiotic nuclear division 5 homolog A	Nucleus	other	
[illegible]	PPIL4	PPIL4	peptidylprolyl isomerase like 4	Nucleus	enzyme	
[illegible]	ULK1	ULK1	unc-51 like autophagy activating kinase 1	Cytoplasm	kinase	
[illegible]	TMEM88	TMEM88	transmembrane protein 88	Plasma Membrane	other	
[illegible]	CDC14A	CDC14A	cell division cycle 14A	Nucleus	phosphatase	
[illegible]	ZBTB17	ZBTB17	zinc finger and BTB domain containing 17	Nucleus	transcription regulator	
[illegible]	BRD1	BRD1	bromodomain containing 1	Nucleus	other	
[illegible]	INTS1	INTS1	integrator complex subunit 1	Nucleus	other	
[illegible]	MOB1A	MOB1A	MOB kinase activator 1A	Plasma Membrane	other	
[illegible]	SAMHD1	SAMHD1	SAM and HD domain containing deoxynucleoside tripho	Nucleus	enzyme	
[illegible]	PHF20L1	PHF20L1	PHD finger protein 20-like 1	Other	other	
[illegible]	RRM1	RRM1	ribonucleotide reductase catalytic subunit M1	Nucleus	enzyme	cisplatin, cladribine/cy
[illegible]	ANAPC7	ANAPC7	anaphase promoting complex subunit 7	Nucleus	other	
[illegible]	KDM5C	KDM5C	lysine demethylase 5C	Nucleus	enzyme	
[illegible]	ENO3	ENO3	enolase 3	Cytoplasm	enzyme	
[illegible]	MITD1	MITD1	mit domain containing 1	Other	other	
[illegible]	TRAPPC1	TRAPPC1	trafficking protein particle complex 1	Cytoplasm	other	
[illegible]	RBM6	RBM6	RNA binding motif protein 6	Nucleus	other	
[illegible]	MORN3	MORN3	MORN repeat containing 3	Nucleus	other	
[illegible]	DCAF15	DCAF15	DDB1 and CUL4 associated factor 15	Other	other	
[illegible]	TRABD	TRABD	TraB domain containing	Extracellular Space	other	
[illegible]	TAGLN2	TAGLN2	transgelin 2	Cytoplasm	other	
[illegible]	STRIP1	STRIP1	striatin interacting protein 1	Nucleus	other	
[illegible]	DUSP22	DUSP22	dual specificity phosphatase 22	Cytoplasm	phosphatase	
[illegible]	[illegible]	PTOV1-AS2	PTOV1 antisense RNA 2	Other	other	
[illegible]	HADHA	HADHA	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiola	Cytoplasm	enzyme	
[illegible]	UNC93B1	UNC93B1	unc-93 homolog B1 (C. elegans)	Cytoplasm	transporter	
[illegible]	DUSP7	DUSP7	dual specificity phosphatase 7	Cytoplasm	phosphatase	
[illegible]	PPM1F	PPM1F	protein phosphatase, Mg2+/Mn2+ dependent 1F	Cytoplasm	phosphatase	
[illegible]	SYNJ1	SYNJ1	synaptojanin 1	Cytoplasm	phosphatase	
[illegible]	PNN	PNN	pinin, desmosome associated protein	Plasma Membrane	other	
[illegible]	FNBP4	FNBP4	formin binding protein 4	Nucleus	other	
[illegible]	NPIPB4	NPIPB4 (includes others)	nuclear pore complex interacting protein family memb	Nucleus	other	
[illegible]	DDX28	DDX28	DEAD-box helicase 28	Nucleus	enzyme	
[illegible]	SLC39A13	SLC39A13	solute carrier family 39 member 13	Cytoplasm	transporter	
[illegible]	CLASP2	CLASP2	cytoplasmic linker associated protein 2	Cytoplasm	other	
[illegible]	CYB5D1	CYB5D1	cytochrome b5 domain containing 1	Other	other	
[illegible]	[illegible]					
[illegible]	[illegible]					
[illegible]	RAD51-AS1	RAD51-AS1	RAD51 antisense RNA 1 (head to head)	Other	other	
[illegible]	NA					
[illegible]	SNX1	SNX1	sorting nexin 1	Cytoplasm	transporter	
[illegible]	SPNS1	SPNS1	sphingolipid transporter 1 (putative)	Cytoplasm	transporter	
[illegible]	LAIR1	LAIR1	leukocyte associated immunoglobulin like receptor 1	Plasma Membrane	transmembrane recepto	
[illegible]	TXN	TXN	thioredoxin	Cytoplasm	enzyme	PX-12
[illegible]	TIMM44	TIMM44	translocase of inner mitochondrial membrane 44	Cytoplasm	transporter	
[illegible]	SCFD1	SCFD1	sec1 family domain containing 1	Cytoplasm	transporter	
[illegible]	ADAM9	ADAM9	ADAM metallopeptidase domain 9	Plasma Membrane	peptidase	
[illegible]	ATP1B1	ATP1B1	ATPase Na+/K+ transporting subunit beta 1	Plasma Membrane	transporter	
[illegible]	PPAN	PPAN	peter pan homolog (Drosophila)	Nucleus	other	
[illegible]	[illegible]					
[illegible]	PARP12	PARP12	poly(ADP-ribose) polymerase family member 12	Nucleus	other	
[illegible]	ZNF300	ZNF300	zinc finger protein 300	Extracellular Space	other	
[illegible]	ACSL1	ACSL1	acyl-CoA synthetase long-chain family member 1	Cytoplasm	enzyme	
[illegible]	DROSHA	DROSHA	drosha ribonuclease III	Nucleus	enzyme	
[illegible]	COPRS	COPRS	coordinator of PRMT5 and differentiation stimulator	Nucleus	other	
[illegible]	ZNF668	ZNF668	zinc finger protein 668	Nucleus	other	
[illegible]	PDXDC1	PDXDC1	pyridoxal dependent decarboxylase domain containing	Cytoplasm	other	
[illegible]	ADA	ADA	adenosine deaminase	Cytoplasm	enzyme	[illegible]
[illegible]	VPS39	VPS39	VPS39, HOPS complex subunit	Cytoplasm	transporter	
[illegible]	ATP10A	ATP10A	ATPase phospholipid transporting 10A (putative)	Plasma Membrane	transporter	
[illegible]	PSME4	PSME4	proteasome activator subunit 4	Cytoplasm	other	
[illegible]	SERINC3	SERINC3	serine incorporator 3	Plasma Membrane	transporter	
[illegible]	UBE2K	UBE2K	ubiquitin conjugating enzyme E2 K	Cytoplasm	enzyme	
[illegible]	PICALM	PICALM	phosphatidylinositol binding clathrin assembly protein	Cytoplasm	other	
[illegible]	PYGB	PYGB	glycogen phosphorylase B	Cytoplasm	enzyme	
[illegible]	FN3KRP	FN3KRP	fructosamine 3 kinase related protein	Cytoplasm	kinase	
[illegible]	EHBP1L1	EHBP1L1	EH domain binding protein 1 like 1	Other	other	
[illegible]	GET4	GET4	golgi to ER traffic protein 4	Cytoplasm	other	
[illegible]	NCAPD3	NCAPD3	non-SMC condensin II complex subunit D3	Nucleus	other	
[illegible]	UHRF1BP1	UHRF1BP1	UHRF1 binding protein 1	Other	other	
[illegible]	TGFB1	TGFB1	transforming growth factor beta 1	Extracellular Space	growth factor	dalantercept
[illegible]	RABAC1	RABAC1	Rab acceptor 1	Cytoplasm	other	
[illegible]	XPO1	XPO1	exportin 1	Nucleus	transporter	verdinexor, SL-801, leptomy
[illegible]	ERCC3	ERCC3	ERCC excision repair 3, TFIIH core complex helicase sul	Nucleus	enzyme	
[illegible]	RAPGEF1	RAPGEF1	Rap guanine nucleotide exchange factor 1	Cytoplasm	other	
[illegible]	TXK	TXK	TXK tyrosine kinase	Cytoplasm	kinase	
[illegible]	CCAR1	CCAR1	cell division cycle and apoptosis regulator 1	Nucleus	transcription regulator	
[illegible]	HIGD1A	HIGD1A	HIG1 hypoxia inducible domain family member 1A	Cytoplasm	other	
[illegible]	NA					
[illegible]	ARL6IP1	ARL6IP1	ADP ribosylation factor like GTPase 6 interacting protei	Cytoplasm	other	
[illegible]	REC8	REC8	REC8 meiotic recombination protein	Nucleus	other	
[illegible]	VPS16	VPS16	VPS16, CORVET/HOPS core subunit	Cytoplasm	transporter	
[illegible]	IQCB1	IQCB1	IQ motif containing B1	Extracellular Space	other	
[illegible]	UVSSA	UVSSA	UV stimulated scaffold protein A	Nucleus	other	
[illegible]	ZBTB7A	ZBTB7A	zinc finger and BTB domain containing 7A	Nucleus	transcription regulator	
[illegible]	B2M	B2M	beta-2-microglobulin	Plasma Membrane	transmembrane receptor	[illegible]

[illegible]	HARS2	HARS2	histidyl-tRNA synthetase 2, mitochondrial	Cytoplasm	enzyme	
[illegible]	IVD	IVD	isovaleryl-CoA dehydrogenase	Cytoplasm	enzyme	
[illegible]	YBX1	YBX1	Y-box binding protein 1	Nucleus	transcription regulator	
[illegible]	CHCHD10	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	Cytoplasm	other	
[illegible]	MUT	MUT	methylmalonyl-CoA mutase	Cytoplasm	enzyme	[illegible]
[illegible]	SLC50A1	SLC50A1	solute carrier family 50 member 1	Plasma Membrane	transporter	
[illegible]	HMGB3	HMGB3	high mobility group box 3	Nucleus	other	
[illegible]	ASAP1	ASAP1 (includes others)	ArfGAP with SH3 domain, ankyrin repeat and PH do	Other	other	
[illegible]	NA					
[illegible]	PSMB4	PSMB4	proteasome subunit beta 4	Cytoplasm	peptidase	
[illegible]	PEPD	PEPD	peptidase D	Cytoplasm	peptidase	
[illegible]	MT-CO3	MT-CO3	cytochrome c oxidase III	Cytoplasm	enzyme	
[illegible]	NIPA2	NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2	Cytoplasm	other	
[illegible]	USP14	USP14	ubiquitin specific peptidase 14	Cytoplasm	peptidase	VLX1570
[illegible]	CECR1	CECR1	cat eye syndrome chromosome region, candidate 1	Extracellular Space	enzyme	
[illegible]	GHDC	GHDC	GH3 domain containing	Cytoplasm	other	
[illegible]	ZFP36	ZFP36	ZFP36 ring finger protein	Nucleus	transcription regulator	
[illegible]	[illegible]					
[illegible]	FAM69C	FAM69C	family with sequence similarity 69 member C	Extracellular Space	other	
[illegible]	GMCL1	GMCL1	germ cell-less, spermatogenesis associated 1	Nucleus	other	
[illegible]	AAMP	AAMP	angio associated migratory cell protein	Plasma Membrane	other	
[illegible]	FAM91A1	FAM91A1	family with sequence similarity 91 member A1	Other	other	
[illegible]	FMR1	FMR1	fragile X mental retardation 1	Cytoplasm	translation regulator	
[illegible]	CHRAC1	CHRAC1	chromatin accessibility complex 1	Nucleus	enzyme	
[illegible]	WNT7A	WNT7A	Wnt family member 7A	Extracellular Space	cytokine	
[illegible]	MT-CO2	MT-CO2	cytochrome c oxidase subunit II	Cytoplasm	enzyme	
[illegible]	TP53BP1	TP53BP1	tumor protein p53 binding protein 1	Nucleus	transcription regulator	
[illegible]	SYTL1	SYTL1	synaptotagmin like 1	Cytoplasm	enzyme	
[illegible]	SH2D1A	SH2D1A	SH2 domain containing 1A	Cytoplasm	other	
[illegible]	ABHD2	ABHD2	abhydrolase domain containing 2	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	CELF1	CELF1	CUGBP Elav-like family member 1	Cytoplasm	translation regulator	
[illegible]	SEC61B	SEC61B	Sec61 translocon beta subunit	Cytoplasm	transporter	
[illegible]	C8orf58	C8orf58	chromosome 8 open reading frame 58	Cytoplasm	other	
[illegible]	KCTD13	KCTD13	potassium channel tetramerization domain containing :	Nucleus	ion channel	
[illegible]	QKI	QKI	QKI, KH domain containing RNA binding	Nucleus	other	
[illegible]	PMPCB	PMPCB	peptidase, mitochondrial processing beta subunit	Cytoplasm	peptidase	
[illegible]	ZNF587B	ZNF587B	zinc finger protein 587B	Other	other	
[illegible]	RCOR1	RCOR1	REST corepressor 1	Nucleus	transcription regulator	
[illegible]	EVL	EVL	Enah/Vasp-like	Plasma Membrane	other	
[illegible]	CD58	CD58	CD58 molecule	Plasma Membrane	other	
[illegible]	ANO8	ANO8	anoctamin 8	Plasma Membrane	ion channel	
[illegible]	[illegible]					
[illegible]	BANF1	BANF1	barrier to autointegration factor 1	Nucleus	other	
[illegible]	BLVRA	BLVRA	biliverdin reductase A	Cytoplasm	enzyme	
[illegible]	SET	SET	SET nuclear proto-oncogene	Nucleus	phosphatase	
[illegible]	UBFD1	UBFD1	ubiquitin family domain containing 1	Other	other	
[illegible]	LPPR2	PLPPR2	phospholipid phosphatase related 2	Other	phosphatase	
[illegible]	APH1A	APH1A	aph-1 homolog A, gamma-secretase subunit	Cytoplasm	peptidase	
[illegible]	NA					
[illegible]	CHORDC1	CHORDC1	cysteine and histidine rich domain containing 1	Other	other	
[illegible]	PRKDC	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	Nucleus	kinase	7D, CC-115, MSC24
[illegible]	TECPR1	TECPR1	tectonin beta-propeller repeat containing 1	Cytoplasm	other	
[illegible]	PSIP1	PSIP1	PC4 and SFRS1 interacting protein 1	Nucleus	transcription regulator	
[illegible]	SUPT5H	SUPT5H	SPT5 homolog, DSIF elongation factor subunit	Nucleus	transcription regulator	
[illegible]	C7orf55-LUC7L2	LUC7L2	LUC7 like 2, pre-mRNA splicing factor	Other	other	
[illegible]	COX8A	COX8A	cytochrome c oxidase subunit 8A	Cytoplasm	enzyme	
[illegible]	TMEM198B	TMEM198B	transmembrane protein 198B (pseudogene)	Other	other	
[illegible]	LAMTOR1	LAMTOR1	late endosomal/lysosomal adaptor, MAPK and MTOR a	Plasma Membrane	other	
[illegible]	CERK	CERK	ceramide kinase	Plasma Membrane	kinase	
[illegible]	NFS1	NFS1	NFS1, cysteine desulfurase	Cytoplasm	enzyme	
[illegible]	FOS	FOS	Fos proto-oncogene, AP-1 transcription factor subunit	Nucleus	transcription regulator	
[illegible]	U2AF1	U2AF1/U2AF1L5	U2 small nuclear RNA auxiliary factor 1	Nucleus	other	
[illegible]	ZBTB40	ZBTB40	zinc finger and BTB domain containing 40	Nucleus	other	
[illegible]	SOAT1	SOAT1	sterol O-acyltransferase 1	Cytoplasm	enzyme	[illegible]
[illegible]	WASH6P	WASH6P	WAS protein family homolog 6 pseudogene	Cytoplasm	other	
[illegible]	PAF1	PAF1	PAF1 homolog, Paf1/RNA polymerase II complex compo	Nucleus	other	
[illegible]	CKLF	CKLF	chemokine like factor	Extracellular Space	cytokine	
[illegible]	GALNT1	GALNT1	polypeptide N-acetylgalactosaminyltransferase 1	Cytoplasm	enzyme	
[illegible]	SMS	SMS	spermine synthase	Cytoplasm	enzyme	[illegible]
[illegible]	CNPPD1	CNPPD1	cyclin Pas1/PHO80 domain containing 1	Other	other	
[illegible]	FUOM	FUOM	fucose mutarotase	Cytoplasm	enzyme	
[illegible]	SERPINB8	SERPINB8	serpin family B member 8	Cytoplasm	other	
[illegible]	NSUN5P1	NSUN5P1	NOP2/Sun RNA methyltransferase family member 5 pse	Other	other	
[illegible]	PCED1A	PCED1A	PC-esterase domain containing 1A	Other	other	
[illegible]	UBE2F	UBE2F	ubiquitin conjugating enzyme E2 F (putative)	Cytoplasm	enzyme	
[illegible]	GPR18	GPR18	G protein-coupled receptor 18	Plasma Membrane	G-protein coupled recept	
[illegible]	ARL17A	ARL17A/ARL17B	ADP ribosylation factor like GTPase 17B	Other	other	
[illegible]	FAM118A	FAM118A	family with sequence similarity 118 member A	Nucleus	enzyme	
[illegible]	CAMKK1	CAMKK1	calcium/calmodulin dependent protein kinase kinase 1	Cytoplasm	kinase	
[illegible]	CYSTM1	CYSTM1	cysteine rich transmembrane module containing 1	Cytoplasm	other	
[illegible]	OPTN	OPTN	optineurin	Cytoplasm	other	
[illegible]	ALKBH5	ALKBH5	alkB homolog 5, RNA demethylase	Nucleus	enzyme	
[illegible]	ST8SIA4	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransfe	Cytoplasm	enzyme	
[illegible]	CSGALNACT1	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase :	Cytoplasm	enzyme	
[illegible]	TRABD2A					
[illegible]	THAP4	THAP4	THAP domain containing 4	Extracellular Space	other	
[illegible]	CCT6P1	CCT6P1	chaperonin containing TCP1 subunit 6 pseudogene 1	Other	other	
[illegible]	GNPTAB	GNPTAB	N-acetylglucosamine-1-phosphate transferase alpha an	Cytoplasm	enzyme	
[illegible]	IFIT3	IFIT3	interferon induced protein with tetratricopeptide repea	Cytoplasm	other	
[illegible]	CACTIN	CACTIN	cactin, spliceosome C complex subunit	Nucleus	other	
[illegible]	RASAL3	RASAL3	RAS protein activator like 3	Cytoplasm	other	
[illegible]	SATB1	SATB1	SATB homeobox 1	Nucleus	transcription regulator	
[illegible]	PAFAH2	PAFAH2	platelet activating factor acetylhydrolase 2	Cytoplasm	enzyme	
[illegible]	RHEB	RHEB	Ras homolog enriched in brain	Cytoplasm	enzyme	
[illegible]	PPP4R1L	PPP4R1L	protein phosphatase 4 regulatory subunit 1-like (pseud	Other	other	
[illegible]	HIST1H2BK	HIST1H2BK	histone cluster 1 H2B family member k	Nucleus	other	
[illegible]	VCPIP1	VCPIP1	valosin containing protein interacting protein 1	Cytoplasm	peptidase	
[illegible]	ZNF689	ZNF689	zinc finger protein 689	Other	other	
[illegible]	BAP1	BAP1	BRCA1 associated protein 1	Nucleus	peptidase	
[illegible]	EVI2A	EVI2A	ecotropic viral integration site 2A	Plasma Membrane	transmembrane recepto	
[illegible]	GPS1	GPS1	G protein pathway suppressor 1	Nucleus	other	
[illegible]	TBRG4	TBRG4	transforming growth factor beta regulator 4	Cytoplasm	other	
[illegible]	FAM193A	FAM193A	family with sequence similarity 193 member A	Nucleus	other	
[illegible]	WHAMMP3	WHAMMP3	WAS protein homolog associated with actin, golgi mem	Other	other	
[illegible]	VMAC	VMAC	vimentin-type intermediate filament associated coiled-	Cytoplasm	other	
[illegible]	MEX3C	MEX3C	mex-3 RNA binding family member C	Cytoplasm	other	
[illegible]	MBTPS1	MBTPS1	membrane bound transcription factor peptidase, site 1	Cytoplasm	peptidase	[illegible]
[illegible]	HPS4	HPS4	HPS4, biogenesis of lysosomal organelles complex 3 sul	Cytoplasm	other	
[illegible]	SMURF1	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	Cytoplasm	enzyme	
[illegible]	PGK1	PGK1	phosphoglycerate kinase 1	Cytoplasm	kinase	
[illegible]	CTSA	CTSA	cathepsin A	Cytoplasm	peptidase	
[illegible]	DHX35	DHX35	DEAH-box helicase 35	Other	enzyme	
[illegible]	TMX3	TMX3	thioredoxin related transmembrane protein 3	Cytoplasm	enzyme	
[illegible]	FLNA	FLNA	filamin A	Cytoplasm	other	
[illegible]	FAM101B	RFLNB	refilin B	Other	other	
[illegible]	SPRY1	SPRY1	sprouty RTK signaling antagonist 1	Cytoplasm	other	
[illegible]	RRAS2	RRAS2	related RAS viral (r-ras) oncogene homolog 2	Plasma Membrane	enzyme	
[illegible]	GIGYF2	GIGYF2	GRB10 interacting GYF protein 2	Cytoplasm	other	
[illegible]	NUP98	NUP98	nucleoporin 98	Nucleus	transporter	
[illegible]	NICN1	NICN1	nicolin 1	Nucleus	other	
[illegible]	TBC1D5	TBC1D5	TBC1 domain family member 5	Extracellular Space	other	
[illegible]	FLT3LG	FLT3LG	fms related tyrosine kinase 3 ligand	Extracellular Space	cytokine	
[illegible]	DDOST	DDOST	dolichyl-diphosphooligosaccharide--protein glycosyltran	Cytoplasm	enzyme	
[illegible]	HKR1	HKR1	HKR1, GLI-Kruppel zinc finger family member	Nucleus	other	
[illegible]	CAP1	CAP1	adenylate cyclase associated protein 1	Plasma Membrane	other	
[illegible]	PTPRJ	PTPRJ	protein tyrosine phosphatase, receptor type J	Plasma Membrane	phosphatase	
[illegible]	TMEM219	TMEM219	transmembrane protein 219	Plasma Membrane	other	
[illegible]	PBXIP1	PBXIP1	PBX homeobox interacting protein 1	Nucleus	transcription regulator	
[illegible]	DCHS1	DCHS1	dachsous cadherin-related 1	Plasma Membrane	other	
[illegible]	[illegible]					
[illegible]	HN1	HN1	hematological and neurological expressed 1	Nucleus	other	
[illegible]	TMEM104	TMEM104	transmembrane protein 104	Other	transporter	
[illegible]	HTT	HTT	huntingtin	Cytoplasm	transcription regulator	
[illegible]	TYW5	TYW5	tRNA-yW synthesizing protein 5	Cytoplasm	enzyme	
[illegible]	SLC37A1	SLC37A1	solute carrier family 37 member 1	Plasma Membrane	transporter	
[illegible]	UBL4A	UBL4A	ubiquitin like 4A	Cytoplasm	enzyme	
[illegible]	NLRC3	NLRC3	NLR family CARD domain containing 3	Cytoplasm	other	
[illegible]	NA					
[illegible]	NEIL1	NEIL1	nei like DNA glycosylase 1	Nucleus	enzyme	
[illegible]	RBM14	RBM14	RNA binding motif protein 14	Nucleus	transcription regulator	
[illegible]	SNX10	SNX10	sorting nexin 10	Cytoplasm	transporter	
[illegible]	RILPL2	RILPL2	Rab interacting lysosomal protein like 2	Cytoplasm	other	
[illegible]	RAB5A	RAB5A	RAB5A, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	TSPYL4	TSPYL4	TSPY like 4	Nucleus	other	
[illegible]	CLASRP	CLASRP	CLK4 associating serine/arginine rich protein	Nucleus	other	
[illegible]	PAFAH1B2	PAFAH1B2	platelet activating factor acetylhydrolase 1b catalytic s	Cytoplasm	enzyme	
[illegible]	ATP2B1	ATP2B1	ATPase plasma membrane Ca2+ transporting 1	Plasma Membrane	transporter	
[illegible]	NDUFS3	NDUFS3	NADH:ubiquinone oxidoreductase core subunit S3	Cytoplasm	enzyme	
[illegible]	GTF3C3	GTF3C3	general transcription factor IIIC subunit 3	Nucleus	transcription regulator	
[illegible]	PIK3CD	PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic	Cytoplasm	kinase	-1202, PQR309, AMG
[illegible]	COMMD5	COMMD5	COMM domain containing 5	Nucleus	other	
[illegible]	GUCD1	GUCD1	guanylyl cyclase domain containing 1	Other	other	
[illegible]	H3F3AP4	H3F3AP4	H3 histone, family 3A, pseudogene 4	Other	other	
[illegible]	FAM13A	FAM13A	family with sequence similarity 13 member A	Other	other	
[illegible]	TACC1	TACC1	transforming acidic coiled-coil containing protein 1	Nucleus	other	
[illegible]	TCF7	TCF7	transcription factor 7 (T-cell specific, HMG-box)	Nucleus	transcription regulator	
[illegible]	WDR45B	WDR45B	WD repeat domain 45B	Other	other	
[illegible]	TBC1D10B	TBC1D10B	TBC1 domain family member 10B	Plasma Membrane	enzyme	
[illegible]	AVPI1	AVPI1	arginine vasopressin induced 1	Other	other	
[illegible]	NXT1	NXT1	nuclear transport factor 2 like export factor 1	Nucleus	transporter	
[illegible]	DYNLT1	DYNLT1	dynein light chain Tctex-type 1	Cytoplasm	other	
[illegible]	LHPP	LHPP	phospholysine phosphohistidine inorganic pyrophosphat	Cytoplasm	phosphatase	
[illegible]	MSN	MSN	moesin	Plasma Membrane	other	
[illegible]	XYLT1	XYLT1	xylosyltransferase 1	Cytoplasm	enzyme	
[illegible]	SPAST	SPAST	spastin	Nucleus	enzyme	
[illegible]	DENND1A	DENND1A	DENN domain containing 1A	Plasma Membrane	other	
[illegible]	ATG16L1	ATG16L1	autophagy related 16 like 1	Cytoplasm	enzyme	
[illegible]	NASP	NASP	nuclear autoantigenic sperm protein	Nucleus	other	
[illegible]	TMBIM1					
[illegible]	SNN	SNN	stannin	Plasma Membrane	other	
[illegible]	GSPT1	GSPT1	G1 to S phase transition 1	Cytoplasm	translation regulator	
[illegible]	AAK1	AAK1	AP2 associated kinase 1	Cytoplasm	kinase	
[illegible]	MAP3K1	MAP3K1	mitogen-activated protein kinase kinase kinase 1	Cytoplasm	kinase	[illegible]
[illegible]	IL23A	IL23A	interleukin 23 subunit alpha	Extracellular Space	cytokine	
[illegible]	PMPCA	PMPCA	peptidase, mitochondrial processing alpha subunit	Cytoplasm	peptidase	
[illegible]	VPS33B	VPS33B	VPS33B, late endosome and lysosome associated	Cytoplasm	transporter	
[illegible]	GIMAP7	GIMAP7	GTPase, IMAP family member 7	Cytoplasm	enzyme	
[illegible]	POLG2	POLG2	DNA polymerase gamma 2, accessory subunit	Cytoplasm	enzyme	
[illegible]	MT-ND3	MTND3	MTND3	Cytoplasm	enzyme	
[illegible]	ZUFSP	ZUFSP	zinc finger with UFM1 specific peptidase domain	Other	other	
[illegible]	CDK10	CDK10	cyclin dependent kinase 10	Nucleus	kinase	alvocidib
[illegible]	SERPINB9	SERPINB9	serpin family B member 9	Cytoplasm	other	
[illegible]	ZDHHC8	ZDHHC8	zinc finger DHHC-type containing 8	Nucleus	enzyme	
[illegible]	TRGC2	TRGC2	T cell receptor gamma constant 2	Other	other	
[illegible]	NEU1	NEU1	neuraminidase 1	Cytoplasm	enzyme	
[illegible]	OSBPL7	OSBPL7	oxysterol binding protein like 7	Cytoplasm	transporter	
[illegible]	CTU2	CTU2	cytosolic thiouridylase subunit 2	Cytoplasm	other	
[illegible]	USF1	USF1	upstream transcription factor 1	Nucleus	transcription regulator	
[illegible]	MYO18A	MYO18A	myosin XVIIIA	Cytoplasm	other	
[illegible]	NOTCH2	NOTCH2	notch 2	Plasma Membrane	transcription regulator	
[illegible]	CLN3	CLN3	CLN3, battenin	Cytoplasm	other	
[illegible]	USP47	USP47	ubiquitin specific peptidase 47	Cytoplasm	peptidase	
[illegible]	FAM98A	FAM98A	family with sequence similarity 98 member A	Cytoplasm	other	
[illegible]	SNX2	SNX2	sorting nexin 2	Cytoplasm	transporter	
[illegible]	APOE	APOE	apolipoprotein E	Extracellular Space	transporter	
[illegible]	MOGS	MOGS	mannosyl-oligosaccharide glucosidase	Cytoplasm	enzyme	
[illegible]	MICAL1	MICAL1	microtubule associated monooxygenase, calponin and l	Cytoplasm	enzyme	
[illegible]	RAB27A	RAB27A	RAB27A, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	TRMT2A	TRMT2A	tRNA methyltransferase 2 homolog A	Other	kinase	
[illegible]	MYL12A	MYL12A	myosin light chain 12A	Cytoplasm	other	
[illegible]	PYGM	PYGM	glycogen phosphorylase, muscle associated	Cytoplasm	enzyme	
[illegible]	PI4KA	PI4KA	phosphatidylinositol 4-kinase alpha	Cytoplasm	kinase	
[illegible]	POLR2J3	POLR2J2/POLR2J3	RNA polymerase II subunit J3	Other	transcription regulator	
[illegible]	LPHN1	ADGRL1	adhesion G protein-coupled receptor L1	Plasma Membrane	G-protein coupled recept	
[illegible]	NCLN	NCLN	nicalin	Cytoplasm	peptidase	
[illegible]	MAPKAPK2	MAPKAPK2	mitogen-activated protein kinase-activated protein kina	Nucleus	kinase	[illegible]
[illegible]	HMGN4	HMGN4	high mobility group nucleosomal binding domain 4	Nucleus	other	
[illegible]	DHX15	DHX15	DEAH-box helicase 15	Nucleus	enzyme	
[illegible]	IL7R	IL7R	interleukin 7 receptor	Plasma Membrane	transmembrane recepto	[illegible]
[illegible]	ARPC4	ARPC4	actin related protein 2/3 complex subunit 4	Cytoplasm	other	
[illegible]	RASA4	RASA4	RAS p21 protein activator 4	Cytoplasm	other	
[illegible]	NR4A3	NR4A3	nuclear receptor subfamily 4 group A member 3	Nucleus	ligand-dependent nuclear rec	
[illegible]	UFL1	UFL1	UFM1 specific ligase 1	Cytoplasm	enzyme	
[illegible]	HIF1AN	HIF1AN	hypoxia inducible factor 1 alpha subunit inhibitor	Nucleus	enzyme	
[illegible]	AP4B1	AP4B1	adaptor related protein complex 4 beta 1 subunit	Cytoplasm	transporter	
[illegible]	MYD88	MYD88	myeloid differentiation primary response 88	Plasma Membrane	other	[illegible]
[illegible]	SUGP1	SUGP1	SURP and G-patch domain containing 1	Nucleus	other	
[illegible]	[illegible]	WASHC1	WASH complex subunit 1	Cytoplasm	other	
[illegible]	NDUFAF7	NDUFAF7	NADH:ubiquinone oxidoreductase complex assembly fa	Cytoplasm	enzyme	
[illegible]	CAMSAP1	CAMSAP1	calmodulin regulated spectrin associated protein 1	Cytoplasm	other	
[illegible]	UTP20	UTP20	UTP20, small subunit processome component	Nucleus	other	
[illegible]	TMEM120A	TMEM120A	transmembrane protein 120A	Other	other	
[illegible]	RBL1	RBL1	RB transcriptional corepressor like 1	Nucleus	transcription regulator	
[illegible]	DNPEP	DNPEP	aspartyl aminopeptidase	Cytoplasm	peptidase	

[illegible]	RNPC3	RNPC3	RNA binding region (RNP1, RRM) containing 3	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PRD						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EXOC3	EXOC3	exocyst complex component 3	Plasma Membrane	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MYL5	MYL5	myosin light chain 5	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PLCB2	PLCB2	phospholipase C beta 2	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TADA2B	TADA2B	transcriptional adaptor 2B	Nucleus	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	H3F3A	H3F3A/H3F3B	H3 histone family member 3A	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PHF10	PHF10	PHD finger protein 10	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NFAT5	NFAT5	nuclear factor of activated T-cells 5	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZDHHC2	ZDHHC2	zinc finger DHHC-type containing 2	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TBL1XR1	TBL1XR1	transducin beta like 1 X-linked receptor 1	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GATAD2A	GATAD2A	GATA zinc finger domain containing 2A	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF281	ZNF281	zinc finger protein 281	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LONP2	LONP2	lon peptidase 2, peroxisomal	Cytoplasm	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ICAM3	ICAM3	intercellular adhesion molecule 3	Plasma Membrane	transmembrane receptor		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CCDC6	CCDC6	coiled-coil domain containing 6	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NCKAP5L	NCKAP5L	NCK associated protein 5 like	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CASP4	CASP4	caspase 4	Cytoplasm	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	IGF1R	IGF1R	insulin like growth factor 1 receptor	Plasma Membrane	transmembrane receptor	BIIB022, IGF1, dalotuzum	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CDC23	CDC23	cell division cycle 23	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	C9orf89	CARD19	caspase recruitment domain family member 19	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	VWA8						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZCCHC8	ZCCHC8	zinc finger CCHC-type containing 8	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TMED7	TMED7	transmembrane p24 trafficking protein 7	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CTDSP1	CTDSP1	CTD small phosphatase 1	Nucleus	phosphatase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MEF2D	MEF2D	myocyte enhancer factor 2D	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	POLR3B	POLR3B	RNA polymerase III subunit B	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CGRRF1	CGRRF1	cell growth regulator with ring finger domain 1	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ANKRD13C	ANKRD13C	ankyrin repeat domain 13C	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RP11-[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NANS	NANS	N-acetylneuraminate synthase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DAGLB	DAGLB	diacylglycerol lipase beta	Plasma Membrane	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PRKCD	PRKCD	protein kinase C delta	Cytoplasm	kinase	ingenol mebutate	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MB21D1	MB21D1	Mab-21 domain containing 1	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	C16orf70	C16orf70	chromosome 16 open reading frame 70	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PDE1B	PDE1B	phosphodiesterase 1B	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KIAA1468	KIAA1468	KIAA1468	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RP11-[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TTC14	TTC14	tetratricopeptide repeat domain 14	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CHMP2B	CHMP2B	charged multivesicular body protein 2B	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CDK8	CDK8	cyclin dependent kinase 8	Nucleus	kinase	alvocidib, [illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GON4L	GON4L	gon-4 like	Cytoplasm	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CENPB	CENPB	centromere protein B	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	VNN2	VNN2	vanin 2	Other	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MAEA	MAEA	macrophage erythroblast attacher	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF613	ZNF613	zinc finger protein 613	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SMCHD1	SMCHD1	structural maintenance of chromosomes flexible hinge	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SUSD3	SUSD3	sushi domain containing 3	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CTSC	CTSC	cathepsin C	Cytoplasm	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LPIN2	LPIN2	lipin 2	Nucleus	phosphatase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DENND1A	DENND1A	DENN domain containing 1A	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CPD	CPD	carboxypeptidase D	Extracellular Space	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	AC[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SZT2	SZT2	seizure threshold 2 homolog (mouse)	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TPM4	TPM4	tropomyosin 4	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RAB3B	RAB3B	RAB3B, member RAS oncogene family	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	IL27RA	IL27RA	interleukin 27 receptor subunit alpha	Plasma Membrane	transmembrane receptor		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	OTUD3	OTUD3	OTU deubiquitinase 3	Cytoplasm	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF569	ZNF569	zinc finger protein 569	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CTLA4	CTLA4	cytotoxic T-lymphocyte associated protein 4	Plasma Membrane	transmembrane receptor	ipilimumab/[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PSMB2	PSMB2	proteasome subunit beta 2	Cytoplasm	peptidase	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ITSN2	ITSN2	intersectin 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RP11-[illegible]	[illegible]-AS1	[illegible] antisense RNA 1	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CLUH	CLUH	clustered mitochondria homolog	Cytoplasm	translation regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SPTY2D1	SPTY2D1	SPT2 domain containing 1	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FLII	FLII	FLII, actin remodeling protein	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RALGAPB	RALGAPB	Ral GTPase activating protein non-catalytic beta subunit	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TMEM170A	TMEM170A	transmembrane protein 170A	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MED11	MED11	mediator complex subunit 11	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	HACL1	HACL1	2-hydroxyacyl-CoA lyase 1	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	USP16	USP16	ubiquitin specific peptidase 16	Cytoplasm	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LSR	LSR	lipolysis stimulated lipoprotein receptor	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRI1	MRI1	methylthioribose-1-phosphate isomerase 1	Cytoplasm	translation regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CAMK2G	CAMK2G	calcium/calmodulin dependent protein kinase II gamma	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SNRNP25	SNRNP25	small nuclear ribonucleoprotein U11/U12 subunit 25	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CCNI	CCNI	cyclin I	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NA						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CARD16	CARD16	caspase recruitment domain family member 16	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SNRPA1	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SLC35D2	SLC35D2	solute carrier family 35 member D2	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ERMN	ERMN	ermin	Extracellular Space	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LY96	LY96	lymphocyte antigen 96	Plasma Membrane	transmembrane receptor		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ACTR1B	ACTR1B	ARP1 actin-related protein 1 homolog B, centractin bet	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF664	ZNF664	zinc finger protein 664	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SLC22A23	SLC22A23	solute carrier family 22 member 23	Other	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PDPK1	PDPK1	3-phosphoinositide dependent protein kinase 1	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NME1-NME2	NME2	NME/NM23 nucleoside diphosphate kinase 2	Nucleus	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PIK3R4	PIK3R4	phosphoinositide-3-kinase regulatory subunit 4	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	IFNGR1	IFNGR1	interferon gamma receptor 1	Plasma Membrane	transmembrane receptor	interferon gamma-1b	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GANAB	GANAB	glucosidase II alpha subunit	Cytoplasm	enzyme	miglitol	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	BNIP2	BNIP2	BCL2 interacting protein 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	AIM1	AIM1	absent in melanoma 1	Extracellular Space	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	C10orf32	BORCS7	BLOC-1 related complex subunit 7	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PANX1	PANX1	pannexin 1	Plasma Membrane	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FBXW2	FBXW2	F-box and WD repeat domain containing 2	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PPIB	PPIB	peptidylprolyl isomerase B	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CTD-[illegible]	LOC[illegible]	[illegible] repressor factor-like	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TRAM1	TRAM1	translocation associated membrane protein 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MEN1	MEN1	menin 1	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RIF1	RIF1	replication timing regulatory factor 1	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TSC22D3	TSC22D3	TSC22 domain family member 3	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF92	ZNF92	zinc finger protein 92	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	OBSCN	OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting R	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF831	ZNF831	zinc finger protein 831	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZBTB25	ZBTB25	zinc finger and BTB domain containing 25	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SELT	SELENOT	selenoprotein T	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ARFIP2	ARFIP2	ADP ribosylation factor interacting protein 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LYRM2	LYRM2	LYR motif containing 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FOXRED1	FOXRED1	FAD dependent oxidoreductase domain containing 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ITPR1	ITPR1	inositol 1,4,5-trisphosphate receptor type 1	Cytoplasm	ion channel		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZMYM4	ZMYM4	zinc finger MYM-type containing 4	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SRPK1	SRPK1	SRSF protein kinase 1	Nucleus	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ARFGEF1	ARFGEF1	ADP ribosylation factor guanine nucleotide exchange fa	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RGCC	RGCC	regulator of cell cycle	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CXCR4	CXCR4	C-X-C motif chemokine receptor 4	Plasma Membrane	G-protein coupled receptor	POL6326, BL-8040, [illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SMC1A	SMC1A	structural maintenance of chromosomes 1A	Nucleus	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FBXO5	FBXO5	F-box protein 5	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TMEM88	TMEM88	transmembrane protein 88	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CLDN15	CLDN15	claudin 15	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CAMK2D	CAMK2D	calcium/calmodulin dependent protein kinase II delta	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	AHR	AHR	aryl hydrocarbon receptor	Nucleus	ligand-dependent nuclear rec		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FBXO9	FBXO9	F-box protein 9	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CARS	CARS	cysteinyl-tRNA synthetase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MPC1	MPC1	mitochondrial pyruvate carrier 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LPAR6	LPAR6	lysophosphatidic acid receptor 6	Plasma Membrane	G-protein coupled recepto		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PAXBP1	PAXBP1	PAX3 and PAX7 binding protein 1	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZKSCAN8	ZKSCAN8	zinc finger with KRAB and SCAN domains 8	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	BTG2	BTG2	BTG anti-proliferation factor 2	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LTB4R	LTB4R	leukotriene B4 receptor	Plasma Membrane	G-protein coupled recepto	etalocib	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	APP	APP	amyloid beta precursor protein	Plasma Membrane	other	[illegible], florbetapir F18, [illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RUFY3	RUFY3	RUN and FYVE domain containing 3	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CIRBP-AS1	CIRBP-AS1	CIRBP antisense RNA 1	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SLC25A33	SLC25A33	solute carrier family 25 member 33	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	UBR5	UBR5	ubiquitin protein ligase E3 component n-recognin 5	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	HIPK3	HIPK3	homeodomain interacting protein kinase 3	Nucleus	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PIP4K2A	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase type 2 alpha	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CNNM4	CNNM4	cyclin and CBS domain divalent metal cation transport	Plasma Membrane	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ISCU	ISCU	iron-sulfur cluster assembly enzyme	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	AP2M1	AP2M1	adaptor related protein complex 2 mu 1 subunit	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RBM3	RBM3	RNA binding motif (RNP1, RRM) protein 3	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ACADS	ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPL17	RPL17	ribosomal protein L17	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SAE1	SAE1	SUMO1 activating enzyme subunit 1	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SUPT7L	SUPT7L	SPT7-like STAGA complex gamma subunit	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FOSB	FOSB	FosB proto-oncogene, AP-1 transcription factor subunit	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EZH2	EZH2	enhancer of zeste 2 polycomb repressive complex 2 sub	Nucleus	transcription regulator	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SIL1	SIL1	SIL1 nucleotide exchange factor	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RASGRF2	RASGRF2	Ras protein specific guanine nucleotide releasing factor	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MBD1	MBD1	methyl-CpG binding domain protein 1	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	UROD	UROD	uroporphyrinogen decarboxylase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CTB-[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TIFA	TIFA	TRAF interacting protein with forkhead associated domain	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	IL10RB	IL10RB	interleukin 10 receptor subunit beta	Plasma Membrane	transmembrane receptor		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRPS25	MRPS25	mitochondrial ribosomal protein S25	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PGRMC1	PGRMC1	progesterone receptor membrane component 1	Plasma Membrane	transmembrane receptor		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SNRPN	SNRPN	small nuclear ribonucleoprotein polypeptide N	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ARFGAP2	ARFGAP2	ADP ribosylation factor GTPase activating protein 2	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MLLT11	MLLT11	myeloid/lymphoid or mixed-lineage leukemia; translocat	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DPH7	DPH7	diphthamide biosynthesis 7	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF668	ZNF668	zinc finger protein 668	Cytoplasm	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RAB29	RAB29	RAB29, member RAS oncogene family	Plasma Membrane	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SGTA	SGTA	small glutamine rich tetratricopeptide repeat containin	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ILF3	ILF3	interleukin enhancer binding factor 3	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TNF	TNF	tumor necrosis factor	Extracellular Space	cytokine	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	OXNAD1	OXNAD1	oxidoreductase NAD binding domain containing 1	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZMYND8	ZMYND8	zinc finger MYND-type containing 8	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SARS	SARS	seryl-tRNA synthetase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PGLS	PGLS	6-phosphogluconolactonase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NADK	NADK	NAD kinase	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RNF19B	RNF19B	ring finger protein 19B	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GNB2	GNB2	G protein subunit beta 2	Plasma Membrane	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PIGH	PIGH	phosphatidylinositol glycan anchor biosynthesis class H	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MTRF1	MTRF1	mitochondrial translational release factor 1	Cytoplasm	translation regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CAT	CAT	catalase	Cytoplasm	enzyme	fomepizole	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TET3	TET3	tet methylcytosine dioxygenase 3	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	COG4	COG4	component of oligomeric golgi complex 4	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RARS2	RARS2	arginyl-tRNA synthetase 2, mitochondrial	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ARL4A	ARL4A	ADP ribosylation factor like GTPase 4A	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KIAA2013	KIAA2013	KIAA2013	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	INTS4	INTS4	integrator complex subunit 4	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NPIP[illegible]	NPIP[illegible] (includes others)	nuclear pore complex interacting protein family memb	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KDM1B	KDM1B	lysine demethylase 1B	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZBTB38	ZBTB38	zinc finger and BTB domain containing 38	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TRADD	TRADD	TNFRSF1A associated via death domain	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	S100PBP	S100PBP	S100P binding protein	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	IRF9	IRF9	interferon regulatory factor 9	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CTB-[illegible]	LOC[illegible]	uncharacterized LOC[illegible]	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KIAA[illegible]	USF3	upstream transcription factor family member 3	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RRAD	RRAD	RRAD, Ras related glycolysis inhibitor and calcium chan	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ANP32A	ANP32A	acidic nuclear phosphoprotein 32 family member A	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	XXbac-BPG299F13.17	HCG27	HLA complex group 27 (non-protein coding)	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TRIM14	TRIM14	tripartite motif containing 14	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GPR137B	GPR137B	G protein-coupled receptor 137B	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PCYT1A	PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PIK3C2A	PIK3C2A	phosphatidylinositol-4-phosphate 3-kinase catalytic sub	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ARGLU1	ARGLU1	arginine and glutamate rich 1	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CTD-[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MYSM1	MYSM1	Myb like, SWIRM and MPN domains 1	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MGAT5	MGAT5	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetylg	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TRIM28	TRIM28	tripartite motif containing 28	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SNX29	SNX29	sorting nexin 29	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RETSAT	RETSAT	retinol saturase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FAM49A	FAM49A	family with sequence similarity 49 member A	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PTGES2	PTGES2	prostaglandin E synthase 2	Cytoplasm	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MPZL3	MPZL3	myelin protein zero like 3	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PSME1	PSME1	proteasome activator subunit 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GLB1	GLB1	galactosidase beta 1	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DNAJC11	DNAJC11	DnaJ heat shock protein family (Hsp40) member C11	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SUMO3	SUMO3	small ubiquitin-like modifier 3	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CREBZF	CREBZF	CREB/ATF bZIP transcription factor	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NUP35	NUP35	nucleoporin 35	Nucleus	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NOL8	NOL8	nucleolar protein 8	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EEF2K	EEF2K	eukaryotic elongation factor 2 kinase	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KSR1	KSR1	kinase suppressor of ras 1	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF665	ZNF665	zinc finger protein 665	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TSC22D4	TSC22D4	TSC22 domain family member 4	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CNIH[illegible]	CNIH[illegible]	cornichon family AMPA receptor auxiliary protein 1	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CSNK1G2	CSNK1G2	casein kinase 1 gamma 2	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MAU2	MAU2	MAU2 sister chromatid cohesion factor	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FBXO32	FBXO32	F-box protein 32	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

[illegible]	SLC12A6	SLC12A6	solute carrier family 12 member 6	Plasma Membrane	transporter	
[illegible]	HDAC5	HDAC5	histone deacetylase 5	Nucleus	transcription regulator	[illegible], belinostat, [illegible]
[illegible]	CWC22	CWC22	CWC22 spliceosome associated protein homolog	Nucleus	other	
[illegible]	[illegible]	NPIPB4 (includes others)	nuclear pore complex interacting protein family memb	Nucleus	other	
[illegible]	[illegible]					
[illegible]	ZNF212	ZNF212	zinc finger protein 212	Nucleus	other	
[illegible]	STT3A	STT3A	STT3A, catalytic subunit of the oligosaccharyltransferas	Plasma Membrane	enzyme	
[illegible]	CASP1	CASP1	caspase 1	Cytoplasm	peptidase	caspase 1 inhibitor
[illegible]	SEC14L1	SEC14L1	SEC14 like lipid binding 1	Cytoplasm	transporter	
[illegible]	SH2B1	SH2B1	SH2B adaptor protein 1	Cytoplasm	other	
[illegible]	NDUFV1	NDUFV1	NADH:ubiquinone oxidoreductase core subunit V1	Cytoplasm	enzyme	
[illegible]	MT-ATP8	MT-ATP8	ATP synthase F0 subunit 8	Cytoplasm	enzyme	
[illegible]	MYO18B	MYO18B	myosin XVIIIB	Other	other	
[illegible]	C1orf228	C1orf228	chromosome 1 open reading frame 228	Other	other	
[illegible]	YWHAQ	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygena	Cytoplasm	other	
[illegible]	TPR	TPR	translocated promoter region, nuclear basket protein	Nucleus	transporter	
[illegible]	RBM26	RBM26	RNA binding motif protein 26	Other	other	
[illegible]	ANKRD12	ANKRD12	ankyrin repeat domain 12	Nucleus	transcription regulator	
[illegible]	PRKCQ	PRKCQ	protein kinase C theta	Cytoplasm	kinase	[illegible]
[illegible]	NDST2	NDST2	N-deacetylase and N-sulfotransferase 2	Cytoplasm	enzyme	
[illegible]	ZC3H18	ZC3H18	zinc finger CCCH-type containing 18	Nucleus	other	
[illegible]	CD247	CD247	CD247 molecule	Plasma Membrane	transmembrane receptor	blinatumomab
[illegible]	PIK3R1	PIK3R1	phosphoinositide-3-kinase regulatory subunit 1	Cytoplasm	kinase	
[illegible]	CDK2	CDK2	cyclin dependent kinase 2	Nucleus	kinase	[illegible]
[illegible]	ANP32B	ANP32B	acidic nuclear phosphoprotein 32 family member B	Nucleus	other	
[illegible]	SDHAP1	SDHAP1	succinate dehydrogenase complex flavoprotein subunit	Other	other	
[illegible]	HIGD1A	HIGD1A	HIG1 hypoxia inducible domain family member 1A	Cytoplasm	other	
[illegible]	HAUS6	HAUS6	HAUS augmin like complex subunit 6	Cytoplasm	other	
[illegible]	TMEM147	TMEM147	transmembrane protein 147	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	[illegible]					
[illegible]	ILVBL	ILVBL	ilvB acetolactate synthase like	Cytoplasm	enzyme	
[illegible]	MPPE1	MPPE1	metallophosphoesterase 1	Cytoplasm	enzyme	
[illegible]	POLR3A	POLR3A	RNA polymerase III subunit A	Nucleus	enzyme	
[illegible]	PQLC3	PQLC3	PQ loop repeat containing 3	Other	other	
[illegible]	FAM98B	FAM98B	family with sequence similarity 98 member B	Cytoplasm	other	
[illegible]	GNB1	GNB1	G protein subunit beta 1	Plasma Membrane	enzyme	
[illegible]	ABHD17A	ABHD17A	abhydrolase domain containing 17A	Other	other	
[illegible]	LEPRE1	P3H1	prolyl 3-hydroxylase 1	Nucleus	enzyme	
[illegible]	GLOD4	GLOD4	glyoxalase domain containing 4	Cytoplasm	enzyme	
[illegible]	UHRF1BP1L	UHRF1BP1L	UHRF1 binding protein 1 like	Other	other	
[illegible]	ANXA6	ANXA6	annexin A6	Plasma Membrane	ion channel	
[illegible]	GCC2	GCC2	GRIP and coiled-coil domain containing 2	Cytoplasm	other	
[illegible]	RRP7B	RRP7BP	ribosomal RNA processing 7 homolog B, pseudogene	Other	other	
[illegible]	GOPC	GOPC	golgi associated PDZ and coiled-coil motif containing	Cytoplasm	transporter	
[illegible]	TCIRG1	TCIRG1	T-cell immune regulator 1, ATPase H+ transporting V0	Plasma Membrane	enzyme	
[illegible]	REEP6	REEP6	receptor accessory protein 6	Extracellular Space	transporter	
[illegible]	MKRN1	MKRN1	makorin ring finger protein 1	Other	enzyme	
[illegible]	COPS5	COPS5	COP9 signalosome subunit 5	Nucleus	transcription regulator	
[illegible]	MTA1	MTA1	metastasis associated 1	Nucleus	transcription regulator	
[illegible]	CCNDBP1	CCNDBP1	cyclin D1 binding protein 1	Nucleus	enzyme	
[illegible]	HEATR1	HEATR1	HEAT repeat containing 1	Nucleus	other	
[illegible]	HCG4P5	HCG4P5	HLA complex group 4 pseudogene 5	Other	other	
[illegible]	TSC2	TSC2	tuberous sclerosis 2	Cytoplasm	other	
[illegible]	CHEK1	CHEK1	checkpoint kinase 1	Nucleus	kinase	[illegible]
[illegible]	RAD23B	RAD23B	RAD23 homolog B, nucleotide excision repair protein	Nucleus	other	
[illegible]	MTHFD2	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dep	Cytoplasm	enzyme	
[illegible]	ARAF	ARAF	A-Raf proto-oncogene, serine/threonine kinase	Cytoplasm	kinase	[illegible]
[illegible]	ZNF619	ZNF619	zinc finger protein 619	Nucleus	other	
[illegible]	TNFSF12	TNFSF12	tumor necrosis factor superfamily member 12	Extracellular Space	cytokine	
[illegible]	PAPSS1	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	Cytoplasm	enzyme	
[illegible]	LYAR	LYAR	Ly1 antibody reactive	Plasma Membrane	other	
[illegible]	SLC25A6	SLC25A6	solute carrier family 25 member 6	Cytoplasm	transporter	clodronic acid
[illegible]	ZBTB43	ZBTB43	zinc finger and BTB domain containing 43	Nucleus	other	
[illegible]	ANAPC13	ANAPC13	anaphase promoting complex subunit 13	Nucleus	other	
[illegible]	RBL2	RBL2	RB transcriptional corepressor like 2	Nucleus	other	
[illegible]	HELB	HELB	DNA helicase B	Nucleus	enzyme	[illegible]
[illegible]	ZNF767P	ZNF767P	zinc finger family member 767, pseudogene	Other	other	
[illegible]	BPGM	BPGM	bisphosphoglycerate mutase	Extracellular Space	phosphatase	
[illegible]	DENND4C	DENND4C	DENN domain containing 4C	Cytoplasm	other	
[illegible]	RRBP1	RRBP1	ribosome binding protein 1	Cytoplasm	other	
[illegible]	MBD2	MBD2	methyl-CpG binding domain protein 2	Nucleus	transcription regulator	
[illegible]	VPS9D1	VPS9D1	VPS9 domain containing 1	Other	transporter	
[illegible]	RANBP3	RANBP3	RAN binding protein 3	Nucleus	other	
[illegible]	ATP6V0E1	ATP6V0E1	ATPase H+ transporting V0 subunit e1	Cytoplasm	transporter	
[illegible]	PTBP2	PTBP2	polypyrimidine tract binding protein 2	Nucleus	other	
[illegible]	FTSJ3	FTSJ3	FtsJ homolog 3	Nucleus	enzyme	
[illegible]	STK35	STK35	serine/threonine kinase 35	Cytoplasm	kinase	
[illegible]	MIEF1	MIEF1	mitochondrial elongation factor 1	Cytoplasm	other	
[illegible]	CCZ1	CCZ1/CCZ1B	CCZ1 homolog B, vacuolar protein trafficking and bioge	Cytoplasm	other	
[illegible]	MAGT1	MAGT1	magnesium transporter 1	Plasma Membrane	enzyme	
[illegible]	[illegible]					
[illegible]	DENND4A	DENND4A	DENN domain containing 4A	Nucleus	other	
[illegible]	TMED8	TMED8	transmembrane p24 trafficking protein family member	Other	other	
[illegible]	MTMR4	MTMR4	myotubularin related protein 4	Cytoplasm	phosphatase	
[illegible]	SPTLC2	SPTLC2	serine palmitoyltransferase long chain base subunit 2	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	ZNF687	ZNF687	zinc finger protein 687	Nucleus	other	
[illegible]	PHF20	PHF20	PHD finger protein 20	Nucleus	other	
[illegible]	DEC1					
[illegible]	[illegible]	[illegible]	WAS protein family homolog 3-like	Other	other	
[illegible]	ZNF286A	ZNF286A	zinc finger protein 286A	Nucleus	other	
[illegible]	[illegible]					
[illegible]	HPS6	HPS6	HPS6, biogenesis of lysosomal organelles complex 2 sul	Cytoplasm	other	
[illegible]	ING1	ING1	inhibitor of growth family member 1	Nucleus	transcription regulator	
[illegible]	SIRT3	SIRT3	sirtuin 3	Cytoplasm	enzyme	
[illegible]	PIBF1	PIBF1	progesterone immunomodulatory binding factor 1	Nucleus	other	
[illegible]	[illegible]	PSMA3-AS1	PSMA3 antisense RNA 1	Other	other	
[illegible]	ZNF833P	ZNF833P	zinc finger protein 833, pseudogene	Other	other	
[illegible]	ADO	ADO	2-aminoethanethiol dioxygenase	Cytoplasm	enzyme	
[illegible]	LYPD3	LYPD3	LY6/PLAUR domain containing 3	Plasma Membrane	other	
[illegible]	ANKRD13A	ANKRD13A	ankyrin repeat domain 13A	Plasma Membrane	other	
[illegible]	TMEM128	TMEM128	transmembrane protein 128	Other	other	
[illegible]	NRIP2	NRIP2	nuclear receptor interacting protein 2	Nucleus	transcription regulator	
[illegible]	DGKZ	DGKZ	diacylglycerol kinase zeta	Cytoplasm	kinase	
[illegible]	BCL2L13	BCL2L13	BCL2 like 13	Cytoplasm	other	
[illegible]	DIRC2	DIRC2	disrupted in renal carcinoma 2	Other	other	
[illegible]	FCHSD2	FCHSD2	FCH and double SH3 domains 2	Other	other	
[illegible]	SESN1	SESN1	sestrin 1	Nucleus	other	
[illegible]	RAB8B	RAB8B	RAB8B, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	[illegible]	[illegible]	[illegible] intracellular binding protein	Nucleus	other	
[illegible]	ULBP2	ULBP2	UL16 binding protein 2	Plasma Membrane	transmembrane receptor	
[illegible]	TAF2	TAF2	TATA-box binding protein associated factor 2	Nucleus	transcription regulator	
[illegible]	[illegible]					
[illegible]	NAT9	NAT9	N-acetyltransferase 9 (putative)	Other	other	
[illegible]	PIK3C2B	PIK3C2B	phosphatidylinositol-4-phosphate 3-kinase catalytic sub	Cytoplasm	kinase	
[illegible]	PFKL	PFKL	phosphofructokinase, liver type	Cytoplasm	kinase	
[illegible]	HSPA13	HSPA13	heat shock protein family A (Hsp70) member 13	Cytoplasm	other	
[illegible]	SEC16A	SEC16A	SEC16 homolog A, endoplasmic reticulum export factor	Cytoplasm	phosphatase	
[illegible]	BAG1	BAG1	BCL2 associated athanogene 1	Cytoplasm	other	
[illegible]	TSTD2	TSTD2	thiosulfate sulfurtransferase like domain containing 2	Other	other	
[illegible]	UBALD2	UBALD2	UBA like domain containing 2	Other	other	
[illegible]	PCNA	PCNA	proliferating cell nuclear antigen	Nucleus	enzyme	
[illegible]	[illegible]					
[illegible]	BTBD11	BTBD11	BTB domain containing 11	Other	transcription regulator	
[illegible]	[illegible]					
[illegible]	CCDC108	CFAP65	cilia and flagella associated protein 65	Other	other	
[illegible]	SLC25A5	SLC25A5	solute carrier family 25 member 5	Cytoplasm	transporter	clodronic acid
[illegible]	DOT1L	DOT1L	DOT1 like histone lysine methyltransferase	Nucleus	phosphatase	EPZ-5676
[illegible]	ISYNA1	ISYNA1	inositol-3-phosphate synthase 1	Cytoplasm	enzyme	
[illegible]	FNTA	FNTA	farnesyltransferase, CAAX box, alpha	Cytoplasm	enzyme	lonafarnib
[illegible]	MTND2P28	MTND2P28	mitochondrially encoded NADH:ubiquinone oxidoreduct	Other	other	
[illegible]	IMPAD1	IMPAD1	inositol monophosphatase domain containing 1	Cytoplasm	enzyme	
[illegible]	PLA2G6	PLA2G6	phospholipase A2 group VI	Cytoplasm	enzyme	quinacrine
[illegible]	ATG4D	ATG4D	autophagy related 4D cysteine peptidase	Cytoplasm	peptidase	
[illegible]	RAB6C	RAB6C	RAB6C, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	FAM110A	FAM110A	family with sequence similarity 110 member A	Other	other	
[illegible]	DOCK9	DOCK9	dedicator of cytokinesis 9	Cytoplasm	other	
[illegible]	SCML4	SCML4	sex comb on midleg-like 4 (Drosophila)	Nucleus	other	
[illegible]	AGAP3	AGAP3	ArfGAP with GTPase domain, ankyrin repeat and PH do	Nucleus	transcription regulator	
[illegible]	GNG2	GNG2	G protein subunit gamma 2	Plasma Membrane	enzyme	
[illegible]	PDE9A	PDE9A	phosphodiesterase 9A	Cytoplasm	enzyme	
[illegible]	CCNY	CCNY	cyclin Y	Nucleus	other	
[illegible]	IDH3B	IDH3B	isocitrate dehydrogenase 3 (NAD(+)) beta	Cytoplasm	enzyme	
[illegible]	PDE4DIP	PDE4DIP	phosphodiesterase 4D interacting protein	Cytoplasm	enzyme	
[illegible]	MGRN1	MGRN1	mahogunin ring finger 1	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	SGTB	SGTB	small glutamine rich tetratricopeptide repeat containin	Other	other	
[illegible]	ZBED5	ZBED5	zinc finger BED-type containing 5	Nucleus	other	
[illegible]	[illegible]					
[illegible]	UCP2	UCP2	uncoupling protein 2	Cytoplasm	transporter	
[illegible]	TNRC6A	TNRC6A	trinucleotide repeat containing 6A	Nucleus	other	
[illegible]	FUT4	FUT4	fucosyltransferase 4	Cytoplasm	enzyme	
[illegible]	KDM4A	KDM4A	lysine demethylase 4A	Nucleus	transcription regulator	
[illegible]	NDFIP1	NDFIP1	Nedd4 family interacting protein 1	Cytoplasm	other	
[illegible]	LRPPRC	LRPPRC	leucine rich pentatricopeptide repeat containing	Cytoplasm	other	
[illegible]	ZBTB39	ZBTB39	zinc finger and BTB domain containing 39	Nucleus	other	
[illegible]	RNF103	RNF103	ring finger protein 103	Cytoplasm	enzyme	
[illegible]	ANAPC5	ANAPC5	anaphase promoting complex subunit 5	Nucleus	other	
[illegible]	MDC1	MDC1	mediator of DNA damage checkpoint 1	Nucleus	other	
[illegible]	[illegible]	[illegible]	SPT2 domain containing 2	Cytoplasm	other	
[illegible]	CLN8	CLN8	ceroid-lipofuscinosis, neuronal 8, late infantile, variant	Cytoplasm	other	
[illegible]	VAMP8	VAMP8	vesicle associated membrane protein 8	Plasma Membrane	transporter	
[illegible]	ZBTB11	ZBTB11	zinc finger and BTB domain containing 11	Nucleus	other	
[illegible]	ISG20	ISG20	interferon stimulated exonuclease gene 20	Nucleus	enzyme	
[illegible]	LRRC40	LRRC40	leucine rich repeat containing 40	Nucleus	other	
[illegible]	OS9	OS9	OS9, endoplasmic reticulum lectin	Nucleus	other	
[illegible]	XBP1	XBP1	X-box binding protein 1	Nucleus	transcription regulator	
[illegible]	SNORA72	RPL30	ribosomal protein L30	Cytoplasm	other	
[illegible]	NEMF	NEMF	nuclear export mediator factor	Nucleus	other	
[illegible]	PRKCA	PRKCA	protein kinase C alpha	Cytoplasm	kinase	[illegible]
[illegible]	[illegible]					
[illegible]	POU2F2	POU2F2	POU class 2 homeobox 2	Nucleus	transcription regulator	
[illegible]	DAD1	DAD1	defender against cell death 1	Cytoplasm	other	
[illegible]	ADI1	ADI1	acireductone dioxygenase 1	Nucleus	enzyme	
[illegible]	CHAF1A	CHAF1A	chromatin assembly factor 1 subunit A	Nucleus	other	
[illegible]	RC3H1	RC3H1	ring finger and CCCH-type domains 1	Cytoplasm	enzyme	
[illegible]	PITPNM2	PITPNM2	phosphatidylinositol transfer protein membrane associat	Cytoplasm	enzyme	
[illegible]	ARHGAP9	ARHGAP9	Rho GTPase activating protein 9	Cytoplasm	other	
[illegible]	TELO2	TELO2	telomere maintenance 2	Cytoplasm	other	
[illegible]	C17orf59	BORCS6	BLOC-1 related complex subunit 6	Cytoplasm	other	
[illegible]	GNL3	GNL3	G protein nucleolar 3	Nucleus	other	
[illegible]	ZGPAT	ZGPAT	zinc finger CCCH-type and G-patch domain containing	Nucleus	transcription regulator	
[illegible]	GOLGA2	GOLGA2	golgin A2	Cytoplasm	other	
[illegible]	TMEM123	TMEM123	transmembrane protein 123	Plasma Membrane	other	
[illegible]	OTULIN	OTULIN	OTU deubiquitinase with linear linkage specificity	Cytoplasm	peptidase	
[illegible]	[illegible]					
[illegible]	MSH3	MSH3	mutS homolog 3	Nucleus	enzyme	
[illegible]	RPRD1A	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	Extracellular Space	other	
[illegible]	FBXL5	FBXL5	F-box and leucine rich repeat protein 5	Cytoplasm	enzyme	
[illegible]	XPO6	XPO6	exportin 6	Cytoplasm	transporter	
[illegible]	AUP1	AUP1	ancient ubiquitous protein 1	Cytoplasm	other	
[illegible]	NA					
[illegible]	SLC6A6	SLC6A6	solute carrier family 6 member 6	Plasma Membrane	transporter	
[illegible]	GPI	GPI	glucose-6-phosphate isomerase	Extracellular Space	enzyme	
[illegible]	NUCB1	NUCB1	nucleobindin 1	Cytoplasm	other	
[illegible]	ACAP3	ACAP3	ArfGAP with coiled-coil, ankyrin repeat and PH domain	Nucleus	transcription regulator	
[illegible]	MED14	MED14	mediator complex subunit 14	Nucleus	transcription regulator	
[illegible]	FTSJ1	FTSJ1	FtsJ RNA methyltransferase homolog 1 (E. coli)	Cytoplasm	enzyme	
[illegible]	UBR4	UBR4	ubiquitin protein ligase E3 component n-recognin 4	Nucleus	enzyme	
[illegible]	KCNAB2	KCNAB2	potassium voltage-gated channel subfamily A regulator	Plasma Membrane	ion channel	
[illegible]	OCIAD2	OCIAD2	OCIA domain containing 2	Cytoplasm	other	
[illegible]	PURB					
[illegible]	UBB	UBB	ubiquitin B	Cytoplasm	enzyme	
[illegible]	G6PD	G6PD	glucose-6-phosphate dehydrogenase	Cytoplasm	enzyme	
[illegible]	TAF1	TAF1	TATA-box binding protein associated factor 1	Nucleus	transcription regulator	
[illegible]	SLC35F6	SLC35F6	solute carrier family 35 member F6	Cytoplasm	other	
[illegible]	TRMT61B	TRMT61B	tRNA methyltransferase 61B	Cytoplasm	enzyme	
[illegible]	[illegible]	TOX2	TOX high mobility group box family member 2	Nucleus	transcription regulator	
[illegible]	SMARCD3	SMARCD3	SWI/SNF related, matrix associated, actin dependent re	Nucleus	transcription regulator	
[illegible]	HK1	HK1	hexokinase 1	Cytoplasm	kinase	
[illegible]	LAMTOR2	LAMTOR2	late endosomal/lysosomal adaptor, MAPK and MTOR a	Cytoplasm	other	
[illegible]	LIG3	LIG3	DNA ligase 3	Nucleus	enzyme	
[illegible]	WIPF2	WIPF2	WAS/WASL interacting protein family member 2	Cytoplasm	other	
[illegible]	NUTF2	NUTF2	nuclear transport factor 2	Nucleus	transporter	
[illegible]	RCOR3	RCOR3	REST corepressor 3	Nucleus	other	
[illegible]	C17orf75	C17orf75	chromosome 17 open reading frame 75	Extracellular Space	other	
[illegible]	PPAPDC1B	PLPP5	phospholipid phosphatase 5	Other	phosphatase	
[illegible]	ACTL6A	ACTL6A	actin like 6A	Nucleus	other	
[illegible]	GID8	GID8	GID complex subunit 8 homolog	Nucleus	other	
[illegible]	CTDNEP1	CTDNEP1	CTD nuclear envelope phosphatase 1	Extracellular Space	phosphatase	
[illegible]	SNHG11	SNHG11	small nucleolar RNA host gene 11	Other	other	
[illegible]	CCDC132	VPS50	VPS50, EARP/GARPII complex subunit	Cytoplasm	other	
[illegible]	KPNA5	KPNA5	karyopherin subunit alpha 5	Cytoplasm	other	

[illegible]	IER3IP1	IER3IP1	immediate early response 3 interacting protein 1	Cytoplasm	other	-0.90	-0.82	-0.50	0.00	0.00	0.00	0	3	5	100	97	95
[illegible]	ACTR5	ACTR5	ARP5 actin-related protein 5 homolog	Nucleus	other	1.08	1.13	0.75	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	WDR1	WDR1	WD repeat domain 1	Extracellular Space	other	-0.66	-0.82	0.06	0.00	0.00	0.11	0	11	68	100	89	32
[illegible]	NSUN5	NSUN5	NOP2/Sun RNA methyltransferase family member 5	Nucleus	other	0.95	0.74	0.11	0.00	0.00	0.16	100	100	70	0	0	30
[illegible]	ACIN1	ACIN1	apoptotic chromatin condensation inducer 1	Nucleus	enzyme	0.81	0.98	0.55	0.00	0.00	0.00	100	100	97	0	0	3
[illegible]	NA					1.33	1.64		0.00	0.00		97	97		3	3	
[illegible]	FUT11	FUT11	fucosyltransferase 11	Cytoplasm	enzyme	-0.86	-0.29	-0.05	0.00	0.00	0.10	0	19	41	100	81	59
[illegible]	[illegible]					0.88	0.81	0.28	0.00	0.00	0.01	94	94	[illegible]	6	6	[illegible]
[illegible]	MPG	MPG	N-methylpurine DNA glycosylase	Nucleus	enzyme	-0.95	-1.09	-0.48	0.00	0.00	0.00	0	3	16	100	97	84
[illegible]	CD4	CD4	CD4 molecule	Plasma Membrane	transmembrane receptor	-0.92	-0.83	-0.89	0.00	0.00	0.00	3	0	0	97	100	100
[illegible]	BMS1	BMS1	BMS1, ribosome biogenesis factor	Nucleus	other	0.79	0.65	0.47	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	DPM3	DPM3	dolichyl-phosphate mannosyltransferase subunit 3, regu	Cytoplasm	enzyme	1.00	0.66	-0.37	0.00	0.00	0.00	100	94	16	0	6	84
[illegible]	TRGV10	TRGV10	T cell receptor gamma variable 10 (non-functional)	Other	other	-1.57	1.21	-0.94	0.00	0.00	0.00	6	97	3	94	3	97
[illegible]	[illegible]	[illegible]	[illegible]	Cytoplasm	other	0.86	0.86	0.40	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	UBE4B	UBE4B	ubiquitination factor E4B	Cytoplasm	enzyme	0.89	0.83	0.38	0.00	0.00	0.00	100	100	95	0	0	5
[illegible]	RPN2	RPN2	ribophorin II	Cytoplasm	enzyme	-0.72	-0.88	-0.17	0.00	0.00	0.00	0	0	30	100	100	70
[illegible]	CDK2AP2	CDK2AP2	cyclin dependent kinase 2 associated protein 2	Nucleus	other	1.04	1.48	0.73	0.00	0.00	0.00	100	100	97	0	0	3
[illegible]	SMARCC2	SMARCC2	SWI/SNF related, matrix associated, actin dependent re	Nucleus	transcription regulator	0.85	0.74	0.58	0.00	0.00	0.00	100	94	97	0	6	3
[illegible]	SDHAF1	SDHAF1	succinate dehydrogenase complex assembly factor 1	Cytoplasm	other	-1.16	-0.88	-0.04	0.00	0.00	0.09	0	3	41	100	97	59
[illegible]	SURF6	SURF6	surfeit 6	Nucleus	other	0.82	0.75	0.45	0.00	0.00	0.00	100	100	95	0	0	5
[illegible]	PTPN6	PTPN6	protein tyrosine phosphatase, non-receptor type 6	Cytoplasm	phosphatase	-0.66	-1.09	0.38	0.00	0.00	0.00	3	0	16	97	100	14

[illegible]	TCP1	TCP1	t-complex 1	Cytoplasm	other	
[illegible]	TMEM167B	TMEM167B	transmembrane protein 167B	Other	other	
[illegible]	CTSF	CTSF	cathepsin F	Cytoplasm	peptidase	
[illegible]	ZNF287	ZNF287	zinc finger protein 287	Nucleus	other	
[illegible]	HDGF	HDGF	hepatoma derived growth factor	Extracellular Space	growth factor	
[illegible]	SNX12	SNX12	sorting nexin 12	Cytoplasm	transporter	
[illegible]	RANGAP1					
[illegible]	[illegible]					
[illegible]	SLC39A8	SLC39A8	solute carrier family 39 member 8	Plasma Membrane	transporter	
[illegible]	SLC12A7	SLC12A7	solute carrier family 12 member 7	Plasma Membrane	transporter	
[illegible]	MLLT10	MLLT10	myeloid/lymphoid or mixed-lineage leukemia; translocat	Nucleus	transcription regulator	
[illegible]	UNKL	UNKL	unkempt family like zinc finger	Cytoplasm	enzyme	
[illegible]	CLK3	CLK3	CDC like kinase 3	Nucleus	kinase	
[illegible]	USP11	USP11	ubiquitin specific peptidase 11	Nucleus	peptidase	
[illegible]	[illegible]					
[illegible]	CC2D1B	CC2D1B	coiled-coil and C2 domain containing 1B	Nucleus	transcription regulator	
[illegible]	ROMO1	ROMO1	reactive oxygen species modulator 1	Cytoplasm	other	
[illegible]	TSC22D3	TSC22D3	TSC22 domain family member 3	Extracellular Space	other	
[illegible]	MED15	MED15	mediator complex subunit 15	Nucleus	transcription regulator	
[illegible]	RCC2	RCC2	regulator of chromosome condensation 2	Nucleus	other	
[illegible]	VPRBP	DCAF1	DDB1 and CUL4 associated factor 1	Nucleus	kinase	
[illegible]	LRRC59	LRRC59	leucine rich repeat containing 59	Cytoplasm	other	
[illegible]	AP2A2	AP2A2	adaptor related protein complex 2 alpha 2 subunit	Cytoplasm	transporter	
[illegible]	ACAA2	ACAA2	acetyl-CoA acyltransferase 2	Cytoplasm	enzyme	
[illegible]	PHLPP1	PHLPP1	PH domain and leucine rich repeat protein phosphatase	Cytoplasm	enzyme	
[illegible]	PIM1	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	Cytoplasm	kinase	[illegible], AZD-1208, LGH
[illegible]	UBE2E2	UBE2E2	ubiquitin conjugating enzyme E2 E2	Cytoplasm	enzyme	
[illegible]	SEL1L	SEL1L	SEL1L ERAD E3 ligase adaptor subunit	Cytoplasm	other	
[illegible]	KPNA3	KPNA3	karyopherin subunit alpha 3	Nucleus	transporter	
[illegible]	LUZP1	LUZP1	leucine zipper protein 1	Nucleus	other	
[illegible]	SREBF1	SREBF1	sterol regulatory element binding transcription factor 1	Nucleus	transcription regulator	
[illegible]	DMXL1	DMXL1	Dmx like 1	Extracellular Space	other	
[illegible]	ZNF682	ZNF682	zinc finger protein 682	Other	other	
[illegible]	STK19	STK19	serine/threonine kinase 19	Nucleus	kinase	
[illegible]	C7orf73	C7orf73	chromosome 7 open reading frame 73	Other	other	
[illegible]	[illegible]					
[illegible]	FAM3C	FAM3C	family with sequence similarity 3 member C	Extracellular Space	cytokine	
[illegible]	TCTA	TCTA	T-cell leukemia translocation altered	Other	other	
[illegible]	GALNT10	GALNT10	polypeptide N-acetylgalactosaminyltransferase 10	Cytoplasm	enzyme	
[illegible]	ZMYM3	ZMYM3	zinc finger MYM-type containing 3	Nucleus	other	
[illegible]	RASSF2	RASSF2	Ras association domain family member 2	Nucleus	kinase	
[illegible]	PHAX	PHAX	phosphorylated adaptor for RNA export	Cytoplasm	other	
[illegible]	SPATA2L	SPATA2L	spermatogenesis associated 2 like	Other	other	
[illegible]	TMEM62	TMEM62	transmembrane protein 62	Other	enzyme	
[illegible]	POMP	POMP	proteasome maturation protein	Nucleus	other	
[illegible]	XYLT2	XYLT2	xylosyltransferase 2	Cytoplasm	enzyme	
[illegible]	FAR1	FAR1	fatty acyl-CoA reductase 1	Cytoplasm	enzyme	
[illegible]	AFF1	AFF1	AF4/FMR2 family member 1	Nucleus	transcription regulator	
[illegible]	RPP30	RPP30	ribonuclease P/MRP subunit p30	Nucleus	enzyme	
[illegible]	SHISA5	SHISA5	shisa family member 5	Nucleus	other	
[illegible]	POLE4	POLE4	DNA polymerase epsilon 4, accessory subunit	Nucleus	enzyme	[illegible]
[illegible]	MARK3	MARK3	microtubule affinity regulating kinase 3	Cytoplasm	kinase	[illegible]
[illegible]	CD58	CD58	CD58 molecule	Plasma Membrane	other	
[illegible]	FLOT2	FLOT2	flotillin 2	Plasma Membrane	other	
[illegible]	RAB6A	RAB6A	RAB6A, member RAS oncogene family	Plasma Membrane	enzyme	
[illegible]	GPAA1	GPAA1	glycosylphosphatidylinositol anchor attachment 1	Cytoplasm	enzyme	
[illegible]	SND1	SND1	staphylococcal nuclease and tudor domain containing 1	Nucleus	enzyme	
[illegible]	PIAS2	PIAS2	protein inhibitor of activated STAT 2	Nucleus	transcription regulator	
[illegible]	NLRP6	NLRP6	NLR family pyrin domain containing 6	Plasma Membrane	G-protein coupled receptor	
[illegible]	AQR	AQR	aquarius intron-binding spliceosomal factor	Nucleus	other	
[illegible]	ACTR3	ACTR3	ARP3 actin related protein 3 homolog	Plasma Membrane	other	
[illegible]	MED4	MED4	mediator complex subunit 4	Nucleus	transcription regulator	
[illegible]	CD5	CD5	CD5 molecule	Plasma Membrane	transmembrane receptor	
[illegible]	MAPRE1	MAPRE1	microtubule associated protein RP/EB family member 1	Cytoplasm	other	
[illegible]	C7orf43					
[illegible]	ZC3H4	ZC3H4	zinc finger CCCH-type containing 4	Nucleus	other	
[illegible]	SLC38A2	SLC38A2	solute carrier family 38 member 2	Plasma Membrane	transporter	
[illegible]	FCHSD1	FCHSD1	FCH and double SH3 domains 1	Other	other	
[illegible]	CMTM6	CMTM6	CKLF like MARVEL transmembrane domain containing 6	Extracellular Space	cytokine	
[illegible]	[illegible]					
[illegible]	DNAJB14	DNAJB14	DnaJ heat shock protein family (Hsp40) member B14	Other	enzyme	
[illegible]	DDX5					
[illegible]	NUBP1	NUBP1	nucleotide binding protein 1	Cytoplasm	other	
[illegible]	AQP3	AQP3	aquaporin 3 (Gill blood group)	Plasma Membrane	transporter	
[illegible]	ZNF326	ZNF326	zinc finger protein 326	Cytoplasm	other	
[illegible]	SLC4A1AP	SLC4A1AP	solute carrier family 4 member 1 adaptor protein	Nucleus	transporter	
[illegible]	ZNF775	ZNF775	zinc finger protein 775	Other	other	
[illegible]	TRAF6	TRAF6	TNF receptor associated factor 6	Cytoplasm	enzyme	
[illegible]	ZNF143	ZNF143	zinc finger protein 143	Nucleus	transcription regulator	
[illegible]	DAPP1	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositi	Cytoplasm	other	
[illegible]	XRCC3	XRCC3	X-ray repair cross complementing 3	Nucleus	enzyme	
[illegible]	UBC	UBC	ubiquitin C	Cytoplasm	enzyme	
[illegible]	UNC119	UNC119	unc-119 lipid binding chaperone	Cytoplasm	other	
[illegible]	YWHAB	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygena	Cytoplasm	transcription regulator	
[illegible]	AP1G1	AP1G1	adaptor related protein complex 1 gamma 1 subunit	Cytoplasm	transporter	
[illegible]	RNF44	RNF44	ring finger protein 44	Other	other	
[illegible]	IFT52	IFT52	intraflagellar transport 52	Cytoplasm	other	
[illegible]	CD69	CD69	CD69 molecule	Plasma Membrane	transmembrane receptor	
[illegible]	WAC-AS1	WAC-AS1	WAC antisense RNA 1 (head to head)	Other	other	
[illegible]	ARID4A	ARID4A	AT-rich interaction domain 4A	Nucleus	transcription regulator	
[illegible]	SEC24D	SEC24D	SEC24 homolog D, COPII coat complex component	Cytoplasm	transporter	
[illegible]	ABCA1	ABCA1	ATP binding cassette subfamily A member 1	Plasma Membrane	transporter	probucol
[illegible]	FNDC3A	FNDC3A	fibronectin type III domain containing 3A	Cytoplasm	other	
[illegible]	NOP58	NOP58	NOP58 ribonucleoprotein	Nucleus	enzyme	
[illegible]	SECISBP2L	SECISBP2L	SECIS binding protein 2 like	Other	other	
[illegible]	TLE2	TLE2	transducin like enhancer of split 2	Nucleus	transcription regulator	
[illegible]	FUNDC2	FUNDC2	FUN14 domain containing 2	Cytoplasm	other	
[illegible]	[illegible]	INAFM2	InaF motif containing 2	Other	other	
[illegible]	THBS3	THBS3	thrombospondin 3	Extracellular Space	other	
[illegible]	HSH2D	HSH2D	hematopoietic SH2 domain containing	Cytoplasm	other	
[illegible]	M6PR	M6PR	mannose-6-phosphate receptor, cation dependent	Cytoplasm	transporter	alglucosidase alfa
[illegible]	UVRAG	UVRAG	UV radiation resistance associated	Nucleus	other	
[illegible]	MED17	MED17	mediator complex subunit 17	Nucleus	transcription regulator	
[illegible]	WAS	WAS	Wiskott-Aldrich syndrome	Cytoplasm	other	
[illegible]	THAP9-AS1	THAP9-AS1	THAP9 antisense RNA 1	Other	other	
[illegible]	GNPAT	GNPAT	glyceronephosphate O-acyltransferase	Cytoplasm	enzyme	
[illegible]	SFXN1	SFXN1	sideroflexin 1	Cytoplasm	transporter	
[illegible]	BSDC1	BSDC1	BSD domain containing 1	Other	other	
[illegible]	[illegible]					
[illegible]	MMGT1	MMGT1	membrane magnesium transporter 1	Cytoplasm	transporter	
[illegible]	PPP1R12C	PPP1R12C	protein phosphatase 1 regulatory subunit 12C	Cytoplasm	phosphatase	
[illegible]	SQSTM1	SQSTM1	sequestosome 1	Cytoplasm	transcription regulator	
[illegible]	PRR13	PRR13	proline rich 13	Nucleus	other	
[illegible]	PSMD5-AS1	PSMD5-AS1	PSMD5 antisense RNA 1 (head to head)	Other	other	
[illegible]	ACAP1	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH domains	Plasma Membrane	other	
[illegible]	DYNLL1	DYNLL1	dynein light chain LC8-type 1	Cytoplasm	other	
[illegible]	PSMD5	PSMD5	proteasome 26S subunit, non-ATPase 5	Other	other	
[illegible]	HARS	HARS	histidyl-tRNA synthetase	Cytoplasm	enzyme	
[illegible]	PYGO2	PYGO2	pygopus family PHD finger 2	Nucleus	other	
[illegible]	AKR7A2	AKR7A2	aldo-keto reductase family 7 member A2	Cytoplasm	enzyme	
[illegible]	MORC3	MORC3	MORC family CW-type zinc finger 3	Nucleus	other	
[illegible]	[illegible]	[illegible]	uncharacterized [illegible]	Other	other	
[illegible]	INO80B	INO80B	INO80 complex subunit B	Nucleus	other	
[illegible]	CMTR2	CMTR2	cap methyltransferase 2	Other	enzyme	
[illegible]	SC5D	SC5D	sterol-C5-desaturase	Cytoplasm	enzyme	
[illegible]	PGM1	PGM1	phosphoglucomutase 1	Cytoplasm	enzyme	
[illegible]	RALGAPA2	RALGAPA2	Ral GTPase activating protein catalytic alpha subunit 2	Cytoplasm	other	
[illegible]	RBM19	RBM19	RNA binding motif protein 19	Nucleus	other	
[illegible]	NA					
[illegible]	NCOA3	NCOA3	nuclear receptor coactivator 3	Nucleus	transcription regulator	
[illegible]	LAS1L	LAS1L	LAS1 like, ribosome biogenesis factor	Nucleus	other	
[illegible]	TMEM66	TMEM66	transmembrane protein 66	Cytoplasm	other	
[illegible]	DHX29	DHX29	DExH-box helicase 29	Cytoplasm	enzyme	
[illegible]	UBR3	UBR3	ubiquitin protein ligase E3 component n-recognin 3 (pu	Other	enzyme	
[illegible]	CES2	CES2	carboxylesterase 2	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	NAGPA	NAGPA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylg	Cytoplasm	enzyme	
[illegible]	NAA15	NAA15	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	Cytoplasm	other	
[illegible]	UBA6	UBA6	ubiquitin like modifier activating enzyme 6	Cytoplasm	enzyme	
[illegible]	ZNF24	ZNF24	zinc finger protein 24	Nucleus	transcription regulator	
[illegible]	IKZF2	IKZF2	IKAROS family zinc finger 2	Nucleus	transcription regulator	
[illegible]	TCF25	TCF25	transcription factor 25	Nucleus	transcription regulator	
[illegible]	LRPAP1	LRPAP1	LDL receptor related protein associated protein 1	Plasma Membrane	other	
[illegible]	ORC3	ORC3	origin recognition complex subunit 3	Nucleus	other	
[illegible]	ID3	ID3	inhibitor of DNA binding 3, HLH protein	Nucleus	transcription regulator	
[illegible]	PRKRIP1	PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	Nucleus	other	
[illegible]	VIMP	SELENOS	selenoprotein S	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	TNRC6C-AS1	TNRC6C-AS1	TNRC6C antisense RNA 1	Other	other	
[illegible]	IER2	IER2	immediate early response 2	Cytoplasm	other	
[illegible]	DEF8	DEF8	differentially expressed in FDCP 8 homolog	Other	other	
[illegible]	RASA4CP	RASA4CP	RAS p21 protein activator 4C, pseudogene	Other	other	
[illegible]	RABL6	RABL6	RAB, member RAS oncogene family like 6	Cytoplasm	other	
[illegible]	TRPM7	TRPM7	transient receptor potential cation channel subfamily M	Plasma Membrane	kinase	
[illegible]	CNOT6	CNOT6	CCR4-NOT transcription complex subunit 6	Nucleus	enzyme	
[illegible]	CDC37L1	CDC37L1	cell division cycle 37 like 1	Cytoplasm	other	
[illegible]	MAF1	MAF1	MAF1 homolog, negative regulator of RNA polymerase	Nucleus	other	
[illegible]	DDX18	DDX18	DEAD-box helicase 18	Nucleus	enzyme	
[illegible]	BAX	BAX	BCL2 associated X, apoptosis regulator	Cytoplasm	transporter	
[illegible]	HSBP1L1	HSBP1L1	heat shock factor binding protein 1 like 1	Other	other	
[illegible]	PRDM4	PRDM4	PR/SET domain 4	Nucleus	transcription regulator	
[illegible]	CSNK1D	CSNK1D	casein kinase 1 delta	Cytoplasm	kinase	
[illegible]	AGFG1	AGFG1	ArfGAP with FG repeats 1	Nucleus	other	
[illegible]	CEP135	CEP135	centrosomal protein 135	Cytoplasm	other	
[illegible]	LY9	LY9	lymphocyte antigen 9	Plasma Membrane	other	
[illegible]	RAB7A	RAB7A	RAB7A, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	TCEAL8	TCEAL8	transcription elongation factor A like 8	Other	other	
[illegible]	TMEM14C	TMEM14C	transmembrane protein 14C	Plasma Membrane	other	
[illegible]	OSBPL2	OSBPL2	oxysterol binding protein like 2	Cytoplasm	transporter	
[illegible]	TSG101	TSG101	tumor susceptibility 101	Cytoplasm	transcription regulator	
[illegible]	TXNDC12	TXNDC12	thioredoxin domain containing 12	Cytoplasm	enzyme	
[illegible]	MAN1A1	MAN1A1	mannosidase alpha class 1A member 1	Cytoplasm	enzyme	
[illegible]	PDS5A	PDS5A	PDS5 cohesin associated factor A	Nucleus	other	
[illegible]	GDPD5	GDPD5	glycerophosphodiester phosphodiesterase domain contai	Plasma Membrane	enzyme	
[illegible]	PTMA					
[illegible]	CNTRL	CNTRL	centriolin	Nucleus	transcription regulator	
[illegible]	SNHG14	SNHG14		Other	other	
[illegible]	VPS13B	VPS13B	vacuolar protein sorting 13 homolog B	Nucleus	transporter	
[illegible]	SAMD9	SAMD9	sterile alpha motif domain containing 9	Cytoplasm	other	
[illegible]	NAPG	NAPG	NSF attachment protein gamma	Cytoplasm	transporter	
[illegible]	MZF1	MZF1	myeloid zinc finger 1	Nucleus	transcription regulator	
[illegible]	VEZF1	VEZF1	vascular endothelial zinc finger 1	Nucleus	transcription regulator	
[illegible]	USP38	USP38	ubiquitin specific peptidase 38	Other	peptidase	
[illegible]	ETFA	ETFA	electron transfer flavoprotein alpha subunit	Cytoplasm	transporter	
[illegible]	TMEM30A	TMEM30A	transmembrane protein 30A	Plasma Membrane	other	
[illegible]	CAPZB	CAPZB	capping actin protein of muscle Z-line beta subunit	Cytoplasm	other	
[illegible]	COX7A2L	COX7A2L	cytochrome c oxidase subunit 7A2 like	Cytoplasm	enzyme	
[illegible]	RCAN3	RCAN3	RCAN family member 3	Other	other	
[illegible]	TCEB2	ELOB	elongin B	Nucleus	transcription regulator	
[illegible]	MTERFD1	MTERF3	mitochondrial transcription termination factor 3	Cytoplasm	other	
[illegible]	PHF19	PHF19	PHD finger protein 19	Nucleus	other	
[illegible]	OGDH	OGDH	oxoglutarate dehydrogenase	Cytoplasm	enzyme	
[illegible]	COMMD8	COMMD8	COMM domain containing 8	Other	other	
[illegible]	EMC1	EMC1	ER membrane protein complex subunit 1	Plasma Membrane	other	
[illegible]	GTF3C6	GTF3C6	general transcription factor IIIC subunit 6	Nucleus	transcription regulator	
[illegible]	NUP62	NUP62	nucleoporin 62	Nucleus	transporter	
[illegible]	ELOF1	ELOF1	elongation factor 1 homolog	Nucleus	other	
[illegible]	SAP30	SAP30	Sin3A associated protein 30	Nucleus	transcription regulator	
[illegible]	EPHX2	EPHX2	epoxide hydrolase 2	Cytoplasm	enzyme	
[illegible]	FAM98A	FAM98A	family with sequence similarity 98 member A	Extracellular Space	other	
[illegible]	HIPK1	HIPK1	homeodomain interacting protein kinase 1	Nucleus	kinase	
[illegible]	ZNF608	ZNF608	zinc finger protein 608	Nucleus	other	
[illegible]	USP12	USP12	ubiquitin specific peptidase 12	Cytoplasm	peptidase	
[illegible]	PCNXL2	PCNXL2	pecanex homolog 2 (Drosophila)	Other	other	
[illegible]	SMURF2	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	Cytoplasm	enzyme	
[illegible]	DDX24	DDX24	DEAD-box helicase 24	Nucleus	enzyme	
[illegible]	CUL4B	CUL4B	cullin 4B	Nucleus	other	
[illegible]	IFNAR2	IFNAR2	interferon alpha and beta receptor subunit 2	Plasma Membrane	transmembrane receptor	[illegible]
[illegible]	SIT1	SIT1	signaling threshold regulating transmembrane adaptor	Plasma Membrane	other	
[illegible]	[illegible]					
[illegible]	NOP10	NOP10	NOP10 ribonucleoprotein	Nucleus	other	
[illegible]	ZNF703	ZNF703	zinc finger family member 703	Other	other	
[illegible]	GCDH	GCDH	glutaryl-CoA dehydrogenase	Cytoplasm	enzyme	
[illegible]	WDR45	WDR45	WD repeat domain 45	Other	other	
[illegible]	SLC35C2	SLC35C2	solute carrier family 35 member C2	Cytoplasm	transporter	
[illegible]	NME1	NME1	NME/NM23 nucleoside diphosphate kinase 1	Cytoplasm	kinase	
[illegible]	PRPF8	PRPF8	pre-mRNA processing factor 8	Nucleus	other	
[illegible]	C22orf39	C22orf39	chromosome 22 open reading frame 39	Cytoplasm	other	
[illegible]	EIF4B	EIF4B	eukaryotic translation initiation factor 4B	Cytoplasm	translation regulator	
[illegible]	MFSD1	MFSD1	major facilitator superfamily domain containing 1	Other	transporter	
[illegible]	DYM	DYM	dymeclin	Cytoplasm	other	
[illegible]	SLC25A37	SLC25A37	solute carrier family 25 member 37	Cytoplasm	transporter	
[illegible]	PRRC2C	PRRC2C	proline rich coiled-coil 2C	Other	other	
[illegible]	CARS2	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	Cytoplasm	enzyme	
[illegible]	TCERG1	TCERG1	transcription elongation regulator 1	Nucleus	transcription regulator	

[illegible]	ZBTB22	ZBTB22	zinc finger and BTB domain containing 22	Nucleus	other	
[illegible]	CD44	CD44	CD44 molecule (Indian blood group)	Plasma Membrane	other	anti-CD44v7 antibody
[illegible]	DHX37	DHX37	DEAH-box helicase 37	Nucleus	enzyme	
[illegible]	MAN1A2	MAN1A2	mannosidase alpha class 1A member 2	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	ZCCHC4	ZCCHC4	zinc finger CCHC-type containing 4	Other	enzyme	
[illegible]	RREB1	RREB1	ras responsive element binding protein 1	Nucleus	transcription regulator	
[illegible]	SAFB2	SAFB2	scaffold attachment factor B2	Cytoplasm	other	
[illegible]	EXOSC8	EXOSC8	exosome component 8	Nucleus	enzyme	
[illegible]	DNM1L	DNM1L	dynamin 1 like	Cytoplasm	enzyme	
[illegible]	TFE3	TFE3	transcription factor binding to IGHM enhancer 3	Nucleus	transcription regulator	
[illegible]	ZNF883	ZNF883	zinc finger protein 883	Other	other	
[illegible]	HLA-B	HLA-B	major histocompatibility complex, class I, B	Plasma Membrane	transmembrane receptor	
[illegible]	GUF1	GUF1	GUF1 homolog, GTPase	Cytoplasm	other	
[illegible]	MMP24-AS1	MMP24-AS1	MMP24 antisense RNA 1	Other	other	
[illegible]	SNAP29	SNAP29	synaptosome associated protein 29	Cytoplasm	transporter	
[illegible]	ADD3	ADD3	adducin 3	Cytoplasm	other	
[illegible]	F11R	F11R	F11 receptor	Plasma Membrane	other	
[illegible]	SCP2	SCP2	sterol carrier protein 2	Cytoplasm	transporter	
[illegible]	LMAN1	LMAN1	lectin, mannose binding 1	Cytoplasm	other	
[illegible]	RABGGTA	RABGGTA	Rab geranylgeranyltransferase alpha subunit	Extracellular Space	enzyme	
[illegible]	YTHDF3	YTHDF3	YTH N6-methyladenosine RNA binding protein 3	Cytoplasm	other	
[illegible]	CCDC88B	CCDC88B	coiled-coil domain containing 88B	Cytoplasm	other	
[illegible]	CHD8	CHD8	chromodomain helicase DNA binding protein 8	Nucleus	enzyme	
[illegible]	KLHL22	KLHL22	kelch like family member 22	Cytoplasm	other	
[illegible]	PRDX6	PRDX6	peroxiredoxin 6	Cytoplasm	enzyme	
[illegible]	INO80	INO80	INO80 complex subunit	Nucleus	enzyme	
[illegible]	GOLGB1	GOLGB1	golgin B1	Cytoplasm	other	
[illegible]	LSM8	LSM8	LSM8 homolog, U6 small nuclear RNA associated	Nucleus	other	
[illegible]	CHMP6	CHMP6	charged multivesicular body protein 6	Cytoplasm	other	
[illegible]	CASC4	CASC4	cancer susceptibility 4	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	UTP3	UTP3	UTP3, small subunit processome component homolog (	Nucleus	other	
[illegible]	VAPA	VAPA	VAMP associated protein A	Plasma Membrane	other	
[illegible]	NA					
[illegible]	KIZ	KIZ	kizuna centrosomal protein	Cytoplasm	other	
[illegible]	C12orf5	TIGAR	TP53 induced glycolysis regulatory phosphatase	Cytoplasm	enzyme	
[illegible]	PDCD11	PDCD11	programmed cell death 11	Nucleus	other	
[illegible]	MXD1	MXD1	MAX dimerization protein 1	Nucleus	transcription regulator	
[illegible]	SSBP1	SSBP1	single stranded DNA binding protein 1	Cytoplasm	other	
[illegible]	PPP2CA	PPP2CA	protein phosphatase 2 catalytic subunit alpha	Cytoplasm	phosphatase	
[illegible]	TOR1A	TOR1A	torsin family 1 member A	Cytoplasm	enzyme	
[illegible]	PPP1R35	PPP1R35	protein phosphatase 1 regulatory subunit 35	Other	other	
[illegible]	U2AF1L4	U2AF1L4	U2 small nuclear RNA auxiliary factor 1 like 4	Nucleus	other	
[illegible]	PPM1D	PPM1D	protein phosphatase, Mg2+/Mn2+ dependent 1D	Cytoplasm	phosphatase	
[illegible]	TRIM13	TRIM13	tripartite motif containing 13	Cytoplasm	enzyme	
[illegible]	ARPC5L	ARPC5L	actin related protein 2/3 complex subunit 5 like	Cytoplasm	other	
[illegible]	CLEC2B	CLEC2B	C-type lectin domain family 2 member B	Plasma Membrane	other	
[illegible]	MARK2	MARK2	microtubule affinity regulating kinase 2	Cytoplasm	kinase	
[illegible]	PRKAG2	PRKAG2	protein kinase AMP-activated non-catalytic subunit ga	Cytoplasm	kinase	
[illegible]	LINC00641	LINC00641	long intergenic non-protein coding RNA 641	Other	other	
[illegible]	XRN1	XRN1	5'-3' exoribonuclease 1	Cytoplasm	enzyme	
[illegible]	LSM2	LSM2	LSM2 homolog, U6 small nuclear RNA and mRNA degra	Nucleus	other	
[illegible]	LPAR2	LPAR2	lysophosphatidic acid receptor 2	Plasma Membrane	G-protein coupled recepto	
[illegible]	NDUFAF6	NDUFAF6	NADH:ubiquinone oxidoreductase complex assembly fa	Cytoplasm	other	
[illegible]	[illegible]	[illegible]	U5 small nuclear ribonucleoprotein 200 kDa helicase p	Other	other	
[illegible]	TBCB	TBCB	tubulin folding cofactor B	Cytoplasm	other	
[illegible]	DCTN6	DCTN6	dynactin subunit 6	Cytoplasm	enzyme	
[illegible]	APOA1BP	NAXE	NAD(P)HX epimerase	Extracellular Space	enzyme	
[illegible]	TUBGCP2	TUBGCP2	tubulin gamma complex associated protein 2	Cytoplasm	peptidase	
[illegible]	ABHD3	ABHD3	abhydrolase domain containing 3	Plasma Membrane	enzyme	
[illegible]	LOH12CR1	BORCS5	BLOC-1 related complex subunit 5	Cytoplasm	other	
[illegible]	PTAR1	PTAR1	protein prenyltransferase alpha subunit repeat contai	Other	other	
[illegible]	MRGBP	MRGBP	MRG domain binding protein	Nucleus	other	
[illegible]	CINP	CINP	cyclin dependent kinase 2 interacting protein	Nucleus	other	
[illegible]	HNRNPH2	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2	Nucleus	other	
[illegible]	UBE2O	UBE2O	ubiquitin conjugating enzyme E2 O	Nucleus	enzyme	
[illegible]	NTAN1	NTAN1	N-terminal asparagine amidase	Nucleus	enzyme	
[illegible]	SIVA1	SIVA1	SIVA1 apoptosis inducing factor	Cytoplasm	other	
[illegible]	RPL13P3	RPL13P3	ribosomal protein L13 pseudogene 3	Other	other	
[illegible]	ID1	ID1	inhibitor of DNA binding 1, HLH protein	Nucleus	transcription regulator	
[illegible]	[illegible]					
[illegible]	PRDX5	PRDX5	peroxiredoxin 5	Cytoplasm	enzyme	auranofin
[illegible]	[illegible]					
[illegible]	UBTF	UBTF	upstream binding transcription factor, RNA polymerase	Nucleus	transcription regulator	
[illegible]	TMEM109	TMEM109	transmembrane protein 109	Cytoplasm	other	
[illegible]	CYTH1	CYTH1	cytohesin 1	Cytoplasm	other	
[illegible]	CYHR1	CYHR1	cysteine and histidine rich 1	Nucleus	other	
[illegible]	NBAS	NBAS	neuroblastoma amplified sequence	Nucleus	other	
[illegible]	PAG1	PAG1	phosphoprotein membrane anchor with glycosphingolip	Plasma Membrane	other	
[illegible]	TAF8	TAF8	TATA-box binding protein associated factor 8	Nucleus	transcription regulator	
[illegible]	CMPK1	CMPK1	cytidine/uridine monophosphate kinase 1	Nucleus	kinase	
[illegible]	AP5S1	AP5S1	adaptor related protein complex 5 sigma 1 subunit	Nucleus	other	
[illegible]	[illegible]					
[illegible]	ABHD13	ABHD13	abhydrolase domain containing 13	Other	peptidase	
[illegible]	TNK2	TNK2	tyrosine kinase non receptor 2	Cytoplasm	kinase	[illegible]
[illegible]	MPND	MPND	MPN domain containing	Other	other	
[illegible]	ZC3H7A	ZC3H7A	zinc finger CCCH-type containing 7A	Extracellular Space	other	
[illegible]	SGPP1	SGPP1	sphingosine-1-phosphate phosphatase 1	Cytoplasm	phosphatase	
[illegible]	ORC5	ORC5	origin recognition complex subunit 5	Nucleus	other	
[illegible]	UBA5	UBA5	ubiquitin like modifier activating enzyme 5	Cytoplasm	enzyme	
[illegible]	PEBP1	PEBP1	phosphatidylethanolamine binding protein 1	Cytoplasm	other	
[illegible]	SORBS3	SORBS3	sorbin and SH3 domain containing 3	Cytoplasm	other	
[illegible]	RAVER1	RAVER1	ribonucleoprotein, PTB binding 1	Nucleus	other	
[illegible]	HOOK3	HOOK3	hook microtubule tethering protein 3	Cytoplasm	other	
[illegible]	VEGFB	VEGFB	vascular endothelial growth factor B	Extracellular Space	growth factor	[illegible]
[illegible]	TRAF7	TRAF7	TNF receptor associated factor 7	Cytoplasm	enzyme	
[illegible]	ARHGDIA	ARHGDIA	Rho GDP dissociation inhibitor alpha	Cytoplasm	other	
[illegible]	ACSL4	ACSL4	acyl-CoA synthetase long-chain family member 4	Cytoplasm	enzyme	
[illegible]	RALGAPA1	RALGAPA1	Ral GTPase activating protein catalytic alpha subunit 1	Cytoplasm	other	
[illegible]	TMBIM6	TMBIM6	transmembrane BAX inhibitor motif containing 6	Nucleus	other	
[illegible]	SAP30BP	SAP30BP	SAP30 binding protein	Nucleus	transcription regulator	
[illegible]	ATP2C1	ATP2C1	ATPase secretory pathway Ca2+ transporting 1	Cytoplasm	transporter	[illegible]
[illegible]	TFDP1	TFDP1	transcription factor Dp-1	Nucleus	transcription regulator	
[illegible]	NAT6	NAT6	N-acetyltransferase 6	Cytoplasm	other	
[illegible]	PPP2R3D	PPP2R3D	protein phosphatase 2 regulatory subunit B''delta	Nucleus	phosphatase	
[illegible]	AEN	AEN	apoptosis enhancing nuclease	Nucleus	enzyme	
[illegible]	MLLT1	MLLT1	MLLT1, super elongation complex subunit	Nucleus	other	
[illegible]	LINS1	LINS1	lines homolog 1	Other	other	
[illegible]	SF3B1	SF3B1	splicing factor 3b subunit 1	Nucleus	other	
[illegible]	CEP192	CEP192	centrosomal protein 192	Cytoplasm	other	
[illegible]	ZFYVE26	ZFYVE26	zinc finger FYVE-type containing 26	Cytoplasm	other	
[illegible]	HERC6	HERC6	HECT and RLD domain containing E3 ubiquitin protein l	Cytoplasm	enzyme	
[illegible]	ZNF711	ZNF711	zinc finger protein 711	Nucleus	other	
[illegible]	[illegible]	[illegible]	[illegible] associated lipid domain containing 1	Plasma Membrane	other	
[illegible]	FAM214A	FAM214A	family with sequence similarity 214 member A	Other	other	
[illegible]	ZSWIM8	ZSWIM8	zinc finger SWIM-type containing 8	Extracellular Space	other	
[illegible]	ADSL	ADSL	adenylosuccinate lyase	Cytoplasm	enzyme	
[illegible]	TP53RK	TP53RK	TP53 regulating kinase	Nucleus	kinase	
[illegible]	UFD1L	UFD1L	ubiquitin fusion degradation 1 like (yeast)	Cytoplasm	peptidase	
[illegible]	ABHD12	ABHD12	abhydrolase domain containing 12	Plasma Membrane	enzyme	
[illegible]	ZNF581	ZNF581	zinc finger protein 581	Nucleus	other	
[illegible]	TMEM230	TMEM230	transmembrane protein 230	Other	other	
[illegible]	EWSR1	EWSR1	EWS RNA binding protein 1	Nucleus	other	
[illegible]	ZMYM2	ZMYM2	zinc finger MYM-type containing 2	Nucleus	kinase	
[illegible]	ATP5D	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 compl	Cytoplasm	transporter	
[illegible]	[illegible]	[illegible]	uncharacterized [illegible]	Other	other	
[illegible]	PER2	PER2	period circadian clock 2	Nucleus	transcription regulator	
[illegible]	VAMP5	VAMP5	vesicle associated membrane protein 5	Plasma Membrane	transporter	
[illegible]	IRF2BPL	IRF2BPL	interferon regulatory factor 2 binding protein like	Nucleus	other	
[illegible]	UBE2E3	UBE2E3	ubiquitin conjugating enzyme E2 E3	Nucleus	enzyme	
[illegible]	PPM1K	PPM1K	protein phosphatase, Mg2+/Mn2+ dependent 1K	Cytoplasm	phosphatase	
[illegible]	[illegible]	[illegible]	[illegible] kinase 1	Cytoplasm	kinase	
[illegible]	ATXN7L3	ATXN7L3	ataxin 7 like 3	Nucleus	transcription regulator	
[illegible]	METTL9	METTL9	methyltransferase like 9	Other	other	
[illegible]	ICK	ICK	intestinal cell kinase	Cytoplasm	kinase	
[illegible]	EXT2	EXT2	exostosin glycosyltransferase 2	Cytoplasm	enzyme	
[illegible]	PARK7	PARK7	Parkinsonism associated deglycase	Nucleus	enzyme	
[illegible]	NME3	NME3	NME/NM23 nucleoside diphosphate kinase 3	Cytoplasm	kinase	
[illegible]	TMEM140	TMEM140	transmembrane protein 140	Other	other	
[illegible]	CLCN6	CLCN6	chloride voltage-gated channel 6	Plasma Membrane	ion channel	
[illegible]	DLST	DLST	dihydrolipoamide S-succinyltransferase	Cytoplasm	enzyme	
[illegible]	PLEKHB2	PLEKHB2	pleckstrin homology domain containing B2	Other	other	
[illegible]	SSBP4	SSBP4	single stranded DNA binding protein 4	Nucleus	transcription regulator	
[illegible]	ARHGEF18	ARHGEF18	Rho/Rac guanine nucleotide exchange factor 18	Cytoplasm	other	
[illegible]	CBWD1	CBWD1	COBW domain containing 1	Other	other	
[illegible]	PARP10	PARP10	poly(ADP-ribose) polymerase family member 10	Cytoplasm	enzyme	
[illegible]	TMEM139	TMEM139	transmembrane protein 139	Other	other	
[illegible]	SFPQ	SFPQ	splicing factor proline and glutamine rich	Nucleus	other	
[illegible]	RRAGA	RRAGA	Ras related GTP binding A	Cytoplasm	enzyme	
[illegible]	PEX13	PEX13	peroxisomal biogenesis factor 13	Cytoplasm	transporter	
[illegible]	PPP1R16B	PPP1R16B	protein phosphatase 1 regulatory subunit 16B	Plasma Membrane	phosphatase	
[illegible]	TAPBPL	TAPBPL	TAP binding protein like	Cytoplasm	other	
[illegible]	DESI2	DESI2	desumoylating isopeptidase 2	Cytoplasm	other	
[illegible]	TUBA1B	TUBA1B	tubulin alpha 1b	Cytoplasm	other	
[illegible]	SEC24B	SEC24B	SEC24 homolog B, COPII coat complex component	Cytoplasm	transporter	
[illegible]	PRDM2	PRDM2	PR/SET domain 2	Nucleus	transcription regulator	
[illegible]	PPP6C	PPP6C	protein phosphatase 6 catalytic subunit	Nucleus	phosphatase	
[illegible]	POLR3D	POLR3D	RNA polymerase III subunit D	Nucleus	enzyme	
[illegible]	ORMDL1	ORMDL1	ORMDL sphingolipid biosynthesis regulator 1	Cytoplasm	other	
[illegible]	SQRDL	SQRDL	sulfide quinone reductase-like (yeast)	Cytoplasm	enzyme	
[illegible]	ABHD17B	ABHD17B	abhydrolase domain containing 17B	Other	peptidase	
[illegible]	FAM13B	FAM13B	family with sequence similarity 13 member B	Cytoplasm	other	
[illegible]	PPP2R4	PTPA	protein phosphatase 2 phosphatase activator	Cytoplasm	phosphatase	
[illegible]	TOMM22	TOMM22	translocase of outer mitochondrial membrane 22	Cytoplasm	transporter	
[illegible]	MAL	MAL	mal, T-cell differentiation protein	Plasma Membrane	transporter	
[illegible]	MRPL2	MRPL2	mitochondrial ribosomal protein L2	Extracellular Space	other	
[illegible]	CBFB	CBFB	core-binding factor beta subunit	Nucleus	transcription regulator	
[illegible]	GLIPR1	GLIPR1	GLI pathogenesis related 1	Extracellular Space	other	
[illegible]	RAP1GAP2	RAP1GAP2	RAP1 GTPase activating protein 2	Cytoplasm	other	
[illegible]	TMX1	TMX1	thioredoxin related transmembrane protein 1	Cytoplasm	enzyme	
[illegible]	NXF1	NXF1	nuclear RNA export factor 1	Nucleus	transporter	
[illegible]	TRAPPC12	TRAPPC12	trafficking protein particle complex 12	Nucleus	other	
[illegible]	ETFDH	ETFDH	electron transfer flavoprotein dehydrogenase	Cytoplasm	enzyme	
[illegible]	METTL3	METTL3	methyltransferase like 3	Nucleus	enzyme	
[illegible]	LSM10	LSM10	LSM10, U7 small nuclear RNA associated	Nucleus	other	
[illegible]	SEC61A2	SEC61A2	Sec61 translocon alpha 2 subunit	Cytoplasm	transporter	
[illegible]	TESK1	TESK1	testis-specific kinase 1	Nucleus	kinase	
[illegible]	PRDX1	PRDX1	peroxiredoxin 1	Cytoplasm	enzyme	
[illegible]	DRAM2	DRAM2	DNA damage regulated autophagy modulator 2	Cytoplasm	other	
[illegible]	SIK1	LOC102724428/SIK1	salt inducible kinase 1	Nucleus	kinase	[illegible]
[illegible]	AP5M1	AP5M1	adaptor related protein complex 5 mu 1 subunit	Cytoplasm	other	
[illegible]	ANKRA2	ANKRA2	ankyrin repeat family A member 2	Cytoplasm	transcription regulator	
[illegible]	RAD23A	RAD23A	RAD23 homolog A, nucleotide excision repair protein	Nucleus	other	
[illegible]	DSN1	DSN1	DSN1 homolog, MIS12 kinetochore complex component	Nucleus	other	
[illegible]	PARVB	PARVB	parvin beta	Cytoplasm	other	
[illegible]	ABCA7	ABCA7	ATP binding cassette subfamily A member 7	Plasma Membrane	transporter	
[illegible]	EDRF1	EDRF1	erythroid differentiation regulatory factor 1	Other	other	
[illegible]	ERCC1	ERCC1	ERCC excision repair 1, endonuclease non-catalytic sub	Nucleus	enzyme	
[illegible]	CCDC117	CCDC117	coiled-coil domain containing 117	Other	other	
[illegible]	NAGK	NAGK	N-acetylglucosamine kinase	Cytoplasm	kinase	
[illegible]	PEX11B	PEX11B	peroxisomal biogenesis factor 11 beta	Cytoplasm	other	
[illegible]	APEH	APEH	acylaminoacyl-peptide hydrolase	Cytoplasm	peptidase	
[illegible]	UBL3	UBL3	ubiquitin like 3	Cytoplasm	other	
[illegible]	ANXA11	ANXA11	annexin A11	Nucleus	other	
[illegible]	RRP9	RRP9	ribosomal RNA processing 9, small subunit (SSU) proce	Nucleus	other	
[illegible]	COPZ1	COPZ1	coatomer protein complex subunit zeta 1	Cytoplasm	transporter	
[illegible]	UBL7	UBL7	ubiquitin like 7	Other	other	
[illegible]	ZNF22	ZNF22	zinc finger protein 22	Nucleus	other	
[illegible]	PKD1P6	PKD1P6	polycystin 1, transient receptor potential channel intera	Other	other	
[illegible]	NDUFB2	NDUFB2	NADH:ubiquinone oxidoreductase subunit B2	Cytoplasm	enzyme	
[illegible]	SELM	SELENOM	selenoprotein M	Cytoplasm	other	
[illegible]	MRPL9	MRPL9	mitochondrial ribosomal protein L9	Cytoplasm	translation regulator	
[illegible]	MAP2K7	MAP2K7	mitogen-activated protein kinase kinase 7	Cytoplasm	kinase	
[illegible]	CEP85L	CEP85L	centrosomal protein 85 like	Cytoplasm	other	
[illegible]	PLXND1	PLXND1	plexin D1	Plasma Membrane	transmembrane receptor	
[illegible]	NUDT1	NUDT1	nudix hydrolase 1	Extracellular Space	phosphatase	
[illegible]	MCRS1	MCRS1	microspherule protein 1	Nucleus	other	
[illegible]	PITPNA	PITPNA	phosphatidylinositol transfer protein alpha	Cytoplasm	transporter	
[illegible]	SZRD1	SZRD1	SUZ RNA binding domain containing 1	Other	other	
[illegible]	RAB8A	RAB8A	RAB8A, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	TAB1	TAB1	TGF-beta activated kinase 1 (MAP3K7) binding protein 1	Cytoplasm	enzyme	
[illegible]	PIGBOS1	PIGBOS1	PIGB opposite strand 1	Other	other	
[illegible]	CRY1	CRY1	cryptochrome circadian clock 1	Nucleus	enzyme	
[illegible]	MTX3	MTX3	metaxin 3	Other	other	
[illegible]	CKAP2	CKAP2	cytoskeleton associated protein 2	Cytoplasm	other	
[illegible]	KPNA4	KPNA4	karyopherin subunit alpha 4	Nucleus	transporter	
[illegible]	ARFGEF3	ARFGEF3	ADP ribosylation factor guanine nucleotide exchange fa	Cytoplasm	other	
[illegible]	CHD9	CHD9	chromodomain helicase DNA binding protein 9	Cytoplasm	other	
[illegible]	CCRL2	CCRL2	C-C motif chemokine receptor like 2	Plasma Membrane	G-protein coupled recepto	
[illegible]	[illegible]	[illegible]	chromosome 18 open reading frame [illegible]	Other	other	
[illegible]	HCFC2	HCFC2	host cell factor C2	Nucleus	transcription regulator	
[illegible]	CAPZA2	CAPZA2	capping actin protein of muscle Z-line alpha subunit 2	Cytoplasm	other	
[illegible]	SDAD1	SDAD1	SDA1 domain containing 1	Nucleus	other	
[illegible]	MSH3	MSH3	mutS homolog 3	Nucleus	enzyme	

[illegible]	GEMIN7	GEMIN7	gem nuclear organelle associated protein 7	Nucleus	other	
[illegible]	CHCHD2	CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 2	Cytoplasm	other	
[illegible]	SCAMP3	SCAMP3	secretory carrier membrane protein 3	Cytoplasm	transporter	
[illegible]	ARIH1					
[illegible]	ARFGAP3	ARFGAP3	ADP ribosylation factor GTPase activating protein 3	Cytoplasm	transporter	
[illegible]	EPHA4	EPHA4	EPH receptor A4	Plasma Membrane	kinase	
[illegible]	SUMO2	SUMO2	small ubiquitin-like modifier 2	Nucleus	enzyme	
[illegible]	ATP5F1	ATP5F1	ATP synthase, H+ transporting, mitochondrial Fo compl	Cytoplasm	transporter	
[illegible]	CRCP	CRCP	CGRP receptor component	Plasma Membrane	transmembrane recepto	
[illegible]	SRSF6	SRSF6	serine and arginine rich splicing factor 6	Nucleus	other	
[illegible]	VPS54	VPS54	VPS54, GARP complex subunit	Extracellular Space	other	
[illegible]	MDH2	MDH2	malate dehydrogenase 2	Cytoplasm	enzyme	
[illegible]	TRAPPC6A	TRAPPC6A	trafficking protein particle complex 6A	Cytoplasm	other	
[illegible]	CREB3	CREB3	cAMP responsive element binding protein 3	Nucleus	transcription regulator	
[illegible]	C11orf68	C11orf68	chromosome 11 open reading frame 68	Other	other	
[illegible]	LCOR	LCOR	ligand dependent nuclear receptor corepressor	Nucleus	transcription regulator	
[illegible]	HAUS3	HAUS3	HAUS augmin like complex subunit 3	Cytoplasm	other	
[illegible]	ZNF689	ZNF689	zinc finger protein 689	Nucleus	transcription regulator	
[illegible]	ING4	ING4	inhibitor of growth family member 4	Nucleus	transcription regulator	
[illegible]	IMP4	IMP4	IMP4 homolog, U3 small nucleolar ribonucleoprotein	Nucleus	other	
[illegible]	POFUT2	POFUT2	protein O-fucosyltransferase 2	Cytoplasm	enzyme	
[illegible]	RFK	RFK	riboflavin kinase	Cytoplasm	kinase	
[illegible]	USP25	USP25	ubiquitin specific peptidase 25	Cytoplasm	peptidase	
[illegible]	SDF4	SDF4	stromal cell derived factor 4	Cytoplasm	other	
[illegible]	ADRBK1	GRK2	G protein-coupled receptor kinase 2	Cytoplasm	kinase	
[illegible]	KEAP1	KEAP1	kelch like ECH associated protein 1	Cytoplasm	transcription regulator	dimethyl fumarate
[illegible]	EIF2AK4	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	Cytoplasm	kinase	
[illegible]	ABCD3	ABCD3	ATP binding cassette subfamily D member 3	Cytoplasm	transporter	
[illegible]	CAND1	CAND1	cullin associated and neddylation dissociated 1	Cytoplasm	transcription regulator	
[illegible]	PTRHD1	PTRHD1	peptidyl-tRNA hydrolase domain containing 1	Cytoplasm	other	
[illegible]	IFIT5	IFIT5	interferon induced protein with tetratricopeptide repea	Plasma Membrane	other	
[illegible]	DDX28	DDX28	DEAD-box helicase 28	Nucleus	enzyme	
[illegible]	DLG1	DLG1	discs large MAGUK scaffold protein 1	Plasma Membrane	kinase	
[illegible]	PSD4	PSD4	pleckstrin and Sec7 domain containing 4	Cytoplasm	other	
[illegible]	TMBIM4	TMBIM4	transmembrane BAX inhibitor motif containing 4	Nucleus	other	
[illegible]	BCL7B	BCL7B	BCL tumor suppressor 7B	Nucleus	other	
[illegible]	SHKBP1	SHKBP1	SH3KBP1 binding protein 1	Other	other	
[illegible]	RAF1	RAF1	Raf-1 proto-oncogene, serine/threonine kinase	Cytoplasm	kinase	[illegible]/sorafenib, t
[illegible]	[illegible]					
[illegible]	BRWD3	BRWD3	bromodomain and WD repeat domain containing 3	Other	other	
[illegible]	USP36	USP36	ubiquitin specific peptidase 36	Nucleus	peptidase	
[illegible]	TET2	TET2	tet methylcytosine dioxygenase 2	Nucleus	enzyme	
[illegible]	PTGES3P1	PTGES3P1	prostaglandin E synthase 3 pseudogene 1	Other	other	
[illegible]	BZW1P2	BZW1P2	basic leucine zipper and W2 domains 1 pseudogene 2	Other	other	
[illegible]	UBALD1	UBALD1	UBA like domain containing 1	Other	other	
[illegible]	MCM8	MCM8	minichromosome maintenance complex component 8	Nucleus	enzyme	
[illegible]	CCT8	CCT8	chaperonin containing TCP1 subunit 8	Cytoplasm	other	
[illegible]	TADA3	TADA3	transcriptional adaptor 3	Nucleus	transcription regulator	
[illegible]	TMED9	TMED9	transmembrane p24 trafficking protein 9	Cytoplasm	transporter	
[illegible]	MYC	MYC	v-myc avian myelocytomatosis viral oncogene homolog	Nucleus	transcription regulator	
[illegible]	CDKN2D	CDKN2D	cyclin dependent kinase inhibitor 2D	Cytoplasm	transcription regulator	
[illegible]	RNF7	RNF7	ring finger protein 7	Nucleus	enzyme	
[illegible]	CHD8	CHD8	chromodomain helicase DNA binding protein 8	Nucleus	enzyme	
[illegible]	HCCS	HCCS	holocytochrome c synthase	Cytoplasm	enzyme	
[illegible]	BAG5	BAG5	BCL2 associated athanogene 5	Cytoplasm	other	
[illegible]	PIP5K1A	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase type 1 alpha	Cytoplasm	kinase	
[illegible]	FGD3	FGD3	FYVE, RhoGEF and PH domain containing 3	Cytoplasm	other	
[illegible]	GLTSCR1L	GLTSCR1L	GLTSCR1 like	Other	other	
[illegible]	AGK	AGK	acylglycerol kinase	Cytoplasm	kinase	
[illegible]	FAM213B	FAM213B	family with sequence similarity 213 member B	Cytoplasm	enzyme	
[illegible]	ARF4	ARF4	ADP ribosylation factor 4	Cytoplasm	enzyme	
[illegible]	FAM177A1	FAM177A1	family with sequence similarity 177 member A1	Other	other	
[illegible]	PAPOLG	PAPOLG	poly(A) polymerase gamma	Nucleus	enzyme	
[illegible]	YTHDC1	YTHDC1	YTH domain containing 1	Cytoplasm	other	
[illegible]	DDHD2	DDHD2	DDHD domain containing 2	Cytoplasm	enzyme	
[illegible]	MSRA	MSRA	methionine sulfoxide reductase A	Cytoplasm	enzyme	
[illegible]	PUM1	PUM1	pumilio RNA binding family member 1	Cytoplasm	other	
[illegible]	RGL2	RGL2	ral guanine nucleotide dissociation stimulator like 2	Cytoplasm	other	
[illegible]	NUP50	NUP50	nucleoporin 50	Nucleus	transporter	
[illegible]	ACTR1A	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alph	Cytoplasm	other	
[illegible]	JOSD2	JOSD2	Josephin domain containing 2	Cytoplasm	enzyme	
[illegible]	TPMT	TPMT	thiopurine S-methyltransferase	Cytoplasm	enzyme	olsalazine
[illegible]	PRKCSH	PRKCSH	protein kinase C substrate 80K-H	Cytoplasm	enzyme	
[illegible]	USP50	USP50	ubiquitin specific peptidase 50	Extracellular Space	enzyme	
[illegible]	FAM204A	FAM204A	family with sequence similarity 204 member A	Other	other	
[illegible]	SRSF5	SRSF5	serine and arginine rich splicing factor 5	Nucleus	other	
[illegible]	PHKA2	PHKA2	phosphorylase kinase regulatory subunit alpha 2	Cytoplasm	kinase	
[illegible]	KLC1	KLC1	kinesin light chain 1	Cytoplasm	other	
[illegible]	YPEL5	YPEL5	yippee like 5	Nucleus	other	
[illegible]	CTSK	CTSK	cathepsin K	Cytoplasm	peptidase	[illegible] inhibitor, odana
[illegible]	KIAA0141	KIAA0141	KIAA0141	Cytoplasm	other	
[illegible]	ZBTB2	ZBTB2	zinc finger and BTB domain containing 2	Nucleus	other	
[illegible]	NOP9	NOP9	NOP9 nucleolar protein	Nucleus	other	
[illegible]	UBE2Z	UBE2Z	ubiquitin conjugating enzyme E2 Z	Other	other	
[illegible]	ZNF180	ZNF180	zinc finger protein 180	Nucleus	other	
[illegible]	ABCC10	ABCC10	ATP binding cassette subfamily C member 10	Plasma Membrane	transporter	
[illegible]	SAFB	SAFB	scaffold attachment factor B	Nucleus	other	
[illegible]	PRPSAP2	PRPSAP2	phosphoribosyl pyrophosphate synthetase associated pr	Other	other	
[illegible]	RBM15	RBM15	RNA binding motif protein 15	Nucleus	other	
[illegible]	COX17	COX17	COX17, cytochrome c oxidase copper chaperone	Cytoplasm	enzyme	
[illegible]	EEF2	EEF2	eukaryotic translation elongation factor 2	Cytoplasm	translation regulator	
[illegible]	B3GAT3	B3GAT3	beta-1,3-glucuronyltransferase 3	Cytoplasm	enzyme	
[illegible]	VAPB	VAPB	VAMP associated protein B and C	Plasma Membrane	other	
[illegible]	SOCS3	SOCS3	suppressor of cytokine signaling 3	Cytoplasm	phosphatase	
[illegible]	COPG1	COPG1	coatomer protein complex subunit gamma 1	Cytoplasm	transporter	
[illegible]	PTPN4	PTPN4	protein tyrosine phosphatase, non-receptor type 4	Cytoplasm	phosphatase	
[illegible]	EXOSC7	EXOSC7	exosome component 7	Nucleus	enzyme	
[illegible]	STX16	STX16	syntaxin 16	Cytoplasm	transporter	
[illegible]	DUSP23	DUSP23	dual specificity phosphatase 23	Cytoplasm	phosphatase	
[illegible]	KCTD9	KCTD9	potassium channel tetramerization domain containing !	Other	other	
[illegible]	LRRC58	LRRC58	leucine rich repeat containing 58	Other	other	
[illegible]	DSTN	DSTN	destrin, actin depolymerizing factor	Cytoplasm	other	
[illegible]	PHACTR4	PHACTR4	phosphatase and actin regulator 4	Plasma Membrane	other	
[illegible]	TSR1	TSR1	TSR1, ribosome maturation factor	Nucleus	other	
[illegible]	VAMP3	VAMP3	vesicle associated membrane protein 3	Plasma Membrane	other	
[illegible]	DDHD1	DDHD1	DDHD domain containing 1	Extracellular Space	enzyme	
[illegible]	DDIT3	DDIT3	DNA damage inducible transcript 3	Nucleus	transcription regulator	
[illegible]	MIIP	MIIP	migration and invasion inhibitory protein	Other	other	
[illegible]	MTA2	MTA2	metastasis associated 1 family member 2	Nucleus	transcription regulator	
[illegible]	KIAA1430	CFAP97	cilia and flagella associated protein 97	Other	other	
[illegible]	KANSL2	KANSL2	KAT8 regulatory NSL complex subunit 2	Nucleus	other	
[illegible]	PLEKHM1					
[illegible]	BAZ1A	BAZ1A	bromodomain adjacent to zinc finger domain 1A	Nucleus	other	
[illegible]	C6orf203	C6orf203	chromosome 6 open reading frame 203	Cytoplasm	other	
[illegible]	CCT5	CCT5	chaperonin containing TCP1 subunit 5	Cytoplasm	other	
[illegible]	BCL7C	BCL7C	BCL tumor suppressor 7C	Nucleus	other	
[illegible]	MED6	MED6	mediator complex subunit 6	Nucleus	transcription regulator	
[illegible]	COX6B1	COX6B1	cytochrome c oxidase subunit 6B1	Cytoplasm	enzyme	
[illegible]	SRRT	SRRT	serrate, RNA effector molecule	Nucleus	other	
[illegible]	CDC42	CDC42	cell division cycle 42	Cytoplasm	enzyme	
[illegible]	DTX3L	DTX3L	deltex E3 ubiquitin ligase 3L	Cytoplasm	enzyme	
[illegible]	KLHL8	KLHL8	kelch like family member 8	Other	other	
[illegible]	ZDHHC3	ZDHHC3	zinc finger DHHC-type containing 3	Cytoplasm	peptidase	
[illegible]	NKAP	NKAP	NFKB activating protein	Nucleus	transcription regulator	
[illegible]	HIST3H2A	HIST3H2A	histone cluster 3 H2A	Nucleus	other	
[illegible]	TMEM168	TMEM168	transmembrane protein 168	Other	other	
[illegible]	RNH1	RNH1	ribonuclease/angiogenin inhibitor 1	Cytoplasm	other	
[illegible]	STK16	STK16	serine/threonine kinase 16	Cytoplasm	kinase	
[illegible]	[illegible]					
[illegible]	CASP8	CASP8	caspase 8	Cytoplasm	peptidase	[illegible] inhibitor, emrica
[illegible]	TXN2	TXN2	thioredoxin 2	Cytoplasm	enzyme	
[illegible]	PHC3	PHC3	polyhomeotic homolog 3	Nucleus	transcription regulator	
[illegible]	MTRF1L	MTRF1L	mitochondrial translational release factor 1 like	Cytoplasm	translation regulator	
[illegible]	TMED3	TMED3	transmembrane p24 trafficking protein 3	Cytoplasm	transporter	
[illegible]	AKAP1	AKAP1	A-kinase anchoring protein 1	Cytoplasm	other	
[illegible]	BYSL	BYSL	bystin like	Nucleus	other	
[illegible]	ACAP2	ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domain	Nucleus	other	
[illegible]	VPS37B	VPS37B	VPS37B, ESCRT-I subunit	Cytoplasm	other	
[illegible]	PPP1R37	PPP1R37	protein phosphatase 1 regulatory subunit 37	Other	other	
[illegible]	GRAMD3	GRAMD3	GRAM domain containing 3	Extracellular Space	other	
[illegible]	HDAC4	HDAC4	histone deacetylase 4	Nucleus	transcription regulator	[illegible], belinostat, pyroxa
[illegible]	SRI	SRI	sorcin	Cytoplasm	transporter	
[illegible]	CLSTN3	CLSTN3	calsyntenin 3	Plasma Membrane	other	
[illegible]	ERCC6L2	ERCC6L2	ERCC excision repair 6 like 2	Other	enzyme	
[illegible]	TIA1	TIA1	TIA1 cytotoxic granule associated RNA binding protein	Nucleus	other	
[illegible]	NXT2	NXT2	nuclear transport factor 2 like export factor 2	Nucleus	transporter	
[illegible]	NACC1	NACC1	nucleus accumbens associated 1	Nucleus	transcription regulator	
[illegible]	TCEB1P29	ELOCP29	elongin C pseudogene 29	Other	other	
[illegible]	BLZF1	BLZF1	basic leucine zipper nuclear factor 1	Cytoplasm	transcription regulator	
[illegible]	EID1	EID1	EP300 interacting inhibitor of differentiation 1	Nucleus	transcription regulator	
[illegible]	[illegible]	[illegible]	[illegible] interacting protein 1	Cytoplasm	other	
[illegible]	KIAA1683	KIAA1683	KIAA1683	Other	other	
[illegible]	SDHAP1	SDHAP1	succinate dehydrogenase complex flavoprotein subunit	Other	other	
[illegible]	RNF34	RNF34	ring finger protein 34	Cytoplasm	enzyme	
[illegible]	CCSER2	CCSER2	coiled-coil serine rich protein 2	Other	other	
[illegible]	SPOP	SPOP	speckle type BTB/POZ protein	Extracellular Space	other	
[illegible]	APPBP2	APPBP2	amyloid beta precursor protein binding protein 2	Cytoplasm	other	
[illegible]	VRK2	VRK2	vaccinia related kinase 2	Nucleus	kinase	
[illegible]	HLA-B	HLA-B	major histocompatibility complex, class I, B	Plasma Membrane	transmembrane recepto	
[illegible]	CISD3	CISD3	CDGSH iron sulfur domain 3	Cytoplasm	other	
[illegible]	ZNF428	ZNF428	zinc finger protein 428	Nucleus	transcription regulator	
[illegible]	SATB1-AS1	SATB1-AS1	SATB1 antisense RNA 1	Other	other	
[illegible]	ADNP2	ADNP2	ADNP homeobox 2	Other	other	
[illegible]	C12orf4	C12orf4	chromosome 12 open reading frame 4	Cytoplasm	other	
[illegible]	PNKP	PNKP	polynucleotide kinase 3'-phosphatase	Nucleus	kinase	
[illegible]	N4BP1	N4BP1	NEDD4 binding protein 1	Cytoplasm	other	
[illegible]	GNE	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylman	Cytoplasm	kinase	
[illegible]	PGGT1B	PGGT1B	protein geranylgeranyltransferase type I subunit beta	Cytoplasm	enzyme	
[illegible]	TAF11	TAF11	TATA-box binding protein associated factor 11	Nucleus	transcription regulator	
[illegible]	CDR2	CDR2	cerebellar degeneration related protein 2	Cytoplasm	other	
[illegible]	SCAF1	SCAF1	SR-related CTD associated factor 1	Extracellular Space	other	
[illegible]	SPATA13	SPATA13	spermatogenesis associated 13	Plasma Membrane	other	
[illegible]	REEP4	REEP4	receptor accessory protein 4	Cytoplasm	other	
[illegible]	SCAPER	SCAPER	S-phase cyclin A associated protein in the ER	Extracellular Space	other	
[illegible]	ZNF280D					
[illegible]	KIAA1033	WASHC4	WASH complex subunit 4	Cytoplasm	other	
[illegible]	PPP6R2	PPP6R2	protein phosphatase 6 regulatory subunit 2	Cytoplasm	other	
[illegible]	JKAMP	JKAMP	JNK1/MAPK8-associated membrane protein	Cytoplasm	other	
[illegible]	MAGEH1	MAGEH1	MAGE family member H1	Cytoplasm	other	
[illegible]	TSN	TSN	translin	Nucleus	other	
[illegible]	EIF3B	EIF3B	eukaryotic translation initiation factor 3 subunit B	Cytoplasm	translation regulator	
[illegible]	TRNAU1AP	TRNAU1AP	tRNA selenocysteine 1 associated protein 1	Nucleus	other	
[illegible]	NUP214	NUP214	nucleoporin 214	Nucleus	transporter	
[illegible]	CENPU	CENPU	centromere protein U	Nucleus	other	
[illegible]	ELMO2	ELMO2	engulfment and cell motility 2	Cytoplasm	other	
[illegible]	WHAMM	WHAMM	WAS protein homolog associated with actin, golgi mem	Cytoplasm	other	
[illegible]	MED12	MED12	mediator complex subunit 12	Nucleus	transcription regulator	
[illegible]	HAX1	HAX1	HCLS1 associated protein X-1	Cytoplasm	other	
[illegible]	ZNF281	ZNF281	zinc finger protein 281	Nucleus	other	
[illegible]	OXLD1	OXLD1	oxidoreductase like domain containing 1	Cytoplasm	other	
[illegible]	NOL8	NOL8	nucleolar protein 8	Nucleus	other	
[illegible]	NOM1	NOM1	nucleolar protein with MIF4G domain 1	Nucleus	other	
[illegible]	MAPK8	MAPK8	mitogen-activated protein kinase 8	Cytoplasm	kinase	aplidine
[illegible]	GAPVD1	GAPVD1	GTPase activating protein and VPS9 domains 1	Cytoplasm	other	
[illegible]	UAP1	UAP1	UDP-N-acetylglucosamine pyrophosphorylase 1	Nucleus	enzyme	
[illegible]	DVL2	DVL2	dishevelled segment polarity protein 2	Cytoplasm	other	
[illegible]	SH3RF3	SH3RF3	SH3 domain containing ring finger 3	Other	other	
[illegible]	RCE1	RCE1	Ras converting CAAX endopeptidase 1	Cytoplasm	peptidase	
[illegible]	ASCC2	ASCC2	activating signal cointegrator 1 complex subunit 2	Nucleus	other	
[illegible]	TSPAN17	TSPAN17	tetraspanin 17	Other	enzyme	
[illegible]	DUT	DUT	deoxyuridine triphosphatase	Nucleus	enzyme	TAS-114
[illegible]	[illegible]	[illegible]	ATP synthase, H+ transporting, mitochondrial F1 compl	Cytoplasm	other	
[illegible]	SLC9A8	SLC9A8	solute carrier family 9 member A8	Plasma Membrane	transporter	
[illegible]	TMEM183A	TMEM183A	transmembrane protein 183A	Other	other	
[illegible]	CDC16	CDC16	cell division cycle 16	Nucleus	other	
[illegible]	DHX40	DHX40	DEAH-box helicase 40	Other	enzyme	
[illegible]	ARID4A	ARID4A	AT-rich interaction domain 4A	Nucleus	transcription regulator	
[illegible]	CAPZA1	CAPZA1	capping actin protein of muscle Z-line alpha subunit 1	Cytoplasm	other	
[illegible]	PLEKHM1P	PLEKHM1P	pleckstrin homology and RUN domain containing M1 ps	Other	other	
[illegible]	PCNT	PCNT	pericentrin	Cytoplasm	other	
[illegible]	RPL36AL	RPL36AL	ribosomal protein L36a like	Cytoplasm	other	
[illegible]	ATAD1	ATAD1	ATPase family, AAA domain containing 1	Other	enzyme	
[illegible]	VAMP7	VAMP7	vesicle associated membrane protein 7	Cytoplasm	transporter	
[illegible]	FOXN3	FOXN3	forkhead box N3	Nucleus	other	
[illegible]	JAGN1	JAGN1	jagunal homolog 1	Cytoplasm	other	
[illegible]	CTNNBL1	CTNNBL1	catenin beta like 1	Nucleus	other	
[illegible]	GMPR2	GMPR2	guanosine monophosphate reductase 2	Cytoplasm	enzyme	
[illegible]	EBLN2	EBLN2	endogenous Bornavirus like nucleoprotein 2	Other	other	
[illegible]	[illegible]	[illegible]	[illegible] domain containing 2	Other	other	
[illegible]	WDR48	WDR48	WD repeat domain 48	Cytoplasm	peptidase	
[illegible]	NR2C2	NR2C2	nuclear receptor subfamily 2 group C member 2	Nucleus	ligand-dependent nuclear rec	
[illegible]	IK					
[illegible]	NUDT22	NUDT22	nudix hydrolase 22	Nucleus	other	
[illegible]	TAF13	TAF13	TATA-box binding protein associated factor 13	Nucleus	transcription regulator	
[illegible]	BUB3	BUB3	BUB3, mitotic checkpoint protein	Nucleus	other	

[illegible]	VAC14	VAC14	Vac14, PIKFYVE complex component	Cytoplasm	other	
[illegible]	ARID2	ARID2	AT-rich interaction domain 2	Nucleus	transcription regulator	
[illegible]	PIM3	PIM3	Pim-3 proto-oncogene, serine/threonine kinase	Cytoplasm	kinase	[illegible], AZD-1208, LGH
[illegible]	ZNF800	ZNF800	zinc finger protein 800	Other	other	
[illegible]	CRTC2	CRTC2	CREB regulated transcription coactivator 2	Nucleus	other	
[illegible]	ASCC3	ASCC3	activating signal cointegrator 1 complex subunit 3	Cytoplasm	enzyme	
[illegible]	WDR33	WDR33	WD repeat domain 33	Nucleus	other	
[illegible]	AP3B1	AP3B1	adaptor related protein complex 3 beta 1 subunit	Plasma Membrane	transporter	
[illegible]	[illegible]	LINC01578	long intergenic non-protein coding RNA 1578	Other	other	
[illegible]	SEC22C	SEC22C	SEC22 homolog C, vesicle trafficking protein	Cytoplasm	other	
[illegible]	FAM98C	FAM98C	family with sequence similarity 98 member C	Other	other	
[illegible]	DNASE1L1	DNASE1L1	deoxyribonuclease 1 like 1	Cytoplasm	enzyme	
[illegible]	MAP4K2	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	Cytoplasm	kinase	
[illegible]	SCRIB					
[illegible]	CAMK4	CAMK4	calcium/calmodulin dependent protein kinase IV	Nucleus	kinase	
[illegible]	WRNIP1	WRNIP1	Werner helicase interacting protein 1	Nucleus	enzyme	
[illegible]	SNAPC3	SNAPC3	small nuclear RNA activating complex polypeptide 3	Nucleus	transcription regulator	
[illegible]	GTF3C2	GTF3C2	general transcription factor IIIC subunit 2	Nucleus	transcription regulator	
[illegible]	WWP1	WWP1	WW domain containing E3 ubiquitin protein ligase 1	Cytoplasm	enzyme	
[illegible]	DTD1	DTD1	D-tyrosyl-tRNA deacylase 1	Cytoplasm	enzyme	
[illegible]	KIAA1147	KIAA1147	KIAA1147	Other	other	
[illegible]	ZNF614	ZNF614	zinc finger protein 614	Other	other	
[illegible]	PSMD6	PSMD6	proteasome 26S subunit, non-ATPase 6	Cytoplasm	enzyme	
[illegible]	TGOLN2	TGOLN2	trans-golgi network protein 2	Cytoplasm	other	
[illegible]	SYNE3	SYNE3	spectrin repeat containing nuclear envelope family me	Nucleus	other	
[illegible]	NCBP2	NCBP2	nuclear cap binding protein subunit 2	Nucleus	other	
[illegible]	SMARCE1	SMARCE1	SWI/SNF related, matrix associated, actin dependent re	Nucleus	transcription regulator	
[illegible]	IFFO1	IFFO1	intermediate filament family orphan 1	Other	other	
[illegible]	PARP15	PARP15	poly(ADP-ribose) polymerase family member 15	Other	other	
[illegible]	AAGAB	AAGAB	alpha and gamma adaptin binding protein	Cytoplasm	other	
[illegible]	ECHS1	ECHS1	enoyl-CoA hydratase, short chain 1	Cytoplasm	enzyme	
[illegible]	MSANTD3	MSANTD3	Myb/SANT DNA binding domain containing 3	Other	other	
[illegible]	SH3BP5L	SH3BP5L	SH3 binding domain protein 5 like	Other	other	
[illegible]	DHX37	DHX37	DEAH-box helicase 37	Extracellular Space	other	
[illegible]	VTI1B	VTI1B	vesicle transport through interaction with t-SNAREs 1B	Plasma Membrane	transporter	
[illegible]	COPB1	COPB1	coatomer protein complex subunit beta 1	Cytoplasm	transporter	
[illegible]	NOSIP	NOSIP	nitric oxide synthase interacting protein	Cytoplasm	other	
[illegible]	COPS7B	COPS7B	COP9 signalosome subunit 7B	Cytoplasm	other	
[illegible]	RCC1	RCC1	regulator of chromosome condensation 1	Cytoplasm	other	
[illegible]	[illegible]	[illegible]	PMS1 homolog 2, mismatch repair system component p	Other	other	
[illegible]	ARHGAP12	ARHGAP12	Rho GTPase activating protein 12	Cytoplasm	other	
[illegible]	SRSF1	SRSF1	serine and arginine rich splicing factor 1	Nucleus	other	
[illegible]	ATXN2L	ATXN2L	ataxin 2 like	Nucleus	other	
[illegible]	DDX39	DDX39	DEAD-box helicase 39	Other	enzyme	
[illegible]	ZDBF2	ZDBF2	zinc finger DBF-type containing 2	Other	other	
[illegible]	IL12RB1	IL12RB1	interleukin 12 receptor subunit beta 1	Plasma Membrane	transmembrane recepto	
[illegible]	PIK3C3	PIK3C3	phosphatidylinositol 3-kinase catalytic subunit type 3	Cytoplasm	kinase	
[illegible]	ORC4	ORC4	origin recognition complex subunit 4	Nucleus	other	
[illegible]	ELF1	ELF1	E74 like ETS transcription factor 1	Nucleus	transcription regulator	
[illegible]	ZNF821	ZNF821	zinc finger protein 821	Other	other	
[illegible]	MDK	MDK	midkine (neurite growth-promoting factor 2)	Extracellular Space	growth factor	
[illegible]	AHCTF1	AHCTF1	AT-hook containing transcription factor 1	Nucleus	transcription regulator	
[illegible]	CHFR	CHFR	checkpoint with forkhead and ring finger domains	Nucleus	enzyme	
[illegible]	NA					
[illegible]	[illegible]					
[illegible]	RPL7AP6	RPL7AP6	ribosomal protein L7a pseudogene 6	Other	other	
[illegible]	MRPS9	MRPS9	mitochondrial ribosomal protein S9	Cytoplasm	other	
[illegible]	CUL4A	CUL4A	cullin 4A	Nucleus	other	
[illegible]	FGFR1OP2	FGFR1OP2	FGFR1 oncogene partner 2	Cytoplasm	kinase	
[illegible]	CCDC59	CCDC59	coiled-coil domain containing 59	Nucleus	other	
[illegible]	SP140	SP140	SP140 nuclear body protein	Nucleus	transcription regulator	
[illegible]	FASTKD3	FASTKD3	FAST kinase domains 3	Cytoplasm	other	
[illegible]	SBDSP1	SBDSP1	Shwachman-Bodian-Diamond syndrome pseudogene 1	Other	other	
[illegible]	ZKSCAN5	ZKSCAN5	zinc finger with KRAB and SCAN domains 5	Nucleus	transcription regulator	
[illegible]	FARSB	FARSB	phenylalanyl-tRNA synthetase beta subunit	Cytoplasm	enzyme	
[illegible]	LDLRAP1	LDLRAP1	low density lipoprotein receptor adaptor protein 1	Cytoplasm	transporter	
[illegible]	VIPAS39	VIPAS39	VPS33B interacting protein, apical-basolateral polarity	Plasma Membrane	other	
[illegible]	GPR132	GPR132	G protein-coupled receptor 132	Plasma Membrane	-protein coupled recepto	
[illegible]	[illegible]	MRNIP	MRN complex interacting protein	Nucleus	other	
[illegible]	SLC25A12	SLC25A12	solute carrier family 25 member 12	Cytoplasm	transporter	
[illegible]	RFXAP	RFXAP	regulatory factor X associated protein	Nucleus	transcription regulator	
[illegible]	RPA2	RPA2	replication protein A2	Nucleus	other	
[illegible]	RCN2	RCN2	reticulocalbin 2	Cytoplasm	other	
[illegible]	ZNF608	ZNF608	zinc finger protein 608	Other	other	
[illegible]	EHMT1	EHMT1	euchromatic histone lysine methyltransferase 1	Nucleus	transcription regulator	
[illegible]	NAF1	NAF1	nuclear assembly factor 1 ribonucleoprotein	Cytoplasm	other	
[illegible]	LTV1	LTV1	LTV1 ribosome biogenesis factor	Other	other	
[illegible]	ZEB1	ZEB1	zinc finger E-box binding homeobox 1	Nucleus	transcription regulator	
[illegible]	THAP3	THAP3	THAP domain containing 3	Nucleus	other	
[illegible]	SERPINF1	SERPINF1	serpin family F member 1	Extracellular Space	other	
[illegible]	EFTUD2	EFTUD2	elongation factor Tu GTP binding domain containing 2	Nucleus	enzyme	
[illegible]	PMM1	PMM1	phosphomannomutase 1	Cytoplasm	enzyme	
[illegible]	AKAP10	AKAP10	A-kinase anchoring protein 10	Cytoplasm	other	
[illegible]	ATL2	ATL2	atlastin GTPase 2	Cytoplasm	other	
[illegible]	ZNF292	ZNF292	zinc finger protein 292	Nucleus	transcription regulator	
[illegible]	CENPC	CENPC	centromere protein C	Nucleus	other	
[illegible]	ARF5	ARF5	ADP ribosylation factor 5	Cytoplasm	enzyme	
[illegible]	IGSF8	IGSF8	immunoglobulin superfamily member 8	Plasma Membrane	other	
[illegible]	CD97	ADGRE5	adhesion G protein-coupled receptor E5	Plasma Membrane	-protein coupled recepto	
[illegible]	TRIM52	TRIM52	tripartite motif containing 52	Other	other	
[illegible]	MRPL4	MRPL4	mitochondrial ribosomal protein L4	Cytoplasm	other	
[illegible]	PARP2	PARP2	poly(ADP-ribose) polymerase 2	Nucleus	enzyme	[illegible], E7449, ABT-767, C
[illegible]	SRSF8	SRSF8	serine and arginine rich splicing factor 8	Nucleus	other	
[illegible]	EIF3L	EIF3L	eukaryotic translation initiation factor 3 subunit L	Cytoplasm	other	
[illegible]	AKAP8L	AKAP8L	A-kinase anchoring protein 8 like	Nucleus	other	
[illegible]	TMEM108	TMEM108	transmembrane protein 108	Extracellular Space	other	
[illegible]	RPUSD4	RPUSD4	RNA pseudouridylate synthase domain containing 4	Cytoplasm	other	
[illegible]	SMYD5	SMYD5	SMYD family member 5	Other	other	
[illegible]	CAPN10	CAPN10	calpain 10	Cytoplasm	peptidase	
[illegible]	RNF2	RNF2	ring finger protein 2	Nucleus	transcription regulator	
[illegible]	ZNF44	ZNF44	zinc finger protein 44	Nucleus	other	
[illegible]	BICD2	BICD2	BICD cargo adaptor 2	Cytoplasm	other	
[illegible]	UGGT1	UGGT1	UDP-glucose glycoprotein glucosyltransferase 1	Cytoplasm	enzyme	
[illegible]	SLC9A8	SLC9A8	solute carrier family 9 member A8	Cytoplasm	transporter	
[illegible]	TBC1D22A	TBC1D22A	TBC1 domain family member 22A	Other	other	
[illegible]	CERS4	CERS4	ceramide synthase 4	Cytoplasm	transcription regulator	
[illegible]	MAFG	MAFG	MAF bZIP transcription factor G	Nucleus	transcription regulator	
[illegible]	PIGB	PIGB	phosphatidylinositol glycan anchor biosynthesis class B	Cytoplasm	enzyme	
[illegible]	NBEAL2	NBEAL2	neurobeachin like 2	Cytoplasm	other	
[illegible]	ZNF526	ZNF526	zinc finger protein 526	Nucleus	transcription regulator	
[illegible]	ZNF865	ZNF865	zinc finger protein 865	Other	other	
[illegible]	SEC23A	SEC23A	Sec23 homolog A, coat complex II component	Cytoplasm	transporter	
[illegible]	NOTCH1	NOTCH1	notch 1	Plasma Membrane	transcription regulator	OMP-52M51
[illegible]	WDR83	WDR83	WD repeat domain 83	Nucleus	other	
[illegible]	THYN1	THYN1	thymocyte nuclear protein 1	Nucleus	other	
[illegible]	RBM34	RBM34	RNA binding motif protein 34	Nucleus	other	
[illegible]	IPCEF1	IPCEF1	interaction protein for cytohesin exchange factors 1	Cytoplasm	enzyme	
[illegible]	FRAT2	FRAT2	FRAT2, WNT signaling pathway regulator	Cytoplasm	other	
[illegible]	[illegible]	[illegible]	SH3 domain containing GRB2 like 1, endophilin A2 pseu	Other	other	
[illegible]	SCYL2	SCYL2	SCY1 like pseudokinase 2	Cytoplasm	other	
[illegible]	ZMAT2	ZMAT2	zinc finger matrin-type 2	Nucleus	other	
[illegible]	PHF3	PHF3	PHD finger protein 3	Nucleus	other	
[illegible]	CCDC126	CCDC126	coiled-coil domain containing 126	Other	other	
[illegible]	MAT2A	MAT2A	methionine adenosyltransferase 2A	Cytoplasm	enzyme	
[illegible]	VWA9	INTS14	integrator complex subunit 14	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	PRR7	PRR7	proline rich 7, synaptic	Other	other	
[illegible]	USP42	USP42	ubiquitin specific peptidase 42	Nucleus	peptidase	
[illegible]	PDE7A	PDE7A	phosphodiesterase 7A	Cytoplasm	enzyme	e, dipyridamole, ketot
[illegible]	OAT	OAT	ornithine aminotransferase	Cytoplasm	enzyme	
[illegible]	SPG11	SPG11	spastic paraplegia 11 (autosomal recessive)	Cytoplasm	other	
[illegible]	IPO9	IPO9	importin 9	Nucleus	transporter	
[illegible]	UBE2L3	UBE2L3	ubiquitin conjugating enzyme E2 L3	Nucleus	enzyme	
[illegible]	AGTPBP1	AGTPBP1	ATP/GTP binding protein 1	Nucleus	peptidase	
[illegible]	STAT5B	STAT5B	signal transducer and activator of transcription 5B	Nucleus	transcription regulator	
[illegible]	NPEPPS	NPEPPS	aminopeptidase puromycin sensitive	Cytoplasm	peptidase	
[illegible]	TRAPPC2	TRAPPC2	trafficking protein particle complex 2	Cytoplasm	other	
[illegible]	ZNHIT1	ZNHIT1	zinc finger HIT-type containing 1	Nucleus	other	
[illegible]	MRPL23	MRPL23	mitochondrial ribosomal protein L23	Cytoplasm	other	
[illegible]	NDUFB10	NDUFB10	NADH:ubiquinone oxidoreductase subunit B10	Cytoplasm	enzyme	
[illegible]	PRDX3P1	PRDX3P1	peroxiredoxin 3 pseudogene 1	Other	other	
[illegible]	DPF2	DPF2	double PHD fingers 2	Nucleus	other	
[illegible]	LSM12	LSM12	LSM12 homolog	Other	other	
[illegible]	BRE	BRE	brain and reproductive organ-expressed (TNFRSF1A mo	Cytoplasm	other	
[illegible]	RNF126	RNF126	ring finger protein 126	Other	enzyme	
[illegible]	C17orf70	FAAP100	Fanconi anemia core complex associated protein 100	Nucleus	other	
[illegible]	KPNB1	KPNB1	karyopherin subunit beta 1	Nucleus	transporter	
[illegible]	TAF6	TAF6	TATA-box binding protein associated factor 6	Nucleus	transcription regulator	
[illegible]	NOG	NOG	noggin	Extracellular Space	growth factor	
[illegible]	CRABP2	CRABP2	cellular retinoic acid binding protein 2	Cytoplasm	transporter	
[illegible]	[illegible]	[illegible]	uncharacterized LOC[illegible]	Other	other	
[illegible]	UQCR11	UQCR11	ubiquinol-cytochrome c reductase, complex III subunit)	Cytoplasm	enzyme	
[illegible]	COASY	COASY	Coenzyme A synthase	Cytoplasm	kinase	
[illegible]	SNHG7	SNHG7	small nucleolar RNA host gene 7	Other	other	
[illegible]	TPCN1	TPCN1	two pore segment channel 1	Plasma Membrane	ion channel	
[illegible]	OXCT1	OXCT1	3-oxoacid CoA-transferase 1	Cytoplasm	enzyme	
[illegible]	ZNF776	ZNF776	zinc finger protein 776	Other	other	
[illegible]	C2CD3	C2CD3	C2 calcium dependent domain containing 3	Cytoplasm	other	
[illegible]	MRPL40	MRPL40	mitochondrial ribosomal protein L40	Cytoplasm	other	
[illegible]	HGSNAT	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	Cytoplasm	enzyme	
[illegible]	C18orf21	C18orf21	chromosome 18 open reading frame 21	Other	other	
[illegible]	CDYL	CDYL	chromodomain Y-like	Nucleus	transcription regulator	
[illegible]	ITPKB	ITPKB	inositol-trisphosphate 3-kinase B	Cytoplasm	kinase	
[illegible]	HERC3	HERC3	HECT and RLD domain containing E3 ubiquitin protein l	Cytoplasm	enzyme	
[illegible]	[illegible]	RPS27AP16	ribosomal protein S27a pseudogene 16	Other	other	
[illegible]	PIP4K2C	PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase type 2 gamm	Cytoplasm	kinase	
[illegible]	RAD54L2	RAD54L2	RAD54-like 2 (S. cerevisiae)	Nucleus	transcription regulator	
[illegible]	RPRD1B	RPRD1B	regulation of nuclear pre-mRNA domain containing 1B	Nucleus	other	
[illegible]	RAB11B	RAB11B	RAB11B, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	DNAJB2	DNAJB2	DnaJ heat shock protein family (Hsp40) member B2	Nucleus	other	
[illegible]	DPP4	DPP4	dipeptidyl peptidase 4	Plasma Membrane	peptidase	tin/alogliptin, alogli
[illegible]	PEX6	PEX6	peroxisomal biogenesis factor 6	Cytoplasm	enzyme	
[illegible]	[illegible]	[illegible]	ATP synthase, H+ transporting, mitochondrial Fo compl	Cytoplasm	transporter	
[illegible]	[illegible]					
[illegible]	ATP1A1	ATP1A1	ATPase Na+/K+ transporting subunit alpha 1	Plasma Membrane	transporter	ne, ethacrynic acid, r
[illegible]	GCFC2	GCFC2	GC-rich sequence DNA-binding factor 2	Nucleus	transcription regulator	
[illegible]	VRK3	VRK3	vaccinia related kinase 3	Nucleus	kinase	
[illegible]	ARHGEF7	ARHGEF7	Rho guanine nucleotide exchange factor 7	Cytoplasm	other	
[illegible]	CCDC43	CCDC43	coiled-coil domain containing 43	Other	other	
[illegible]	OAS3	OAS3	2'-5'-oligoadenylate synthetase 3	Cytoplasm	enzyme	
[illegible]	SMG9	SMG9	SMG9, nonsense mediated mRNA decay factor	Cytoplasm	other	
[illegible]	DNAJC1	DNAJC1	DnaJ heat shock protein family (Hsp40) member C1	Cytoplasm	other	
[illegible]	PARP14	PARP14	poly(ADP-ribose) polymerase family member 14	Cytoplasm	other	
[illegible]	L3MBTL2	L3MBTL2	L3MBTL2 polycomb repressive complex 1 subunit	Nucleus	transcription regulator	
[illegible]	C9orf114	SPOUT1	SPOUT domain containing methyltransferase 1	Nucleus	other	
[illegible]	XPO5	XPO5	exportin 5	Nucleus	transporter	
[illegible]	SLC25A44	SLC25A44	solute carrier family 25 member 44	Cytoplasm	transporter	
[illegible]	FAM104A	FAM104A	family with sequence similarity 104 member A	Other	other	
[illegible]	CAPN7	CAPN7	calpain 7	Cytoplasm	peptidase	
[illegible]	STARD7	STARD7	StAR related lipid transfer domain containing 7	Cytoplasm	other	
[illegible]	DRAP1	DRAP1	DR1 associated protein 1	Nucleus	transcription regulator	
[illegible]	[illegible]	[illegible]	SH3 domain containing [illegible]	Cytoplasm	other	
[illegible]	RBM48	RBM48	RNA binding motif protein 48	Nucleus	other	
[illegible]	ECI1	ECI1	enoyl-CoA delta isomerase 1	Cytoplasm	enzyme	
[illegible]	PSMD2	PSMD2	proteasome 26S subunit, non-ATPase 2	Cytoplasm	other	[illegible]
[illegible]	MAPKAPK5	MAPKAPK5	mitogen-activated protein kinase-activated protein kina	Cytoplasm	kinase	
[illegible]	[illegible]	[illegible]	[illegible] binding protein 2	Cytoplasm	enzyme	
[illegible]	TXLNA	TXLNA	taxilin alpha	Extracellular Space	cytokine	
[illegible]	[illegible]					
[illegible]	U2SURP	U2SURP	U2 snRNP associated SURP domain containing	Nucleus	other	
[illegible]	ZNF282	ZNF282	zinc finger protein 282	Nucleus	transcription regulator	
[illegible]	KIAA0020	PUM3	pumilio RNA binding family member 3	Nucleus	other	
[illegible]	SDF2L1	SDF2L1	stromal cell derived factor 2 like 1	Cytoplasm	other	
[illegible]	XPO7	XPO7	exportin 7	Nucleus	transporter	
[illegible]	WASH7P	WASH7P	WAS protein family homolog 7 pseudogene	Other	other	
[illegible]	ETFB	ETFB	electron transfer flavoprotein beta subunit	Cytoplasm	transporter	
[illegible]	[illegible]	[illegible]	transmembrane and immunoglobulin domain containin	Other	other	
[illegible]	UBE4A	UBE4A	ubiquitination factor E4A	Cytoplasm	enzyme	
[illegible]	TOB2	TOB2	transducer of ERBB2, 2	Nucleus	other	
[illegible]	RBM43	RBM43	RNA binding motif protein 43	Other	other	
[illegible]	FAM98B	FAM98B	family with sequence similarity 98 member B	Nucleus	other	
[illegible]	COL6A2	COL6A2	collagen type VI alpha 2 chain	Extracellular Space	other	ase clostridium histo
[illegible]	KIAA0355	KIAA0355	KIAA0355	Extracellular Space	other	
[illegible]	[illegible]	[illegible]	[illegible] domain containing 1	Other	other	
[illegible]	[illegible]	[illegible]	ATP binding cassette subfamily [illegible] member 1	Plasma Membrane	transporter	
[illegible]	TRIB2	TRIB2	tribbles pseudokinase 2	Plasma Membrane	kinase	
[illegible]	SPTBN1	SPTBN1	spectrin beta, non-erythrocytic 1	Plasma Membrane	other	
[illegible]	XKR8	XKR8	XK related 8	Plasma Membrane	other	
[illegible]	ZFPM1	ZFPM1	zinc finger protein, FOG family member 1	Nucleus	transcription regulator	
[illegible]	ZNF529	ZNF529	zinc finger protein 529	Other	other	
[illegible]	CETN2	CETN2	centrin 2	Nucleus	enzyme	
[illegible]	REXO2	REXO2	RNA exonuclease 2	Cytoplasm	enzyme	
[illegible]	TP53INP2	TP53INP2	tumor protein p53 inducible nuclear protein 2	Nucleus	other	
[illegible]	HNRNPA1L2	HNRNPA1L2	heterogeneous nuclear ribonucleoprotein A1 like 2	Other	other	
[illegible]	POC5	POC5	POC5 centriolar protein	Cytoplasm	other	

[illegible]	NUP54	NUP54	nucleoporin 54	Nucleus	transporter	
[illegible]	AIFM1	AIFM1	apoptosis inducing factor mitochondria associated 1	Cytoplasm	enzyme	
[illegible]	ZC3H13	ZC3H13	zinc finger CCCH-type containing 13	Extracellular Space	other	
[illegible]	C4orf46	C4orf46	chromosome 4 open reading frame 46	Other	other	
[illegible]	COMMD3	COMMD3	COMM domain containing 3	Extracellular Space	other	
[illegible]	AGGF1	AGGF1	angiogenic factor with G-patch and FHA domains 1	Cytoplasm	other	
[illegible]	KDM8	KDM8	lysine demethylase 8	Nucleus	enzyme	
[illegible]	WDR36	WDR36	WD repeat domain 36	Extracellular Space	other	
[illegible]	KATNB1	KATNB1	katanin regulatory subunit B1	Cytoplasm	enzyme	
[illegible]	WDFY2	WDFY2	WD repeat and FYVE domain containing 2	Cytoplasm	other	
[illegible]	CELF2	CELF2	CUGBP Elav-like family member 2	Nucleus	other	
[illegible]	RSPRY1	RSPRY1	ring finger and SPRY domain containing 1	Other	other	
[illegible]	BRD8	BRD8	bromodomain containing 8	Nucleus	transcription regulator	
[illegible]	CNDP2	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)	Cytoplasm	peptidase	
[illegible]	BATF	BATF	basic leucine zipper ATF-like transcription factor	Nucleus	transcription regulator	
[illegible]	ATG14	ATG14	autophagy related 14	Cytoplasm	other	
[illegible]	TMEM214	TMEM214	transmembrane protein 214	Extracellular Space	other	
[illegible]	ZNF350	ZNF350	zinc finger protein 350	Other	other	
[illegible]	GIMAP5	GIMAP5	GTPase, IMAP family member 5	Cytoplasm	other	
[illegible]	TEX10	TEX10	testis expressed 10	Nucleus	other	
[illegible]	GCNT4	GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2	Cytoplasm	enzyme	
[illegible]	ZNF471	ZNF471	zinc finger protein 471	Nucleus	other	
[illegible]	RASA2	RASA2	RAS p21 protein activator 2	Cytoplasm	other	
[illegible]	PRRC2B	PRRC2B	proline rich coiled-coil 2B	Other	other	
[illegible]	TPGS2	TPGS2	tubulin polyglutamylase complex subunit 2	Nucleus	other	
[illegible]	KDM4A	KDM4A	lysine demethylase 4A	Nucleus	enzyme	
[illegible]	MCM8	MCM8	minichromosome maintenance complex component 8	Nucleus	enzyme	
[illegible]	NDUFS2	NDUFS2	NADH:ubiquinone oxidoreductase core subunit S2	Cytoplasm	enzyme	
[illegible]	BTBD7	BTBD7	BTB domain containing 7	Nucleus	other	
[illegible]	CLEC2D	CLEC2D	C-type lectin domain family 2 member D	Plasma Membrane	transmembrane receptor	
[illegible]	MAPK13	MAPK13	mitogen-activated protein kinase 13	Cytoplasm	kinase	talmapimod
[illegible]	SENP6	SENP6	SUMO1/sentrin specific peptidase 6	Cytoplasm	peptidase	
[illegible]	SOD1	SOD1	superoxide dismutase 1	Cytoplasm	enzyme	
[illegible]	LINC00[illegible]	LINC00[illegible]		Other	other	
[illegible]	EXOSC9	EXOSC9	exosome component 9	Nucleus	enzyme	
[illegible]	REM2	REM2	RRAD and GEM like GTPase 2	Plasma Membrane	enzyme	
[illegible]	OSTC	OSTC	oligosaccharyltransferase complex non-catalytic subunit	Cytoplasm	enzyme	
[illegible]	PDLIM2	PDLIM2	PDZ and LIM domain 2	Cytoplasm	other	
[illegible]	MPHOSPH8	MPHOSPH8	M-phase phosphoprotein 8	Nucleus	transcription regulator	
[illegible]	ARRDC2	ARRDC2	arrestin domain containing 2	Other	other	
[illegible]	CD7	CD7	CD7 molecule	Plasma Membrane	other	
[illegible]	ZER1	ZER1	zyg-11 related cell cycle regulator	Other	enzyme	
[illegible]	SLC2A4RG	SLC2A4RG	SLC2A4 regulator	Cytoplasm	transcription regulator	
[illegible]	EPB41	EPB41	erythrocyte membrane protein band 4.1	Plasma Membrane	other	
[illegible]	TRMT44	TRMT44	tRNA methyltransferase 44 homolog (S. cerevisiae)	Other	other	
[illegible]	STX4	STX4	syntaxin 4	Plasma Membrane	transporter	
[illegible]	TMEM141	TMEM141	transmembrane protein 141	Other	other	
[illegible]	YIPF5	YIPF5	Yip1 domain family member 5	Cytoplasm	other	
[illegible]	SNX29	SNX29	sorting nexin 29	Cytoplasm	transporter	
[illegible]	TCEA3	TCEA3	transcription elongation factor A3	Nucleus	transcription regulator	
[illegible]	COX16	COX16	COX16, cytochrome c oxidase assembly homolog	Cytoplasm	other	
[illegible]	H2AFJ	H2AFJ	H2A histone family member J	Cytoplasm	other	
[illegible]	GIMAP4	GIMAP4	GTPase, IMAP family member 4	Nucleus	other	
[illegible]	SOX13	SOX13	SRY-box 13	Nucleus	transcription regulator	
[illegible]	YEATS2	YEATS2	YEATS domain containing 2	Nucleus	transcription regulator	
[illegible]	PTPN7	PTPN7	protein tyrosine phosphatase, non-receptor type 7	Cytoplasm	phosphatase	
[illegible]	SLC12A2	SLC12A2	solute carrier family 12 member 2	Plasma Membrane	transporter	[illegible]
[illegible]	PTPMT1	PTPMT1	protein tyrosine phosphatase, mitochondrial 1	Cytoplasm	phosphatase	
[illegible]	TUBA1A	TUBA1A	tubulin alpha 1a	Cytoplasm	other	[illegible]
[illegible]	AIP	AIP	aryl hydrocarbon receptor interacting protein	Nucleus	transcription regulator	
[illegible]	GADD45A	GADD45A	growth arrest and DNA damage inducible alpha	Nucleus	other	
[illegible]	SMARCAD1	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent re	Nucleus	enzyme	
[illegible]	[illegible]	TRIM73/TRIM74	tripartite motif containing 74	Cytoplasm	other	
[illegible]	MCTS1	MCTS1	MCTS1, re-initiation and release factor	Cytoplasm	other	
[illegible]	LPCAT4	LPCAT4	lysophosphatidylcholine acyltransferase 4	Cytoplasm	enzyme	
[illegible]	NAE1	NAE1	NEDD8 activating enzyme E1 subunit 1	Cytoplasm	enzyme	
[illegible]	LSG1	LSG1	large 60S subunit nuclear export GTPase 1	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	RBPJ	RBPJ	recombination signal binding protein for immunoglobul	Nucleus	transcription regulator	
[illegible]	NONO	NONO	non-POU domain containing, octamer-binding	Nucleus	other	
[illegible]	FCHO1	FCHO1	FCH domain only 1	Plasma Membrane	other	
[illegible]	CNST	CNST	consortin, connexin sorting protein	Cytoplasm	other	
[illegible]	USP5	USP5	ubiquitin specific peptidase 5	Cytoplasm	peptidase	
[illegible]	DRG2	DRG2	developmentally regulated GTP binding protein 2	Cytoplasm	other	
[illegible]	KLF5	KLF5	Kruppel like factor 5	Nucleus	transcription regulator	
[illegible]	REV1	REV1	REV1, DNA directed polymerase	Nucleus	enzyme	
[illegible]	TTC32	TTC32	tetratricopeptide repeat domain 32	Other	other	
[illegible]	NPM1P26	NPM1P26	nucleophosmin 1 pseudogene 26	Other	other	
[illegible]	RPL7P1	RPL7P1	ribosomal protein L7 pseudogene 1	Other	other	
[illegible]	ZCCHC1	ZCCHC1	zinc finger CCHC-type containing 1	Nucleus	other	
[illegible]	GLCCI1	GLCCI1	glucocorticoid induced 1	Cytoplasm	other	
[illegible]	MRPL15	MRPL15	mitochondrial ribosomal protein L15	Cytoplasm	other	
[illegible]	TMEM101	TMEM101	transmembrane protein 101	Extracellular Space	other	
[illegible]	RBBP5	RBBP5	RB binding protein 5, histone lysine methyltransferase c	Nucleus	enzyme	
[illegible]	NARF	NARF	nuclear prelamin A recognition factor	Nucleus	enzyme	
[illegible]	PRKAR1B	PRKAR1B	protein kinase cAMP-dependent type I regulatory subun	Cytoplasm	kinase	
[illegible]	BNIP3	BNIP3	BCL2 interacting protein 3	Cytoplasm	other	
[illegible]	PDE4D	PDE4D	phosphodiesterase 4D	Cytoplasm	enzyme	[illegible]
[illegible]	C8orf82	C8orf82	chromosome 8 open reading frame 82	Other	other	
[illegible]	YARS2	YARS2	tyrosyl-tRNA synthetase 2	Cytoplasm	enzyme	
[illegible]	TMEM106C	TMEM106C	transmembrane protein 106C	Other	other	
[illegible]	[illegible]					
[illegible]	FBXO18	FBXO18	F-box protein, helicase, 18	Nucleus	enzyme	
[illegible]	MIA3	MIA3	MIA family member 3, ER export factor	Cytoplasm	transporter	
[illegible]	WBP4	WBP4	WW domain binding protein 4	Cytoplasm	other	
[illegible]	ADAM10	ADAM10	ADAM metallopeptidase domain 10	Plasma Membrane	peptidase	
[illegible]	[illegible]	BEX3	brain expressed X-linked 3	Cytoplasm	other	
[illegible]	CASP2	CASP2	caspase 2	Cytoplasm	peptidase	
[illegible]	TMEM156	TMEM156	transmembrane protein 156	Other	kinase	
[illegible]	[illegible]	[illegible]	[illegible] domain containing	Other	other	
[illegible]	C19orf60	C19orf60	chromosome 19 open reading frame 60	Other	other	
[illegible]	C12orf29	C12orf29	chromosome 12 open reading frame 29	Other	other	
[illegible]	PDHA1	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	Cytoplasm	enzyme	
[illegible]	PPP2R5A	PPP2R5A	protein phosphatase 2 regulatory subunit B'alpha	Cytoplasm	phosphatase	
[illegible]	GTF3C5	GTF3C5	general transcription factor IIIC subunit 5	Nucleus	transcription regulator	
[illegible]	RAB32	RAB32	RAB32, member RAS oncogene family	Cytoplasm	enzyme	
[illegible]	[illegible]	[illegible]	[illegible] related protein	Cytoplasm	other	
[illegible]	MORC3	MORC3	MORC family CW-type zinc finger 3	Nucleus	other	
[illegible]	ZMIZ2	ZMIZ2	zinc finger MIZ-type containing 2	Nucleus	transcription regulator	
[illegible]	CCDC159	CCDC159	coiled-coil domain containing 159	Other	other	
[illegible]	NHP2	NHP2	NHP2 ribonucleoprotein	Nucleus	other	
[illegible]	DHX16	DHX16	DEAH-box helicase 16	Nucleus	enzyme	
[illegible]	TUBGCP3	TUBGCP3	tubulin gamma complex associated protein 3	Cytoplasm	other	
[illegible]	RRP8	RRP8	ribosomal RNA processing 8, methyltransferase, homol	Nucleus	enzyme	
[illegible]	LANCL1	LANCL1	LanC like 1	Plasma Membrane	other	
[illegible]	TMEM80	TMEM80	transmembrane protein 80	Other	other	
[illegible]	CRNKL1	CRNKL1	crooked neck pre-mRNA splicing factor 1	Nucleus	other	
[illegible]	PHF8	PHF8	PHD finger protein 8	Nucleus	enzyme	
[illegible]	PRDX2	PRDX2	peroxiredoxin 2	Cytoplasm	enzyme	
[illegible]	MBIP	MBIP	MAP3K12 binding inhibitory protein 1	Nucleus	other	
[illegible]	SFMBT2	SFMBT2	Scm-like with four mbt domains 2	Nucleus	other	
[illegible]	SLC25A32	SLC25A32	solute carrier family 25 member 32	Cytoplasm	transporter	
[illegible]	CCDC88C	CCDC88C	coiled-coil domain containing 88C	Cytoplasm	other	
[illegible]	RBMX	RBMX	RNA binding motif protein, X-linked	Nucleus	other	
[illegible]	NUMA1	NUMA1	nuclear mitotic apparatus protein 1	Nucleus	other	
[illegible]	TMEM43	TMEM43	transmembrane protein 43	Nucleus	other	
[illegible]	WDR5	WDR5	WD repeat domain 5	Nucleus	enzyme	
[illegible]	TAZ	TAZ	tafazzin	Nucleus	enzyme	
[illegible]	FYN	FYN	FYN proto-oncogene, Src family tyrosine kinase	Plasma Membrane	kinase	[illegible]
[illegible]	YIF1B	YIF1B	Yip1 interacting factor homolog B, membrane traffick	Cytoplasm	other	
[illegible]	ABHD5	ABHD5	abhydrolase domain containing 5	Cytoplasm	enzyme	
[illegible]	STK25	STK25	serine/threonine kinase 25	Cytoplasm	kinase	
[illegible]	C1orf52	C1orf52	chromosome 1 open reading frame 52	Nucleus	other	
[illegible]	ZFYVE19	ZFYVE19	zinc finger FYVE-type containing 19	Cytoplasm	other	
[illegible]	FBXO45	FBXO45	F-box protein 45	Plasma Membrane	other	
[illegible]	BABAM1	BABAM1	BRISC and BRCA1 A complex member 1	Nucleus	other	
[illegible]	UNC13D	UNC13D	unc-13 homolog D	Cytoplasm	other	
[illegible]	DCAF6	DCAF6	DDB1 and CUL4 associated factor 6	Nucleus	transcription regulator	
[illegible]	ORAOV1	ORAOV1	oral cancer overexpressed 1	Other	other	
[illegible]	RWDD4	RWDD4	RWD domain containing 4	Other	other	
[illegible]	BUD13	BUD13	BUD13 homolog	Nucleus	other	
[illegible]	MON2	MON2	MON2 homolog, regulator of endosome-to-Golgi traffi	Cytoplasm	other	
[illegible]	MASTL	MASTL	microtubule associated serine/threonine kinase like	Cytoplasm	kinase	
[illegible]	AASDH	AASDH	aminoadipate-semialdehyde dehydrogenase	Other	enzyme	
[illegible]	SAAL1	SAAL1	serum amyloid A like 1	Other	other	
[illegible]	TBC1D23	TBC1D23	TBC1 domain family member 23	Cytoplasm	other	
[illegible]	ZNF827	ZNF827	zinc finger protein 827	Other	other	
[illegible]	PYURF	PYURF	PIGY upstream reading frame	Cytoplasm	other	
[illegible]	SBDS	SBDS	SBDS ribosome assembly guanine nucleotide exchange	Nucleus	other	
[illegible]	TGDS	TGDS	TDP-glucose 4,6-dehydratase	Extracellular Space	enzyme	
[illegible]	NIF3L1	NIF3L1	NGG1 interacting factor 3 like 1	Cytoplasm	other	
[illegible]	YAF2	YAF2	YY1 associated factor 2	Nucleus	transcription regulator	
[illegible]	ANKIB1	ANKIB1	ankyrin repeat and IBR domain containing 1	Nucleus	transcription regulator	
[illegible]	RP11-[illegible]					
[illegible]	GARS	GARS	glycyl-tRNA synthetase	Cytoplasm	enzyme	
[illegible]	PPP2R5B	PPP2R5B	protein phosphatase 2 regulatory subunit B'beta	Cytoplasm	phosphatase	
[illegible]	NDUFA7	NDUFA7	NADH:ubiquinone oxidoreductase subunit A7	Cytoplasm	enzyme	
[illegible]	DIDO1	DIDO1	death inducer-obliterator 1	Nucleus	other	
[illegible]	PSMC5	PSMC5	proteasome 26S subunit, ATPase 5	Nucleus	transcription regulator	
[illegible]	TMEM160	TMEM160	transmembrane protein 160	Cytoplasm	other	
[illegible]	ADAM8	ADAM8	ADAM metallopeptidase domain 8	Plasma Membrane	peptidase	
[illegible]	TRIM33	TRIM33	tripartite motif containing 33	Nucleus	transcription regulator	
[illegible]	[illegible]	LOC[illegible]	uncharacterized LOC[illegible]	Other	other	
[illegible]	DCAF4	DCAF4	DDB1 and CUL4 associated factor 4	Other	other	
[illegible]	SNRNP40	SNRNP40	small nuclear ribonucleoprotein U5 subunit 40	Nucleus	other	
[illegible]	NUDC	NUDC	nuclear distribution C, dynein complex regulator	Cytoplasm	other	
[illegible]	RYK	RYK	receptor-like tyrosine kinase	Plasma Membrane	kinase	
[illegible]	MOSPD3	MOSPD3	motile sperm domain containing 3	Other	other	
[illegible]	UROS	UROS	uroporphyrinogen III synthase	Cytoplasm	enzyme	
[illegible]	RCBTB1	RCBTB1	RCC1 and BTB domain containing protein 1	Nucleus	other	
[illegible]	PUM2	PUM2	pumilio RNA binding family member 2	Cytoplasm	other	
[illegible]	PABPN1	PABPN1	poly(A) binding protein nuclear 1	Nucleus	enzyme	
[illegible]	ITGB2-AS1	ITGB2-AS1	ITGB2 antisense RNA 1	Other	other	
[illegible]	MRPS18A	MRPS18A	mitochondrial ribosomal protein S18A	Cytoplasm	other	
[illegible]	CCDC101	SGF29	SAGA complex associated factor 29	Nucleus	other	
[illegible]	PCMTD2	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransfera	Cytoplasm	enzyme	
[illegible]	RNF25	RNF25	ring finger protein 25	Nucleus	transcription regulator	
[illegible]	[illegible]					
[illegible]	HPGD	HPGD	hydroxyprostaglandin dehydrogenase 15 (NAD)	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	EP400	EP400	E1A binding protein p400	Nucleus	other	
[illegible]	GIPC1	GIPC1	GIPC PDZ domain containing family member 1	Cytoplasm	other	
[illegible]	MFSD11	MFSD11	major facilitator superfamily domain containing 11	Other	other	
[illegible]	[illegible]	[illegible]	solute carrier family 35 member [illegible]	Other	other	
[illegible]	JMJD1C	JMJD1C	jumonji domain containing 1C	Nucleus	enzyme	
[illegible]	SUCLA2	SUCLA2	succinate-CoA ligase ADP-forming beta subunit	Cytoplasm	enzyme	
[illegible]	UBL5	UBL5	ubiquitin like 5	Cytoplasm	other	
[illegible]	TCEAL4	TCEAL4	transcription elongation factor A like 4	Other	other	
[illegible]	PACS2	PACS2	phosphofurin acidic cluster sorting protein 2	Cytoplasm	other	
[illegible]	IST1	IST1	IST1, ESCRT-III associated factor	Cytoplasm	other	
[illegible]	POLE3	POLE3	DNA polymerase epsilon 3, accessory subunit	Nucleus	enzyme	[illegible]
[illegible]	TMEM128	TMEM128	transmembrane protein 128	Other	other	
[illegible]	DGCR2	DGCR2	DiGeorge syndrome critical region gene 2	Plasma Membrane	other	
[illegible]	INPPL1	INPPL1	inositol polyphosphate phosphatase like 1	Cytoplasm	phosphatase	
[illegible]	[illegible]	[illegible]	ribosomal protein L[illegible] pseudogene 4	Other	other	
[illegible]	CSRNP2	CSRNP2	cysteine and serine rich nuclear protein 2	Nucleus	transcription regulator	
[illegible]	ZNF3	ZNF3	zinc finger protein 3	Nucleus	transcription regulator	
[illegible]	TRIM24	TRIM24	tripartite motif containing 24	Nucleus	transcription regulator	
[illegible]	TBP	TBP	TATA-box binding protein	Nucleus	transcription regulator	
[illegible]	CARD8	CARD8	caspase recruitment domain family member 8	Nucleus	other	
[illegible]	TP53	TP53	tumor protein p53	Nucleus	transcription regulator	[illegible]
[illegible]	RFT1	RFT1	RFT1 homolog	Other	other	
[illegible]	GGPS1	GGPS1	geranylgeranyl diphosphate synthase 1	Cytoplasm	enzyme	zoledronic acid
[illegible]	TUBB2A	TUBB2A	tubulin beta 2A class IIa	Cytoplasm	other	[illegible]
[illegible]	[illegible]	[illegible]	zinc finger protein [illegible]	Nucleus	other	
[illegible]	TRBV5-1	TRBV5-1	T cell receptor beta variable 5-1	Other	other	
[illegible]	ITPA	ITPA	inosine triphosphatase	Cytoplasm	enzyme	
[illegible]	METAP1	METAP1	methionyl aminopeptidase 1	Cytoplasm	peptidase	
[illegible]	NABP2	NABP2	nucleic acid binding protein 2	Nucleus	other	
[illegible]	GLT8D1	GLT8D1	glycosyltransferase 8 domain containing 1	Cytoplasm	enzyme	
[illegible]	SYNJ2	SYNJ2	synaptojanin 2	Cytoplasm	phosphatase	
[illegible]	RFX5	RFX5	regulatory factor X5	Nucleus	transcription regulator	
[illegible]	CRBN	CRBN	cereblon	Cytoplasm	enzyme	[illegible]
[illegible]	PFKP	PFKP	phosphofructokinase, platelet	Cytoplasm	kinase	
[illegible]	APOM	APOM	apolipoprotein M	Plasma Membrane	transporter	
[illegible]	[illegible]					
[illegible]	GNAQ	GNAQ	G protein subunit alpha q	Plasma Membrane	enzyme	
[illegible]	NVL	NVL	nuclear VCP-like	Nucleus	other	
[illegible]	GAS5	GAS5	growth arrest specific 5 (non-protein coding)	Other	other	
[illegible]	ZNF525	ZNF525	zinc finger protein 525	Nucleus	other	
[illegible]	UPF2	UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)	Cytoplasm	other	
[illegible]	HIST1H1E	HIST1H1E	histone cluster 1 H1 family member e	Nucleus	other	
[illegible]	IER5L	IER5L	immediate early response 5 like	Other	other	
[illegible]	PRR29	PRR29	proline rich 29	Other	other	
[illegible]	DSEL	DSEL	DSE like [illegible]	Cytoplasm	enzyme	

[illegible]	LIMS3	LIMS3	LIM domain containing 3	Nucleus	other		0.32	0.40	0.36	0.00	0.00	0.00	97	94	81	3	6	19
[illegible]	DDX39A	DDX39A	DEAD-box helicase 39A	Nucleus	enzyme		0.32	0.35	0.21	0.00	0.00	0.81	100	97	94	0	3	6
[illegible]	MTERFD2	MTERF4	mitochondrial transcription termination factor 4	Cytoplasm	other		0.32	0.28	-0.33	0.00	0.00	0.00	97	75	8	3	25	92
[illegible]	SLC7A1	SLC7A1	solute carrier family 7 member 1	Plasma Membrane	transporter		-0.50	-0.08	0.07	0.00	0.00	0.00	17	31	39	83	69	61
[illegible]	SELO	SELENOO	selenoprotein O	Extracellular Space	enzyme		0.82	0.57	1.45	0.00	0.00	0.00	89	89	100	11	11	0
[illegible]	DCXR	DCXR	dicarbonyl and L-xylulose reductase	Cytoplasm	enzyme		0.36	0.35	0.09	0.00	0.00	0.37	97	97	86	3	3	14
[illegible]	VEZT	VEZT	vezatin, adherens junctions transmembrane protein	Plasma Membrane	other		0.31	0.32	0.39	0.00	0.00	0.00	100	81	86	0	19	14
[illegible]	MCOLN1	MCOLN1	mucolipin 1	Cytoplasm	ion channel		0.42	0.34	0.36	0.00	0.00	0.00	94	81	100	6	19	0
[illegible]	TAGLN	TAGLN	transgelin	Cytoplasm	other		0.40	0.30	1.30	0.00	0.00	0.00	94	89	100	6	11	0
[illegible]	TMSB4XP8	TMSB4XP8	thymosin beta 4, X-linked pseudogene 8	Other	other		-0.39	-0.58	-0.57	0.00	0.00	0.00	9	17	36	91	83	64
[illegible]	PPP1R12A	PPP1R12A	protein phosphatase 1 regulatory subunit 12A	Cytoplasm	phosphatase		0.30	0.32	0.32	0.00	0.00	0.00	100	94	97	0	6	3
[illegible]	GATA3	GATA3	GATA binding protein 3	Nucleus	transcription regulator		0.39	0.48	-0.66	0.00	0.00	0.00	94	89	0	6	11	100
[illegible]	NA						0.36	0.13	-0.63	0.00	0.00	0.00	97	72	0	3	28	100
[illegible]	GNB5	GNB5	G protein subunit beta 5	Plasma Membrane	enzyme		0.31	0.35	0.25	0.00	0.00	0.00	97	81	86	3	19	14
[illegible]	KLHL36	KLHL36	kelch like family member 36	Cytoplasm	other		0.34	0.01	-0.34	0.00	0.01	0.00	100	53	8	0	47	92
[illegible]	AKTIP	AKTIP	AKT interacting protein	Cytoplasm	other		0.36	0.26		0.00	0.00		97	97		3	3	
[illegible]	GATC	GATC	glutamyl-tRNA amidotransferase subunit C	Nucleus	enzyme		0.75	0.34		0.00	0.00		100	75		0	25	
[illegible]	COPS6	COPS6	COP9 signalosome subunit 6	Nucleus	other		0.37	0.48	0.08	0.00	0.00	0.38	89	78	31	11	22	69
[illegible]	SUCLG1	SUCLG1	succinate-CoA ligase alpha subunit	Cytoplasm	enzyme		0.38	0.51	-0.01	0.00	0.00	0.30	97	94	69	3	6	31
[illegible]	PLEKHJ1						-0.32	-0.06	-0.35	0.00	0.00	0.00	3	8	14	97	92	86
[illegible]	DPM3	DPM3	dolichyl-phosphate mannosyltransferase subunit 3	Cytoplasm	enzyme		-0.36	-0.60	-0.52	0.00	0.00	0.00	9	8	19	91	92	81
[illegible]	UBQLN4	UBQLN4	ubiquilin 4	Cytoplasm	other		-0.38	-0.18	0.86	0.00	0.14	0.00	0	25	70	100	75	30
[illegible]	SLC28A3	SLC28A3	solute carrier family 28 member 3	Plasma Membrane	transporter		0.31	0.35	0.25	0.00	0.00	0.00	97	78	89	3	22	11
[illegible]	MRPL49	MRPL49	mitochondrial ribosomal protein L49	Cytoplasm	enzyme		0.31	0.37	-0.43	0.00	0.00	0.00	100	92	0	0	8	100
[illegible]	MAP4K5	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	Cytoplasm	kinase	vemurafenib, dabrafe	0.34	0.46	0.97	0.00	0.00	0.00	100	94	100	0	6	0
[illegible]	EBAG9	EBAG9	estrogen receptor binding site associated, antigen, 9	Cytoplasm	other		0.31	0.21	0.13	0.00	0.00	0.19	97	81	73	3	19	27
[illegible]	MLEC	MLEC	malectin	Plasma Membrane	other		0.31	0.32	0.12	0.00	0.00	0.04	100	92	73	0	8	27
[illegible]	SLC35A3	SLC35A3	solute carrier family 35 member A3	Cytoplasm	transporter		0.31	0.58	0.01	0.00	0.00	0.72	100	92	31	0	8	69
[illegible]	NUDT16L1	NUDT16L1	nudix hydrolase 16 like 1	Cytoplasm	other		0.31	0.34	-0.38	0.00	0.00	0.00	100	86	0	0	14	100
[illegible]	DHRS12	DHRS12	dehydrogenase/reductase 12	Nucleus	other		0.42	0.32		0.00	0.00		97	75		3	25	
[illegible]	DKFZP686I15220						0.34	0.30	0.75	0.00	0.00	0.00	100	89	100	0	11	0
[illegible]	NA						0.31	0.48	-0.21	0.00	0.00	0.00	100	86	39	0	14	61
[illegible]	RNF111	RNF111	ring finger protein 111	Nucleus	enzyme		0.34	0.18	0.09	0.00	0.00	0.86	100	78	64	0	22	36
[illegible]	SART3	SART3	squamous cell carcinoma antigen recognized by T cells	Nucleus	other		0.30	0.46	0.21	0.00	0.00	0.00	97	94	89	3	6	11
[illegible]	MEI1	MEI1	meiotic double-stranded break formation protein 1	Other	other		0.37	0.15		0.00	0.05		100	72		0	28	
[illegible]	UBP1	UBP1	upstream binding protein 1 (LBP-1a)	Cytoplasm	transcription regulator		0.34	0.30	0.28	0.00	0.00	0.00	97	78	95	3	22	5
[illegible]	ORMDL2	ORMDL2	ORMDL sphingolipid biosynthesis regulator 2	Cytoplasm	other		-0.32	-0.06	0.07	0.00	0.00	0.48	3	11	57	97	89	43
[illegible]	HAUS8	HAUS8	HAUS augmin like complex subunit 8	Cytoplasm	other		0.32	0.34	0.21	0.00	0.00	0.00	97	97	89	3	3	11
[illegible]	ATRX	ATRX	ATRX, chromatin remodeler	Nucleus	transcription regulator		0.32	0.17	0.39	0.00	0.00	0.11	97	64	62	3	36	38
[illegible]	DGKE	DGKE	diacylglycerol kinase epsilon	Cytoplasm	kinase		0.39			0.00			94			6		
[illegible]	MAML1	MAML1	mastermind like transcriptional coactivator 1	Nucleus	transcription regulator		0.30	0.35	0.13	0.00	0.00	0.06	97	94	68	3	6	32
[illegible]	C9orf106	C9orf106	chromosome 9 open reading frame 106	Cytoplasm	other		0.36	0.58	0.30	0.00	0.00	0.00	100	100	95	0	0	5
[illegible]	WSB1	WSB1	WD repeat and SOCS box containing 1	Cytoplasm	enzyme		0.32	0.59	0.97	0.00	0.00	0.00	91	97	100	9	3	0
[illegible]	TSTA3	TSTA3	tissue specific transplantation antigen P35B	Plasma Membrane	enzyme		-0.32	-0.47	0.08	0.00	0.00	0.39	11	17	59	89	83	41
[illegible]	TARBP2	TARBP2	TARBP2, RISC loading complex RNA binding subunit	Nucleus	other		0.39	0.62	0.13	0.00	0.00	0.17	100	97	76	0	3	24
[illegible]	NUP160	NUP160	nucleoporin 160	Nucleus	transporter		0.38	0.45	0.42	0.00	0.00	0.00	97	94	97	3	6	3
[illegible]	RAD9A	RAD9A	RAD9 checkpoint clamp component A	Nucleus	enzyme		0.70	0.65		0.00	0.00		94	94		6	6	
[illegible]	C12orf66	C12orf66	chromosome 12 open reading frame 66	Other	other		0.38	0.28	-0.75	0.00	0.00	0.00	97	89	0	3	11	100
[illegible]	ACP5	ACP5	acid phosphatase 5, tartrate resistant	Cytoplasm	phosphatase		-0.58	-1.09	0.76	0.00	0.00	0.00	23	0	100	77	100	0
[illegible]	NT5C	NT5C	5', 3'-nucleotidase, cytosolic	Cytoplasm	phosphatase		-0.39	-0.32	0.41	0.00	0.76	0.00	11	39	95	89	61	5
[illegible]	WHSC1	NSD2	nuclear receptor binding SET domain protein 2	Nucleus	enzyme		0.36	0.13	-0.01	0.00	0.00	0.41	97	64	46	3	36	54
[illegible]	PPP6R1	PPP6R1	protein phosphatase 6 regulatory subunit 1	Cytoplasm	other		0.31	0.47	0.42	0.00	0.00	0.00	94	89	95	6	11	5
[illegible]	KRT8P33	KRT8P33	keratin 8 pseudogene 33	Other	other		0.70	0.68		0.00	0.00		97	94		3	6	
[illegible]	C1orf159	C1orf159	chromosome 1 open reading frame 159	Other	other		0.48	0.41	0.46	0.00	0.00	0.00	94	89	92	6	11	8
[illegible]	STX17	STX17	syntaxin 17	Plasma Membrane	transporter		0.87			0.00			100			0		
[illegible]	SLC38A11	SLC38A11	solute carrier family 38 member 11	Other	other		0.46	0.06	0.41	0.00	0.08	0.00	91	53	78	9	47	22
[illegible]	NA						0.37	0.32	-0.10	0.00	0.00	0.00	97	86	27	3	14	73
[illegible]	KIDINS220	KIDINS220	kinase D interacting substrate 220	Nucleus	transcription regulator		0.31	0.21	0.31	0.00	0.00	0.00	97	92	86	3	8	14
[illegible]	C9orf16	C9orf16	chromosome 9 open reading frame 16	Other	other		0.38	0.35	0.14	0.00	0.00	0.03	100	83	68	0	17	32
[illegible]	C9orf130	C9orf130	chromosome 9 open reading frame 130	Cytoplasm	other		0.34	0.07	-0.25	0.00	0.02	0.00	100	64	11	0	36	89
[illegible]	TRBV29-1	TRBV29-1	T cell receptor beta variable 29-1	Other	other		0.31	0.30	-1.28	0.00	0.00	0.00	100	78	0	0	22	100
[illegible]	IARS2	IARS2	isoleucyl-tRNA synthetase 2, mitochondrial	Cytoplasm	enzyme		0.36	0.17	-0.08	0.00	0.00	0.00	91	69	5	9	31	95
[illegible]	PMS2CL	PMS2CL	PMS2 C-terminal like pseudogene	Other	other		0.31	0.45	-0.02	0.00	0.00	0.34	91	89	46	9	11	54
[illegible]	RRN3	RRN3	RRN3 homolog, RNA polymerase I transcription factor	Nucleus	transcription regulator		0.32	0.34	0.36	0.00	0.00	0.00	89	83	95	11	17	5
[illegible]	USP8	USP8	ubiquitin specific peptidase 8	Cytoplasm	peptidase		0.32	0.24	-0.08	0.00	0.00	0.45	100	83	43	0	17	57
[illegible]	HEATR3	HEATR3	HEAT repeat containing 3	Other	other		0.36		0.96	0.00		0.00	97		100	3		0
[illegible]	ZBTB48	ZBTB48	zinc finger and BTB domain containing 48	Nucleus	transcription regulator		0.36	0.65	0.86	0.00	0.00	0.00	97	100	100	3	0	0
[illegible]	IREB2	IREB2	iron responsive element binding protein 2	Cytoplasm	translation regulator		0.31	0.18	-0.20	0.00	0.00	0.00	97	75	11	3	25	89
[illegible]	ABHD10	ABHD10	abhydrolase domain containing 10	Cytoplasm	enzyme		0.30	0.15	-0.65	0.00	0.00	0.00	97	75	0	3	25	100
[illegible]	GBP5	GBP5	guanylate binding protein 5	Plasma Membrane	enzyme		0.31	0.65	0.80	0.00	0.00	0.00	80	97	95	20	3	5
[illegible]	HCFC1R1	HCFC1R1	host cell factor C1 regulator 1	Nucleus	other		-0.34	-0.78	0.06	0.00	0.00	0.91	8	8	57	92	92	43
[illegible]	TRAF2	TRAF2	TNF receptor associated factor 2	Cytoplasm	enzyme		0.32	0.07	-0.17	0.00	0.04	0.00	100	61	26	0	39	74
[illegible]	LL22NC03-N64E9.1						-0.40	-0.59	0.86	0.00	0.00	0.00	0	8	86	100	92	14
[illegible]	C4orf?	GLMP	glycosylated lysosomal membrane protein	Cytoplasm	transcription regulator		-0.38	-0.59	-0.57	0.00	0.00	0.00	11	6	11	89	94	89
[illegible]	NA						0.78	0.93		0.00	0.00		100	92		0	8	
[illegible]	RP11-[illegible]						0.71	0.15	-1.08	0.00	0.00	0.00	100	78	0	0	22	100
[illegible]	ETAA1	ETAA1	Ewing tumor associated antigen 1	Nucleus	other		0.37	0.35	-0.37	0.00	0.00	0.00	97	72	30	3	28	70
[illegible]	UNK	UNK	unkempt family zinc finger	Nucleus	transporter		0.32	0.50	-0.08	0.00	0.00	0.37	100	100	49	0	0	51
[illegible]	RNF144A	RNF144A	ring finger protein 144A	Nucleus	enzyme		0.50			0.00			97			3		
[illegible]	ZNF84	ZNF84	zinc finger protein 84	Nucleus	transcription regulator		0.30	0.52	0.50	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	NPDC1	NPDC1	neural proliferation, differentiation and control 1	Extracellular Space	other		0.80	1.19		0.00	0.00		80	97		20	3	
[illegible]	TIMM13	TIMM13	translocase of inner mitochondrial membrane 13	Cytoplasm	transporter		-0.38	-0.66	-0.88	0.00	0.00	0.00	6	8	19	94	92	81
[illegible]	DNAJC13	DNAJC13	DnaJ heat shock protein family (Hsp40) member C13	Cytoplasm	other		0.32	0.21		0.00	0.00		94	75		6	25	
[illegible]	PMS2	PMS2	PMS1 homolog 2, mismatch repair system component	Nucleus	enzyme		0.39	0.38		0.00	0.00		100	92		0	8	
[illegible]	[illegible]	[illegible]	[illegible]	Cytoplasm	other		0.38	0.94	0.49	0.00	0.00	0.00	89	97	100	11	3	0
[illegible]	ARMCX5	ARMCX5	armadillo repeat containing, X-linked 5	Other	other		0.37	0.28		0.00	0.00		94	81		6	19	
[illegible]	SETDB1	SETDB1	SET domain bifurcated 1	Nucleus	enzyme		0.30	0.49	0.26	0.00	0.00	0.00	100	100	92	0	0	8
[illegible]	RPL21P75	RPL21P75	ribosomal protein L21 pseudogene 75	Other	other		0.35			0.00			89			11		
[illegible]	ERO1LB	ERO1B	endoplasmic reticulum oxidoreductase 1 beta	Cytoplasm	enzyme		0.31	0.34	0.76	0.00	0.00	0.00	91	92	95	9	8	5
[illegible]	TMEM204	TMEM204	transmembrane protein 204	Plasma Membrane	other		0.38	-0.20	-1.96	0.00	0.30	0.00	97	81	0	3	19	100
[illegible]	GABBR1	GABBR1	gamma-aminobutyric acid type B receptor subunit 1	Plasma Membrane	G-protein coupled receptor	baclofen, arbaclofen, bacl	0.38	-1.08	0.91	0.00	0.00	0.00	80	3	100	20	97	0
[illegible]	HIVEP2	HIVEP2	human immunodeficiency virus type I enhancer binding	Nucleus	transcription regulator		0.32	0.07	-0.14	0.00	0.30	0.00	94	61	11	6	39	89
[illegible]	TIMM8B	TIMM8B	translocase of inner mitochondrial membrane 8 homolog	Cytoplasm	transporter		-0.37	-0.59	-0.29	0.00	0.00	0.00	11	8	22	89	92	78
[illegible]	NA						1.27	0.61		0.00	0.00		86	83		14	17	
[illegible]	CCS	CCS	copper chaperone for superoxide dismutase	Cytoplasm	enzyme		0.48	0.37	0.06	0.00	0.00	0.34	91	72	54	9	28	46
[illegible]	TM2D3	TM2D3	TM2 domain containing 3	Other	other		0.34	0.21	0.17	0.00	0.00	0.03	100	81	81	0	19	19
[illegible]	SLAIN1	SLAIN1	SLAIN motif family member 1	Other	other		0.32	0.17	-0.93	0.00	0.01	0.00	91	67	0	9	33	100
[illegible]	KLHDC3	KLHDC3	kelch domain containing 3	Cytoplasm	other		0.30	0.38	-0.69	0.00	0.00	0.00	94	86	0	6	14	100
[illegible]	NA						0.86	1.05	0.92	0.00	0.00	0.00	91	97	97	9	3	3
[illegible]	ALDH16A1	ALDH16A1	aldehyde dehydrogenase 16 family member A1	Cytoplasm	enzyme		0.38	0.51	0.98	0.00	0.00	0.00	77	86	97	23	14	3
[illegible]	WDR81	WDR81	WD repeat domain 81	Nucleus	other		0.37	0.28		0.00	0.00		97	94		3	6	
[illegible]	ATRIP	ATRIP	ATR interacting protein	Nucleus	kinase		0.39	0.51	0.08	0.00	0.00	0.06	97	89	68	3	11	32
[illegible]	C1orf131	C1orf131	chromosome 1 open reading frame 131	Nucleus	other		0.36	0.50	0.13	0.00	0.00	0.30	100	100	68	0	0	32
[illegible]	TAP1	TAP1	transporter 1, ATP binding cassette subfamily B membe	Cytoplasm	transporter		0.32	0.28	0.05	0.00	0.00	0.93	89	89	65	11	11	35
[illegible]	MRPL55	MRPL55	mitochondrial ribosomal protein L55	Cytoplasm	other		0.34	0.28	-0.43	0.00	0.00	0.00	97	86	0	3	14	100
[illegible]	CYTH4	CYTH4	cytohesin 4	Cytoplasm	other		0.31	-0.07	0.41	0.00	0.00	0.00	86	11	92	14	89	8
[illegible]	RP4-694A12.2						0.77			0.00			100			0		
[illegible]	SDCCAG8	SDCCAG8	serologically defined colon cancer antigen 8	Cytoplasm	other		0.38	0.13	0.05	0.00	0.02	0.48	100	64	62	0	36	38
[illegible]	RNASEH2B	RNASEH2B	ribonuclease H2 subunit B	Nucleus	enzyme		0.31	0.15	0.02	0.00	0.00	0.87	83	69	54	17	31	46
[illegible]	ALKBH3	ALKBH3	alkB homolog 3, alpha-ketoglutarate dependent dioxyg	Nucleus	enzyme		0.48	0.41	-0.44	0.00	0.00	0.00	97	92	0	3	8	100
[illegible]	ALDOC	ALDOC	aldolase, fructose-bisphosphate C	Cytoplasm	enzyme		0.86			0.00			94			6		
[illegible]	FAM209A	FAM209A	family with sequence similarity 209 member A	Other	other		0.76	0.89	0.70	0.00	0.00	0.00	100	100	100	0	0	0
[illegible]	SLC7A5P1	SLC7A5P1	solute carrier family 7 member 5 pseudogene 1	Other	other		0.48	1.59	1.36	0.00	0.00	0.00	91	97	97	9	3	3
[illegible]	TSSK4	TSSK4	testis specific serine kinase 4	Cytoplasm	kinase		0.82	0.45		0.00	0.00		97	81		3	19	
[illegible]	TRAV2	TRAV2	T cell receptor alpha variable 2	Other	other		0.77	0.03	-1.28	0.00	0.48	0.00	100	53	0	0	47	100
[illegible]	TMEM101	TMEM101	transmembrane protein 101	Extracellular Space	other		0.34	0.24	0.61	0.00	0.00	0.00	94	81	100	6	19	0
[illegible]	HLA-H	HLA-H	major histocompatibility complex, class I, H (pseudogen	Plasma Membrane	other		0.38	1.01	0.99	0.00	0.00	0.00	86	83	89	14	17	11
[illegible]	SNX13	SNX13	sorting nexin 13	Cytoplasm	transporter		0.37	0.29	0.08	0.00	0.00	0.68	97	86	62	3	14	38
[illegible]	NA						0.36	0.42		0.00	0.00		89	89		11	11	
[illegible]	RP11-[illegible]						-0.38	-0.08	-0.27	0.00	0.01	0.00	6	47	36	94	53	64
[illegible]	C1orf50	C1orf50	chromosome 1 open reading frame 50	Other	other		0.48	0.44	0.09	0.00	0.00	0.79	100	83	62	0	17	38
[illegible]	AC010463.3	LOC220729	succinate dehydrogenase complex flavoprotein subunit A	Other	other		0.40			0.00			97			3		
[illegible]	NAPRT	NAPRT	nicotinate phosphoribosyltransferase	Cytoplasm	enzyme		0.37	-0.27	0.32	0.00	0.21	0.00	74	36	97	26	64	3
[illegible]	ANXA2R	ANXA2R	annexin A2 receptor	Plasma Membrane	other		0.36	0.57	-0.50	0.00	0.00	0.00	100	97	3	0	3	97
[illegible]	MCEE	MCEE	methylmalonyl-CoA epimerase	Cytoplasm	enzyme		0.72			0.00			100			0		
[illegible]	GTF2H1	GTF2H1	general transcription factor IIH subunit 1	Nucleus	transcription regulator		0.34	-0.05	-0.22	0.00	0.68	0.00	100	39	14	0	61	86
[illegible]	SYTL3	SYTL3	synaptotagmin like 3	Cytoplasm	other		0.40	0.80	0.34	0.00	0.00	0.14	80	94	68	20	6	32
[illegible]	PTP4A3	PTP4A3	protein tyrosine phosphatase type IVA, member 3	Plasma Membrane	phosphatase		0.31			0.00			100			0		
[illegible]	TCTN3	TCTN3	tectonic family member 3	Cytoplasm	other		0.40	0.28	-0.18	0.00	0.00	0.00	94	75	30	6	25	70
[illegible]	FAM38B	FAM38B	family with sequence similarity 38 member B	Plasma Membrane	other		0.31	0.41	-0.12	0.00	0.00	0.00	86	81	36	14	19	64
[illegible]	FBRSL1	FBRSL1	fibrosin like 1	Nucleus	other		0.30	0.18	0.49	0.00	0.00	0.00	83	72	92	17	28	8
[illegible]	MRPL20	MRPL20	mitochondrial ribosomal protein L20	Cytoplasm	other		0.31	0.47	0.08	0.00	0.00	0.00	100	100	89	0	0	11
[illegible]	CCDC53	WASHC3	WASH complex subunit 3	Cytoplasm	other		0.39	0.34	0.05	0.00	0.00	0.87	97	86	54	3	14	46
[illegible]	CD80	CD80	CD80 molecule	Plasma Membrane	transporter		0.36	0.52	-0.18	0.00	0.00	0.00	97	94	30	3	6	70
[illegible]	CCDC39	CFAP69	cilia and flagella associated protein 69	Nucleus	other		0.37		0.92	0.00		0.00	91		100	9		0
[illegible]	TTC13	TTC13	tetratricopeptide repeat domain 13	Other	other		0.36			0.00			91			9		
[illegible]	PTTG1	PTTG1	pituitary tumor-transforming 1	Nucleus	transcription regulator		-0.42	-0.44	-0.38	0.00	0.00	0.00	11	14	22	89	86	78
[illegible]	ZNF12	ZNF12	zinc finger protein 12	Nucleus	transcription regulator		0.36	0.28	0.27	0.00	0.00	0.00	100	78	81	0	22	19
[illegible]	SLC30A5	SLC30A5	solute carrier family 30 member 5	Plasma Membrane	transporter		0.31	0.41	0.86	0.00	0.00	0.00	100	97	100	0	3	0
[illegible]	FHL1	FHL1	four and a half LIM domains 1	Cytoplasm	other		0.40	-1.32	-1.23	0.00	0.00	0.00	91	0	0	9	100	100
[illegible]	FLAD1	FLAD1	flavin adenine dinucleotide synthetase 1	Cytoplasm	enzyme		0.34	0.30	0.30	0.00	0.00	0.09	100	92	73	0	8	27
[illegible]	ZFPL1	ZFPL1	zinc finger protein like 1	Cytoplasm	other		0.37	0.26	0.18	0.00	0.00	0.10	100	92	78	0	8	22
[illegible]	C9orf78	C9orf78	chromosome 9 open reading frame 78	Other	other		0.31	0.57	0.82	0.00	0.00	0.00	94	89	86	6	11	14
[illegible]	RP5-[illegible]	MTCO3P12		Other	other		-1.00	-0.99	-0.57	0.00	0.00	0.00	11	33	14	89	67	86
[illegible]	MRPL41	MRPL41	mitochondrial ribosomal protein L41	Cytoplasm	other		0.32	-0.07	-0.36	0.00	0.06	0.00	97	42	11	3	58	89
[illegible]	MTRF1L	MTRF1L	mitochondrial translation release factor 1 like	Other	other		0.38	0.38		0.00	0.00		91	89		9	11	
[illegible]	POLR3F	POLR3F	RNA polymerase III subunit F	Nucleus	enzyme		0.39	0.32	-0.04	0.00	0.00	0.09	97	86	38	3	14	62
[illegible]	CA11	CA11	carbonic anhydrase 11	Extracellular Space	enzyme		0.36	0.08	-0.67	0.00	0.01	0.00	100	61	5	0	39	95
[illegible]	NELL2	NELL2	neural EGFL like 2	Extracellular Space	other		0.34	1.72	-1.80	0.00	0.00	0.00	80	100	0	20	0	100
[illegible]	TSNARE1	TSNARE1	t-SNARE domain containing 1	Other	other		0.36	0.12		0.00	0.11		94	89		6	11	
[illegible]	MIR142	mir-142	microRNA 142	Cytoplasm	microRNA		0.48	1.05	1.47	0.00	0.00	0.00	83	86	89	17	14	11
[illegible]	MIS18A	MIS18A	MIS18 kinetochore protein A	Nucleus	other		0.31	0.48		0.00	0.00		97	92		3	8	
[illegible]	RFC2	RFC2	replication factor C subunit 2	Nucleus	other		0.38	0.35	-0.17	0.00	0.00	0.00	100	67	30	0	33	70
[illegible]	MAGEF1	MAGEF1	MAGE family member F1	Cytoplasm	other		-0.38	-0.89	-1.03	0.00	0.00	0.00	14	0	0	86	100	100
[illegible]	CTD-2228K2.5	PP7080	uncharacterized LOC25845	Other	other		0.80			0.00			100			0		
[illegible]	ALKBH1	ALKBH1	alkB homolog 1, histone H2A dioxygenase	Cytoplasm	enzyme		0.38	0.58	0.28	0.00	0.00	0.00	100	97	92	0	3	8
[illegible]	CNPY2	CNPY2	canopy FGF signaling regulator 2	Plasma Membrane	other		0.36	0.34	0.17	0.00	0.00	0.87	97	92	70	3	8	30
[illegible]	ALKBH2	ALKBH2	alkB homolog 2, alpha-ketoglutarate dependent dioxyg	Nucleus	enzyme		0.42	0.31		0.00	0.00		94	83		6	17	
[illegible]	ASCC1	ASCC1	activating signal cointegrator 1 complex subunit 1	Nucleus	transcription regulator		0.31	0.63		0.00	0.00		97	97		3	3	
[illegible]	CNOT10	CNOT10	CCR4-NOT transcription complex subunit 10	Cytoplasm	other		0.34	0.50	0.11	0.00	0.00	0.56	97	94	65	3	6	35
[illegible]	CCR9	CCR9	C-C motif chemokine receptor 9	Plasma Membrane	G-protein coupled recept		0.38			0.00			91			9		
[illegible]	HDHD3	HDHD3	haloacid dehalogenase like hydrolase domain containin	Cytoplasm	enzyme		0.37	0.25	-0.35	0.00	0.00	0.00	100	78	14	0	22	86
[illegible]	RP11-[illegible]	LOC100289561	uncharacterized LOC100289561	Other	other		0.42			0.00			100			0		
[illegible]	LEO1	LEO1	LEO1 homolog, Paf1/RNA polymerase II complex comp	Nucleus	other		0.34	0.67		0.00	0.00		100	100		0	0	
[illegible]	SUZ12P1	SUZ12P1	SUZ12 polycomb repressive complex 2 subunit pseudog	Other	other		0.89	0.54	0.75	0.00	0.00	0.00	100	89	95	0	11	5
[illegible]	CLEC2D						0.38	0.55	0.02	0.00	0.00	0.87	94	92	31	6	8	69
[illegible]	TDRD7	TDRD7	tudor domain containing 7	Cytoplasm	other		0.32		1.28	0.00		0.00	97		100	3		0
[illegible]	AK5	AK5	adenylate kinase 5	Cytoplasm	kinase		0.36			0.00			94			6		
[illegible]	METTL22	METTL22	methyltransferase like 22	Nucleus	enzyme		0.32	0.51	0.28	0.00	0.00	0.00	100	97	92	0	3	8
[illegible]	HADH	HADH	hydroxyacyl-CoA dehydrogenase	Cytoplasm	enzyme		0.36			0.00			86			14		
[illegible]	UBE2Q2P1	UBE2Q2P1	ubiquitin conjugating enzyme E2 Q2 (putative) pseudoge	Other	other		-0.42	-0.08	0.99	0.00	0.26	0.00	3	44	97	97	56	3
[illegible]	LAGE3	LAGE3	L antigen family member 3	Nucleus	other		-0.36	-0.81		0.00	0.09		11	25		89	75	
[illegible]	LTA	LTA	lymphotoxin alpha	Extracellular Space	cytokine	ept, etanercept/metho	0.32	0.16	-0.48	0.00	0.00	0.00	89	69	8	11	31	92
[illegible]	AC068580.1						0.77			0.00			94			6		
[illegible]	HELQ	HELQ	helicase, POLQ like	Nucleus	enzyme		0.38	0.26	0.11	0.00	0.00	0.04	91	81	76	9	19	24
[illegible]	TRAV26-1	TRAV26-1	T cell receptor alpha variable 26-1	Other	other		0.42			0.00			97			3		
[illegible]	XRCC1	XRCC1	X-ray repair cross complementing 1	Nucleus	enzyme		0.32	0.30		0.00	0.05		91	64		9	36	
[illegible]	TRPV2	TRPV2	transient receptor potential cation channel subfamily V	Plasma Membrane	ion channel		0.34	0.52	0.21	0.00	0.00	0.03	89	89	70	11	11	30
[illegible]	CYB5R1	CYB5R1	cytochrome b5 reductase 1	Cytoplasm	enzyme		0.30		0.12	0.00		0.80	97		70	3		30
[illegible]	YIPF3	YIPF3	Yip1 domain family member 3	Cytoplasm	other		0.31	0.34	0.18	0.00	0.00	0.34	97	94	65	3	6	35
[illegible]	C3orf62	C3orf62	chromosome 3 open reading frame 62	Nucleus	other		0.34	0.47		0.00	0.00		100	100		0	0	
[illegible]	STK11IP	STK11IP	serine/threonine kinase 11 interacting protein	Cytoplasm	other		0.30	0.65	1.11	0.00	0.00	0.00	94	86	100	6	14	0
[illegible]	COX18	COX18	COX18, cytochrome c oxidase assembly factor	Cytoplasm	transporter		0.34			0.00			94			6		
[illegible]	NA						0.75	0.67		0.00	0.00		94	89		6	11	
[illegible]	LIME1	LIME1	Lck interacting transmembrane adaptor 1	Extracellular Space	other		0.32	0.47		0.00	0.00		94	89		6	11	
[illegible]	RP11-[illegible]	HMGB1P6	high mobility group box 1 pseudogene 6	Other	other		-0.36	-0.14	0.18	0.00	0.14	0.14	20	36	65	80	64	35
[illegible]	RP11-[illegible]						0.75	0.60		0.00	0.00		91	94		9	6	
[illegible]	RP11-[illegible]						0.38	-0.15	-1.55	0.00	0.35	0.00	97	28	0	3	72	100
[illegible]	MAP3K4	MAP3K4	mitogen-activated protein kinase kinase kinase 4	Cytoplasm	kinase		0.31	0.63		0.00	0.00		94	97		6	3	
[illegible]	ZBTB9	ZBTB9	zinc finger and BTB domain containing 9	Nucleus	other		0.38	0.59		0.00	0.00		94	89		6	11	
[illegible]	NMRAL1	NMRAL1	NmrA like redox sensor 1	Nucleus	other		0.37			0.00			89			11		
[illegible]	MLH1	MLH1	mutL homolog 1	Nucleus	enzyme		0.30	0.35	0.26	0.00	0.00	0.00	100	94	86	0	6	14
[illegible]	SNORD4A						0.37	0.68	0.27	0.00	0.00	0.00	91	89	68	9	11	32
[illegible]	B4GALT7	B4GALT7	beta-1,4-galactosyltransferase 7	Cytoplasm	enzyme		0.32	0.49	0.58	0.00	0.00	0.00	91	89	92	9	11	8
[illegible]	BRI3	BRI3	[illegible] family member 3	Plasma Membrane	other		0.31	0.01	-0.33	0.00	0.01	0.00	89	50	36	11	50	64
[illegible]	PHYH	PHYH	phytanoyl-CoA 2-hydroxylase	Cytoplasm	enzyme		0.30	0.29		0.00	0.00		100	86		0	14	
[illegible]	GEMIN2	GEMIN2	gem nuclear organelle associated protein 2	Nucleus	other		0.37	0.49		0.00	0.00		97	83		3	17	
[illegible]	YPEL2	YPEL2	yippee like 2	Nucleus	other		0.31	0.06	-0.60	0.00	0.08	0.00	89	56	5	11	44	95
[illegible]	RP11-[illegible]						0.31	0.49	-0.37	0.00	0.00	0.00	100	94	39	0	6	61
[illegible]	NR4A2	NR4A2	nuclear receptor subfamily 4 group A member 2	Nucleus	ligand-dependent nuclear rec		0.38	1.08	0.86	0.00	0.00	0.00	74	92	89	26	8	11
[illegible]	TRAV41	TRAV41	T cell receptor alpha variable 41	Other	other		0.36			0.00			91			9		
[illegible]	HEXDC	HEXDC	hexosaminidase D	Other	enzyme		0.30	-0.08	-0.11	0.00	0.09	0.03	86	42	41	14	58	59
[illegible]	ACP2	ACP2	acid phosphatase 2, lysosomal	Cytoplasm	phosphatase		0.31			0.00			94			6		
[illegible]	SNRNP35	SNRNP35	small nuclear ribonucleoprotein U11/U12 subunit 35	Nucleus	other		0.30	0.03	-0.21	0.00	0.07	0.00	94	53	24	6	47	76
[illegible]	RNFT1	RNFT1	ring finger protein, transmembrane 1	Other	other		0.31	0.19	0.42	0.00	0.05	0.00	94	64	97	6	36	3
[illegible]	FAM133C	FAM133C	family with sequence similarity 133 C	Other	other		0.34	0.51		0.00	0.00		91	92		9	8	
[illegible]	RPL15P1	RPL15P1	ribosomal protein L15 pseudogene 1	Other	other		0.36			0.00			100			0		
[illegible]	PATL2	PATL2	PAT1 homolog 2	Cytoplasm	translation regulator		0.37	0.98	0.60	0.00	0.00	0.00	83	97	89	17	3	11
[illegible]	FAM20A	FAM20A	family with sequence similarity 20 member A	Extracellular Space	other		0.31			0.00			94			6		
[illegible]	RP11-[illegible]						0.40	0.48	0.06	0.00	0.00	0.47	91	86	54	9	14	46
[illegible]	TRBV21-1	TRBV21-1	T cell receptor beta variable 21-1 (pseudogene)	Plasma Membrane	other		0.32	0.55		0.00	0.00		94	83		6	17	
[illegible]	TRAV8-1	TRAV8-1	T cell receptor alpha variable 8-1	Other	other		0.36			0.00			94			6		
[illegible]	TRAV13-2	TRAV13-2	T cell receptor alpha variable 13-2	Other	other		0.34	-0.21	-1.22	0.00	0.36	0.00	80	31	3	20	69	97
[illegible]	STAB1	STAB1	stabilin 1	Plasma Membrane	transporter			-5.01	1.31		0.00	0.00		0	97		100	3
[illegible]	RAB32	RAB32	RAB32, member RAS oncogene family	Cytoplasm	enzyme		-6.52	-4.88	0.34	5.63E-06	0.00	0.01	0	0	75	100	100	26
[illegible]	RIN2	RIN2	Ras and Rab interactor 2	Cytoplasm	other			-6.36	0.82		0.00	0.00		0	89		100	11
[illegible]	TTYH3	TTYH3	tweety family member 3	Plasma Membrane	ion channel		-5.48	-3.18	0.92	0.00	0.00	0.00	0	0	89	100	100	11
[illegible]	FAM129B	FAM129B	family with sequence similarity 129 member B	Cytoplasm	other		-6.05	-4.85	1.34	0.00	0.00	0.00	0	0	97	100	100	3
[illegible]	CD33	CD33	CD33 molecule	Plasma Membrane	other		-6.36	-4.91	0.41	0.00	0.00	0.00	0	0	84	100	100	16
[illegible]	CXCL1	CXCL1	C-X-C motif chemokine ligand 1	Extracellular Space	cytokine		-6.98	-5.87	0.80	0.00	0.00	0.00	0	0	88	100	100	12
[illegible]	CSF1R	CSF1R	colony stimulating factor 1 receptor	Plasma Membrane	kinase	tinib, PLX3397, ARR	-6.85	-4.70	0.26	0.00	0.00	0.03	0	0	62	100	100	38
[illegible]	HCAR2	HCAR2	hydroxycarboxylic acid receptor 2	Plasma Membrane	G-protein coupled recept	acid/niacin, nia	-6.10	-5.39	1.76	0.00	0.00	0.00	0	0	100	100	100	0
[illegible]	RP11-[illegible]						-6.28	-5.88	0.22	0.00	0.00	0.03	0	0	65	100	100	35
[illegible]	CXCR5	CXCR5	C-X-C motif chemokine receptor 5	Plasma Membrane	G-protein coupled recept		-6.44	-4.08	0.76	0.00	0.00	0.00	0	0	86	100	100	14
[illegible]	TUBB8	TUBB8	tubulin beta 8 class V	Cytoplasm	other		-5.91	-5.01	1.44	0.00	0.00	0.00	0	0	100	100	100	0

[illegible]	CYP1B1	CYP1B1	cytochrome P450 family 1 subfamily B member 1	Cytoplasm	enzyme			-1.05	2.16		0.00	0.00		0	97		100	8
[illegible]	SEMA4A	SEMA4A	semaphorin 4A	Plasma Membrane	other		-0.81	-0.65	0.06	0.00	0.00	0.49	0	0	97	100	100	63
[illegible]	C3AR1	C3AR1	complement C3a receptor 1	Plasma Membrane	G-protein coupled receptor		-0.56	-0.68	0.09	0.00	0.00	0.67	0	0	97	100	100	63
[illegible]	SYNPO2	SYNPO2	synaptopodin 2	Cytoplasm	other		-1.27	-1.42	0.80	0.00	0.00	0.00	0	0	92	100	100	8
[illegible]	IGLV8-10	IGLV8-10	immunoglobulin lambda variable 8-10	Other	other		"-99"	"-99"	-0.88	0.00	0.00	0.00	0	0	80	100	100	70
[illegible]	SERPINB1	SERPINB1	serpin family B member 1	Extracellular Space	other			-6.16	-0.71		0.00	0.00		0	22		100	78
[illegible]	ZAP70	ZAP70	zeta chain of T cell receptor associated protein kinase 70	Plasma Membrane	kinase		2.89	1.21	0.50	0.00	0.00	0.00	100	100	81	0	0	39
[illegible]	NEK6	NEK6	NIMA related kinase 6	Nucleus	kinase		-6.50	-2.98	0.37	0.00	0.00	0.00	0	0	89	100	100	14
[illegible]	MGAT1	MGAT1	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglu	Cytoplasm	enzyme		-1.95	-1.26	-0.12	0.00	0.00	0.00	0	0	24	100	100	76
[illegible]	RALB	RALB	RAS like proto-oncogene B	Cytoplasm	enzyme		-6.28	-2.90	-0.04	0.00	0.00	0.67	0	0	66	100	100	94
[illegible]	KLRK1	KLRC4-KLRK1/KLRK1	killer cell lectin like receptor K1	Plasma Membrane	transmembrane receptor			6.41			0.00			100			0	
[illegible]	NKTR	NKTR	natural killer cell triggering receptor	Plasma Membrane	other		2.56	2.12	1.86	0.00	0.00	0.00	97	100	92	8	0	8
[illegible]	C1QA	C1QA	complement C1q A chain	Extracellular Space	peptidase			-6.20	-0.41		0.00	0.00		0	38		100	76
[illegible]	IGLV7-43	IGLV7-43	immunoglobulin lambda variable 7-43	Extracellular Space	peptidase		"-99"	-5.99	-0.43	0.00	0.00	0.00	0	0	22	100	100	78
[illegible]	IGKV1-9	IGKV1-9	immunoglobulin kappa variable 1-9	Other	other		"-99"	-5.98	-0.70	0.00	0.00	0.00	0	0	27	100	100	79
[illegible]	HOMER3	HOMER3	homer scaffolding protein 3	Plasma Membrane	other			-3.06	0.72		0.00	0.00		0	95		100	5
[illegible]	ABCB1	ABCB1	ATP binding cassette subfamily B member 1	Plasma Membrane	transporter	tariquidar, OC 144-093, valspodar		3.05	1.10		0.00	0.00		100	95		0	5
[illegible]	FOXJ1	FOXJ1	forkhead box J1	Nucleus	transcription regulator			2.79			0.00			100			0	
[illegible]	MAPK8IP1	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	Cytoplasm	other			2.52	1.98		0.00	0.00		100	100		0	0
[illegible]	VPREB3	VPREB3	pre-B lymphocyte 3	Cytoplasm	other		-6.14	-4.99	0.02	0.00	0.00	0.81	0	0	91	100	100	69
[illegible]	SETD7	SETD7	SET domain containing lysine methyltransferase 7	Nucleus	enzyme		0.86	-2.39	-0.06	0.00	0.00	0.00	83	0	82	17	100	68
[illegible]	EMR1	ADGRE1	adhesion G protein-coupled receptor E1	Plasma Membrane	G-protein coupled receptor		-0.28	-3.60	-0.39	0.00	0.00	0.00	26	0	11	76	100	89
[illegible]	COL1A1	COL1A1	collagen type I alpha 1 chain	Extracellular Space	other	collagenase clostridium histolyticum		3.28			0.00			100			0	
[illegible]	PTK7	PTK7	protein tyrosine kinase 7 (inactive)	Plasma Membrane	kinase			2.15			0.00			100			0	
[illegible]	SH2B2	SH2B2	SH2B adaptor protein 2	Cytoplasm	other			-3.15	0.16		0.00	0.48		0	99		100	41
[illegible]	SESN3	SESN3	sestrin 3	Extracellular Space	other		-0.12	-1.67	-0.48	0.00	0.00	0.00	81	0	8	99	100	92
[illegible]	TSPAN32	TSPAN32	tetraspanin 32	Plasma Membrane	other		0.82	1.83	0.67	0.00	0.00	0.00	71	100	95	29	0	5
[illegible]	RGS2	RGS2	regulator of G-protein signaling 2	Nucleus	other		-1.81	-1.77	0.46	0.00	0.00	0.00	0	0	78	100	100	22
[illegible]	CCDC157	CCDC157	coiled-coil domain containing 157	Other	other			2.10			0.00			100			0	
[illegible]	DGKA	DGKA	diacylglycerol kinase alpha	Cytoplasm	kinase		2.52	1.85	0.86	0.00	0.00	0.00	100	97	78	0	3	22
[illegible]	ABCA2	ABCA2	ATP binding cassette subfamily A member 2	Plasma Membrane	transporter		0.49	1.53	0.86	0.00	0.00	0.00	71	100	89	29	0	11
[illegible]	RNASET2	RNASET2	ribonuclease T2	Cytoplasm	enzyme		0.06	-1.68	-0.15	0.01	0.00	0.00	54	0	26	46	100	84
[illegible]	CORO1B	CORO1B	coronin 1B	Cytoplasm	other		-0.21	-1.11	-0.61	0.00	0.00	0.00	87	0	5	88	100	95
[illegible]	TP53INP1	TP53INP1	tumor protein p53 inducible nuclear protein 1	Nucleus	other		-0.17	-1.52	-0.42	0.00	0.00	0.00	63	0	14	97	100	86
[illegible]	LAYN	LAYN	layilin	Plasma Membrane	other			1.94			0.00			100			0	
[illegible]	TNFRSF25	TNFRSF25	TNF receptor superfamily member 25	Plasma Membrane	transmembrane receptor		2.57	1.46	0.28	0.00	0.00	0.01	100	100	91	0	0	69
[illegible]	TSEN34	TSEN34	tRNA splicing endonuclease subunit 34	Nucleus	enzyme		0.39	1.46	0.30	0.30	0.00	0.15	66	100	94	34	0	66
[illegible]	OSBPL5	OSBPL5	oxysterol binding protein like 5	Cytoplasm	transporter			1.67	1.01		0.00	0.00		100	97		0	3
[illegible]	UBASH3B	UBASH3B	ubiquitin associated and SH3 domain containing B	Other	enzyme		-0.39	-1.70	-0.88	0.00	0.00	0.00	3	0	11	97	100	89
[illegible]	SPAG5	SPAG5	sperm associated antigen 5	Nucleus	peptidase			1.95	1.07		0.00	0.00		100	100		0	0
[illegible]	CD200	CD200	CD200 molecule	Plasma Membrane	other		0.40	-1.13	-0.13	0.00	0.00	0.01	83	0	38	17	100	62
[illegible]	MTSS1L	MTSS1L	MTSS1L, I-BAR domain containing	Plasma Membrane	other			1.50			0.00			100			0	
[illegible]	SESTD1	SESTD1	SEC14 and spectrin domain containing 1	Extracellular Space	other			-1.50	0.48		0.00	0.00		0	100		100	0
[illegible]	ATP8A1	ATP8A1	ATPase phospholipid transporting 8A1	Cytoplasm	transporter		0.29	1.36	-0.80	0.00	0.00	0.00	83	97	14	17	3	86
[illegible]	DUSP8	DUSP8	dual specificity phosphatase 8	Cytoplasm	phosphatase			-1.75	0.15		0.00	0.04		0	78		100	27
[illegible]	CRTAM	CRTAM	cytotoxic and regulatory T-cell molecule	Plasma Membrane	other			1.38			0.00			100			0	
[illegible]	[illegible]						-1.96	-1.60	0.61	0.00	0.00	0.00	0	3	97	100	97	3
[illegible]	UBE2S	UBE2S	ubiquitin conjugating enzyme E2 S	Nucleus	enzyme		0.41	1.19	0.75	0.00	0.00	0.00	77	100	97	23	0	3
[illegible]	LLGL2	LLGL2	LLGL2, scribble cell polarity complex component	Cytoplasm	other		0.35	1.52	0.76	0.48	0.00	0.00	63	97	97	37	3	3
[illegible]	[illegible]	[illegible]	[illegible] binding protein 11	Cytoplasm	enzyme		-0.13	1.18	0.06	0.37	0.00	0.51	81	0	99	99	0	61
[illegible]	SLC31A1	SLC31A1	solute carrier family 31 member 1	Plasma Membrane	transporter		-0.60	-1.88	-0.60	0.00	0.00	0.00	17	0	11	83	100	89
[illegible]	TNFSF10	TNFSF10	tumor necrosis factor superfamily member 10	Extracellular Space	cytokine		-0.66	-1.56	-0.77	0.00	0.00	0.00	20	0	0	80	100	100
[illegible]	GTF3C1	GTF3C1	general transcription factor IIIC subunit 1	Nucleus	transcription regulator		0.46	1.01	0.88	0.00	0.00	0.00	97	100	97	3	0	3
[illegible]	DFNB31	WHRN	whirlin	Plasma Membrane	other			1.41	1.22		0.00	0.00		100	100		0	0
[illegible]	TNFRSF10D	TNFRSF10D	TNF receptor superfamily member 10d	Plasma Membrane	transmembrane receptor		0.35	-1.85	-0.21	0.30	0.00	0.00	71	0	80	29	100	20
[illegible]	GALNT11	GALNT11	polypeptide N-acetylgalactosaminyltransferase 11	Cytoplasm	enzyme		0.11	1.19	-0.80	0.04	0.00	0.00	66	100	3	34	0	97
[illegible]	NBL1	MINOS1-NBL1/NBL1	neuroblastoma 1, DAN family BMP antagonist	Nucleus	other		-0.67	1.23	-0.87	0.00	0.00	0.00	23	100	0	77	0	100
[illegible]	NEU4	NEU4	neuraminidase 4	Cytoplasm	enzyme			-1.68	1.39		0.00	0.00		3	97		97	3
[illegible]	ZBED3	ZBED3	zinc finger BED-type containing 3	Cytoplasm	other			1.14			0.00			100			0	
[illegible]	TRIM8	TRIM8	tripartite motif containing 8	Nucleus	other		-0.35	-1.08	-0.27	0.00	0.00	0.00	20	0	14	80	100	86
[illegible]	SPAG4	SPAG4	sperm associated antigen 4	Cytoplasm	other			1.67	2.38		0.00	0.00		100	100		0	0
[illegible]	ELK3	ELK3	ELK3, ETS transcription factor	Nucleus	transcription regulator		-0.16	-1.17	-0.44	0.00	0.00	0.00	29	0	11	71	100	89
[illegible]	ARID5B	ARID5B	AT-rich interaction domain 5B	Nucleus	transcription regulator		-0.10	-1.17	-0.25	0.00	0.00	0.00	43	3	14	57	97	86
[illegible]	PDZD4	PDZD4	PDZ domain containing 4	Cytoplasm	other		0.02	-1.46	-1.00	0.01	0.00	0.00	51	3	3	49	97	97
[illegible]	SIRT2	SIRT2	sirtuin 2	Nucleus	transcription regulator		-0.16	1.03	0.56	0.01	0.00	0.00	29	100	100	71	0	0
[illegible]	MVD	MVD	mevalonate diphosphate decarboxylase	Cytoplasm	enzyme		0.01	1.13	0.21	0.48	0.00	0.04	51	100	62	49	0	38
[illegible]	DGKQ	DGKQ	diacylglycerol kinase theta	Cytoplasm	kinase		-0.31	1.08	0.06	0.00	0.00	0.67	34	94	99	66	6	61
[illegible]	PLK3	PLK3	polo like kinase 3	Nucleus	kinase		0.46	0.91	0.66	0.00	0.00	0.00	83	97	81	17	3	19
[illegible]	OAS1	OAS1	2'-5'-oligoadenylate synthetase 1	Cytoplasm	enzyme			-1.81	0.06		0.00	0.69		3	94		97	6
[illegible]	LMNA	LMNA	lamin A/C	Nucleus	other		-0.09	1.15	2.16	0.00	0.00	0.00	43	89	100	57	11	0
[illegible]	TMEM97	TMEM97	transmembrane protein 97	Nucleus	other		0.46	0.95	0.21	0.00	0.00	0.00	100	100	86	0	0	14
[illegible]	POGLUT1	POGLUT1	protein O-glucosyltransferase 1	Extracellular Space	enzyme			1.81			0.00			100			0	
[illegible]	TPM2	TPM2	tropomyosin 2 (beta)	Other	other		2.28	1.48		0.00	0.00	0.00	100	97		0	3	
[illegible]	H2AFX	H2AFX	H2A histone family member X	Nucleus	transcription regulator		0.44	1.04	0.29	0.00	0.00	0.08	77	100	86	23	0	14
[illegible]	KCNQ1	KCNQ1	potassium voltage-gated channel subfamily Q member 1	Plasma Membrane	ion channel	[illegible], indapamide	-0.32	-1.08	-0.78	0.00	0.00	0.00	9	0	0	91	100	100
[illegible]	TUBB6	TUBB6	tubulin beta 6 class V	Cytoplasm	other	[illegible]/vinorelbine,	0.45	0.97	1.06	0.00	0.00	0.00	66	97	97	34	3	3
[illegible]	RP3-395M20.9							1.15			0.00			100			0	
[illegible]	HEXB	HEXB	hexosaminidase subunit beta	Cytoplasm	enzyme		-0.48	-1.39	0.76	0.00	0.00	0.00	26	3	95	74	97	5
[illegible]	DBN1	DBN1	drebrin 1	Cytoplasm	other			1.24			0.00			94			6	
[illegible]	TNFRSF10A	TNFRSF10A	TNF receptor superfamily member 10a	Plasma Membrane	transmembrane receptor	[illegible]	-0.06	-1.36	-0.05	0.01	0.00	0.36	40	0	63	60	100	37
[illegible]	CDCA7L	CDCA7L	cell division cycle associated 7 like	Nucleus	other		-0.49	-1.36	-0.02	0.00	0.00	0.47	17	0	69	83	100	31
[illegible]	SLAMF1	SLAMF1	signaling lymphocytic activation molecule family member 1	Plasma Membrane	transmembrane receptor		0.27	-1.30	-0.08	0.00	0.00	0.46	83	0	69	17	100	31
[illegible]	TOB1	TOB1	transducer of ERBB2, 1	Nucleus	transcription regulator		0.49	0.91	-0.41	0.00	0.00	0.00	91	97	26	9	3	74
[illegible]	CAMK1D	CAMK1D	calcium/calmodulin dependent protein kinase ID	Cytoplasm	kinase		-0.41	-1.07	-0.35	0.00	0.00	0.00	6	0	3	94	100	97
[illegible]	MYO1F	MYO1F	myosin IF	Cytoplasm	other		-1.50	-0.87	0.68	0.00	0.00	0.00	0	14	95	100	86	5
[illegible]	ZNF384	ZNF384	zinc finger protein 384	Nucleus	other		0.38	1.08	0.32	0.00	0.00	0.03	80	94	70	20	6	30
[illegible]	ANO6	ANO6	anoctamin 6	Plasma Membrane	ion channel		-0.37	-1.10	-0.35	0.00	0.00	0.00	9	0	8	91	100	92
[illegible]	MDFIC	MDFIC	MyoD family inhibitor domain containing	Nucleus	other		-0.15	-1.14	-0.99	0.01	0.00	0.00	31	0	0	69	100	100
[illegible]	TUBA4A	TUBA4A	tubulin alpha 4a	Cytoplasm	other	[illegible]/vinorelbine, [illegible]	-0.18	0.98	0.05	0.00	0.00	0.62	40	92	57	60	8	43
[illegible]	BIRC3	BIRC3	baculoviral IAP repeat containing 3	Cytoplasm	enzyme	birinapant	0.24	-0.99	-0.59	0.00	0.00	0.00	80	0	3	20	100	97
[illegible]	PHGDH	PHGDH	phosphoglycerate dehydrogenase	Cytoplasm	enzyme			1.16			0.00			100			0	
[illegible]	MXI1	MXI1	MAX interactor 1, dimerization protein	Nucleus	transcription regulator		0.01	-0.98	-0.88	0.06	0.00	0.00	51	0	0	49	100	100
[illegible]	NA							1.52	1.16		0.00	0.00		97	84		3	16
[illegible]	MADD	MADD	MAP kinase activating death domain	Cytoplasm	other		0.31	0.86	0.48	0.00	0.00	0.00	80	94	97	20	6	3
[illegible]	GUK1	GUK1	guanylate kinase 1	Cytoplasm	kinase		0.10	0.85	0.16	0.27	0.00	0.00	57	100	89	43	0	11
[illegible]	ZNF624	ZNF624	zinc finger protein 624	Other	other		-0.44	-1.47	-0.68	0.00	0.00	0.00	6	0	8	94	100	92
[illegible]	KLHL18	KLHL18	kelch like family member 18	Other	other		0.26	0.93	0.66	0.00	0.00	0.00	86	97	100	14	3	0
[illegible]	DGKD	DGKD	diacylglycerol kinase delta	Cytoplasm	kinase		0.38	0.90	1.27	0.00	0.00	0.00	86	97	100	14	3	0
[illegible]	PTPN23	PTPN23	protein tyrosine phosphatase, non-receptor type 23	Cytoplasm	phosphatase		0.40	0.88	0.86	0.00	0.00	0.00	91	97	100	9	3	0
[illegible]	DYRK1B	DYRK1B	dual specificity tyrosine phosphorylation regulated kinase 1B	Nucleus	kinase		0.26	1.10	0.89	0.00	0.00	0.00	83	100	100	17	0	0
[illegible]	RB1	RB1	RB transcriptional corepressor 1	Nucleus	transcription regulator		-0.17	-0.96	-0.28	0.00	0.00	0.00	17	0	26	83	100	84
[illegible]	RAC2	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family,	Cytoplasm	enzyme		-0.45	-0.96	-0.82	0.00	0.00	0.00	14	0	3	86	100	97
[illegible]	RAB6B	RAB6B	RAB6B, member RAS oncogene family	Cytoplasm	enzyme		-0.50	-0.88	-0.10	0.00	0.00	0.01	3	0	38	97	100	62
[illegible]	CMTM7	CMTM7	CKLF like MARVEL transmembrane domain containing 7	Extracellular Space	cytokine		-0.50	-1.11	-0.51	0.00	0.00	0.00	14	0	5	86	100	95
[illegible]	WDR47	WDR47	WD repeat domain 47	Other	other		0.50	1.03	0.72	0.00	0.00	0.00	57	92	100	43	8	0
[illegible]	HIPK2	HIPK2	homeodomain interacting protein kinase 2	Nucleus	kinase		-0.12	-0.92	-0.65	0.00	0.00	0.00	31	0	3	69	100	97
[illegible]	ZBTB49	ZBTB49	zinc finger and BTB domain containing 49	Nucleus	other		0.42	0.94	0.37	0.00	0.00	0.00	89	100	89	11	0	11
[illegible]	PIK3CB	PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic	Cytoplasm	kinase	[illegible], SAR260301,	-0.02	-0.98	-0.16	0.00	0.00	0.00	40	0	30	60	100	70
[illegible]	MAP4K4	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	Cytoplasm	kinase		-0.17	-0.96	0.06	0.00	0.00	0.18	6	0	73	94	100	27
[illegible]	CCDC120	CCDC120	coiled-coil domain containing 120	Plasma Membrane	other		0.48	0.95		0.00	0.00		94	100		6	0	
[illegible]	ZNF318	ZNF318	zinc finger protein 318	Other	other		-0.31	-0.86	-0.83	0.00	0.00	0.00	29	0	0	71	100	100
[illegible]	[illegible]	[illegible]	[illegible]	Other	other		-0.26	-0.91	-0.77	0.00	0.00	0.00	23	0	0	77	100	100
[illegible]	JAM3	JAM3	junctional adhesion molecule 3	Plasma Membrane	other			0.92	0.86		0.00	0.00		94	100		6	0
[illegible]	SESN2	SESN2	sestrin 2	Cytoplasm	enzyme		-0.19	0.80	1.00	0.00	0.00	0.00	40	92	97	60	8	3
[illegible]	BIRC2	BIRC2	baculoviral IAP repeat containing 2	Cytoplasm	enzyme	birinapant	0.36	0.88	0.06	0.00	0.00	0.21	91	94	68	9	6	32
[illegible]	CALM1	CALM1 (includes others)	calmodulin 1	Cytoplasm	other		-0.48	-0.90	-0.49	0.00	0.00	0.00	6	0	3	94	100	97
[illegible]	EPHB6	EPHB6	EPH receptor B6	Plasma Membrane	kinase		0.26	-0.96	-0.17	0.00	0.00	0.00	77	0	39	23	100	61
[illegible]	ZNF696	ZNF696	zinc finger protein 696	Nucleus	transcription regulator		-0.21	0.82	-0.52	0.00	0.00	0.00	17	100	3	83	0	97
[illegible]	EPSTI1	EPSTI1	epithelial stromal interaction 1	Other	other		-0.25	-0.91	0.16	0.00	0.00	0.21	17	3	68	83	97	32
[illegible]	TNFAIP8	TNFAIP8	TNF alpha induced protein 8	Cytoplasm	other		0.13	-0.88	-0.15	0.39	0.00	0.12	69	0	61	31	100	39
[illegible]	PTPLAD2	HACD4	3-hydroxyacyl-CoA dehydratase 4	Cytoplasm	enzyme		-0.35	-0.91	-0.82	0.00	0.00	0.00	17	0	0	83	100	100
[illegible]	ARHGAP9	ARHGAP9	Rho GTPase activating protein 9	Cytoplasm	enzyme		-0.38	-0.78	-0.27	0.00	0.00	0.00	6	0	14	94	100	86
[illegible]	ANXA1	ANXA1	annexin A1	Plasma Membrane	enzyme	[illegible], hyd	-0.36	-0.88	1.31	0.00	0.00	0.00	14	6	100	86	94	0
[illegible]	MAP3K1	MAP3K1	mitogen-activated protein kinase kinase kinase 1	Cytoplasm	kinase	E6201	-0.12	-0.78	0.09	0.00	0.00	0.17	34	3	78	66	97	22
[illegible]	MEF2A	MEF2A	myocyte enhancer factor 2A	Nucleus	transcription regulator		-0.38	-0.86	0.16	0.00	0.00	0.04	14	0	84	86	100	16
[illegible]	MFSD12	MFSD12	major facilitator superfamily domain containing 12	Cytoplasm	other		-0.06	-0.86	0.61	0.00	0.00	0.00	46	8	92	54	92	8
[illegible]	GRPEL2	GRPEL2	GrpE like 2, mitochondrial	Cytoplasm	other		-0.06	-1.00	-1.08	0.10	0.00	0.00	46	3	0	54	97	100
[illegible]	SLC30A1	SLC30A1	solute carrier family 30 member 1	Plasma Membrane	transporter		0.49	0.86	0.87	0.00	0.00	0.00	97	97	100	3	3	0
[illegible]	BCL9L	BCL9L	B-cell CLL/lymphoma 9-like	Cytoplasm	other		0.38	0.83	-0.75	0.00	0.00	0.00	89	97	3	11	3	97
[illegible]	JMJD6	JMJD6	arginine demethylase and lysine hydroxylase	Plasma Membrane	transmembrane receptor		-0.44	0.75	0.48	0.00	0.00	0.00	17	100	86	83	0	14
[illegible]	DNAJA1	DNAJA1	DnaJ heat shock protein family (Hsp40) member A1	Nucleus	other		0.36	0.81	0.56	0.00	0.00	0.00	77	89	92	23	11	8
[illegible]	ABLIM1	ABLIM1	actin binding LIM protein 1	Cytoplasm	other		0.49	0.83	-1.08	0.00	0.00	0.00	100	97	0	0	3	100
[illegible]	CTDSP2	CTDSP2	CTD small phosphatase 2	Nucleus	phosphatase		-0.44	-0.86	-0.74	0.00	0.00	0.00	3	0	0	97	100	100
[illegible]	HEXIM1	HEXIM1	hexamethylene bisacetamide inducible 1	Nucleus	transcription regulator		0.37	0.71	0.06	0.00	0.00	0.38	80	97	62	20	3	38
[illegible]	ATXN7L2	ATXN7L2	ataxin 7 like 2	Other	other		0.25	0.83	0.92	0.00	0.00	0.00	77	100	100	23	0	0
[illegible]	RAP1GDS1	RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1	Cytoplasm	other		-0.44	-1.05	-0.82	0.00	0.00	0.00	11	0	19	89	100	81
[illegible]	SAMSN1	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	Nucleus	other		-0.25	-0.86	0.56	0.00	0.00	0.00	23	3	95	77	97	5
[illegible]	AGO4	AGO4	argonaute 4, RISC catalytic component	Cytoplasm	translation regulator		-0.26	-0.82	0.25	0.00	0.00	0.00	14	0	70	86	100	30
[illegible]	CTPS1	CTPS1	CTP synthase 1	Nucleus	enzyme	[illegible]	0.12	0.70	0.95	0.22	0.00	0.00	66	100	100	34	0	0
[illegible]	NET1	NET1	neuroepithelial cell transforming 1	Nucleus	other		0.32	-0.96	-0.42	0.00	0.00	0.00	63	0	8	37	100	92
[illegible]	FAM78A	FAM78A	family with sequence similarity 78 member A	Other	other		-0.46	-0.86	-1.08	0.00	0.00	0.00	23	3	0	77	97	100
[illegible]	STAT1	STAT1	signal transducer and activator of transcription 1	Nucleus	transcription regulator		-0.36	-0.75	0.09	0.00	0.00	0.96	20	0	34	80	100	66
[illegible]	PSTK	PSTK	phosphoseryl-tRNA kinase	Cytoplasm	kinase			0.98			0.00			97			3	
[illegible]	PHTF2	PHTF2	putative homeodomain transcription factor 2	Cytoplasm	other		-0.12	-0.96	0.56	0.00	0.00	0.00	34	0	95	66	100	5
[illegible]	CTDP1	CTDP1	CTD phosphatase subunit 1	Nucleus	phosphatase		0.31	0.71	0.06	0.00	0.00	0.30	17	100	86	83	0	14
[illegible]	RAB3B	RAB3B	RAB3B, member RAS oncogene family	Plasma Membrane	enzyme		0.22	0.83	0.75	0.06	0.00	0.00	77	100	97	23	0	3
[illegible]	ACVR1B	ACVR1B	activin A receptor type 1B	Plasma Membrane	kinase		-0.12	-0.89	-0.58	0.00	0.00	0.00	29	0	3	71	100	97
[illegible]	FAM63A	FAM63A	family with sequence similarity 63 member A	Extracellular Space	other		-0.50	-0.75	-0.88	0.00	0.00	0.00	6	0	5	94	100	95
[illegible]	PCNX3	PCNX3	pecanex homolog 3 (Drosophila)	Other	other		0.46	0.70	0.48	0.00	0.00	0.00	91	97	95	9	3	5
[illegible]	GLRX	GLRX	glutaredoxin	Cytoplasm	enzyme		-0.47	-0.97	-0.16	0.00	0.00	0.00	20	0	22	80	100	78
[illegible]	C9orf142	C9orf142	chromosome 9 open reading frame 142	Cytoplasm	other		0.26	0.89	-0.14	0.01	0.00	0.00	71	100	30	29	0	70
[illegible]	ERG	ERG	ERG proto-oncogene	Nucleus	transcription regulator		-0.36	-0.78	-0.84	0.00	0.00	0.00	6	0	5	94	100	95
[illegible]	PARP8	PARP8	poly(ADP-ribose) polymerase family member 8	Other	other		0.12	0.72	0.10	0.39	0.00	0.80	71	97	73	29	3	27
[illegible]	KAT5	KAT5	lysine acetyltransferase 5	Nucleus	transcription regulator		0.41	0.70	0.76	0.00	0.00	0.00	94	100	100	6	0	0
[illegible]	SLCO4A1	SLCO4A1	solute carrier organic anion transporter family member	Plasma Membrane	transporter		-0.50	-0.81	-0.04	0.00	0.00	0.15	6	0	66	94	100	34
[illegible]	[illegible]						0.37	0.71	0.86	0.00	0.00	0.00	77	97	92	23	3	8
[illegible]	LRP10	LRP10	LDL receptor related protein 10	Plasma Membrane	transmembrane receptor		-0.48	-0.86	-0.34	0.00	0.00	0.00	3	0	5	97	100	95
[illegible]	APOL6	APOL6	apolipoprotein L6	Extracellular Space	transporter		0.47	0.89	-0.18	0.00	0.00	0.00	86	89	39	14	11	61
[illegible]	FOXP1	FOXP1	forkhead box P1	Nucleus	other		-0.38	-0.81	-0.48	0.00	0.00	0.00	0	0	0	100	100	100
[illegible]	TRIM39	TRIM39	tripartite motif containing 39	Cytoplasm	other		0.25	0.74	0.76	0.00	0.00	0.00	71	100	100	29	0	0
[illegible]	CCRN4L	NOCT	nocturnin	Nucleus	transcription regulator		-0.14	0.72	1.17	0.00	0.00	0.00	40	89	100	60	11	0
[illegible]	GOT1	GOT1	glutamic-oxaloacetic transaminase 1	Cytoplasm	enzyme			1.08			0.00			100			0	
[illegible]	TMEM2	TMEM2	transmembrane protein 2	Cytoplasm	other		0.21	0.88	0.32	0.01	0.00	0.01	83	94	86	17	6	14
[illegible]	DHRS1	DHRS1	dehydrogenase/reductase 1	Cytoplasm	enzyme			0.98			0.00			100			0	
[illegible]	MTFP1	MTFP1	mitochondrial fission process 1	Cytoplasm	other		0.48	0.97	-0.92	0.00	0.00	0.00	94	100	0	6	0	100
[illegible]	DNAJC5	DNAJC5	DnaJ heat shock protein family (Hsp40) member C5	Plasma Membrane	other		-0.42	-0.79	-0.37	0.00	0.00	0.00	0	0	14	100	100	86
[illegible]	ITM2B	ITM2B	integral membrane protein 2B	Plasma Membrane	other		-0.38	-0.78	-0.88	0.00	0.00	0.00	9	0	0	91	100	100
[illegible]	PRKCH	PRKCH	protein kinase C eta	Cytoplasm	kinase	ingenol mebutate	0.50	0.67	-0.97	0.00	0.00	0.00	94	97	0	6	3	100
[illegible]	IL21R	IL21R	interleukin 21 receptor	Plasma Membrane	transmembrane receptor		-0.17	0.65	0.27	0.00	0.00	0.00	31	94	78	69	6	22
[illegible]	DYNC1H1	DYNC1H1	dynein cytoplasmic 1 heavy chain 1	Cytoplasm	peptidase		0.13	0.67	0.86	0.28	0.00	0.00	71	97	92	29	3	8
[illegible]	TMEM109	TMEM109	transmembrane protein 109	Cytoplasm	other		-0.44	-0.89	-0.03	0.00	0.00	0.56	3	0	69	97	100	31
[illegible]	ZNF471	ZNF471	zinc finger protein 471	Nucleus	other			0.78	0.44		0.00	0.00		94	92		6	8
[illegible]	KDM8	KDM8	lysine demethylase 8	Extracellular Space	enzyme		0.31	0.75	1.16	0.00	0.00	0.00	71	92	100	29	8	0
[illegible]	GIMAP6	GIMAP6	GTPase, IMAP family member 6	Cytoplasm	other		-0.14	-0.95	-1.47	0.00	0.00	0.00	31	0	0	69	100	100
[illegible]	ATPIF1	ATPIF1	ATPase inhibitory factor 1	Cytoplasm	other		0.48	0.78	-0.57	0.00	0.00	0.00	94	97	3	6	3	97
[illegible]	CNOT2	CNOT2	CCR4-NOT transcription complex subunit 2	Nucleus	transcription regulator		0.42	0.88	0.86	0.00	0.00	0.00	97	97	100	3	3	0
[illegible]	GAK	GAK	cyclin G associated kinase	Nucleus	kinase		0.41	0.88	0.91	0.00	0.00	0.00	86	97	100	14	3	0
[illegible]	LEPROT	LEPROT	leptin receptor overlapping transcript	Plasma Membrane	other		-0.48	-0.78	0.06	0.00	0.00	0.45	9	0	57	91	100	43
[illegible]	PLA2G15	PLA2G15	phospholipase A2 group XV	Cytoplasm	enzyme			-1.15	-0.85		0.00	0.00		0	19		100	81
[illegible]	CMPK2	CMPK2	cytidine/uridine monophosphate kinase 2	Cytoplasm	kinase		-0.38	-1.10	-0.41	0.00	0.00	0.00	20	6	5	80	94	95
[illegible]	FAM210B	FAM210B	family with sequence similarity 210 member B	Extracellular Space	other		-0.17	-0.82	-1.08	0.00	0.00	0.00	37	0	0	63	100	100
[illegible]	WASF2	WASF2	WAS protein family member 2	Plasma Membrane	other		-0.48	-0.79	-0.63	0.00	0.00	0.00	3	0	0	97	100	100
[illegible]	NCK2	NCK2	NCK adaptor protein 2	Cytoplasm	kinase		0.00	-0.78	-0.74	0.06	0.00	0.00	49	6	8	51	94	92
[illegible]	PPFIBP2	PPFIBP2	PPFIA binding protein 2	Nucleus	phosphatase		-0.15	0.76	1.02	0.00	0.00	0.00	17	92	100	83	8	0
[illegible]	SBK1	SBK1	SH3 domain binding kinase 1	Other	kinase		0.27	0.71	-0.76	0.00	0.00	0.00	83	94	0	17	6	100
[illegible]	FBXO34	FBXO34	F-box protein 34	Other	other		-0.15	-0.79	-0.41	0.00	0.00	0.00	34	3	16	66	97	84
[illegible]	LRRFIP1	LRRFIP1	LRR binding FLII interacting protein 1	Cytoplasm	other		-0.47	-0.88	0.30	0.00	0.00	0.00	11	3	84	89	97	16
[illegible]	SMAD7	SMAD7	SMAD family member 7	Nucleus	transcription regulator		0.27	0.71	0.46	0.00	0.00	0.00	83	89	84	17	11	16
[illegible]	SAMD8	SAMD8	sterile alpha motif domain containing 8	Cytoplasm	enzyme		-0.45	-0.70	0.02	0.00	0.00	0.90	0	3	54	100	97	46
[illegible]	POLR1A	POLR1A	RNA polymerase I subunit A	Nucleus	enzyme			0.84			0.00			97			3	
[illegible]	EIF2S3	EIF2S3	eukaryotic translation initiation factor 2 subunit gamma	Cytoplasm	translation regulator		-0.48	-0.79	-0.82	0.00	0.00	0.00	3	0	0	97	100	100
[illegible]	NFKBIZ	NFKBIZ	NFKB inhibitor zeta	Nucleus	transcription regulator		-0.12	0.72	0.96	0.00	0.00	0.00	29	3	97	71	97	3
[illegible]	ABR	ABR	active BCR-related	Cytoplasm	other		-0.30	-0.82	0.86	0.00	0.00	0.00	23	3	100	77	97	0
[illegible]	HYOU1	HYOU1	hypoxia up-regulated 1	Cytoplasm	other		0.29	0.84	0.58	0.00	0.00	0.00	86	100	100	14	0	0
[illegible]	CD226	CD226	CD226 molecule	Plasma Membrane	other		-0.36	-0.96	-0.42	0.00	0.00	0.00	14	6	11	86	94	89
[illegible]	MFN2	MFN2	mitofusin 2	Cytoplasm	enzyme		0.45	0.80	0.40	0.00	0.00	0.00	94	97	92	6	3	8
[illegible]	TNKS2	TNKS2	tankyrase 2	Nucleus	enzyme		0.45	0.69	0.17	0.00	0.00	0.04	100	94	70	0	6	30
[illegible]	C9orf91	C9orf91	chromosome 9 open reading frame 91	Other	other		-0.17	-0.81	-0.68	0.00	0.00	0.00	17	3	3	83	97	97
[illegible]	KANSL3	KANSL3	KAT8 regulatory NSL complex subunit 3	Nucleus	other		0.47	0.80	0.91	0.00	0.00	0.00	97	100	100	3	0	0
[illegible]	CBLB	CBLB	Cbl proto-oncogene B	Nucleus	enzyme		0.28	0.85	0.25	0.00	0.00	0.00	94	97	81	6	3	19
[illegible]	C11orf21	C11orf21	chromosome 11 open reading frame 21	Cytoplasm	other		0.06	0.89	-0.17	0.88	0.00	0.00	63	97	32	37	3	68
[illegible]	SKI	SKI	SKI proto-oncogene	Nucleus	transcription regulator		0.11	0.73	-0.21	0.18	0.00	0.07	63	89	38	37	11	62
[illegible]	KPNA2	KPNA2	karyopherin subunit alpha 2	Nucleus	transporter		-0.06	0.85	0.06	0.02	0.00	0.19	46	92	86	54	8	14
[illegible]	RASL11A	RASL11A	RAS like family 11 member A	Nucleus	other			1.05			0.00			100			0	
[illegible]	BAG5	BAG5	BCL2 associated athanogene 5	Nucleus	enzyme		0.47	0.70	0.91	0.00	0.00	0.00	97	97	97	3	3	3
[illegible]	HIF1A	HIF1A	hypoxia inducible factor 1 alpha subunit	Nucleus	transcription regulator	EZN-2968	-0.37	-0.71	0.81	0.00	0.00	0.00	11	3	78	89	97	22
[illegible]	SOX4	SOX4	SRY-box 4	Nucleus	transcription regulator		-0.09	-0.75	-1.09	0.00	0.00	0.00	46	3	0	54	97	100
[illegible]	COA1	COA1	cytochrome c oxidase assembly factor 1 homolog	Cytoplasm	other		0.41	0.85	-0.17	0.00	0.00	0.00	97	100	22	3	0	78
[illegible]	CHML	CHML	CHM like, Rab escort protein 2	Cytoplasm	enzyme		0.17	-0.71	0.14	0.87	0.00	0.23	66	0	62	34	100	38
[illegible]	RNF213	RNF213	ring finger protein 213	Cytoplasm	enzyme		0.48	0.89	-0.15	0.00	0.00	0.00	91	92	32	9	8	68
[illegible]	ERO1L	ERO1A	endoplasmic reticulum oxidoreductase 1 alpha	Cytoplasm	enzyme		-0.26	-0.89	-0.49	0.00	0.00	0.00	20	0	14	80	100	86
[illegible]	HEG1	HEG1	heart development protein with EGF like domains 1	Plasma Membrane	other		0.29	-0.70	-0.57	0.00	0.00	0.00	91	3	5	9	97	95
[illegible]	AMPD3	AMPD3	adenosine monophosphate deaminase 3	Cytoplasm	enzyme		-0.07	-0.85	0.89	0.00	0.00	0.00	29	0	100	71	100	0
[illegible]	ZFYVE1	ZFYVE1	zinc finger FYVE-type containing 1	Cytoplasm	other		0.42	0.67	0.26	0.00	0.00	0.00	94	100	86	6	0	14
[illegible]	BAG3	BAG3	BCL2 associated athanogene 3	Cytoplasm	other		0.26	-0.91	-0.78	0.00	0.00	0.00	91	8	5	9	92	95
[illegible]	SURF2	SURF2	surfeit 2	Nucleus	other		0.08	0.81	-0.92	0.91	0.00	0.00	63	100	0	37	0	100
[illegible]	STIP1	STIP1	stress induced phosphoprotein 1	Cytoplasm	other	[illegible]	0.00	0.89	0.80	0.09	0.00	0.00	49	97	89	51	3	11
[illegible]	SLMAP	SLMAP	sarcolemma associated protein	Plasma Membrane	other		0.38	0.84	0.90	0.00	0.00	0.00	91	97	100	9	3	0
[illegible]	IL16	IL16	interleukin 16	Extracellular Space	cytokine		-0.15	-0.86	-0.59	0.00	0.00	0.00	23	0	5	77	100	95
[illegible]	[illegible]	[illegible]	[illegible]	Cytoplasm	other			0.83			0.00			94			6	
[illegible]	ERP29	ERP29	endoplasmic reticulum protein 29	Cytoplasm	transporter		-0.48	-0.77	-0.59	0.00	0.00	0.00	6	3	3	94	97	97
[illegible]	LSM14B	LSM14B	LSM family member 14B	Other	other		-0.14	0.81	-0.15	0.00	0.00	0.00	34	100	19	66	0	81
[illegible]	IFNAR1	IFNAR1	interferon alpha and beta receptor subunit 1	Plasma Membrane	transmembrane receptor	recombinant interferon	-0.14	-0.71	-0.39	0.00	0.00	0.00	29	0	14	71	100	86
[illegible]	TRMT6	TRMT6	tRNA methyltransferase 6	Nucleus	other		-0.27	-0.86	1.02	0.00	0.00	0.00	23	0	100	77	100	0
[illegible]	IFFO2	IFFO2	intermediate filament family orphan 2	Other	other		0.27	0.83	0.86	0.00	0.00	0.00	80	86	89	20	14	11

MTOR	MTOR	mechanistic target of rapamycin	Nucleus	kinase	cyclosporine A/sirolim
SUCLG2	SUCLG2	succinate-CoA ligase GDP-forming beta subunit	Cytoplasm	enzyme	
CASZ1	CASZ1	castor zinc finger 1	Nucleus	enzyme	
PTPN22	PTPN22	protein tyrosine phosphatase, non-receptor type 22	Cytoplasm	phosphatase	
CD38	CD38	CD38 molecule	Plasma Membrane	other	
SMPD4	SMPD4	sphingomyelin phosphodiesterase 4	Cytoplasm	enzyme	
MRPL27	MRPL27	mitochondrial ribosomal protein L27	Cytoplasm	other	
PRR5	PRR5	proline rich 5	Cytoplasm	other	
RBM39	RBM39	RNA binding motif protein 39	Nucleus	transcription regulator	
SUPT6H	SUPT6H	SPT6 homolog, histone chaperone	Nucleus	transcription regulator	
CREM	CREM	cAMP responsive element modulator	Nucleus	transcription regulator	
CYTIP	CYTIP	cytohesin 1 interacting protein	Cytoplasm	other	
SLC25A30	SLC25A30	solute carrier family 25 member 30	Cytoplasm	other	
AMBRA1	AMBRA1	autophagy and beclin 1 regulator 1	Cytoplasm	other	
IP6K2	IP6K2	inositol hexakisphosphate kinase 2	Cytoplasm	kinase	
NA					
[illegible]					
TOLLIP	TOLLIP	toll interacting protein	Cytoplasm	other	
IGHMBP2	IGHMBP2	immunoglobulin mu binding protein 2	Nucleus	enzyme	
EFNA1	EFNA1	ephrin A1	Plasma Membrane	other	
FXYD5	FXYD5	FXYD domain containing ion transport regulator 5	Plasma Membrane	ion channel	
TMSB10	TMSB10/TMSB4X	thymosin beta 10	Cytoplasm	other	
CRYL1	CRYL1	crystallin lambda 1	Cytoplasm	enzyme	
KLHL5	KLHL5	kelch like family member 5	Extracellular Space	other	
HTATIP2	HTATIP2	HIV-1 Tat interactive protein 2	Nucleus	transcription regulator	
CEP170	CEP170	centrosomal protein 170	Nucleus	other	
TNFRSF10B	TNFRSF10B	TNF receptor superfamily member 10b	Plasma Membrane	transmembrane receptor	[illegible], conatumum
TREX1	TREX1	three prime repair exonuclease 1	Nucleus	enzyme	
ANAPC16	ANAPC16	anaphase promoting complex subunit 16	Nucleus	other	
FAIM3	FCMR	Fc fragment of IgM receptor	Plasma Membrane	other	
ZNF669	ZNF669	zinc finger protein 669	Nucleus	other	
CD69	CD69	CD69 molecule	Plasma Membrane	other	
RIPK1	RIPK1	receptor interacting serine/threonine kinase 1	Plasma Membrane	kinase	
EPG5	EPG5	ectopic P-granules autophagy protein 5 homolog	Other	other	
PLCXD2	PLCXD2	phosphatidylinositol specific phospholipase C X domain	Other	enzyme	
EGLN2	EGLN2	egl-9 family hypoxia inducible factor 2	Cytoplasm	enzyme	
ANKRD11	ANKRD11	ankyrin repeat domain 11	Nucleus	other	
CHERP	CHERP	calcium homeostasis endoplasmic reticulum protein	Cytoplasm	other	
PLCL2					
AGPAT3	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	Cytoplasm	enzyme	
RNF168	RNF168	ring finger protein 168	Other	other	
CDK17	CDK17	cyclin dependent kinase 17	Cytoplasm	kinase	
PRKX	PRKX	protein kinase, X-linked	Cytoplasm	kinase	
HM13	HM13	histocompatibility minor 13	Cytoplasm	peptidase	
LRMP	LRMP	lymphoid restricted membrane protein	Cytoplasm	other	
HUWE1	HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin	Nucleus	transcription regulator	
WIBG	PYM1	PYM homolog 1, exon junction complex associated fact	Nucleus	other	
ARHGEF6	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor 6	Cytoplasm	other	
DBR1	DBR1	debranching RNA lariats 1	Nucleus	enzyme	
CNOT6L	CNOT6L	CCR4-NOT transcription complex subunit 6 like	Cytoplasm	enzyme	
ATXN3	ATXN3	ataxin 3	Nucleus	peptidase	
UBE2E1	UBE2E1	ubiquitin conjugating enzyme E2 E1	Cytoplasm	enzyme	
RGS18	RGS18	regulator of G-protein signaling 18	Cytoplasm	other	
DDIT4	DDIT4	DNA damage inducible transcript 4	Cytoplasm	other	
CHUK	CHUK	conserved helix-loop-helix ubiquitous kinase	Cytoplasm	kinase	bardoxolone methyl
ADD1	ADD1	adducin 1	Cytoplasm	other	
UGCG	UGCG	UDP-glucose ceramide glucosyltransferase	Cytoplasm	enzyme	[illegible]
GLO1	GLO1	glyoxalase I	Cytoplasm	enzyme	
BNIPL	BNIPL	BCL2 interacting protein like	Cytoplasm	other	
RAB33A	RAB33A	RAB33A, member RAS oncogene family	Cytoplasm	enzyme	
GMFB	GMFB	glia maturation factor beta	Cytoplasm	growth factor	
IMPACT	IMPACT	impact RWD domain protein	Cytoplasm	other	
SMG6	SMG6	SMG6, nonsense mediated mRNA decay factor	Cytoplasm	enzyme	
CENPBD1P1	CENPBD1P1	CENPB DNA-binding domains containing 1, pseudogene	Other	other	
STX12	STX12	syntaxin 12	Cytoplasm	other	
ZNF296	ZNF296	zinc finger protein 296	Nucleus	other	
DNAJB1	DNAJB1	DnaJ heat shock protein family (Hsp40) member B1	Nucleus	transcription regulator	
IPO8	IPO8	importin 8	Nucleus	transporter	
CD2AP	CD2AP	CD2 associated protein	Cytoplasm	other	
PPP1R15A	PPP1R15A	protein phosphatase 1 regulatory subunit 15A	Cytoplasm	other	
TAF8	TAF8	TATA-box binding protein associated factor 8	Nucleus	transcription regulator	
RERE	RERE	arginine-glutamic acid dipeptide repeats	Nucleus	transcription regulator	
LFNG	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltra	Cytoplasm	enzyme	
AKAP11	AKAP11	A-kinase anchoring protein 11	Cytoplasm	other	
CHD4	CHD4	chromodomain helicase DNA binding protein 4	Nucleus	enzyme	
THEMIS	THEMIS	thymocyte selection associated	Cytoplasm	other	
[illegible]	[illegible]	[illegible] assembly factor 2	Cytoplasm	enzyme	
BTF3L4	BTF3L4	basic transcription factor 3 like 4	Other	other	
ZNF695	ZNF695	zinc finger protein 695	Cytoplasm	other	
FAM20B	FAM20B	FAM20B, glycosaminoglycan xylosylkinase	Extracellular Space	enzyme	
[illegible]	ACTG1P20	actin gamma 1 pseudogene 20	Other	other	
CNBP	CNBP	CCHC-type zinc finger nucleic acid binding protein	Nucleus	transcription regulator	
ZYG11B	ZYG11B	zyg-11 family member B, cell cycle regulator	Other	other	
NUDT15	NUDT15	nudix hydrolase 15	Cytoplasm	phosphatase	
SNX20	SNX20	sorting nexin 20	Cytoplasm	other	
ZZEF1	ZZEF1	zinc finger ZZ-type and EF-hand domain containing 1	Other	other	
GBP4	GBP4	guanylate binding protein 4	Cytoplasm	enzyme	
GLS	GLS	glutaminase	Cytoplasm	enzyme	CB-839
SIK3	SIK3	SIK family kinase 3	Cytoplasm	kinase	
SH3KBP1	SH3KBP1	SH3 domain containing kinase binding protein 1	Cytoplasm	other	
PHF12	PHF12	PHD finger protein 12	Nucleus	transcription regulator	
ABCF1	ABCF1	ATP binding cassette subfamily F member 1	Cytoplasm	transporter	
GLA	GLA	galactosidase alpha	Cytoplasm	enzyme	
TIMM17A	TIMM17A	translocase of inner mitochondrial membrane 17A	Cytoplasm	transporter	
TANK	TANK	TRAF family member associated NFKB activator	Cytoplasm	other	
GMNN	GMNN	geminin, DNA replication inhibitor	Nucleus	transcription regulator	
SLC25A3	SLC25A3	solute carrier family 25 member 3	Cytoplasm	transporter	
ATXN10	ATXN10	ataxin 10	Cytoplasm	other	
GRK6	GRK6	G protein-coupled receptor kinase 6	Plasma Membrane	kinase	
DIABLO	DIABLO	diablo IAP-binding mitochondrial protein	Cytoplasm	other	
AKAP17A	AKAP17A	A-kinase anchoring protein 17A	Nucleus	other	
SMG5	SMG5	SMG5, nonsense mediated mRNA decay factor	Nucleus	other	
HTRA2	HTRA2	HtrA serine peptidase 2	Cytoplasm	peptidase	
[illegible]					
ZNF318	ZNF318	zinc finger protein 318	Nucleus	other	
GIMAP2	GIMAP2	GTPase, IMAP family member 2	Cytoplasm	other	
[illegible]	[illegible]	SH3 domain containing [illegible]	Cytoplasm	other	
[illegible]					
HSPD1	HSPD1	heat shock protein family D (Hsp60) member 1	Cytoplasm	enzyme	
MAPKAP1	MAPKAP1	mitogen-activated protein kinase associated protein 1	Cytoplasm	other	
DYNLT3	DYNLT3	dynein light chain Tctex-type 3	Cytoplasm	other	
C1GALT1	C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-	Plasma Membrane	enzyme	
TBL2	TBL2	transducin beta like 2	Plasma Membrane	other	
EXOG	EXOG	exo/endonuclease G	Cytoplasm	enzyme	
RANBP10	RANBP10	RAN binding protein 10	Cytoplasm	other	
MTURN	MTURN	maturin, neural progenitor differentiation regulator ho	Other	other	
POLR2M	POLR2M	RNA polymerase II subunit M	Nucleus	other	
ATF2	ATF2	activating transcription factor 2	Nucleus	transcription regulator	
TMEM208	TMEM208	transmembrane protein 208	Cytoplasm	other	
STK24	STK24	serine/threonine kinase 24	Cytoplasm	kinase	
MORF4L2	MORF4L2	mortality factor 4 like 2	Nucleus	other	
CERS6	CERS6	ceramide synthase 6	Nucleus	transcription regulator	
FLI1	FLI1	Fli-1 proto-oncogene, ETS transcription factor	Nucleus	transcription regulator	
ACD	ACD	ACD, shelterin complex subunit and telomerase recruit	Nucleus	other	
PACSIN2	PACSIN2	protein kinase C and casein kinase substrate in neurons	Cytoplasm	transporter	
UBE2G1	UBE2G1	ubiquitin conjugating enzyme E2 G1	Cytoplasm	enzyme	
BTBD10	BTBD10	BTB domain containing 10	Cytoplasm	other	
PSEN1	PSEN1	presenilin 1	Plasma Membrane	peptidase	tarenflurbil
SERTAD1	SERTAD1	SERTA domain containing 1	Nucleus	transcription regulator	
NIPSNAP3A	NIPSNAP3A	nipsnap homolog 3A	Nucleus	other	
MTM1	MTM1	myotubularin 1	Cytoplasm	phosphatase	
PJA1	PJA1	praja ring finger ubiquitin ligase 1	Cytoplasm	enzyme	
RANBP2	RANBP2	RAN binding protein 2	Nucleus	enzyme	
UBAP2	UBAP2	ubiquitin associated protein 2	Cytoplasm	other	
C18orf32	C18orf32	chromosome 18 open reading frame 32	Other	other	
UBE2A	UBE2A	ubiquitin conjugating enzyme E2 A	Cytoplasm	enzyme	
TIPARP	TIPARP	TCDD inducible poly(ADP-ribose) polymerase	Nucleus	enzyme	
KMT2D	KMT2D	lysine methyltransferase 2D	Nucleus	transcription regulator	
SRRM2	SRRM2	serine/arginine repetitive matrix 2	Nucleus	other	
LTB	LTB	lymphotoxin beta	Extracellular Space	cytokine	
SLC25A33	SLC25A33	solute carrier family 25 member 33	Cytoplasm	transporter	
UTP6	UTP6	UTP6, small subunit processome component	Nucleus	other	
SEPHS2	SEPHS2	selenophosphate synthetase 2	Other	enzyme	
[illegible]	STK38	serine/threonine kinase 38	Nucleus	kinase	
METTL16	METTL16	methyltransferase like 16	Nucleus	enzyme	
COPB2	COPB2	coatomer protein complex subunit beta 2	Cytoplasm	transporter	
PPTC7	PPTC7	PTC7 protein phosphatase homolog	Cytoplasm	phosphatase	
MBNL2	MBNL2	muscleblind like splicing regulator 2	Nucleus	other	
RNF26	RNF26	ring finger protein 26	Other	other	
NA					
SLC39A1	SLC39A1	solute carrier family 39 member 1	Plasma Membrane	transporter	
C7orf49	C7orf49	chromosome 7 open reading frame 49	Other	other	
CCNH	CCNH	cyclin H	Nucleus	transcription regulator	
TFRC	TFRC	transferrin receptor	Plasma Membrane	transporter	CALAA-01
INPP5A	INPP5A	inositol polyphosphate-5-phosphatase A	Plasma Membrane	phosphatase	
EXOC8	EXOC8	exocyst complex component 8	Plasma Membrane	other	
RNASEH2C	RNASEH2C	ribonuclease H2 subunit C	Other	other	
ATG9A	ATG9A	autophagy related 9A	Cytoplasm	other	
RAB21	RAB21	RAB21, member RAS oncogene family	Cytoplasm	enzyme	
SERP1	SERP1	stress associated endoplasmic reticulum protein 1	Cytoplasm	other	
ZNF614	ZNF614	zinc finger protein 614	Other	other	
C9orf72	C9orf72	chromosome 9 open reading frame 72	Cytoplasm	other	
XIAP	XIAP	X-linked inhibitor of apoptosis	Cytoplasm	enzyme	[illegible] nucleotide AEG35156,
NMD3	NMD3	NMD3 ribosome export adaptor	Nucleus	other	
MFSD9	MFSD9	major facilitator superfamily domain containing 9	Other	transporter	
ELMO1	ELMO1	engulfment and cell motility 1	Cytoplasm	other	
ARID1B	ARID1B	AT-rich interaction domain 1B	Nucleus	transcription regulator	
GPSM3	GPSM3	G-protein signaling modulator 3	Cytoplasm	other	
IL17RA	IL17RA	interleukin 17 receptor A	Plasma Membrane	transmembrane receptor	
SNTB1	SNTB1	syntrophin beta 1	Plasma Membrane	other	
WWP2	WWP2	WW domain containing E3 ubiquitin protein ligase 2	Cytoplasm	enzyme	
CD96	CD96	CD96 molecule	Plasma Membrane	other	
FAM189A	FAM189A	family with sequence similarity 189 member A	Other	other	
ARL6IP6	ARL6IP6	ADP ribosylation factor like GTPase 6 interacting prot	Cytoplasm	other	
C18orf54	C18orf54	chromosome 18 open reading frame 54	Extracellular Space	other	
ROCK1	ROCK1	Rho associated coiled-coil containing protein kinase 1	Cytoplasm	kinase	
LMBR1	LMBR1	limb development membrane protein 1	Plasma Membrane	transmembrane receptor	
TXLNG	TXLNG	taxilin gamma	Nucleus	other	
REST	REST	RE1 silencing transcription factor	Nucleus	transcription regulator	
SETD8	KMT5A	lysine methyltransferase 5A	Nucleus	enzyme	
GTF2F1	GTF2F1	general transcription factor IIF subunit 1	Nucleus	transcription regulator	
YDJC	YDJC	YdjC homolog (bacterial)	Other	other	
PGRMC2	PGRMC2	progesterone receptor membrane component 2	Nucleus	other	
ARHGAP30	ARHGAP30	Rho GTPase activating protein 30	Cytoplasm	other	
KDSR	KDSR	3-ketodihydrosphingosine reductase	Plasma Membrane	enzyme	
MICU1	MICU1	mitochondrial calcium uptake 1	Cytoplasm	other	
FTSJ2	MRM2	mitochondrial rRNA methyltransferase 2	Nucleus	enzyme	
RFC4	RFC4	replication factor C subunit 4	Nucleus	other	
ATP5G3	ATP5G3	ATP synthase, H+ transporting, mitochondrial Fo compl	Cytoplasm	transporter	
SUZ12	SUZ12	SUZ12 polycomb repressive complex 2 subunit	Nucleus	enzyme	
SYNE1	SYNE1	spectrin repeat containing nuclear envelope protein 1	Nucleus	other	
ERC1	ERC1	ELKS/RAB6-interacting/CAST family member 1	Cytoplasm	other	
MYL12B	MYL12B	myosin light chain 12B	Cytoplasm	other	
[illegible]					
XAF1	XAF1	XIAP associated factor 1	Nucleus	other	
ATP5J	ATP5J	ATP synthase, H+ transporting, mitochondrial Fo compl	Cytoplasm	transporter	
CHMP1B	CHMP1B	charged multivesicular body protein 1B	Plasma Membrane	enzyme	
15-Sep	SELENOF	selenoprotein F	Cytoplasm	enzyme	
JMY	JMY	junction mediating and regulatory protein, p53 cofacto	Nucleus	transcription regulator	
CCZ1	CCZ1/CCZ1B	CCZ1 homolog, vacuolar protein trafficking and bioge	Cytoplasm	other	
[illegible]	[illegible]	stromal antigen 3-like [illegible], pseudogene	Other	other	
VMP1					
DNAJC27	DNAJC27	DnaJ heat shock protein family (Hsp40) member C27	Cytoplasm	enzyme	
[illegible]					
EEF1A1P6	EEF1A1P6	eukaryotic translation elongation factor 1 alpha 1 pseu	Other	other	
CRK	CRK	CRK proto-oncogene, adaptor protein	Cytoplasm	other	
BCL9	BCL9	B-cell CLL/lymphoma 9	Nucleus	other	
MAPK3	MAPK3	mitogen-activated protein kinase 3	Cytoplasm	kinase	ulixertinib, LY3214996
FAS	FAS	Fas cell surface death receptor	Plasma Membrane	transmembrane receptor	
MESDC2	MESDC2	mesoderm development candidate 2	Extracellular Space	other	
ABHD16A	ABHD16A	abhydrolase domain containing 16A	Cytoplasm	enzyme	
DNAJC14	DNAJC14	DnaJ heat shock protein family (Hsp40) member C14	Cytoplasm	other	
ELF1	ELF1	E74 like ETS transcription factor 1	Nucleus	transcription regulator	
TBC1D9B	TBC1D9B	TBC1 domain family member 9B	Other	other	
SDCBP	SDCBP	syndecan binding protein	Plasma Membrane	enzyme	
AZIN1	AZIN1	antizyme inhibitor 1	Cytoplasm	enzyme	
MFAP3	MFAP3	microfibrillar associated protein 3	Extracellular Space	other	
OLA1	OLA1	Obg like ATPase 1	Cytoplasm	enzyme	
CIDECP	CIDECP	cell death-inducing DFFA-like effector c pseudogene	Other	other	
CSTF2T	CSTF2T	cleavage stimulation factor subunit 2 tau variant	Nucleus	other	
CAST	CAST	calpastatin	Cytoplasm	peptidase	
LAX1	LAX1	lymphocyte transmembrane adaptor 1	Cytoplasm	other	
RNF122	RNF122	ring finger protein 122	Other	other	
DPEP2	DPEP2	dipeptidase 2	Plasma Membrane	peptidase	
IGBP1	IGBP1	immunoglobulin binding protein 1	Cytoplasm	phosphatase	

[illegible]	GPX7	GPX7	glutathione peroxidase 7	Cytoplasm	enzyme		-0.31
[illegible]	[illegible]						0.30
[illegible]	ST3GAL1	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	Cytoplasm	enzyme		-0.33
[illegible]	C21orf91	C21orf91	chromosome 21 open reading frame 91	Other	other		-0.27
[illegible]	CD81	CD81	CD81 molecule	Plasma Membrane	other		-0.27
[illegible]	NA						-0.08
[illegible]	QSOX2	QSOX2	quiescin sulfhydryl oxidase 2	Other	enzyme		-0.30
[illegible]	RBCK1	RBCK1	RANBP2-type and C3HC4-type zinc finger containing 1	Cytoplasm	transcription regulator		-0.33
[illegible]	KCNA3	KCNA3	potassium voltage-gated channel subfamily A member	Plasma Membrane	ion channel	dalfampridine	0.23
[illegible]	POMGNT2	POMGNT2	protein O-linked mannose N-acetylglucosaminyltransferase	Cytoplasm	enzyme		0.36
[illegible]	[illegible]						-0.26
[illegible]	USP22	USP22	ubiquitin specific peptidase 22	Nucleus	peptidase		-0.41
[illegible]	TMEM208	TMEM208	transmembrane protein 208	Other	other		-0.40
[illegible]	WDTC1	WDTC1	WD and tetratricopeptide repeats 1	Other	other		-0.39
[illegible]	ZNF707						
[illegible]	DCK	DCK	deoxycytidine kinase	Nucleus	kinase	[illegible]	-0.17
[illegible]	IGF2R	IGF2R	insulin like growth factor 2 receptor	Plasma Membrane	transmembrane receptor		0.46
[illegible]	GSAP	GSAP	gamma-secretase activating protein	Cytoplasm	peptidase		-0.18
[illegible]	SDHD	SDHD	succinate dehydrogenase complex subunit D	Cytoplasm	enzyme	hexachlorophene	-0.35
[illegible]	KLF2	KLF2	Kruppel like factor 2	Nucleus	transcription regulator		0.38
[illegible]	CYP20A1	CYP20A1	cytochrome P450 family 20 subfamily A member 1	Other	enzyme		0.48
[illegible]	PWP2	LOC102724159/PWP2	PWP2 periodic tryptophan protein homolog (yeast)	Nucleus	other		0.33
[illegible]	CCDC23	SVBP	small vasohibin binding protein	Other	other		-0.36
[illegible]	PELI2	PELI2	pellino E3 ubiquitin protein ligase family member 2	Cytoplasm	kinase		-0.31
[illegible]	TTC9	TTC9	tetratricopeptide repeat domain 9	Extracellular Space	other		-0.06
[illegible]	CCNYL1						-0.30
[illegible]	PAK1	PAK1	p21 (RAC1) activated kinase 1	Cytoplasm	kinase		-0.12
[illegible]	SGSH	SGSH	N-sulfoglucosamine sulfohydrolase	Cytoplasm	enzyme		0.31
[illegible]	CWF19L2	CWF19L2	CWF19-like 2, cell cycle control (S. pombe)	Other	other		0.35
[illegible]	ZNF395	ZNF395	zinc finger protein 395	Nucleus	other		0.47
[illegible]	EDEM1	EDEM1	ER degradation enhancing alpha-mannosidase like prot	Cytoplasm	enzyme		-0.30
[illegible]	ZBED6	ZBED6	zinc finger BED-type containing 6	Nucleus	other		
[illegible]	TGIF1	TGIF1	TGFB induced factor homeobox 1	Nucleus	transcription regulator		-0.33
[illegible]	PIGC	PIGC	phosphatidylinositol glycan anchor biosynthesis class C	Cytoplasm	enzyme		-0.27
[illegible]	ZNF682	ZNF682	zinc finger protein 682	Other	other		-0.39
[illegible]	TCEAL8	TCEAL8	transcription elongation factor A like 8	Other	other		-0.08
[illegible]	DNAJC4	DNAJC4	DnaJ heat shock protein family (Hsp40) member C4	Cytoplasm	other		-0.06
[illegible]	NDRG3	NDRG3	NDRG family member 3	Cytoplasm	other		-0.33
[illegible]	ERP44	ERP44	endoplasmic reticulum protein 44	Cytoplasm	enzyme		-0.05
[illegible]	C19orf10	MYDGF	myeloid derived growth factor	Extracellular Space	cytokine		-0.47
[illegible]	ATG101	ATG101	autophagy related 101	Cytoplasm	other		-0.43
[illegible]	PPP3CB	PPP3CB	protein phosphatase 3 catalytic subunit beta	Plasma Membrane	phosphatase	cyclosporin, pimecrolimus	-0.40
[illegible]	SRP9	SRP9	signal recognition particle 9	Cytoplasm	other		-0.25
[illegible]	MCM4	MCM4	minichromosome maintenance complex component 4	Nucleus	enzyme		
[illegible]	ATP6V1D	ATP6V1D	ATPase H+ transporting V1 subunit D	Cytoplasm	transporter		0.29
[illegible]	FBXW5	FBXW5	F-box and WD repeat domain containing 5	Cytoplasm	enzyme		-0.19
[illegible]	GCHFR	GCHFR	GTP cyclohydrolase I feedback regulator	Cytoplasm	other		-0.36
[illegible]	FAM134A	FAM134A	family with sequence similarity 134 member A	Other	other		-0.26
[illegible]	EIF4E2	EIF4E2	eukaryotic translation initiation factor 4E family memb	Cytoplasm	translation regulator		-0.40
[illegible]	NME4	NME4	NME/NM23 nucleoside diphosphate kinase 4	Cytoplasm	kinase		-0.08
[illegible]	THOC7	THOC7	THO complex 7	Nucleus	other		-0.43
[illegible]	SGMS1	SGMS1	sphingomyelin synthase 1	Cytoplasm	enzyme		-0.15
[illegible]	EPS15L1	EPS15L1	epidermal growth factor receptor pathway substrate 15	Plasma Membrane	other		0.26
[illegible]	OBFC1	STN1	STN1, CST complex subunit	Nucleus	other		-0.36
[illegible]	KCTD10	KCTD10	potassium channel tetramerization domain containing	Cytoplasm	other		-0.40
[illegible]	[illegible]						0.32
[illegible]	SLMO2	PRELID3B	PRELI domain containing 3B	Cytoplasm	other		-0.09
[illegible]	MTHFR	MTHFR	methylenetetrahydrofolate reductase	Cytoplasm	enzyme		-0.26
[illegible]	AIMP2	AIMP2	aminoacyl tRNA synthetase complex interacting multifu	Plasma Membrane	other		
[illegible]	AP3M1	AP3M1	adaptor related protein complex 3 mu 1 subunit	Cytoplasm	transporter		0.29
[illegible]	ETV6	ETV6	ETS variant 6	Nucleus	transcription regulator		0.46
[illegible]	DLGAP4	DLGAP4	DLG associated protein 4	Plasma Membrane	other		-0.16
[illegible]	ZNF277	ZNF277	zinc finger protein 277	Nucleus	transcription regulator		-0.09
[illegible]	SIDT2	SIDT2	SID1 transmembrane family member 2	Cytoplasm	other		-0.08
[illegible]	FRAT1	FRAT1	FRAT1, WNT signaling pathway regulator	Cytoplasm	other		-0.38
[illegible]	ABRACL	ABRACL	ABRA C-terminal like	Other	other		-0.22
[illegible]	ITFG1	ITFG1	integrin alpha FG-GAP repeat containing 1	Plasma Membrane	other		-0.22
[illegible]	ALG2	ALG2	ALG2, alpha-1,3/1,6-mannosyltransferase	Cytoplasm	enzyme		-0.38
[illegible]	PRMT6	PRMT6	protein arginine methyltransferase 6	Nucleus	enzyme		-0.09
[illegible]	PCED1B	PCED1B	PC-esterase domain containing 1B	Other	other		0.22
[illegible]	ADPRM	ADPRM	ADP-ribose/CDP-alcohol diphosphatase, manganese dep	Cytoplasm	enzyme		0.18
[illegible]	SIMC1	SIMC1	SUMO interacting motifs containing 1	Other	other		-0.39
[illegible]	USP32	USP32	ubiquitin specific peptidase 32	Cytoplasm	other		-0.33
[illegible]	ARHGEF2	ARHGEF2	Rho/Rac guanine nucleotide exchange factor 2	Cytoplasm	other		-0.15
[illegible]	DBNL						-0.36
[illegible]	FAM175A	FAM175A	family with sequence similarity 175 member A	Nucleus	other		0.28
[illegible]	PTPN1	PTPN1	protein tyrosine phosphatase, non-receptor type 1	Cytoplasm	phosphatase	phosphatase 1B inhibit	-0.45
[illegible]	UBLCP1	UBLCP1	ubiquitin like domain containing CTD phosphatase 1	Nucleus	phosphatase		-0.49
[illegible]	[illegible]	[illegible]	[illegible] opposite strand	Other	other		-0.26
[illegible]	DDX3X	DDX3X	DEAD-box helicase 3, X-linked	Cytoplasm	enzyme		0.30
[illegible]	POLD4	POLD4	DNA polymerase delta 4, accessory subunit	Nucleus	enzyme		-0.22
[illegible]	IL16	IL16	interleukin 16	Extracellular Space	cytokine		0.31
[illegible]	ITGA8	ITGA8	integrin subunit alpha 8	Plasma Membrane	other		-0.44
[illegible]	TRMT12	TRMT12	tRNA methyltransferase 12 homolog	Other	other		-0.18
[illegible]	PROSC	PROSC	proline synthetase co-transcribed homolog (bacterial)	Cytoplasm	enzyme		-0.29
[illegible]	FDX1	FDX1	ferredoxin 1	Cytoplasm	transporter		-0.49
[illegible]	SLC38A10	SLC38A10	solute carrier family 38 member 10	Cytoplasm	other		-0.30
[illegible]	DHX34	DHX34	DExH-box helicase 34	Other	enzyme		-0.43
[illegible]	STX8	STX8	syntaxin 8	Plasma Membrane	other		-0.48
[illegible]	MRPL14	MRPL14	mitochondrial ribosomal protein L14	Cytoplasm	other		-0.31
[illegible]	NFATC1	NFATC1	nuclear factor of activated T-cells 1	Nucleus	transcription regulator		-0.15
[illegible]	ELOVL5	ELOVL5	ELOVL fatty acid elongase 5	Cytoplasm	enzyme		-0.18
[illegible]	ETHE1	ETHE1	ETHE1, persulfide dioxygenase	Cytoplasm	enzyme		-0.16
[illegible]	NA						0.41
[illegible]	FAM122A	FAM122A	family with sequence similarity 122A	Extracellular Space	other		-0.48
[illegible]	TMEM71	TMEM71	transmembrane protein 71	Cytoplasm	other		0.22
[illegible]	CSK	CSK	c-src tyrosine kinase	Cytoplasm	kinase	bosutinib	0.25
[illegible]	PAICS	PAICS	phosphoribosylaminoimidazole carboxylase and phosph	Cytoplasm	enzyme		0.14
[illegible]	COMMD7	COMMD7	COMM domain containing 7	Cytoplasm	other		-0.38
[illegible]	CA5BP1	CA5BP1	carbonic anhydrase VB pseudogene 1	Other	other		0.29
[illegible]	SLC12A9	SLC12A9	solute carrier family 12 member 9	Plasma Membrane	transporter		-0.32
[illegible]	[illegible]						
[illegible]	C21orf33	C21orf33/LOC102724023	chromosome 21 open reading frame 33	Cytoplasm	other		-0.08
[illegible]	STRA13	CENPX	centromere protein X	Nucleus	other		-0.23
[illegible]	[illegible]	[illegible]	[illegible], member RAS oncogene family	Cytoplasm	enzyme		-0.45
[illegible]	LZIC	LZIC	leucine zipper and CTNNBIP1 domain containing	Other	other		-0.23
[illegible]	SLC25A1	SLC25A1	solute carrier family 25 member 1	Other	transporter		-0.41
[illegible]	ZNF561	ZNF561	zinc finger protein 561	Nucleus	other		0.28
[illegible]	IGHV1OR15-1	IGHV1OR15-1	immunoglobulin heavy variable 1/OR15-1 (non-functio	Other	other		0.28
[illegible]	OGFR	OGFR	opioid growth factor receptor	Plasma Membrane	other	[illegible]	-0.21
[illegible]	MIF	MIF	macrophage migration inhibitory factor (glycosylation-i	Extracellular Space	cytokine		-0.23
[illegible]	MED19	MED19	mediator complex subunit 19	Nucleus	other		0.24
[illegible]	MLLT1	MLLT1	MLLT1, super elongation complex subunit	Nucleus	transcription regulator		-0.45
[illegible]	EBPL	EBPL	emopamil binding protein like	Cytoplasm	enzyme		-0.29
[illegible]	SSBP3	SSBP3	single stranded DNA binding protein 3	Nucleus	transcription regulator		-0.42
[illegible]	SIGMAR1	SIGMAR1	sigma non-opioid intracellular receptor 1	Plasma Membrane	transmembrane receptor	[illegible]	-0.30
[illegible]	MGMT	MGMT	O-6-methylguanine-DNA methyltransferase	Nucleus	enzyme	[illegible]	-0.31
[illegible]	LSM6	LSM6	LSM6 homolog, U6 small nuclear RNA and mRNA degra	Nucleus	other		-0.26
[illegible]	DECR1	DECR1	2,4-dienoyl-CoA reductase 1	Cytoplasm	enzyme		-0.26
[illegible]	GLTPD1	CPTP	ceramide-1-phosphate transfer protein	Cytoplasm	transporter		-0.18
[illegible]	NENF	NENF	neudesin neurotrophic factor	Extracellular Space	growth factor		-0.16
[illegible]	TPRA1	TPRA1	transmembrane protein adipocyte associated 1	Plasma Membrane	G-protein coupled receptor		-0.33
[illegible]	[illegible]						0.31
[illegible]	NFKBIL1	NFKBIL1	NFKB inhibitor like 1	Nucleus	transcription regulator		-0.15
[illegible]	TRBV27	TRBV27	T cell receptor beta variable 27	Other	other		-0.42
[illegible]	NDUFA11	NDUFA11	NADH:ubiquinone oxidoreductase subunit A11	Cytoplasm	enzyme		-0.38
[illegible]	MRPL36	MRPL36	mitochondrial ribosomal protein L36	Cytoplasm	other		-0.36
[illegible]	GPR174	GPR174	G protein-coupled receptor 174	Plasma Membrane	G-protein coupled receptor		0.29
[illegible]	GPANK1	GPANK1	G-patch domain and ankyrin repeats 1	Nucleus	transcription regulator		-0.27
[illegible]	TFPT	TFPT	TCF3 fusion partner	Nucleus	other		-0.45
[illegible]	FAM127B	FAM127B	family with sequence similarity 127 member B	Other	other		
[illegible]	AREG	AREG	amphiregulin	Extracellular Space	growth factor		-0.36
[illegible]	IFI35	IFI35	interferon induced protein 35	Nucleus	other		-0.48
[illegible]	TRBV6-6	TRBV6-6	T cell receptor beta variable 6-6	Other	other		0.45
[illegible]	HIST1H2BD	HIST1H2BD	histone cluster 1 H2B family member d	Nucleus	other		-0.14
[illegible]	[illegible]						-0.06
[illegible]	MYO1C	MYO1C	myosin IC	Cytoplasm	enzyme		
[illegible]	FADS3	FADS3	fatty acid desaturase 3	Plasma Membrane	enzyme		
[illegible]	NA						0.46
[illegible]	CD8B	CD8B	CD8b molecule	Plasma Membrane	transmembrane receptor	[illegible]	-0.17
[illegible]	ADAM28	ADAM28	ADAM metallopeptidase domain 28	Plasma Membrane	peptidase		
[illegible]	BCL11B	BCL11B	B-cell CLL/lymphoma 11B	Nucleus	transcription regulator		0.43
[illegible]	MMP19	MMP19	matrix metallopeptidase 19	Extracellular Space	peptidase	marimastat	
[illegible]	CD3D	CD3D	CD3d molecule	Plasma Membrane	transmembrane receptor	blinatumomab	0.28
[illegible]	ITM2A	ITM2A	integral membrane protein 2A	Plasma Membrane	other		0.43
[illegible]	AMIGO1	AMIGO1	adhesion molecule with Ig like domain 1	Plasma Membrane	other		0.38
[illegible]	TRBC2	TRBC2	T cell receptor beta constant 2	Other	other		0.39
[illegible]	GEN1	GEN1	GEN1, Holliday junction 5' flap endonuclease	Cytoplasm	enzyme		
[illegible]	TRBV28	TRBV28	T cell receptor beta variable 28	Other	other		0.45
[illegible]	MSC	MSC	musculin	Cytoplasm	transcription regulator		
[illegible]	IL32	IL32	interleukin 32	Extracellular Space	cytokine		-0.49
[illegible]	IL1A	IL1A	interleukin 1 alpha	Extracellular Space	cytokine		
[illegible]	CD27	CD27	CD27 molecule	Plasma Membrane	transmembrane receptor	CDX-1127	-0.08
[illegible]	SLFN5	SLFN5	schlafen family member 5	Nucleus	enzyme		-0.22
[illegible]	PNP	PNP	purine nucleoside phosphorylase	Nucleus	enzyme	[illegible]	-0.33
[illegible]	LEPROTL1	LEPROTL1	leptin receptor overlapping transcript-like 1	Plasma Membrane	other		0.44
[illegible]	UAP1L1	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1	Other	other		
[illegible]	ORMDL3	ORMDL3	ORMDL sphingolipid biosynthesis regulator 3	Cytoplasm	other		0.30
[illegible]	[illegible]						
[illegible]	GIMAP1	GIMAP1	GTPase, IMAP family member 1	Cytoplasm	other		0.37
[illegible]	RIN1	RIN1	Ras and Rab interactor 1	Cytoplasm	other		
[illegible]	SELPLG	SELPLG	selectin P ligand	Plasma Membrane	other		-0.22
[illegible]	PCED1B-AS1	PCED1B-AS1	PCED1B antisense RNA 1	Other	other		0.31
[illegible]	AMPD3	AMPD3	adenosine monophosphate deaminase 3	Cytoplasm	enzyme		0.25
[illegible]	TRBV20-1	TRBV20-1	T cell receptor beta variable 20-1	Other	other		0.43
[illegible]	RELT	RELT	RELT tumor necrosis factor receptor	Plasma Membrane	transmembrane receptor		-0.48
[illegible]	FANCD2	FANCD2	Fanconi anemia complementation group D2	Nucleus	other		
[illegible]	SIRPG	SIRPG	signal regulatory protein gamma	Plasma Membrane	other		0.38
[illegible]	F3	F3	coagulation factor III, tissue factor	Plasma Membrane	transmembrane receptor	recombinant human factor VII	
[illegible]	LDHB	LDHB	lactate dehydrogenase B	Cytoplasm	enzyme		0.23
[illegible]	FHOD1	FHOD1	formin homology 2 domain containing 1	Cytoplasm	other		
[illegible]	ABCB4	ABCB4	ATP binding cassette subfamily B member 4	Plasma Membrane	transporter		
[illegible]	RASGRP3	RASGRP3	RAS guanyl releasing protein 3	Cytoplasm	other		
[illegible]	ADCY3	ADCY3	adenylate cyclase 3	Plasma Membrane	enzyme		
[illegible]	MAML2	MAML2	mastermind like transcriptional coactivator 2	Nucleus	transcription regulator		0.36
[illegible]	RRP12	RRP12	ribosomal RNA processing 12 homolog	Nucleus	other		0.22
[illegible]	RASGEF1B	RASGEF1B	RasGEF domain family member 1B	Other	other		-0.33
[illegible]	LRP5L	LRP5L	LDL receptor related protein 5 like	Other	other		
[illegible]	HSPA7	HSPA7	heat shock protein family A (Hsp70) member 7	Cytoplasm	other		
[illegible]	[illegible]						0.41
[illegible]	SLCO4A1	SLCO4A1	solute carrier organic anion transporter family member	Plasma Membrane	transporter		
[illegible]	CLEC17A	CLEC17A	C-type lectin domain family 17 member A	Plasma Membrane	other		
[illegible]	IL1R1	IL1R1	interleukin 1 receptor type 1	Plasma Membrane	transmembrane receptor	anakinra	
[illegible]	FCRL2	FCRL2	Fc receptor like 2	Other	other		
[illegible]	CHI3L2	CHI3L2	chitinase 3 like 2	Extracellular Space	enzyme		0.28
[illegible]	VIM-AS1	VIM-AS1	VIM antisense RNA 1	Other	other		
[illegible]	SMAD3	SMAD3	SMAD family member 3	Nucleus	transcription regulator		-0.10
[illegible]	MANBA	MANBA	mannosidase beta	Cytoplasm	enzyme		
[illegible]	CDKN2B	CDKN2B	cyclin dependent kinase inhibitor 2B	Nucleus	kinase		-0.32
[illegible]	[illegible]						0.25
[illegible]	MGAT4A	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylgl	Cytoplasm	enzyme		0.26
[illegible]	ARHGEF40	ARHGEF40	Rho guanine nucleotide exchange factor 40	Other	other		
[illegible]	KLF6	KLF6	Kruppel like factor 6	Nucleus	transcription regulator		0.27
[illegible]	ZFP36L2	ZFP36L2	ZFP36 ring finger protein like 2	Nucleus	transcription regulator		-0.18
[illegible]	KLF12	KLF12	Kruppel like factor 12	Nucleus	transcription regulator		0.29
[illegible]	UBXN11	UBXN11	UBX domain protein 11	Cytoplasm	other		0.41
[illegible]	NXPE3	NXPE3	neurexophilin and PC-esterase domain family member	Other	other		-0.12
[illegible]	TRBV19	TRBV19	T cell receptor beta variable 19	Other	other		0.31
[illegible]	PRDM8	PRDM8	PR/SET domain 8	Nucleus	transcription regulator		
[illegible]	DMXL2	DMXL2	Dmx like 2	Cytoplasm	other		
[illegible]	JAG1	JAG1	jagged 1	Extracellular Space	growth factor		
[illegible]	PLD3	PLD3	phospholipase D3	Cytoplasm	enzyme		
[illegible]	DYRK2	DYRK2	dual specificity tyrosine phosphorylation regulated kina	Cytoplasm	kinase		0.16
[illegible]	PITPNC1	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	Cytoplasm	transporter		0.27
[illegible]	[illegible]						0.32
[illegible]	NFKBIA	NFKBIA	NFKB inhibitor alpha	Cytoplasm	transcription regulator		0.45
[illegible]	WDR89	WDR89	WD repeat domain 89	Other	other		0.39
[illegible]	NUP88	NUP88	nucleoporin 88	Nucleus	transporter		0.39
[illegible]	MPP7	MPP7	membrane palmitoylated protein 7	Plasma Membrane	other		0.22
[illegible]	PACS1	PACS1	phosphofurin acidic cluster sorting protein 1	Cytoplasm	other		-0.05
[illegible]	IFITM1	IFITM1	interferon induced transmembrane protein 1	Plasma Membrane	transmembrane receptor		-0.18
[illegible]	CCND3	CCND3	cyclin D3	Nucleus	kinase		0.27
[illegible]	ETS1	ETS1	ETS proto-oncogene 1, transcription factor	Nucleus	transcription regulator		0.26
[illegible]	TRBV2	TRBV2	T cell receptor beta variable 2	Other	other		0.47
[illegible]	STYX	STYX	serine/threonine/tyrosine interacting protein	Cytoplasm	phosphatase		0.18
[illegible]	FAM217B	FAM217B	family with sequence similarity 217 member B	Other	other		-0.38
[illegible]	CRTC3	CRTC3	CREB regulated transcription coactivator 3	Nucleus	other		0.20
[illegible]	ZBP1	ZBP1	Z-DNA binding protein 1	Cytoplasm	other		
[illegible]	TOX	TOX	thymocyte selection associated high mobility group box	Nucleus	other		0.30
[illegible]	SUMO4	SUMO4	SUMO family member 4	Nucleus	other		
[illegible]	CYTH3	CYTH3	cytohesin 3	Cytoplasm	other		
[illegible]	TSPAN14	TSPAN14	tetraspanin 14	Plasma Membrane	other		0.21
[illegible]	LONRF3	LONRF3	LON peptidase N-terminal domain and ring finger 3	Other	other		
[illegible]	TRBV6-5	TRBV6-5	T cell receptor beta variable 6-5	Other	other		0.40
[illegible]	USP28	USP28	ubiquitin specific peptidase 28	Nucleus	peptidase		

[illegible]	THEM4	THEM4	thioesterase superfamily member 4	Plasma Membrane	enzyme		0.42	-0.80	-1.30
[illegible]	FCGR2C	FCGR2C	Fc fragment of IgG receptor IIc (gene/pseudogene)	Plasma Membrane	transmembrane receptor	IgG			1.89
[illegible]	DUSP16	DUSP16	dual specificity phosphatase 16	Nucleus	phosphatase		0.46	0.03	-1.17
[illegible]	PTPRR	PTPRR	protein tyrosine phosphatase, receptor type R	Plasma Membrane	phosphatase		-0.18	-0.21	1.18
[illegible]	LGALS3BP	LGALS3BP	galectin 3 binding protein	Plasma Membrane	transmembrane receptor		0.28	-0.15	-1.16
[illegible]	LRRC8D	LRRC8D	leucine rich repeat containing 8 family member D	Plasma Membrane	G-protein coupled receptor		0.12	-0.26	-1.17
[illegible]	SEMA3F	SEMA3F	semaphorin 3F	Extracellular Space	other				1.27
[illegible]	KIF3A	KIF3A	kinesin family member 3A	Cytoplasm	other		0.17	-0.07	-1.10
[illegible]	GYPC	GYPC	glycophorin C (Gerbich blood group)	Plasma Membrane	other		0.21	0.03	-1.06
[illegible]	SKAP1	SKAP1	src kinase associated phosphoprotein 1	Cytoplasm	kinase		0.39	-0.08	-1.17
[illegible]	RARRES3	RARRES3	retinoic acid receptor responder 3	Cytoplasm	enzyme		-0.02	0.17	-1.12
[illegible]	GRASP	GRASP	general receptor for phosphoinositides 1 associated scaffo	Plasma Membrane	other		-0.16	-0.14	1.09
[illegible]	RP11-[illegible]	LOC100288175	uncharacterized LOC100288175	Other	other				1.79
[illegible]	KCTD7	KCTD7	potassium channel tetramerization domain containing 7	Other	ion channel				1.30
[illegible]	PRRC1	PRRC1	proline rich coiled-coil 1	Other	other		0.11	-0.08	-1.07
[illegible]	PDE3A	PDE3A	phosphodiesterase 3A	Cytoplasm	enzyme	e, dipyridamole, ketotifen, tolbutamide, theophylline, pentoxifylline			1.27
[illegible]	IKZF1	IKZF1	IKAROS family zinc finger 1	Nucleus	transcription regulator		0.22	-0.69	-0.99
[illegible]	TSNAX	TSNAX	translin associated factor X	Nucleus	transporter		0.06	-0.65	-1.10
[illegible]	MICAL3	MICAL3	microtubule associated monooxygenase, calponin and LIM	Cytoplasm	enzyme				1.09
[illegible]	DGCR6L	DGCR6L	DiGeorge syndrome critical region gene 6 like	Nucleus	other		-0.25	-0.60	-1.13
[illegible]	DNAAF2	DNAAF2	dynein axonemal assembly factor 2	Cytoplasm	other		-0.08	0.16	1.17
[illegible]	TSHZ1	TSHZ1	teashirt zinc finger homeobox 1	Nucleus	transcription regulator		-0.06	-0.28	-1.05
[illegible]	PRR13	PRR13	proline rich 13	Extracellular Space	other		0.30	-0.08	-0.99
[illegible]	SH3YL1	SH3YL1	SH3 and SYLF domain containing 1	Plasma Membrane	other		0.40	0.00	-1.10
[illegible]	CLCN7	CLCN7	chloride voltage-gated channel 7	Plasma Membrane	ion channel		0.45	0.17	1.14
[illegible]	BIN2	BIN2	bridging integrator 2	Plasma Membrane	other		-0.44	-0.07	-0.99
[illegible]	ITGA5	ITGA5	integrin subunit alpha 5	Plasma Membrane	transmembrane receptor		0.30	0.18	1.11
[illegible]	IRF2BP1	IRF2BP1	interferon regulatory factor 2 binding protein 1	Nucleus	transcription regulator		-0.06	-0.39	-1.09
[illegible]	NSF	NSF	N-ethylmaleimide sensitive factor, vesicle fusing ATPase	Cytoplasm	transporter				1.18
[illegible]	TRBV3-1	TRBV3-1	T cell receptor beta variable 3-1	Other	other		0.40	-0.05	-1.18
[illegible]	CTBP1-AS2	CTBP1-AS2	CTBP1 antisense RNA 2 (head to head)	Other	other		0.24	0.19	-1.06
[illegible]	NA								1.42
[illegible]	SMPD1	SMPD1	sphingomyelin phosphodiesterase 1	Cytoplasm	enzyme	sphingomyelinase inhib	0.46	0.10	-0.96
[illegible]	MYADM	MYADM	myeloid associated differentiation marker	Nucleus	other		-0.14	0.05	1.12
[illegible]	XPNPEP1	XPNPEP1	X-prolyl aminopeptidase 1	Cytoplasm	peptidase		0.15	0.18	1.09
[illegible]	SETD1B	SETD1B	SET domain containing 1B	Nucleus	enzyme		0.49	0.18	-1.05
[illegible]	LBH	LBH	limb bud and heart development	Nucleus	transcription regulator		0.34	0.00	-1.05
[illegible]	CDC37						0.35	0.16	0.96
[illegible]	TRAV13-1	TRAV13-1	T cell receptor alpha variable 13-1	Other	other		0.36	-0.22	-1.44
[illegible]	RRN3P1	RRN3P1	RRN3 homolog, RNA polymerase I transcription factor ;	Other	other				1.23
[illegible]	TPRG1L	TPRG1L	tumor protein p63 regulated 1 like	Cytoplasm	other		-0.10	-0.26	-0.96
[illegible]	ATP6V0E2	ATP6V0E2	ATPase H+ transporting V0 subunit e2	Cytoplasm	enzyme		-0.29	-0.18	-1.17
[illegible]	ASF1A	ASF1A	anti-silencing function 1A histone chaperone	Nucleus	other		0.29	-0.39	-1.17
[illegible]	NGLY1	NGLY1	N-glycanase 1	Cytoplasm	enzyme		-0.21	0.05	1.16
[illegible]	MFSD2A	MFSD2A	major facilitator superfamily domain containing 2A	Plasma Membrane	transporter				1.29
[illegible]	STX1A	STX1A	syntaxin 1A	Cytoplasm	transporter		-0.42	-0.11	1.16
[illegible]	KDM4B	KDM4B	lysine demethylase 4B	Nucleus	enzyme		-0.10	0.21	0.95
[illegible]	GZMM	GZMM	granzyme M	Cytoplasm	peptidase		-0.09	0.16	-0.98
[illegible]	LRRK2	LRRK2	leucine rich repeat kinase 2	Cytoplasm	kinase				1.10
[illegible]	MAP3K3	MAP3K3	mitogen-activated protein kinase kinase kinase 3	Other	kinase		0.10	-0.05	1.10
[illegible]	TRAV12-1	TRAV12-1	T cell receptor alpha variable 12-1	Other	other		0.21	-0.10	-1.41
[illegible]	BOD1L1	BOD1L1	biorientation of chromosomes in cell division 1 like 1	Nucleus	other		0.35	0.47	1.22
[illegible]	PRUNE	PRUNE1	prune exopolyphosphatase	Nucleus	enzyme		0.26	-0.02	-1.11
[illegible]	ST13	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hs	Cytoplasm	other		-0.11	-0.25	-0.97
[illegible]	EIF2AK3	EIF2AK3	eukaryotic translation initiation factor 2 alpha kinase 3	Cytoplasm	kinase		-0.18	-0.06	1.22
[illegible]	HSPB1	HSPB1	heat shock protein family B (small) member 1	Cytoplasm	other		0.27	-0.06	-1.16
[illegible]	NECAP2	NECAP2	NECAP endocytosis associated 2	Cytoplasm	other		0.45	-0.27	-0.84
[illegible]	SERPINB1	SERPINB1	serpin family B member 1	Extracellular Space	other	drotrecogin alfa			1.31
[illegible]	KLHL2	KLHL2	kelch like family member 2	Cytoplasm	other		-0.08	-0.12	1.18
[illegible]	PLEKHG3	PLEKHG3	pleckstrin homology and RhoGEF domain containing G3	Cytoplasm	other		0.30	0.29	0.98
[illegible]	NA						-0.16	0.19	-1.47
[illegible]	NPC1	NPC1	NPC intracellular cholesterol transporter 1	Cytoplasm	transporter		-0.40	0.10	1.06
[illegible]	RABEP2	RABEP2	rabaptin, RAB GTPase binding effector protein 2	Cytoplasm	other		0.18	0.46	1.16
[illegible]	RGS10	RGS10	regulator of G-protein signaling 10	Cytoplasm	other		0.13	-0.08	-0.81
[illegible]	THAP11	THAP11	THAP domain containing 11	Nucleus	other		-0.18	-0.07	-0.99
[illegible]	RHNO1	RHNO1	RAD9-HUS1-RAD1 interacting nuclear orphan 1	Nucleus	other		0.18	-0.07	-0.99
[illegible]	SLC17A9	SLC17A9	solute carrier family 17 member 9	Cytoplasm	other				1.17
[illegible]	COLGALT1	COLGALT1	collagen beta(1-O)galactosyltransferase 1	Cytoplasm	enzyme		0.34	-0.29	1.22
[illegible]	PFKFB2	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	Cytoplasm	kinase				1.18
[illegible]	RALGDS	RALGDS	ral guanine nucleotide dissociation stimulator	Cytoplasm	other		0.26	0.10	1.09
[illegible]	6-Sep	SEPT6	septin 6	Cytoplasm	other		0.00	-0.80	-0.87
[illegible]	ZNF507	ZNF507	zinc finger protein 507	Nucleus	other		0.44	0.12	-0.86
[illegible]	SEPN1	SELENON	selenoprotein N	Cytoplasm	other		0.15	-0.08	-0.87
[illegible]	UPP1	UPP1	uridine phosphorylase 1	Cytoplasm	enzyme		-0.10	-0.09	1.21
[illegible]	VPS26B	VPS26B	VPS26, retromer complex component B	Cytoplasm	transporter		-0.15	0.04	-0.88
[illegible]	TRAV8-2	TRAV8-2	T cell receptor alpha variable 8-2	Other	other		0.42	-0.12	-1.21
[illegible]	SLC9B2						-0.97	-0.60	1.21
[illegible]	ZNF862	ZNF862	zinc finger protein 862	Other	other		0.27	-0.08	-0.89
[illegible]	NAIF1	NAIF1	nuclear apoptosis inducing factor 1	Nucleus	other		0.14	-0.39	-1.01
[illegible]	DVL3	DVL3	dishevelled segment polarity protein 3	Cytoplasm	other		0.27	-0.05	0.96
[illegible]	NIPSNAP1	NIPSNAP1	nipsnap homolog 1	Cytoplasm	enzyme		0.18	0.00	-1.07
[illegible]	THAP2	THAP2	THAP domain containing 2	Nucleus	other				1.11
[illegible]	DENND6A	DENND6A	DENN domain containing 6A	Cytoplasm	other		0.28	0.01	-0.88
[illegible]	AK8	AK8	adenylate kinase 8	Cytoplasm	kinase		0.02	-0.02	-0.93
[illegible]	COX11	COX11	COX11, cytochrome c oxidase copper chaperone	Cytoplasm	enzyme		-0.10	0.01	-0.89
[illegible]	BTN3A2	BTN3A2	butyrophilin subfamily 3 member A2	Plasma Membrane	other		-0.09	-0.18	-0.84
[illegible]	CHAMP1	CHAMP1	chromosome alignment maintaining phosphoprotein 1	Nucleus	other		0.05	-0.02	-0.93
[illegible]	FAM117B	FAM117B	family with sequence similarity 117 member B	Other	other		0.30	0.13	-0.75
[illegible]	CCDC9	CCDC9	coiled-coil domain containing 9	Extracellular Space	other		-0.11	0.02	0.95
[illegible]	ACSL3	ACSL3	acyl-CoA synthetase long-chain family member 3	Cytoplasm	enzyme		0.26	0.15	0.88
[illegible]	SLC22A4	SLC22A4	solute carrier family 22 member 4	Plasma Membrane	transporter				1.02
[illegible]	GGA1	GGA1	golgi associated, gamma adaptin ear containing, ARF b	Cytoplasm	transporter		-0.01	0.00	0.95
[illegible]	TRAV12-3	TRAV12-3	T cell receptor alpha variable 12-3	Other	other		0.24	-0.08	-1.48
[illegible]	NOC3L	NOC3L	NOC3 like DNA replication regulator	Nucleus	other				1.16
[illegible]	ALAS1	ALAS1	5'-aminolevulinate synthase 1	Cytoplasm	enzyme		-0.26	-0.44	0.95
[illegible]	MT2A	MT2A	metallothionein 2A	Cytoplasm	other		-0.28	0.15	-0.91
[illegible]	TRBV5-6	TRBV5-6	T cell receptor beta variable 5-6	Other	other		-0.07	0.09	-1.03
[illegible]	MFNG	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltr	Cytoplasm	enzyme		0.30	-0.39	-0.83
[illegible]	NPM3	NPM3	nucleophosmin/nucleoplasmin 3	Nucleus	other		0.29	0.12	-1.07
[illegible]	TNS3	TNS3	tensin 3	Plasma Membrane	phosphatase				1.10
[illegible]	IQSEC1	IQSEC1	IQ motif and Sec7 domain 1	Cytoplasm	other		0.38	-0.42	0.99
[illegible]	ZBTB4	ZBTB4	zinc finger and BTB domain containing 4	Nucleus	transcription regulator		0.14	0.13	-0.77
[illegible]	SLC38A11	SLC38A11	solute carrier family 38 member 11	Cytoplasm	transporter		0.49	-0.30	0.98
[illegible]	ARAP1	ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH do	Cytoplasm	other		0.29	0.29	0.80
[illegible]	S1PR1	S1PR1	sphingosine-1-phosphate receptor 1	Plasma Membrane	G-protein coupled receptor	fingolimod phosphate	-0.32	-0.60	-0.93
[illegible]	TRBV9	TRBV9	T cell receptor beta variable 9	Plasma Membrane	other		-0.29	0.43	-1.12
[illegible]	ATAD2B	ATAD2B	ATPase family, AAA domain containing 2B	Nucleus	other				0.98
[illegible]	MSR1	MSR1	macrophage scavenger receptor 1	Plasma Membrane	transmembrane receptor				1.12
[illegible]	SVIP	SVIP	small VCP interacting protein	Cytoplasm	other		-0.12	0.08	-0.91
[illegible]	GRAP2	GRAP2	GRB2-related adaptor protein 2	Cytoplasm	other		0.40	0.47	-0.90
[illegible]	MMP9	MMP9	matrix metallopeptidase 9	Extracellular Space	peptidase	D, relamostat, marimastat, prinomastat, glucosamine			1.23
[illegible]	CDC42BPB	CDC42BPB	CDC42 binding protein kinase beta	Cytoplasm	kinase				0.98
[illegible]	IDH2	IDH2	isocitrate dehydrogenase (NADP(+)) 2, mitochondrial	Cytoplasm	enzyme	enasidenib	0.18	-0.22	-0.83
[illegible]	RASSF3	RASSF3	Ras association domain family member 3	Other	other		0.26	-0.29	-0.80
[illegible]	ATP13A3	ATP13A3	ATPase 13A3	Extracellular Space	transporter		-0.11	-0.18	0.86
[illegible]	P2RY8	P2RY8	purinergic receptor P2Y8	Plasma Membrane	G-protein coupled receptor		-0.16	-0.17	-0.88
[illegible]	MIS18BP1	MIS18BP1	MIS18 binding protein 1	Nucleus	other		-0.15	-0.02	0.97
[illegible]	TRBV7-8	TRBV7-8	T cell receptor beta variable 7-8	Other	other		0.12	-0.09	-1.11
[illegible]	TOP1	TOP1	topoisomerase (DNA) I	Nucleus	enzyme	irinotecan/cisplatin	0.34	0.22	0.91
[illegible]	MCTP2	MCTP2	multiple C2 and transmembrane domain containing 2	Other	other				1.18
[illegible]	RP11-[illegible]								2.25
[illegible]	COBLL1	COBLL1	cordon-bleu WH2 repeat protein like 1	Extracellular Space	other				0.96
[illegible]	SMG1P3	SMG1P3	SMG1P3, nonsense mediated mRNA decay associated P	Other	other		0.26	0.44	0.95
[illegible]	TMEM30B	TMEM30B	transmembrane protein 30B	Other	other		0.44	0.20	-0.77
[illegible]	HMG20B	HMG20B	high mobility group 20B	Nucleus	transcription regulator		0.37	-0.08	0.86
[illegible]	NCK1	NCK1	NCK adaptor protein 1	Cytoplasm	kinase		-0.17	-0.02	-0.87
[illegible]	ANKRD18BP	ANKRD18BP	ankyrin repeat domain 18B, pseudogene	Other	other		0.21	-0.06	-1.06
[illegible]	ARL2BP	ARL2BP	ADP ribosylation factor like GTPase 2 binding protein	Cytoplasm	transcription regulator		-0.27	-0.26	-0.82
[illegible]	PLAC8	PLAC8	placenta specific 8	Nucleus	other		0.27	0.00	-0.88
[illegible]	GFI1	GFI1	growth factor independent 1 transcriptional repressor	Nucleus	transcription regulator		0.30	0.27	-0.87
[illegible]	CDC42SE2	CDC42SE2	CDC42 small effector 2	Plasma Membrane	other		-0.97	-0.26	-0.85
[illegible]	KIAA1731	CEP295	centrosomal protein 295	Cytoplasm	other				0.92
[illegible]	EMB	EMB	embigin	Plasma Membrane	transporter		-0.19	-0.25	-0.78
[illegible]	PDE3B	PDE3B	phosphodiesterase 3B	Cytoplasm	enzyme	ol, dipyridamole, amri	0.35	0.49	-0.85
[illegible]	CCDC109B	MCUB	mitochondrial calcium uniporter dominant negative bet	Cytoplasm	other		0.26	-0.17	-0.78
[illegible]	FECH	FECH	ferrochelatase	Cytoplasm	enzyme		-0.15	0.03	-0.91
[illegible]	LRWD1								0.96
[illegible]	DPH5	DPH5	diphthamide biosynthesis 5	Cytoplasm	enzyme		-0.15	-0.12	-0.97
[illegible]	IFI30	IFI30	IFI30, lysosomal thiol reductase	Cytoplasm	enzyme				1.08
[illegible]	FAM102B	FAM102B	family with sequence similarity 102 member B	Other	other		-0.02	0.15	0.82
[illegible]	[illegible]-AS1	[illegible]-AS1	[illegible] antisense RNA 1	Other	other		0.21	-0.08	-0.77
[illegible]	CLEC4E	CLEC4E	C-type lectin domain family 4 member E	Plasma Membrane	other				1.02
[illegible]	DUSP8	DUSP8	dual specificity phosphatase 8	Nucleus	phosphatase		0.36	0.18	-0.81
[illegible]	TRBV4-1	TRBV4-1	T cell receptor beta variable 4-1	Other	other		-0.44	0.21	-1.45
[illegible]	SCOC	SCOC	short coiled-coil protein	Cytoplasm	other		-0.20	-0.02	-0.84
[illegible]	TMPO	TMPO	thymopoietin	Nucleus	other		-0.19	-0.19	-0.75
[illegible]	ZNF321	ZNF321	zinc finger protein 321	Nucleus	other		0.17	-0.15	-0.85
[illegible]	POLR3GL	POLR3GL	RNA polymerase III subunit G like	Nucleus	other		-0.06	-0.01	-0.99
[illegible]	CSF2RA	CSF2RA	colony stimulating factor 2 receptor alpha subunit	Plasma Membrane	transmembrane receptor	[illegible]			1.18
[illegible]	SNAI1	SNAI1	snail family transcriptional repressor 1	Nucleus	transcription regulator		0.36	0.27	1.15
[illegible]	FBXO25	FBXO25	F-box protein 25	Nucleus	enzyme		0.10	-0.39	-0.80
[illegible]	ZFAND1	ZFAND1	zinc finger AN1-type containing 1	Other	other		-0.11	-0.05	-0.83
[illegible]	SLC7A6								0.92
[illegible]	RIOK1	RIOK1	RIO kinase 1	Other	kinase		0.29	0.44	0.85
[illegible]	C12orf57	C12orf57	chromosome 12 open reading frame 57	Other	other		0.49	0.49	-0.84
[illegible]	POFUT1						0.06	-0.08	-0.88
[illegible]	TRAF4	TRAF4	TNF receptor associated factor 4	Cytoplasm	other		-0.08	-0.09	0.86
[illegible]	RHBDD2	RHBDD2	rhomboid domain containing 2	Plasma Membrane	other		0.36	-0.18	-0.73
[illegible]	EPB41L3	EPB41L3	erythrocyte membrane protein band 4.1 like 3	Plasma Membrane	other				0.89
[illegible]	SPAG9	SPAG9	sperm associated antigen 9	Cytoplasm	other		0.37	0.15	0.80
[illegible]	RPL13P1	RPL13P1	ribosomal protein L13 pseudogene 1	Other	other				1.85
[illegible]	PTK2B	PTK2B	protein tyrosine kinase 2 beta	Cytoplasm	kinase	PF-562271, CT-707	0.29	0.15	0.80
[illegible]	CD83						0.22	-0.17	-0.78
[illegible]	MAGED1	MAGED1	MAGE family member D1	Plasma Membrane	transcription regulator		-0.09	0.04	-0.83
[illegible]	SNRK	SNRK	SNF related kinase	Cytoplasm	kinase		-0.10	0.09	-0.82
[illegible]	JADE1	JADE1	jade family PHD finger 1	Nucleus	transcription regulator		0.29	0.13	-0.77
[illegible]	ARHGDIB	ARHGDIB	Rho GDP dissociation inhibitor beta	Cytoplasm	enzyme		-0.26	-0.18	-0.80
[illegible]	GMFG	GMFG	glia maturation factor gamma	Cytoplasm	growth factor		0.11	-0.46	-0.79
[illegible]	DDX54	DDX54	DEAD-box helicase 54	Nucleus	transcription regulator		-0.21	0.11	0.81
[illegible]	FOXJ2	FOXJ2	forkhead box J2	Nucleus	transcription regulator		0.12	-0.05	-0.77
[illegible]	STMN1						0.11	0.11	-0.75
[illegible]	TSR3	TSR3	TSR3, acp transferase ribosome maturation factor	Cytoplasm	enzyme		0.27	-0.29	-0.83
[illegible]	CHMP3	CHMP3	charged multivesicular body protein 3	Cytoplasm	other		-0.14	-0.09	-0.74
[illegible]	PLGRKT	PLGRKT	plasminogen receptor with a C-terminal lysine	Cytoplasm	other		0.27	-0.01	-1.15
[illegible]	PPA1	PPA1	pyrophosphatase (inorganic) 1	Cytoplasm	enzyme		-0.17	-0.16	-0.74
[illegible]	NA						0.20	0.09	-0.83
[illegible]	TRUB1	TRUB1	TruB pseudouridine synthase family member 1	Other	enzyme		0.26	-0.07	-0.85
[illegible]	TAF9B	TAF9B	TATA-box binding protein associated factor 9b	Nucleus	transcription regulator		0.15	-0.27	-0.81
[illegible]	RDH14	RDH14	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	Cytoplasm	enzyme		-0.40	-0.60	-0.87
[illegible]	ATP6V1B2	ATP6V1B2	ATPase H+ transporting V1 subunit B2	Cytoplasm	transporter	gallium nitrate	-0.18	-0.11	0.75
[illegible]	SPOCK2	SPOCK2	SPARC/osteonectin, cwcv and kazal like domains protec	Extracellular Space	other		0.21	0.49	-0.77
[illegible]	LA16c-390E6.4								2.28
[illegible]	PRAF2	PRAF2	PRA1 domain family member 2	Other	other		-0.21	-0.18	-1.04
[illegible]	CACYBP	CACYBP	calcyclin binding protein	Nucleus	other		0.15	-0.05	-0.77
[illegible]	ATP8B2	ATP8B2	ATPase phospholipid transporting 8B2	Plasma Membrane	transporter		0.47	0.42	-0.72
[illegible]	RPS8	RPS8	ribosomal protein S8	Cytoplasm	enzyme		0.21	0.02	-0.74
[illegible]	C18orf8	C18orf8	chromosome 18 open reading frame 8	Cytoplasm	other		0.27	0.22	0.88
[illegible]	NUDT21	NUDT21	nudix hydrolase 21	Nucleus	other		-0.14	-0.28	-0.75
[illegible]	STAT6	STAT6	signal transducer and activator of transcription 6	Nucleus	transcription regulator		0.32	-0.22	0.86
[illegible]	MRPS18A	MRPS18A	mitochondrial ribosomal protein S18A	Cytoplasm	other		-0.26	-0.60	-0.77
[illegible]	FKBP5	FKBP5	FK506 binding protein 5	Nucleus	enzyme		0.35	-0.11	-0.81
[illegible]	CLPTM1L	CLPTM1L	CLPTM1 like	Other	other		0.12	0.04	0.82
[illegible]	NUTM2A						0.37	0.07	-0.74
[illegible]	CCNB1	CCNB1	cyclin B1	Nucleus	other		-0.15	-0.14	-0.74
[illegible]	TRBV20-1	TRBV20-1	T cell receptor beta variable 20-1	Other	other		-0.11	-0.26	-1.20
[illegible]	CLPP	CLPP	caseinolytic mitochondrial matrix peptidase proteolytic	Cytoplasm	peptidase		-0.14	-0.18	-0.80
[illegible]	S1PR4	S1PR4	sphingosine-1-phosphate receptor 4	Plasma Membrane	G-protein coupled receptor	fingolimod phosphate	-0.18	-0.07	-0.77
[illegible]	TPCN2	TPCN2	two pore segment channel 2	Cytoplasm	ion channel				0.91
[illegible]	ATP6V0A1								0.96
[illegible]	RPS12	RPS12	ribosomal protein S12	Cytoplasm	other		0.21	0.16	-0.73
[illegible]	PIKFYVE	PIKFYVE	phosphoinositide kinase, FYVE-type zinc finger containi	Cytoplasm	kinase		0.27	-0.10	0.77
[illegible]	CUTA	CUTA	cutA divalent cation tolerance homolog	Cytoplasm	other		-0.11	-0.18	-0.76
[illegible]	9-Sep	SEPT9	septin 9	Cytoplasm	enzyme		-0.07	-0.06	-0.70
[illegible]	NDNL2	NSMCE3	NSE3 homolog, SMC5-SMC6 complex component	Nucleus	other		0.19	0.43	-0.85
[illegible]	FKBP8	FKBP8	FK506 binding protein 8	Cytoplasm	other		-0.22	-0.07	-0.74
[illegible]	NCKAP1L	NCKAP1L	NCK associated protein 1 like	Plasma Membrane	other		0.31	0.19	0.75
[illegible]	C11orf98	C11orf98	chromosome 11 open reading frame 98	Other	other				1.01
[illegible]	HELZ2	HELZ2	helicase with zinc finger 2	Nucleus	transcription regulator		0.02	0.19	0.80
[illegible]	GTF2H3	GTF2H3	general transcription factor IIH subunit 3	Nucleus	transcription regulator		0.36	-0.18	-0.88
[illegible]	RCHY1	RCHY1	ring finger and CHY zinc finger domain containing 1	Nucleus	enzyme		-0.01	-0.28	-0.70
[illegible]	CTNND1	CTNND1	catenin delta 1	Nucleus	other				0.85
[illegible]	MFSD10	MFSD10	major facilitator superfamily domain containing 10	Other	transporter		-0.01	0.44	0.80
[illegible]	GFOD1	GFOD1	glucose-fructose oxidoreductase domain containing 1	Other	enzyme				0.86
[illegible]	YES1	YES1	YES proto-oncogene 1, Src family tyrosine kinase	Cytoplasm	kinase	dasatinib, JNJ-[illegible]	0.27	0.40	-0.84
[illegible]	BIN3	BIN3	bridging integrator 3	Cytoplasm	other		0.32	0.18	0.78
[illegible]	CTD-[illegible]	LOC100505771	uncharacterized LOC100505771	Other	other		0.29	-0.22	-0.85
[illegible]	SAMD3	SAMD3	sterile alpha motif domain containing 3	Other	other		-0.44	0.24	-0.98
[illegible]	GALNT3	GALNT3	polypeptide N-acetylgalactosaminyltransferase 3	Cytoplasm	enzyme				0.80
[illegible]	RPL3	RPL3	ribosomal protein L3	Nucleus	other	omacetaxine mepesuccin	-0.16	0.00	-0.88
[illegible]	PRKACB	PRKACB	protein kinase cAMP-activated catalytic subunit beta	Cytoplasm	kinase		0.30	0.30	-0.72
[illegible]	PPRC1	PPRC1	peroxisome proliferator-activated receptor gamma, co	Nucleus	transcription regulator		-0.26	0.07	0.75
[illegible]	PTBP3	PTBP3	polypyrimidine tract binding protein 3	Nucleus	other		-0.45	-0.60	-0.71
[illegible]	AP1S3	AP1S3	adaptor related protein complex 1 sigma 3 subunit	Cytoplasm	transporter				0.99
[illegible]	CCL20	CCL20	C-C motif chemokine ligand 20	Extracellular Space	cytokine				1.32
[illegible]	GYLTL1B	LARGE2	LARGE xylosyl- and glucuronyltransferase 2	Cytoplasm	enzyme				1.28

[illegible]	HINT3	HINT3	histidine triad nucleotide binding protein 3	Cytoplasm	other		-0.36	-0.42
[illegible]	TMEM208	TMEM208	transmembrane protein 208	Other	other		0.28	0.15
[illegible]	SPATA6L1	SPATA6L1	spermatogenesis associated 6 like 1	Other	other		0.48	0.05
[illegible]	ADAM17	ADAM17	ADAM metallopeptidase domain 17	Plasma Membrane	peptidase		-0.26	-0.30
[illegible]	STXBP5	STXBP5	syntaxin binding protein 5	Plasma Membrane	other		0.14	0.09
[illegible]	ATMIN	ATMIN	ATM interactor	Nucleus	other		-0.25	-0.22
[illegible]	CNOT7	CNOT7	CCR4-NOT transcription complex subunit 7	Nucleus	transcription regulator		-0.21	-0.02
[illegible]	PIH1D2	PIH1D2	PIH1 domain containing 2	Nucleus	other		-0.08	-0.29
[illegible]	ZXDB	ZXDB	zinc finger, X-linked, duplicated B	Nucleus	other		-0.23	-0.45
[illegible]	SAYSD1	SAYSD1	SAYSVFN motif domain containing 1	Other	other		0.21	0.19
[illegible]	CD72	CD72	CD72 molecule	Plasma Membrane	transmembrane receptor			
[illegible]	NSMCE1	NSMCE1	NSE1 homolog, SMC5-SMC6 complex component	Nucleus	transporter		-0.08	-0.22
[illegible]	[illegible]							
[illegible]	URI1	URI1	URI1, prefoldin like chaperone	Nucleus	transcription regulator		0.39	0.02
[illegible]	GABARAPL1	GABARAPL1	GABA type A receptor associated protein like 1	Cytoplasm	other		-0.41	0.12
[illegible]	PPDPF	PPDPF	pancreatic progenitor cell differentiation and proliferat	Other	other		-0.27	-0.26
[illegible]	PSMB9	PSMB9	proteasome subunit beta 9	Cytoplasm	peptidase	ride, carfilzomib/dexa	-0.45	-0.36
[illegible]	FBXO41	FBXO41	F-box protein 41	Cytoplasm	enzyme		-0.36	-0.26
[illegible]	TGFBR2	TGFBR2	transforming growth factor beta receptor 2	Plasma Membrane	kinase		0.21	0.16
[illegible]	DNAJC25	DNAJC25	DnaJ heat shock protein family (Hsp40) member C25	Other	other		0.05	0.43
[illegible]	TMEM66	SARAF	store-operated calcium entry associated regulatory fac	Cytoplasm	other		0.36	-0.05
[illegible]	EEF1A1	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	Cytoplasm	translation regulator		-0.30	-0.01
[illegible]	BET1L	BET1L	Bet1 golgi vesicular membrane trafficking protein like	Cytoplasm	transporter		0.21	-0.42
[illegible]	EIF2D	EIF2D	eukaryotic translation initiation factor 2D	Cytoplasm	transporter		-0.06	-0.30
[illegible]	MOCS2	MOCS2	molybdenum cofactor synthesis 2	Cytoplasm	enzyme		0.34	0.13
[illegible]	NDUFS5	NDUFS5	NADH:ubiquinone oxidoreductase subunit S5	Cytoplasm	enzyme		0.38	0.10
[illegible]	CFL2	CFL2	cofilin 2	Extracellular Space	other		-0.22	-0.45
[illegible]	EEF1A1P5	EEF1A1P5	eukaryotic translation elongation factor 1 alpha 1 pseu	Extracellular Space	other		0.02	-0.45
[illegible]	RND1	RND1	Rho family GTPase 1	Cytoplasm	enzyme		0.26	0.14
[illegible]	CSTF1	CSTF1	cleavage stimulation factor subunit 1	Nucleus	other		-0.06	-0.14
[illegible]	SLC12A4	SLC12A4	solute carrier family 12 member 4	Plasma Membrane	transporter	bumetanide		
[illegible]	FAM200B	FAM200B	family with sequence similarity 200 member B	Other	other		0.24	-0.27
[illegible]	USP8	USP8	ubiquitin specific peptidase 8	Cytoplasm	peptidase		0.08	0.18
[illegible]	SLC35A4	SLC35A4	solute carrier family 35 member A4	Other	transporter		-0.31	-0.06
[illegible]	HPS6	HPS6	HPS6, biogenesis of lysosomal organelles complex 2 sul	Cytoplasm	other			
[illegible]	ESYT2	ESYT2	extended synaptotagmin 2	Plasma Membrane	other		0.11	-0.30
[illegible]	EIF4E3	EIF4E3	eukaryotic translation initiation factor 4E family memb	Cytoplasm	translation regulator		0.08	-0.30
[illegible]	TSEN15	TSEN15	tRNA splicing endonuclease subunit 15	Nucleus	enzyme		-0.30	-0.26
[illegible]	UBOX5	UBOX5	U-box domain containing 5	Nucleus	enzyme		0.06	-0.23
[illegible]	DAP3	DAP3	death associated protein 3	Cytoplasm	other		0.08	-0.30
[illegible]	MRFAP1L1	MRFAP1L1	Morf4 family associated protein 1 like 1	Other	other		0.20	-0.08
[illegible]	DIMT1	DIMT1	DIM1 dimethyladenosine transferase 1 homolog	Cytoplasm	enzyme		-0.15	-0.36
[illegible]	CCDC25	CCDC25	coiled-coil domain containing 25	Cytoplasm	other		-0.27	-0.05
[illegible]	EIF3E	EIF3E	eukaryotic translation initiation factor 3 subunit E	Cytoplasm	other		-0.08	-0.40
[illegible]	VAMP2	VAMP2	vesicle associated membrane protein 2	Plasma Membrane	other	botulinum toxin type B	-0.02	-0.05
[illegible]	SLC2A6	SLC2A6	solute carrier family 2 member 6	Plasma Membrane	transporter			
[illegible]	RPL36A	RPL36A	ribosomal protein L36a, X-linked	Cytoplasm	other		-0.14	-0.17
[illegible]	RPL13	RPL13	ribosomal protein L13	Nucleus	other		0.08	-0.08
[illegible]	ARMC1	ARMC1	armadillo repeat containing 1	Cytoplasm	other		0.41	0.14
[illegible]	ZNF268	ZNF268	zinc finger protein 268	Nucleus	transcription regulator		0.11	-0.09
[illegible]	RNF38	RNF38	ring finger protein 38	Nucleus	enzyme		0.01	-0.11
[illegible]	SLC25A16	SLC25A16	solute carrier family 25 member 16	Cytoplasm	other		-0.17	-0.24
[illegible]	BAALC	BAALC	BAALC	Cytoplasm	other		0.30	0.30
[illegible]	RPUSD2	RPUSD2	RNA pseudouridylate synthase domain containing 2	Other	enzyme		-0.25	-0.30
[illegible]	CLSTN1	CLSTN1	calsyntenin 1	Plasma Membrane	other		0.17	-0.08
[illegible]	LINC-PINT	LINC-PINT	long intergenic non-protein coding RNA, p53 induced tr	Other	other		-0.01	0.39
[illegible]	CKB	CKB	creatine kinase B	Cytoplasm	kinase			
[illegible]	ZNF777	ZNF777	zinc finger protein 777	Other	other		0.09	0.11
[illegible]	ZNF83	ZNF83	zinc finger protein 83	Nucleus	other		0.24	-0.08
[illegible]	PPCDC	PPCDC	phosphopantothenoylcysteine decarboxylase	Cytoplasm	enzyme			
[illegible]	FAM120A	FAM120A	family with sequence similarity 120 member A	Other	other		0.00	0.05
[illegible]	GOLGA7	GOLGA7	golgin A7	Cytoplasm	other		0.08	0.11
[illegible]	AES	AES	amino-terminal enhancer of split	Nucleus	transcription regulator		-0.15	-0.09
[illegible]	RAPGEF2	RAPGEF2	Rap guanine nucleotide exchange factor 2	Cytoplasm	other		-0.48	0.30
[illegible]	BLNK	BLNK	B-cell linker	Cytoplasm	other			
[illegible]	RP11-[illegible]							
[illegible]	LNPEP	LNPEP	leucyl and cystinyl aminopeptidase	Cytoplasm	peptidase		0.00	0.18
[illegible]	BCAR3	BCAR3	breast cancer anti-estrogen resistance 3	Cytoplasm	other			
[illegible]	MAZ	MAZ	MYC associated zinc finger protein	Nucleus	transcription regulator		-0.05	-0.11
[illegible]	RPIA	RPIA	ribose 5-phosphate isomerase A	Cytoplasm	enzyme		-0.36	-0.16
[illegible]	PIH1D1	PIH1D1	PIH1 domain containing 1	Other	other		0.06	-0.06
[illegible]	JADE2	JADE2	jade family PHD finger 2	Nucleus	enzyme		-0.15	-0.08
[illegible]	DLL1	DLL1	delta like canonical Notch ligand 1	Plasma Membrane	enzyme			
[illegible]	DHCR7	DHCR7	7-dehydrocholesterol reductase	Cytoplasm	enzyme		-0.02	0.18
[illegible]	EIF4B	EIF4B	eukaryotic translation initiation factor 4B	Cytoplasm	translation regulator		-0.25	-0.36
[illegible]	C8orf59	C8orf59	chromosome 8 open reading frame 59	Cytoplasm	other		-0.11	-0.48
[illegible]	RPL13AP5	RPL13AP5	ribosomal protein L13a pseudogene 5	Other	other		0.39	-0.27
[illegible]	TJP2	TJP2	tight junction protein 2	Plasma Membrane	kinase			
[illegible]	NDUFB9	NDUFB9	NADH:ubiquinone oxidoreductase subunit B9	Cytoplasm	enzyme		-0.26	-0.42
[illegible]	ZBTB14	ZBTB14	zinc finger and BTB domain containing 14	Nucleus	transcription regulator		0.01	-0.30
[illegible]	P2RY10	P2RY10	purinergic receptor P2Y10	Plasma Membrane	G-protein coupled recept		0.08	-0.14
[illegible]	EIF5	EIF5	eukaryotic translation initiation factor 5	Cytoplasm	translation regulator		0.05	0.39
[illegible]	TNFRSF18	TNFRSF18	TNF receptor superfamily member 18	Plasma Membrane	transmembrane receptor			
[illegible]	SUN2	SUN2	Sad1 and UNC84 domain containing 2	Nucleus	other		-0.25	-0.12
[illegible]	FAM8A1	FAM8A1	family with sequence similarity 8 member A1	Other	other		0.30	-0.08
[illegible]	RPL13P12	RPL13P12	ribosomal protein L13 pseudogene 12	Other	other		-0.09	-0.01
[illegible]	FBL	FBL	fibrillarin	Nucleus	enzyme		-0.06	0.14
[illegible]	NAP1L5	NAP1L5	nucleosome assembly protein 1 like 5	Other	other		-0.30	-0.29
[illegible]	SFXN3	SFXN3	sideroflexin 3	Cytoplasm	transporter		0.25	0.27
[illegible]	SNX25	SNX25	sorting nexin 25	Cytoplasm	other		-0.02	-0.09
[illegible]	ARHGAP27	ARHGAP27	Rho GTPase activating protein 27	Cytoplasm	other		0.27	-0.02
[illegible]	RPLP2	RPLP2	ribosomal protein lateral stalk subunit P2	Cytoplasm	other		-0.10	-0.01
[illegible]	B3GNT2	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltra	Cytoplasm	enzyme		-0.48	0.14
[illegible]	DDHD1	DDHD1	DDHD domain containing 1	Cytoplasm	other		0.36	0.19
[illegible]	CLNS1A	CLNS1A	chloride nucleotide-sensitive channel 1A	Plasma Membrane	ion channel		-0.18	-0.49
[illegible]	TOMM40L							
[illegible]	SMCR8	SMCR8	Smith-Magenis syndrome chromosome region, candida	Nucleus	other		-0.08	-0.43
[illegible]	SLC9A7	SLC9A7	solute carrier family 9 member A7	Cytoplasm	transporter			
[illegible]	FAM172A						-0.17	-0.43
[illegible]	UBE2E1	UBE2E1	ubiquitin conjugating enzyme E2 E1	Cytoplasm	transcription regulator		-0.21	-0.09
[illegible]	RPSA	RPSA	ribosomal protein SA	Cytoplasm	translation regulator		-0.28	-0.18
[illegible]	NBR1	NBR1	NBR1, autophagy cargo receptor	Cytoplasm	other		0.10	0.15
[illegible]	FMNL1	FMNL1	formin like 1	Cytoplasm	other		0.06	0.04
[illegible]	MAFK	MAFK	MAF bZIP transcription factor K	Nucleus	transcription regulator		0.02	-0.41
[illegible]	WEE1	WEE1	WEE1 G2 checkpoint kinase	Nucleus	kinase	MK-1775		
[illegible]	NUCKS1	NUCKS1	nuclear casein kinase and cyclin dependent kinase subs	Nucleus	kinase		-0.21	-0.30
[illegible]	DDX6	DDX6	DEAD-box helicase 6	Nucleus	enzyme		-0.08	-0.18
[illegible]	MZT2B	MZT2B	mitotic spindle organizing protein 2B	Cytoplasm	other		0.10	-0.05
[illegible]	NDUFC2	NDUFC2	NADH:ubiquinone oxidoreductase subunit C2	Cytoplasm	enzyme		-0.28	-0.41
[illegible]	VPS37C	VPS37C	VPS37C, ESCRT-I subunit	Cytoplasm	other			
[illegible]	USP30	USP30	ubiquitin specific peptidase 30	Cytoplasm	peptidase		-0.21	-0.08
[illegible]	PATZ1	PATZ1	POZ/BTB and AT hook containing zinc finger 1	Nucleus	transcription regulator		0.09	0.00
[illegible]	BTN2A1	BTN2A1	butyrophilin subfamily 2 member A1	Plasma Membrane	other		0.02	0.43
[illegible]	COX7C						-0.29	-0.45
[illegible]	RPL4	RPL4	ribosomal protein L4	Cytoplasm	enzyme		-0.10	-0.15
[illegible]	SEPW1	SELENOW	selenoprotein W	Cytoplasm	enzyme		-0.09	-0.13
[illegible]	TRIM52-AS1	TRIM52-AS1	TRIM52 antisense RNA 1 (head to head)	Other	other		-0.30	-0.29
[illegible]	MPND	MPND	MPN domain containing	Other	other		-0.22	-0.07
[illegible]	THAP5	THAP5	THAP domain containing 5	Nucleus	other		0.35	-0.36
[illegible]	ATP5H	ATP5H	ATP synthase, H+ transporting, mitochondrial Fo compl	Cytoplasm	enzyme		0.02	-0.21
[illegible]	ACADVL	ACADVL	acyl-CoA dehydrogenase, very long chain	Cytoplasm	enzyme		0.22	0.01
[illegible]	ZNRF2	ZNRF2	zinc and ring finger 2	Cytoplasm	enzyme		0.36	0.18
[illegible]	RP11-[illegible].1						-0.02	-0.07
[illegible]	RPL32P3	RPL32P3	ribosomal protein L32 pseudogene 3	Other	other		-0.02	-0.16
[illegible]	ATF4	ATF4	activating transcription factor 4	Nucleus	transcription regulator		0.05	-0.07
[illegible]	EPT1	SELENOI	selenoprotein I	Cytoplasm	enzyme		-0.27	-0.02
[illegible]	RP11-[illegible]	[illegible]	ribosomal protein [illegible] pseudogene 7	Other	other		-0.28	-0.05
[illegible]	DEPDC5	DEPDC5	DEP domain containing 5	Cytoplasm	other			
[illegible]	C8orf33	C8orf33	chromosome 8 open reading frame 33	Other	other		-0.37	-0.07
[illegible]	SNX9	SNX9	sorting nexin 9	Cytoplasm	transporter		0.06	0.01
[illegible]	SPATA20	SPATA20	spermatogenesis associated 20	Other	other		0.41	0.37
[illegible]	GMPS	GMPS	guanine monophosphate synthase	Nucleus	enzyme	ine amidotransferase i	-0.18	-0.17
[illegible]	NAA10	NAA10	N(alpha)-acetyltransferase 10, NatA catalytic subunit	Cytoplasm	enzyme		-0.01	-0.08
[illegible]	POLDIP2	POLDIP2	DNA polymerase delta interacting protein 2	Cytoplasm	other		-0.13	-0.15
[illegible]	KLF3	KLF3	Kruppel like factor 3	Nucleus	transcription regulator		-0.09	-0.36
[illegible]	ANKRD13D	ANKRD13D	ankyrin repeat domain 13D	Plasma Membrane	other		0.22	0.43
[illegible]	GSK3B	GSK3B	glycogen synthase kinase 3 beta	Nucleus	kinase	enzastaurin	-0.23	-0.22
[illegible]	CRLF3	CRLF3	cytokine receptor like factor 3	Cytoplasm	transcription regulator		0.06	-0.02
[illegible]	UQCRB	UQCRB	ubiquinol-cytochrome c reductase binding protein	Cytoplasm	enzyme		-0.10	-0.22
[illegible]	TOR1AIP2	TOR1AIP2	torsin 1A interacting protein 2	Cytoplasm	other		-0.14	0.11
[illegible]	RAB11A	RAB11A	RAB11A, member RAS oncogene family	Cytoplasm	enzyme		-0.26	-0.36
[illegible]	C1QBP	C1QBP	complement C1q binding protein	Cytoplasm	transcription regulator		-0.17	-0.26
[illegible]	TNRC6B	TNRC6B	trinucleotide repeat containing 6B	Other	other		0.26	0.23
[illegible]	BTN3A3	BTN3A3	butyrophilin subfamily 3 member A3	Plasma Membrane	other		0.02	0.11
[illegible]	ZIK1	ZIK1	zinc finger protein interacting with K protein 1	Other	other		0.10	-0.22
[illegible]	TPT1	TPT1	tumor protein, translationally-controlled 1	Cytoplasm	other		0.08	-0.25
[illegible]	TSTD1	TSTD1	thiosulfate sulfurtransferase like domain containing 1	Cytoplasm	other		-0.09	-0.17
[illegible]	SAMD1	SAMD1	sterile alpha motif domain containing 1	Other	other		0.00	-0.08
[illegible]	ZC3H12A						0.06	0.40
[illegible]	CCDC71	CCDC71	coiled-coil domain containing 71	Nucleus	other		-0.40	-0.43
[illegible]	LSM1	LSM1	LSM1 homolog, U6 small nuclear RNA and mRNA degra	Nucleus	other		-0.46	-0.45
[illegible]	RPS14	RPS14	ribosomal protein S14	Cytoplasm	translation regulator		0.09	-0.08
[illegible]	PSMF1	PSMF1	proteasome inhibitor subunit 1	Cytoplasm	other		-0.36	-0.29
[illegible]	ZNF791	ZNF791	zinc finger protein 791	Other	other		0.18	0.11
[illegible]	C9orf16	C9orf16	chromosome 9 open reading frame 16	Other	other		-0.44	-0.16
[illegible]	IRF7	IRF7	interferon regulatory factor 7	Nucleus	transcription regulator		-0.20	-0.27
[illegible]	RPS3AP6	RPS3AP6	ribosomal protein S3A pseudogene 6	Other	other		0.27	-0.08
[illegible]	ZNF428	ZNF428	zinc finger protein 428	Other	other		0.00	0.36
[illegible]	NDUFA6	NDUFA6	NADH:ubiquinone oxidoreductase subunit A6	Cytoplasm	enzyme		-0.22	-0.30
[illegible]	TRAK2	TRAK2	trafficking kinesin protein 2	Plasma Membrane	transporter		0.27	-0.10
[illegible]	MAT2B	MAT2B	methionine adenosyltransferase 2B	Cytoplasm	enzyme		-0.30	-0.08
[illegible]	ALKBH7	ALKBH7	alkB homolog 7	Cytoplasm	other		-0.38	-0.05
[illegible]	BLMH	BLMH	bleomycin hydrolase	Cytoplasm	peptidase		0.18	0.44
[illegible]	RPS2	RPS2	ribosomal protein S2	Cytoplasm	other		-0.18	-0.17
[illegible]	AIDA	AIDA	axin interactor, dorsalization associated	Cytoplasm	other		-0.05	-0.41
[illegible]	LETMD1	LETMD1	LETM1 domain containing 1	Plasma Membrane	other		0.17	-0.08
[illegible]	C14orf1	C14orf1	chromosome 14 open reading frame 1	Cytoplasm	other		0.17	0.20
[illegible]	STAG3L4	STAG3L4	stromal antigen 3-like 4 (pseudogene)	Other	other		-0.17	0.16
[illegible]	LRRC8B	LRRC8B	leucine rich repeat containing 8 family member B	Other	other		0.46	-0.08
[illegible]	MTMR1	MTMR1	myotubularin related protein 1	Cytoplasm	phosphatase		0.39	0.08
[illegible]	UGP2	UGP2	UDP-glucose pyrophosphorylase 2	Cytoplasm	enzyme		-0.09	0.00
[illegible]	TRMT2B	TRMT2B	tRNA methyltransferase 2 homolog B	Cytoplasm	enzyme		0.09	-0.16
[illegible]	CAMLG	CAMLG	calcium modulating ligand	Cytoplasm	other	A/tacrolimus, cyclosp	-0.13	-0.07
[illegible]	SNRPA	SNRPA	small nuclear ribonucleoprotein polypeptide A	Nucleus	other		-0.42	-0.41
[illegible]	RPL38						-0.20	0.03
[illegible]	YY1						-0.25	-0.25
[illegible]	PARP16	PARP16	poly(ADP-ribose) polymerase family member 16	Cytoplasm	enzyme		0.27	-0.02
[illegible]	PITPNM1	PITPNM1	phosphatidylinositol transfer protein membrane associa	Cytoplasm	transporter		-0.45	-0.06
[illegible]	ARCN1	ARCN1	archain 1	Cytoplasm	other		-0.09	-0.16
[illegible]	LRRC8C	LRRC8C	leucine rich repeat containing 8 family member C	Plasma Membrane	ion channel		-0.02	0.06
[illegible]	VPS51	VPS51	VPS51, GARP complex subunit	Cytoplasm	other		-0.27	-0.18
[illegible]	SLC4A2	SLC4A2	solute carrier family 4 member 2	Plasma Membrane	transporter			
[illegible]	FAF1	FAF1	Fas associated factor 1	Nucleus	other		-0.15	-0.17
[illegible]	SNRPD2	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide	Nucleus	other		-0.18	-0.14
[illegible]	FAM115C	TCAF2	TRPM8 channel associated factor 2	Plasma Membrane	other		0.28	-0.05
[illegible]	PFKFB3	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	Cytoplasm	kinase	PFK-158	-0.17	-0.09
[illegible]	IQGAP1	IQGAP1	IQ motif containing GTPase activating protein 1	Cytoplasm	other		-0.48	-0.49
[illegible]	NDUFB6	NDUFB6	NADH:ubiquinone oxidoreductase subunit B6	Cytoplasm	enzyme		0.01	0.04
[illegible]	PNPLA8	PNPLA8	patatin like phospholipase domain containing 8	Cytoplasm	enzyme		-0.22	-0.39
[illegible]	PLEC	PLEC	plectin	Cytoplasm	other		0.47	-0.01
[illegible]	KCTD2	KCTD2	potassium channel tetramerization domain containing :	Other	ion channel		-0.07	-0.21
[illegible]	RPL13A	RPL13A	ribosomal protein L13a	Cytoplasm	other		-0.06	-0.13
[illegible]	CYFIP2	CYFIP2	cytoplasmic FMR1 interacting protein 2	Cytoplasm	other		0.26	0.01
[illegible]	MFSD6	MFSD6	major facilitator superfamily domain containing 6	Other	other		-0.15	0.21
[illegible]	TRAF5	TRAF5	TNF receptor associated factor 5	Cytoplasm	transporter		-0.01	0.14
[illegible]	FDFT1	FDFT1	farnesyl-diphosphate farnesyltransferase 1	Cytoplasm	enzyme	[illegible], alendronic a	-0.30	-0.42
[illegible]	ZDHHC12	ZDHHC12	zinc finger DHHC-type containing 12	Other	enzyme		-0.27	-0.27
[illegible]	VARS	VARS	valyl-tRNA synthetase	Cytoplasm	enzyme		0.49	0.11
[illegible]	LRG1	LRG1	leucine rich alpha-2-glycoprotein 1	Extracellular Space	other			
[illegible]	NDUFA12	NDUFA12	NADH:ubiquinone oxidoreductase subunit A12	Cytoplasm	enzyme		-0.10	-0.22
[illegible]	THRA	THRA	thyroid hormone receptor, alpha	Nucleus	ligand-dependent nuclear receptor	amiodarone, l	0.48	-0.30
[illegible]	LYSMD3	LYSMD3	LysM domain containing 3	Other	other		0.13	-0.14
[illegible]	TMEM55B	TMEM55B	transmembrane protein 55B	Cytoplasm	phosphatase		0.40	0.09
[illegible]	C16orf13	METTL26	methyltransferase like 26	Other	other		-0.19	-0.28
[illegible]	ING5	ING5	inhibitor of growth family member 5	Nucleus	other			
[illegible]	GTF2A1	GTF2A1	general transcription factor IIA subunit 1	Cytoplasm	transcription regulator		0.14	-0.14
[illegible]	THOC6	THOC6	THO complex 6	Nucleus	other		0.27	0.20
[illegible]	PPP1R7	PPP1R7	protein phosphatase 1 regulatory subunit 7	Nucleus	phosphatase		-0.06	-0.07
[illegible]	EIF4G3	EIF4G3	eukaryotic translation initiation factor 4 gamma 3	Cytoplasm	translation regulator		-0.22	-0.08
[illegible]	KIF20B	KIF20B	kinesin family member 20B	Nucleus	enzyme		0.39	0.48
[illegible]	NSL1	NSL1	NSL1, MIS12 kinetochore complex component	Nucleus	other		0.08	-0.08
[illegible]	COMMD6	COMMD6	COMM domain containing 6	Other	other		-0.20	-0.21
[illegible]	ANP32B	ANP32B	acidic nuclear phosphoprotein 32 family member B	Nucleus	other		-0.06	-0.07
[illegible]	NOP16	NOP16	NOP16 nucleolar protein	Nucleus	other		0.18	0.14
[illegible]	PDIK1L	PDIK1L	PDLIM1 interacting kinase 1 like	Nucleus	kinase		0.12	-0.07
[illegible]	ACSL5	ACSL5	acyl-CoA synthetase long-chain family member 5	Cytoplasm	enzyme			
[illegible]	TACO1	TACO1	translational activator of cytochrome c oxidase I	Cytoplasm	other		-0.02	-0.02
[illegible]	NA							
[illegible]	TTC39C	TTC39C	tetratricopeptide repeat domain 39C	Other	other		0.28	-0.01
[illegible]	BACH2	BACH2	BTB domain and CNC homolog 2	Nucleus	transcription regulator		0.15	0.13
[illegible]	MPDU1	MPDU1	mannose-P-dolichol utilization defect 1	Cytoplasm	other		-0.39	-0.08
[illegible]	RPS8	RPS8	ribosomal protein S8	Cytoplasm	other		0.01	-0.02
[illegible]	RPL3	RPL3	ribosomal protein L3	Cytoplasm	other		0.08	-0.15
[illegible]	NSD1	NSD1	nuclear receptor binding SET domain protein 1	Nucleus	transcription regulator		-0.09	-0.06
[illegible]	INTS5	INTS5	integrator complex subunit 5	Nucleus	other		-0.48	-0.08

[illegible]	ZBTB10	ZBTB10	zinc finger and BTB domain containing 10	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ARHGAP1	ARHGAP1	Rho GTPase activating protein 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CCDC93	CCDC93	coiled-coil domain containing 93	Extracellular Space	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TBC1D2	TBC1D2	TBC1 domain family member 2	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRPL34	MRPL34	mitochondrial ribosomal protein L34	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PAFAH1B3	PAFAH1B3	platelet activating factor acetylhydrolase 1b catalytic su	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MS4A7	MS4A7	membrane spanning 4-domains A7	Other	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	PDCD4-AS1	PDCD4-AS1	PDCD4 antisense RNA 1	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MZT1	MZT1	mitotic spindle organizing protein 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CPNE3	CPNE3	copine 3	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS15A	RPS15A	ribosomal protein S15a	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CKS2	CKS2	CDC28 protein kinase regulatory subunit 2	Other	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	WDR11	WDR11	WD repeat domain 11	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	BANP	BANP	BTG3 associated nuclear protein	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GTF3A	GTF3A	general transcription factor IIIA	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KMT2A	KMT2A	lysine methyltransferase 2A	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	BEX2	BEX2	brain expressed X-linked 2	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ESD	ESD	esterase D	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZMYND11	ZMYND11	zinc finger MYND-type containing 11	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SRA1	SRA1	steroid receptor RNA activator 1	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CEP120	CEP120	centrosomal protein 120	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ICAM2	ICAM2	intercellular adhesion molecule 2	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RHOH	RHOH	ras homolog family member H	Plasma Membrane	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	IRF1	IRF1	interferon regulatory factor 1	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PSMD1	PSMD1	proteasome 26S subunit, non-ATPase 1	Cytoplasm	other	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PPP1R2	PPP1R2	protein phosphatase 1 regulatory inhibitor subunit 2	Cytoplasm	phosphatase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DYNLL2	DYNLL2	dynein light chain LC8-type 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPL14	RPL14	ribosomal protein L14	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TFDP2	TFDP2	transcription factor Dp-2	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SH3GLB2	SH3GLB2	SH3 domain containing GRB2 like, endophilin B2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PMP22	PMP22	peripheral myelin protein 22	Plasma Membrane	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	MGAT4B	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylgl	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ATP6V1G1	ATP6V1G1	ATPase H+ transporting V1 subunit G1	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS28	RPS28	ribosomal protein S28	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ATP5A1	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 compl	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TMEM14B	TMEM14B	transmembrane protein 14B	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CEP55	CEP55	centrosomal protein 55	Nucleus	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	OXSR1	OXSR1	oxidative stress responsive 1	Nucleus	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LRRC75A-AS1	LRRC75A-AS1	LRRC75A antisense RNA 1	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	HIVEP1	HIVEP1	human immunodeficiency virus type I enhancer binding	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	INO80C	INO80C	INO80 complex subunit C	Nucleus	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	NUP210	NUP210	nucleoporin 210	Nucleus	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS5	RPS5	ribosomal protein S5	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SLC41A3	SLC41A3	solute carrier family 41 member 3	Plasma Membrane	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	BTBD2	BTBD2	BTB domain containing 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	API5	API5	apoptosis inhibitor 5	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ATP5O	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 compl	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPL22	RPL22	ribosomal protein L22	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SMARCE1	SMARCE1	SWI/SNF related, matrix associated, actin dependent re	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DYNLRB1	DYNLRB1	dynein light chain roadblock-type 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CDIPT	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS29	RPS29	ribosomal protein S29	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRPS35	MRPS35	mitochondrial ribosomal protein S35	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	C7orf60	BMT2	base methyltransferase of 25S rRNA 2 homolog	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CUTC	CUTC	cutC copper transporter	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]								[illegible]						[illegible]			[illegible]
[illegible]	RECQL	RECQL	RecQ like helicase	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CCDC91	CCDC91	coiled-coil domain containing 91	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SMC6	SMC6	structural maintenance of chromosomes 6	Nucleus	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	TMEM59	TMEM59	transmembrane protein 59	Plasma Membrane	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CDS2	CDS2	CDP-diacylglycerol synthase 2	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SAMM50	SAMM50	SAMM50 sorting and assembly machinery component	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SDHC	SDHC	succinate dehydrogenase complex subunit C	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GUSB	GUSB	glucuronidase beta	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LYPLA2	LYPLA2	lysophospholipase II	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NCSTN	NCSTN	nicastrin	Plasma Membrane	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NPRL3	NPRL3	NPR3 like, GATOR1 complex subunit	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NCOA7	NCOA7	nuclear receptor coactivator 7	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	HEBP2	HEBP2	heme binding protein 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GORASP1	GORASP1	golgi reassembly stacking protein 1	Cytoplasm	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	LRRFIP2	LRRFIP2	LRR binding FLII interacting protein 2	Extracellular Space	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DCAF13	DCAF13	DDB1 and CUL4 associated factor 13	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KLHL21	KLHL21	kelch like family member 21	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PSMD10	PSMD10	proteasome 26S subunit, non-ATPase 10	Cytoplasm	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPL7	RPL7	ribosomal protein L7	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ESRRA	ESRRA	estrogen related receptor alpha	Nucleus	ligand-dependent nuclear rec				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	NCOR1	NCOR1	nuclear receptor corepressor 1	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PTPLB	HACD2	3-hydroxyacyl-CoA dehydratase 2	Cytoplasm	phosphatase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SPCS1	SPCS1	signal peptidase complex subunit 1	Cytoplasm	peptidase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GADD45B	GADD45B	growth arrest and DNA damage inducible beta	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	C5orf15	C5orf15	chromosome 5 open reading frame 15	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NUDT2	NUDT2	nudix hydrolase 2	Plasma Membrane	phosphatase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SYNGR3	SYNGR3	synaptogyrin 3	Plasma Membrane	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	SQLE	SQLE	squalene epoxidase	Cytoplasm	enzyme	terbinafine, butenafi	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PEX19	PEX19	peroxisomal biogenesis factor 19	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS18	RPS18	ribosomal protein S18	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CTDSPL2	CTDSPL2	CTD small phosphatase like 2	Nucleus	phosphatase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS4Y1	RPS4Y1	ribosomal protein S4, Y-linked 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CITED4	CITED4	Cbp/p300 interacting transactivator with Glu/Asp rich c	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RRS1	RRS1	ribosome biogenesis regulator homolog	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TOMM20	TOMM20	translocase of outer mitochondrial membrane 20	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	HMGN3	HMGN3	high mobility group nucleosomal binding domain 3	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TMEM9	TMEM9	transmembrane protein 9	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SNRNP27	SNRNP27	small nuclear ribonucleoprotein U4/U6.U5 subunit 27	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	ribosomal protein L[illegible] pseudogene [illegible]	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FAM214B	FAM214B	family with sequence similarity 214 member B	Nucleus	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	RPL34	RPL34	ribosomal protein L34	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ADCK2	ADCK2	aarF domain containing kinase 2	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	BCAS4	BCAS4	breast carcinoma amplified sequence 4	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRPS33	MRPS33	mitochondrial ribosomal protein S33	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GEM	GEM	GTP binding protein overexpressed in skeletal muscle	Plasma Membrane	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	C21orf2	C21orf2	chromosome 21 open reading frame 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	GMDS	GMDS	GDP-mannose 4,6-dehydratase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LSM14A	LSM14A	LSM14A, mRNA processing body assembly factor	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RBM12	RBM12	RNA binding motif protein 12	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FAM162A	FAM162A	family with sequence similarity 162 member A	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TEX261	TEX261	testis expressed 261	Extracellular Space	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CCR7	CCR7	C-C motif chemokine receptor 7	Plasma Membrane	G-protein coupled recept		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRPS23	MRPS23	mitochondrial ribosomal protein S23	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KMT2C	KMT2C	lysine methyltransferase 2C	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CD55	CD55	CD55 molecule (Cromer blood group)	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RSAD1	RSAD1	radical S-adenosyl methionine domain containing 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ARHGAP15	ARHGAP15	Rho GTPase activating protein 15	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SLC31A2	SLC31A2	solute carrier family 31 member 2	Plasma Membrane	transporter				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	STXBP2	STXBP2	syntaxin binding protein 2	Plasma Membrane	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NPM1	NPM1	nucleophosmin	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PTS	PTS	6-pyruvoyltetrahydropterin synthase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZSCAN25	ZSCAN25	zinc finger and SCAN domain containing 25	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	APRT	APRT	adenine phosphoribosyltransferase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	STX3	STX3	syntaxin 3	Plasma Membrane	transporter				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	ZNF764	ZNF764	zinc finger protein 764	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PRR14L	PRR14L	proline rich 14 like	Other	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EIF3E	EIF3E	eukaryotic translation initiation factor 3 subunit E	Cytoplasm	translation regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EAPP	EAPP	E2F associated phosphoprotein	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	C9orf78	C9orf78	chromosome 9 open reading frame 78	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KIAA1143	KIAA1143	KIAA1143	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CBX3	CBX3	chromobox 3	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EEF1D	EEF1D	eukaryotic translation elongation factor 1 delta	Cytoplasm	translation regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EIF1B	EIF1B	eukaryotic translation initiation factor 1B	Cytoplasm	translation regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	UBE2V2	UBE2V2	ubiquitin conjugating enzyme E2 V2	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPL31	RPL31	ribosomal protein L31	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NF2	NF2	neurofibromin 2	Plasma Membrane	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CRELD2	CRELD2	cysteine rich with EGF like domains 2	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPL23A	RPL23A	ribosomal protein L23a	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DANCR	DANCR	differentiation antagonizing non-protein coding RNA	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS21	RPS21	ribosomal protein S21	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	STK17A	STK17A	serine/threonine kinase 17a	Nucleus	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PET117	PET117	PET117 homolog	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPRD2	RPRD2	regulation of nuclear pre-mRNA domain containing 2	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PHC1	PHC1	polyhomeotic homolog 1	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TINF2	TINF2	TERF1 interacting nuclear factor 2	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZNF805	ZNF805	zinc finger protein 805	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PLEKHA1	PLEKHA1	pleckstrin homology domain containing A1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	APBB1IP	APBB1IP	amyloid beta precursor protein binding family B memb	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EIF3H	EIF3H	eukaryotic translation initiation factor 3 subunit H	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RP11-[illegible]								[illegible]									[illegible]
[illegible]	TRERF1	TRERF1	transcriptional regulating factor 1	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TOMM7	TOMM7	translocase of outer mitochondrial membrane 7	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	C6orf22	C6orf22	chromosome 6 open reading frame 22	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	INPP5D	INPP5D	inositol polyphosphate-5-phosphatase D	Cytoplasm	phosphatase	AQX-1125	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TIAM1	TIAM1	T-cell lymphoma invasion and metastasis 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NOLC1	NOLC1	nucleolar and coiled-body phosphoprotein 1	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SMIM20	SMIM20	small integral membrane protein 20	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	USMG5						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MEAF6	MEAF6	MYST/Esa1 associated factor 6	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ZCCHC6	ZCCHC6	zinc finger CCHC-type containing 6	Other	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LMBRD1	LMBRD1	LMBR1 domain containing 1	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CHD1L	CHD1L	chromodomain helicase DNA binding protein 1 like	Nucleus	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CALU	CALU	calumenin	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CNTROB	CNTROB	centrobin, centriole duplication and spindle assembly p	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	EEFSEC	EEFSEC	eukaryotic elongation factor, selenocysteine-tRNA spec	Cytoplasm	translation regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NDUFAB1	NDUFAB1	NADH:ubiquinone oxidoreductase subunit AB1	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PDCD6IP	PDCD6IP	programmed cell death 6 interacting protein	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PSKH1	PSKH1	protein serine kinase H1	Nucleus	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRPS26	MRPS26	mitochondrial ribosomal protein S26	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NDRG1	NDRG1	N-myc downstream regulated 1	Nucleus	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FAM13C	FAM13C	family with sequence similarity 13 member C	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CCND3	CCND3	cyclin D3	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SP4	SP4	Sp4 transcription factor	Nucleus	transcription regulator				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	NA						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS16	RPS16	ribosomal protein S16	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	AHCYL1	AHCYL1	adenosylhomocysteinase like 1	Cytoplasm	enzyme				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	RPL39	RPL39	ribosomal protein L39	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SCRN2	SCRN2	secernin 2	Extracellular Space	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPS2P46	RPS2P46	ribosomal protein S2 pseudogene 46	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MYO9B	MYO9B	myosin IXB	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	KTN1	KTN1	kinectin 1	Plasma Membrane	transmembrane recepto		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TTC3	TTC3	tetratricopeptide repeat domain 3	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	HMBOX1	HMBOX1	HMG-box containing 1	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TRAPPC8	TRAPPC8	trafficking protein particle complex 8	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	P2RX4	P2RX4	purinergic receptor P2X 4	Plasma Membrane	ion channel		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PMVK	PMVK	phosphomevalonate kinase	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NDUFS1	NDUFS1	NADH:ubiquinone oxidoreductase core subunit S1	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	AGPS	AGPS	alkylglycerone phosphate synthase	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RIMKLB	RIMKLB	ribosomal modification protein rimK like family memb	Cytoplasm	enzyme				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	ATP5SL	ATP5SL	ATP5S like	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ETV3	ETV3	ETS variant 3	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RP11-[illegible]						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DGUOK	DGUOK	deoxyguanosine kinase	Cytoplasm	kinase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ATPAF2	ATPAF2	ATP synthase mitochondrial F1 complex assembly facto	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TMEM170B						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	H2AFV	H2AFV	H2A histone family member V	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DHRS4	DHRS4	dehydrogenase/reductase 4	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TRIM59	TRIM59	tripartite motif containing 59	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DOPEY2	DOPEY2	dopey family member 2	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LAMTOR5	LAMTOR5	late endosomal/lysosomal adaptor, MAPK and MTOR a	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FGD2	FGD2	FYVE, RhoGEF and PH domain containing 2	Cytoplasm	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	INO80B	INO80B	INO80 complex subunit B	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NSA2	NSA2	NSA2, ribosome biogenesis homolog	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	BLOC1S4	BLOC1S4	biogenesis of lysosomal organelles complex 1 subunit 4	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	POLM						[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NCS1	NCS1	neuronal calcium sensor 1	Plasma Membrane	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	ZNF273	ZNF273	zinc finger protein 273	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RPA1	RPA1	replication protein A1	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PPP4C	PPP4C	protein phosphatase 4 catalytic subunit	Cytoplasm	phosphatase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	TMEM209	TMEM209	transmembrane protein 209	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PGP	PGP	phosphoglycolate phosphatase	Other	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	PHB	PHB	prohibitin	Nucleus	transcription regulator	[illegible]-targeting peptide	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRTO4	MRTO4	MRT4 homolog, ribosome maturation factor	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LDLRAD4	LDLRAD4	low density lipoprotein receptor class A domain containi	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	NUDT5	NUDT5	nudix hydrolase 5	Cytoplasm	phosphatase		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	FNIP1	FNIP1	folliculin interacting protein 1	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	ATP2A2	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ tran	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CHTF8	CHTF8	chromosome transmission fidelity factor 8	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SP100	SP100	SP100 nuclear antigen	Nucleus	transcription regulator		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SAMD4B	SAMD4B	sterile alpha motif domain containing 4B	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	RNF31	RNF31	ring finger protein 31	Cytoplasm	enzyme		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	LINC01420	NBDY	negative regulator of P-body association	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MRPS12	MRPS12	mitochondrial ribosomal protein S12	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	SLC6A8	SLC6A8	solute carrier family 6 member 8	Extracellular Space	other				[illegible]			[illegible]			[illegible]			[illegible]
[illegible]	WDR83	WDR83	WD repeat domain 83	Nucleus	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	CASS4	CASS4	Cas scaffolding protein family member 4	Other	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	MCL1	MCL1	BCL2 family apoptosis regulator	Cytoplasm	transporter		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	DPH3	DPH3	diphthamide biosynthesis 3	Cytoplasm	other		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

[illegible]	FUNDC1	FUNDC1	FUN14 domain containing 1	Cytoplasm	other	
[illegible]	MRPL19	MRPL19	mitochondrial ribosomal protein L19	Cytoplasm	other	
[illegible]	ZPR1	ZPR1	ZPR1 zinc finger protein	Nucleus	other	
[illegible]	SSR2	SSR2	signal sequence receptor subunit 2	Cytoplasm	other	
[illegible]	RPL13A	RPL13A	ribosomal protein L13a	Cytoplasm	other	
[illegible]	PDCL	PDCL	phosducin like	Cytoplasm	enzyme	
[illegible]	PLEKHM2	PLEKHM2	pleckstrin homology and RUN domain containing M2	Extracellular Space	other	
[illegible]	KCNN4	KCNN4	potassium calcium-activated channel subfamily N mem	Plasma Membrane	ion channel	[illegible]
[illegible]	ID3	ID3	inhibitor of DNA binding 3, HLH protein	Nucleus	transcription regulator	
[illegible]	ISCA2	ISCA2	iron-sulfur cluster assembly 2	Cytoplasm	other	
[illegible]	MVP	MVP	major vault protein	Nucleus	other	
[illegible]	SFR1	SFR1	SWI5 dependent homologous recombination repair pro	Nucleus	transcription regulator	
[illegible]	OGFOD1	OGFOD1	2-oxoglutarate and iron dependent oxygenase domain c	Cytoplasm	enzyme	
[illegible]	PPP1R15B	PPP1R15B	protein phosphatase 1 regulatory subunit 15B	Cytoplasm	phosphatase	
[illegible]	YWHAB	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygena	Cytoplasm	other	
[illegible]	PVRL1	NECTIN1	nectin cell adhesion molecule 1	Plasma Membrane	other	
[illegible]	RP4-[illegible]					
[illegible]	NUMBL	NUMBL	NUMB like, endocytic adaptor protein	Cytoplasm	other	
[illegible]	FAM127B	FAM127B	family with sequence similarity 127 member B	Other	other	
[illegible]	QTRTD1	QTRT2	queuine tRNA-ribosyltransferase accessory subunit 2	Cytoplasm	enzyme	
[illegible]	ING3	ING3	inhibitor of growth family member 3	Nucleus	other	
[illegible]	FLCN	FLCN	folliculin	Cytoplasm	other	
[illegible]	TATDN1					
[illegible]	USP4	USP4	ubiquitin specific peptidase 4	Nucleus	peptidase	
[illegible]	[illegible]	[illegible]	endonuclease/exonuclease/phosphatase family domain c	Other	other	
[illegible]	RRP36	RRP36	ribosomal RNA processing 36	Nucleus	other	
[illegible]	AMDHD2	AMDHD2	amidohydrolase domain containing 2	Nucleus	enzyme	
[illegible]	GRAMD4	GRAMD4	GRAM domain containing 4	Cytoplasm	other	
[illegible]	RPS25	RPS25	ribosomal protein S25	Cytoplasm	other	
[illegible]	SNX5	SNX5	sorting nexin 5	Cytoplasm	transporter	
[illegible]	SYMPK	SYMPK	symplekin	Cytoplasm	other	
[illegible]	TSFM	TSFM	Ts translation elongation factor, mitochondrial	Cytoplasm	translation regulator	
[illegible]	[illegible]					
[illegible]	PGAP2	PGAP2	post-GPI attachment to proteins 2	Other	transporter	
[illegible]	RPTOR	RPTOR	regulatory associated protein of MTOR complex 1	Cytoplasm	other	
[illegible]	FPGS	FPGS	folylpolyglutamate synthase	Cytoplasm	enzyme	pralatrexate
[illegible]	DHRS4L2	DHRS4L2	dehydrogenase/reductase 4 like 2	Other	other	
[illegible]	PPM1M	PPM1M	protein phosphatase, Mg2+/Mn2+ dependent 1M	Nucleus	phosphatase	
[illegible]	ASUN	INTS13	integrator complex subunit 13	Cytoplasm	other	
[illegible]	[illegible]					
[illegible]	OTUD6B	OTUD6B	OTU domain containing 6B	Other	other	
[illegible]	TPST1	TPST1	tyrosylprotein sulfotransferase 1	Cytoplasm	enzyme	
[illegible]	EID3	EID3	EP300 interacting inhibitor of differentiation 3	Cytoplasm	other	
[illegible]	ABCF2	ABCF2	ATP binding cassette subfamily F member 2	Cytoplasm	transporter	
[illegible]	HENMT1	HENMT1	HEN1 methyltransferase homolog 1	Other	enzyme	
[illegible]	RNF6	RNF6	ring finger protein 6	Cytoplasm	enzyme	
[illegible]	THAP1	THAP1	THAP domain containing 1	Nucleus	other	
[illegible]	AFG3L1P	AFG3L1P	AFG3 like matrix AAA peptidase subunit 1, pseudogene	Cytoplasm	other	
[illegible]	METTL1	METTL1	methyltransferase like 1	Nucleus	enzyme	
[illegible]	ISG15	ISG15	ISG15 ubiquitin-like modifier	Extracellular Space	other	
[illegible]	PIAS3	PIAS3	protein inhibitor of activated STAT 3	Nucleus	transcription regulator	
[illegible]	C3orf58	C3orf58	chromosome 3 open reading frame 58	Other	other	
[illegible]	MRPL48	MRPL48	mitochondrial ribosomal protein L48	Cytoplasm	other	
[illegible]	DPH2	DPH2	DPH2 homolog	Cytoplasm	enzyme	
[illegible]	DRAM1	DRAM1	DNA damage regulated autophagy modulator 1	Cytoplasm	other	
[illegible]	ALCAM	ALCAM	activated leukocyte cell adhesion molecule	Plasma Membrane	other	
[illegible]	CTA-29F11.1					
[illegible]	CCT3	CCT3	chaperonin containing TCP1 subunit 3	Cytoplasm	kinase	
[illegible]	ANKRD10	ANKRD10	ankyrin repeat domain 10	Nucleus	transcription regulator	
[illegible]	C19orf52	TIMM29	translocase of inner mitochondrial membrane 29	Cytoplasm	other	
[illegible]	MRPL24	MRPL24	mitochondrial ribosomal protein L24	Cytoplasm	other	
[illegible]	ZNF580	ZNF580	zinc finger protein 580	Nucleus	other	
[illegible]	CSNK2B	CSNK2B	casein kinase 2 beta	Cytoplasm	kinase	
[illegible]	AMZ2P1	AMZ2P1	archaelysin family metallopeptidase 2 pseudogene 1	Other	other	
[illegible]	PROK2	PROK2	prokineticin 2	Extracellular Space	other	
[illegible]	WDR86					
[illegible]	SMPD2	SMPD2	sphingomyelin phosphodiesterase 2	Cytoplasm	enzyme	
[illegible]	RPL9P7	RPL9P7	ribosomal protein L9 pseudogene 7	Other	other	
[illegible]	IFRD2	IFRD2	interferon related developmental regulator 2	Nucleus	other	
[illegible]	MCM5	MCM5	minichromosome maintenance complex component 5	Nucleus	enzyme	
[illegible]	MEF2C	MEF2C	myocyte enhancer factor 2C	Nucleus	transcription regulator	
[illegible]	NDUFA8	NDUFA8	NADH:ubiquinone oxidoreductase subunit A8	Cytoplasm	enzyme	
[illegible]	CHKA	CHKA	choline kinase alpha	Cytoplasm	kinase	TCD-717
[illegible]	MRPS31	MRPS31	mitochondrial ribosomal protein S31	Cytoplasm	other	
[illegible]	CYP2R1	CYP2R1	cytochrome P450 family 2 subfamily R member 1	Cytoplasm	enzyme	
[illegible]	RILP	RILP	Rab interacting lysosomal protein	Cytoplasm	other	
[illegible]	PTK2	PTK2	protein tyrosine kinase 2	Cytoplasm	kinase	CT-707
[illegible]	FEM1C	FEM1C	fem-1 homolog C	Nucleus	transcription regulator	
[illegible]	GTPBP2	GTPBP2	GTP binding protein 2	Extracellular Space	enzyme	
[illegible]	RP13-[illegible]					
[illegible]	CCDC187	CCDC187	coiled-coil domain containing 187	Other	other	
[illegible]	GGCT	GGCT	gamma-glutamylcyclotransferase	Cytoplasm	enzyme	
[illegible]	BRCC3	BRCC3	BRCA1/BRCA2-containing complex subunit 3	Nucleus	enzyme	
[illegible]	FH	FH	fumarate hydratase	Cytoplasm	enzyme	
[illegible]	ERAP2	ERAP2	endoplasmic reticulum aminopeptidase 2	Cytoplasm	peptidase	
[illegible]	SNAPC5	SNAPC5	small nuclear RNA activating complex polypeptide 5	Nucleus	transcription regulator	
[illegible]	RP11-[illegible]					
[illegible]	ALKBH4	ALKBH4	alkB homolog 4, lysine demethylase	Cytoplasm	enzyme	
[illegible]	RPL13AP5	RPL13AP5	ribosomal protein L13a pseudogene 5	Other	other	
[illegible]	CRIP1	CRIP1	cysteine rich protein 1	Cytoplasm	other	
[illegible]	CENPH	CENPH	centromere protein H	Nucleus	other	
[illegible]	RDX	RDX	radixin	Cytoplasm	other	
[illegible]	PSTPIP2	PSTPIP2	proline-serine-threonine phosphatase interacting prote	Cytoplasm	other	
[illegible]	C15orf61	C15orf61	chromosome 15 open reading frame 61	Other	other	
[illegible]	DNPH1	DNPH1	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	Nucleus	enzyme	
[illegible]	PEMT	PEMT	phosphatidylethanolamine N-methyltransferase	Cytoplasm	enzyme	
[illegible]	DENND4B	DENND4B	DENN domain containing 4B	Extracellular Space	other	
[illegible]	RBBP4	RBBP4	RB binding protein 4	Nucleus	enzyme	
[illegible]	METTL18	METTL18	methyltransferase like 18	Other	other	
[illegible]	IRF2	IRF2	interferon regulatory factor 2	Nucleus	transcription regulator	
[illegible]	CNN3	CNN3	calponin 3	Cytoplasm	other	
[illegible]	PRR24	INAFM1	InaF motif containing 1	Other	other	
[illegible]	FFAR2	FFAR2	free fatty acid receptor 2	Plasma Membrane	G-protein coupled receptor	
[illegible]	FAM120A	FAM120A	family with sequence similarity 120 member A	Nucleus	other	
[illegible]	ARHGEF11	ARHGEF11	Rho guanine nucleotide exchange factor 11	Cytoplasm	other	
[illegible]	C6orf226	C6orf226	chromosome 6 open reading frame 226	Other	other	
[illegible]	TOPORS-AS1	TOPORS-AS1	TOPORS antisense RNA 1	Other	other	
[illegible]	RP11-[illegible]					
[illegible]	POLD3	POLD3	DNA polymerase delta 3, accessory subunit	Nucleus	enzyme	
[illegible]	SCARNA9	SCARNA9	small Cajal body-specific RNA 9	Other	other	
[illegible]	CCDC82	CCDC82	coiled-coil domain containing 82	Other	other	
[illegible]	FSCN1	FSCN1	fascin actin-bundling protein 1	Cytoplasm	other	
[illegible]	DNAJC17	DNAJC17	DnaJ heat shock protein family (Hsp40) member C17	Other	other	
[illegible]	ZSCAN9	ZSCAN9	zinc finger and SCAN domain containing 9	Nucleus	transcription regulator	
[illegible]	IER5	IER5	immediate early response 5	Other	other	
[illegible]	FAM127A	FAM127A	family with sequence similarity 127 member A	Other	other	
[illegible]	PGM2	PGM2	phosphoglucomutase 2	Cytoplasm	enzyme	
[illegible]	POP5	POP5	POP5 homolog, ribonuclease P/MRP subunit	Nucleus	enzyme	
[illegible]	RPL13P3	RPL13P3	ribosomal protein L13 pseudogene 3	Other	other	
[illegible]	RPSAP15	RPSAP15	ribosomal protein SA pseudogene 15	Other	other	
[illegible]	RPS23P8	RPS23P8	ribosomal protein S23 pseudogene 8	Other	other	
[illegible]	SRGAP2B	SRGAP2B	SLIT-ROBO Rho GTPase activating protein 2B	Other	other	
[illegible]	RP11-[illegible]					
[illegible]	HES4	HES4	hes family bHLH transcription factor 4	Other	other	
[illegible]	XCL1	XCL1	X-C motif chemokine ligand 1	Extracellular Space	cytokine	
[illegible]	RP11-[illegible]					
[illegible]	NDUFAF3	NDUFAF3	NADH:ubiquinone oxidoreductase complex assembly fa	Cytoplasm	enzyme	
[illegible]	[illegible]					
[illegible]	RP11-[illegible]					
[illegible]	RP11-[illegible]					

Supplementary Table 3B. Differentially expressed non-coding genes in CD4+, CD8+ and CD4-CD8- fraction compared to the original PBMC fraction (using samples from healthy control children only).

							Median LogFC			FDR			Percent Up			Percent Down		
Ensembl Gene IDs	Gene Names	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)	CD4+ vs PBMC	CD8+ vs PBMC	CD4-CD8- vs. PBMC	CD4+ vs PBMC	CD8+ vs PBMC	CD4-CD8- vs. PBMC	CD4+ vs PBMC	CD8+ vs PBMC	CD4-CD8- vs. PBMC	CD4+ vs PBMC	CD8+ vs PBMC	CD4-CD8- vs. PBMC
ENSG00000224137	AC079767.4	LINC01857	long intergenic non-protein coding RNA 1857	Other	other		-7.11	-4.96	0.37	0.00	0.00	0.07	0	0	70	100	100	30
ENSG00000224397	LINC01272	SMIM25	small integral membrane protein 25	Other	other		-4.10	-6.56	0.29	0.00	0.00	0.42	0	0	65	100	100	35
ENSG00000251562	MALAT1	MALAT1	metastasis associated lung adenocarcinoma transcript 1	Nucleus	other		1.78	1.53	1.26	0.00	0.00	0.00	97	100	89	3	0	11
ENSG00000253701	AL928768.3						"-INF"	"-INF"	-0.28	0.00	0.00	0.00	0	0	27	100	100	73
ENSG00000255717	SNHG1	SNHG1	small nucleolar RNA host gene 1	Other	other		1.55	1.57	0.78	0.00	0.00	0.00	100	100	100	0	0	0
ENSG00000256039	RP11-291B21.2						-6.67	1.91	-2.82	0.00	0.00	0.00	0	100	0	100	0	100
ENSG00000260682	7SK	RN7SKP176	RNA, 7SK small nuclear pseudogene 176	Other	other		-4.77	-1.42	1.36	0.00	0.00	0.00	0	0	100	100	100	0
ENSG00000269728	RP11-145M9.4						-3.55	-3.90	-0.04	0.00	0.00	0.00	0	0	43	100	100	57
ENSG00000272379	RP1-257A7.5						-3.81	-4.00	0.87	0.00	0.00	0.00	0	0	95	100	100	5
ENSG00000234184	RP5-887A10.1	LINC01781	long intergenic non-protein coding RNA 1781	Other	other		"-INF"	-5.25	0.01	0.00	0.00	0.30	0	0	51	100	100	49
ENSG00000272016	RP11-215G15.5						-3.76	-3.22	0.61	0.00	0.00	0.00	0	0	95	100	100	5
ENSG00000273472	RP11-102N12.3						-5.34	-4.79	0.75	0.00	0.00	0.00	0	0	97	100	100	3
ENSG00000230709	AC104024.1	LOC284191	uncharacterized LOC284191	Other	other		-6.88	-5.36	1.06	0.00	0.00	0.00	0	0	92	100	100	8
ENSG00000211459	MT-RNR1	MT-RNR1	s-rRNA	Cytoplasm	other		-1.83	-1.14	0.05	0.00	0.00	0.00	0	0	57	100	100	43
ENSG00000250334	LINC00989	LINC00989	long intergenic non-protein coding RNA 989	Other	other		-5.95	"-INF"	-0.98	0.00	0.00	0.00	0	0	16	100	100	84
ENSG00000260655	CTA-250D10.23						-3.67	-2.39	0.83	0.00	0.00	0.00	0	0	97	100	100	3
ENSG00000247982	LINC00926	LINC00926	long intergenic non-protein coding RNA 926	Other	other		-3.46	-2.56	2.02	0.00	0.00	0.00	0	0	100	100	100	0
ENSG00000267174	CTC-510F12.4	HSPC102	uncharacterized HSPC102	Other	other		-4.42	-6.19	0.20	0.00	0.00	0.54	0	0	62	97	100	38
ENSG00000237604	AP001056.1						-4.87	-5.17	0.64	0.00	0.00	0.00	0	0	89	100	100	11
ENSG00000260065	CTA-445C9.15						-2.49	0.08	-0.38	0.00	0.01	0.00	0	56	16	100	44	84
ENSG00000271614	LINC00936	ATP2B1-AS1	ATP2B1 antisense RNA 1	Other	other		-2.56	-2.83	1.16	0.00	0.00	0.00	0	0	100	100	100	0
ENSG00000268734	CTB-61M7.2						-2.94	-4.70	1.95	0.00	0.00	0.00	0	0	100	100	100	0
ENSG00000241163	LINC00877	LINC00877	long intergenic non-protein coding RNA 877	Other	other		-2.97	-4.13	1.51	0.00	0.00	0.00	0	0	100	100	100	0
ENSG00000186594	MIR22HG						-1.86	-1.65	0.84	0.00	0.00	0.00	0	0	95	100	100	5
ENSG00000272523	LINC01023	LINC01023	long intergenic non-protein coding RNA 1023	Other	other		-3.32	-2.07	0.38	0.00	0.00	0.00	0	0	95	100	100	5
ENSG00000230438	SERPINB9P1	SERPINB9P1	serpin family B member 9 pseudogene 1	Other	other		-2.21	-1.92	0.54	0.00	0.00	0.00	0	0	97	100	100	3
ENSG00000253364	RP11-731F5.2						"-INF"	"-INF"	-0.34	0.00	0.00	0.00	0	3	35	100	97	65
ENSG00000260359	NA						-2.20	-1.18	0.31	0.00	0.00	0.00	0	6	76	100	94	24
ENSG00000180422	LINC00304	LINC00304	long intergenic non-protein coding RNA 304	Other	other		2.98	2.09		0.00	0.00		100	100		0	0	
ENSG00000272077	RP11-348P10.2						-2.36	-1.43	0.38	0.00	0.00	0.28	0	6	81	100	94	19
ENSG00000272888	AC013394.2	LINC01578	long intergenic non-protein coding RNA 1578	Other	other		0.66	0.41	-0.11	0.00	0.45	0.00	100	86	32	0	14	68
ENSG00000172965	MIR4435-1HG	MIR4435-2HG	MIR4435-2 host gene	Other	other		-1.79	-1.71	0.28	0.00	0.00	0.40	0	0	73	100	100	27
ENSG00000232931	LINC00342	LINC00342	long intergenic non-protein coding RNA 342	Other	other		2.51	1.92	0.88	0.00	0.00	0.00	100	97	81	0	3	19
ENSG00000233901	RP11-65J3.1	LINC01503	long intergenic non-protein coding RNA 1503	Other	other		-3.39	-4.30	-0.03	0.00	0.00	0.03	0	0	49	100	100	51
ENSG00000255760	RP11-428G5.5	LOC105369723		Other	other		"-INF"		0.32	0.00		0.61	0		59	100		41
ENSG00000175898	CTD-2369P2.2						-1.62	-2.03	0.26	0.00	0.00	0.03	0	0	73	100	100	27
ENSG00000268913	AC026806.2						-2.59	-2.66	-0.18	0.00	0.00	0.01	0	0	43	100	100	57
ENSG00000263126	CTC-479C5.10						2.02	1.90	0.84	0.00	0.00	0.00	100	100	95	0	0	5
ENSG00000233056	ERVH48-1	ERVH48-1	endogenous retrovirus group 48 member 1	racellular Sp	other		2.27	-0.43	-0.96	0.00	0.00	0.00	100	22	5	0	78	95
ENSG00000261005	NA						-1.56	-1.57	0.82	0.00	0.00	0.00	0	3	89	100	97	11
ENSG00000210082	MT-RNR2	MT-RNR2	l-rRNA	Other	other		-1.88	-1.40	-0.54	0.00	0.00	0.00	0	0	16	100	100	84
ENSG00000223511	RP13-297E16.4						2.50	2.17	1.59	0.00	0.00	0.00	100	100	89	0	0	11
ENSG00000259004	RP11-8L8.2	LOC101929422	uncharacterized LOC101929422	Other	other		-3.72	-3.99	0.35	0.00	0.00	0.09	0	0	86	100	100	14
ENSG00000234741	GAS5	GAS5	growth arrest specific 5 (non-protein coding)	Other	other		0.53	0.43	-0.27	0.00	0.18	0.00	100	94	5	0	6	95
ENSG00000223745	RP4-717I23.3	CCDC18-AS1	CCDC18 antisense RNA 1	Other	other		2.43	1.64	1.47	0.00	0.00	0.00	97	97	86	3	3	14
ENSG00000230606	AC159540.1	LOC100506123	uncharacterized LOC100506123	Other	other		2.45	2.13	0.98	0.00	0.00	0.00	100	100	89	0	0	11
ENSG00000272053	RP11-367G6.3						-1.68	-1.13	-0.09	0.00	0.00	0.01	0	3	41	100	97	59
ENSG00000188070	C11orf95	C11orf95	chromosome 11 open reading frame 95	Other	other		-1.68	-0.84	0.23	0.00	0.00	0.35	0	8	73	100	92	27
ENSG00000270055	CTD-3092A11.2						1.70	1.30	0.25	0.00	0.00	0.45	100	100	73	0	0	27
ENSG00000261455	LINC01003	LINC01003	long intergenic non-protein coding RNA 1003	Other	other		-1.42	-1.37	0.28	0.00	0.00	0.17	0	0	76	100	100	24
ENSG00000260807	RP11-161M6.2	LMF1	lipase maturation factor 1	Cytoplasm	other		2.25	0.78	-0.78	0.00	0.00	0.00	100	89	27	0	11	73
ENSG00000240219	RP11-430C7.5	LOC105371692	uncharacterized LOC105371692	Other	other		2.27	1.71	1.32	0.00	0.00	0.00	97	97	95	3	3	5
ENSG00000232891	RP11-136K14.1						-2.44	-2.20	0.99	0.00	0.00	0.00	0	0	100	100	100	0
ENSG00000196295	AC005154.6						2.24	1.68	1.83	0.00	0.00	0.00	97	100	92	3	0	8
ENSG00000225331	AP001055.6	LINC01678		Other	other		-1.54	-2.26	0.16	0.00	0.00	0.81	0	0	73	100	100	27
ENSG00000251301	RP11-81H14.2	LOC100507195	uncharacterized LOC100507195	Other	other		-3.10	-1.34	0.41	0.00	0.00	0.58	3	17	62	97	83	38
ENSG00000267279	RP11-879F14.2						"-INF"		-0.61	0.00		0.00	3		27	97		73
ENSG00000222041	LINC00152	CYTOR	cytoskeleton regulator RNA	Other	other		-1.31	-1.28	0.02	0.00	0.00	0.04	3	6	51	97	94	49
ENSG00000251136	RP11-37B2.1	LOC101929709	uncharacterized LOC101929709	Other	other		-1.47	-1.24	0.78	0.00	0.00	0.00	0	0	100	100	100	0
ENSG00000261490	RP11-448G15.3						2.08	1.08	0.76	0.00	0.00	0.00	97	94	89	3	6	11
ENSG00000188971	RP11-427H3.3						1.35	0.75	-0.77	0.00	0.00	0.00	100	94	3	0	6	97
ENSG00000269290	RP11-869B15.1						2.12	1.32	0.44	0.00	0.00	0.01	97	89	65	3	11	35
ENSG00000260006	RP11-469M7.1						-1.47	-0.74	-0.18	0.00	0.00	0.00	0	0	30	100	100	70
ENSG00000270127	PRKXP1						1.99	1.25		0.00	0.00		100	100		0	0	
ENSG00000260910	LINC00565	LINC00565	long intergenic non-protein coding RNA 565	Other	other		1.66	1.30	-0.44	0.00	0.00	0.00	100	100	19	0	0	81
ENSG00000225783	MIAT	MIAT	myocardial infarction associated transcript (non-protein	Other	other		2.10	2.81	1.05	0.00	0.00	0.00	97	100	86	3	0	14
ENSG00000272316	(bac-BPGBPG55C20.	GUSBP4	glucuronidase, beta pseudogene 4	Other	other		1.62	1.03		0.00	0.00		100	94		0	6	
ENSG00000226137	BAIAP2-AS1	BAIAP2-AS1	BAIAP2 antisense RNA 1 (head to head)	Other	other		-1.38	-2.45	0.02	0.00	0.00	0.03	3	0	51	97	100	49
ENSG00000228784	LINC00954	LINC00954	long intergenic non-protein coding RNA 954	Other	other		1.98	1.45	0.66	0.00	0.00	0.00	100	97	86	0	3	14
ENSG00000270060	RP11-390K5.6						1.78	2.08	1.38	0.00	0.00	0.00	100	100	86	0	0	14
ENSG00000235576	AC092580.4						-2.33	0.78	-1.53	0.00	0.00	0.00	0	81	5	100	19	95
ENSG00000237438	CECR7	CECR7	cat eye syndrome chromosome region, candidate 7 (non-	Other	other		-1.37	-1.08	0.37	0.00	0.00	0.07	0	3	89	100	97	11
ENSG00000260787	NA						1.97	1.50	1.52	0.00	0.00	0.00	100	92	86	0	8	14
ENSG00000266896	RP1-266L20.9						2.36	2.09		0.00	0.00		97	97		3	3	
ENSG00000243650	RN7SL834P	RN7SL834P	RNA, 7SL, cytoplasmic 834, pseudogene	Other	other		2.65	2.30	2.63	0.00	0.00	0.00	97	92	92	3	8	8
ENSG00000235499	AC073046.25						-1.09	-0.71	-0.04	0.00	0.00	0.02	0	3	43	100	97	57
ENSG00000261560	RP11-166B2.3						1.63	1.82	0.45	0.00	0.00	0.66	100	100	59	0	0	41
ENSG00000254419	RP11-261P9.4						2.56	1.94	1.56	0.00	0.00	0.00	100	97	81	0	3	19
ENSG00000272086	CTD-2186M15.3						-1.37	-0.96	0.11	0.00	0.00	0.15	0	0	57	100	100	43
ENSG00000260306	RP11-645C24.5	RRN3P1	RRN3 homolog, RNA polymerase I transcription factor ps	Other	other		2.17	1.40		0.00	0.00		100	92		0	8	
ENSG00000228223	HCG11	HCG11	HLA complex group 11 (non-protein coding)	Other	other		-1.00	-1.72	-0.43	0.00	0.00	0.00	0	0	8	100	100	92
ENSG00000228106	RP11-452F19.3	LOC102724017	uncharacterized LOC102724017	Other	other		-1.06	-0.84	0.30	0.00	0.00	0.93	3	8	68	97	92	32
ENSG00000269640	CTD-2521M24.9						-1.04	-0.82	-0.66	0.00	0.00	0.00	0	6	8	100	94	92
ENSG00000272849	RP11-347I19.8						1.81	1.80	-0.02	0.00	0.00	0.14	97	97	49	3	3	51
ENSG00000142396	ERVK3-1	ERVK3-1		Other	other		1.52	1.66	1.00	0.00	0.00	0.00	100	100	89	0	0	11
ENSG00000197989	SNHG12	SNHG12	small nucleolar RNA host gene 12	Other	other		1.86	1.94	1.42	0.00	0.00	0.00	100	100	100	0	0	0
ENSG00000260101	RP11-568N6.1	LOC101927402	uncharacterized LOC101927402	Other	other		-1.28	-1.59	0.61	0.00	0.00	0.00	3	0	81	97	100	19
ENSG00000266709	MGC12916	MGC12916	uncharacterized protein MGC12916	Other	other		-1.14	-0.90	1.07	0.00	0.00	0.00	17	8	95	83	92	5
ENSG00000240350	AC017002.1						-1.32	-1.23	0.33	0.00	0.00	0.08	11	14	76	89	86	24
ENSG00000267302	RP11-178C3.2	LOC101927755	uncharacterized LOC101927755	Other	other		1.58	1.68	0.70	0.00	0.00	0.00	100	94	76	0	6	24
ENSG00000258559	AC005519.4						1.96	1.97	1.23	0.00	0.00	0.00	100	97	92	0	3	8
ENSG00000263470	RP11-160O5.1						-2.62	-1.73	0.61	0.00	0.00	0.03	0	0	76	100	100	24
ENSG00000238142	RP11-108M9.4	LOC105376805		Other	other		-1.37	-1.15	-0.18	0.00	0.00	0.01	0	6	38	100	94	62
ENSG00000260751	CTD-2196E14.6						1.76	1.79	0.95	0.00	0.00	0.00	100	94	92	0	6	8
ENSG00000266274	RN7SL138P	RN7SL138P		Other	other		"-INF"	"-INF"	0.74	0.00	0.00	0.00	0	0	84	100	100	16
ENSG00000235373	RP11-206L10.3						1.66	1.69	1.32	0.00	0.00	0.00	97	97	89	3	3	11
ENSG00000269928	RP11-849F2.8						1.44	0.96	0.63	0.00	0.00	0.00	100	97	92	0	3	8
ENSG00000261355	NA						1.49	0.56	0.41	0.00	0.00	0.00	97	94	81	3	6	19
ENSG00000272341	RP1-151F17.2						1.88	1.53		0.00	0.00		100	94		0	6	
ENSG00000272168	CASC15	CASC15	cancer susceptibility 15 (non-protein coding)	Other	other		1.41			0.00			100			0		
ENSG00000240905	RN7SL798P	RN7SL798P		Other	other		"-INF"	-3.91	0.47	0.00	0.00	0.00	0	6	65	97	94	35
ENSG00000262370	RP11-473M20.9						1.54	-0.14	1.43	0.00	0.48	0.00	94	44	89	6	56	11
ENSG00000260077	RP11-254F7.2						-1.07	-1.39	0.44	0.00	0.00	0.00	6	0	89	94	100	11
ENSG00000265242	RP11-649A18.7						-0.84	-0.66	-0.60	0.00	0.00	0.00	0	6	5	100	94	95
ENSG00000260948	RP11-552M11.8						1.66	1.00	1.05	0.00	0.00	0.00	97	92	81	3	8	19
ENSG00000234883	MIR155HG						-1.04	-1.06	1.05	0.00	0.00	0.00	17	6	100	83	94	0
ENSG00000260905	RP11-105C19.1						1.89	1.31	0.83	0.00	0.00	0.00	100	89	81	0	11	19
ENSG00000230415	RP5-902P8.10						1.97	1.36	0.61	0.00	0.00	0.00	100	89	76	0	11	24
ENSG00000236871	LINC00106	LINC00106	long intergenic non-protein coding RNA 106	Other	other		3.29	3.02	3.15	0.00	0.00	0.00	100	94	97	0	6	0
ENSG00000237513	RP11-325F22.2	LOC101927902	uncharacterized LOC101927902	Other	other		-0.85	-0.80	0.72	0.00	0.00	0.00	6	11	100	94	89	0
ENSG00000228434	AC004951.6						1.46	1.17	0.49	0.00	0.00	0.00	97	94	84	3	6	16
ENSG00000251867	RP11-48B3.5						-0.93	-0.84	-0.39	0.00	0.00	0.00	6	0	14	94	100	86
ENSG00000264772	SNORA67						1.37	1.47	1.26	0.00	0.00	0.00	100	97	100	0	3	0
ENSG00000236194	AC003104.1						1.68	1.63	0.43	0.00	0.00	0.16	100	89	65	0	11	35
ENSG00000254615	RP11-395G23.3						1.52	1.43	0.34	0.00	0.00	0.03	100	100	76	0	0	24
ENSG00000233261	LINC00264	LINC00264	long intergenic non-protein coding RNA 264	Other	other		1.68	1.33	0.05	0.00	0.00	0.18	97	100	51	3	0	49
ENSG00000224478	RP11-13P5.1						-1.62	-1.66	0.98	0.00	0.00	0.00	9	6	97	91	94	3
ENSG00000231607	DLEU2	mir-15	microRNA 15a	Cytoplasm	microRNA		-0.77	-1.24	0.01	0.00	0.00	0.02	0	0	51	100	100	49
ENSG00000249532	RP11-148B6.1	mir-302	microRNA 302c	Cytoplasm	microRNA		2.15	2.14	1.78	0.00	0.00	0.00	97	100	97	3	0	3
ENSG00000238795	SCARNA12	SCARNA12	small Cajal body-specific RNA 12	Other	other		2.18	1.90	0.99	0.00	0.00	0.00	97	89	84	3	11	16
ENSG00000260114	CTD-2574D22.4	KCTD13	potassium channel tetramerization domain containing 13	Nucleus	n channel		1.46	1.46	0.81	0.00	0.00	0.00	97	97	86	3	3	14
ENSG00000230724	LINC01001	001 (includes	long intergenic non-protein coding RNA 1347	Other	other		1.33	1.28	0.99	0.00	0.00	0.00	100	97	97	0	3	3
ENSG00000269996	NA						-0.75	-1.25	0.35	0.00	0.00	0.00	9	0	81	91	100	19
ENSG00000261220	RP11-629O1.2						-1.13	-0.83	1.41	0.00	0.00	0.00	11	11	97	89	89	3
ENSG00000261114	RP11-325K4.2						-0.88	-0.46	0.66	0.00	0.00	0.00	14	31	86	86	69	14
ENSG00000262766	RP11-196G11.4						1.44	1.54	1.38	0.00	0.00	0.00	97	94	92	3	6	8
ENSG00000261270	RP11-325K4.3						-1.17	-0.38	0.65	0.00	0.00	0.00	11	31	92	89	69	8
ENSG00000267701	RP11-28F1.2						-1.78	-1.73	0.00	0.00	0.00	0.16	0	8	54	100	92	46
ENSG00000260841	CTC-205M6.5						-0.81	-0.15	0.64	0.00	0.00	0.00	11	39	95	89	61	5
ENSG00000261824	LINC00662	LINC00662	long intergenic non-protein coding RNA 662	Other	other		-0.76	-1.00	-0.19	0.00	0.00	0.00	0	0	27	100	100	73
ENSG00000212694	LINC01089	LINC01089	long intergenic non-protein coding RNA 1089	Other	other		1.28	0.79	-0.58	0.00	0.00	0.00	100	97	8	0	3	92
ENSG00000273352	RP11-61I19.3						-0.93	-0.78	-0.08	0.00	0.00	0.00	9	17	43	91	83	57
ENSG00000215908	CROCCP2	CROCCP2	ciliary rootlet coiled-coil, rootletin pseudogene 2	Other	other		1.36	1.39	0.36	0.00	0.00	0.02	100	100	89	0	0	11
ENSG00000254985	RSF1-IT2	RSF1-IT2	RSF1 intronic transcript 2	Other	other		-0.99	-0.16	-0.33	0.00	0.00	0.00	9	39	30	91	61	70
ENSG00000253764	RP11-439C15.4						3.05			0.00			97			3		
ENSG00000206140	TMEM191C	M191B/TMEM	transmembrane protein 191C	Other	other		1.28			0.00			100			0		
ENSG00000240731	RP5-890O3.9						1.74	1.73	1.10	0.00	0.00	0.00	100	97	86	0	3	14
ENSG00000226423	AC093642.4						1.50	0.54	-1.12	0.00	0.02	0.00	97	75	14	3	25	86
ENSG00000259758	CASC7						-0.50	-0.32	-0.27	0.00	0.00	0.00	20	19	32	80	81	68
ENSG00000266918	RP11-798G7.8						1.45	1.27	0.71	0.00	0.00	0.00	94	94	86	6	6	14
ENSG00000232470	RP11-313D6.3						2.25	1.98		0.00	0.00		100	100		0	0	
ENSG00000261338	RP11-378A13.1						-0.78	-0.50	-0.66	0.00	0.00	0.00	9	25	24	91	75	76
ENSG00000261094	RP11-355O1.11						1.21	1.46	0.74	0.00	0.00	0.00	100	100	95	0	0	5
ENSG00000259715	CTD-3110H11.1						2.48	2.06		0.00	0.00		97	89		3	11	
ENSG00000271938	RP11-589C21.6						1.40	1.76	0.24	0.00	0.00	0.33	97	100	62	3	0	38
ENSG00000270172	RP5-1024G6.8						1.41	0.96	0.64	0.00	0.00	0.00	97	97	92	3	3	8
ENSG00000255989	NA						-0.75	-0.76	0.21	0.00	0.00	0.78	9	11	68	91	89	32

ENSG00000241860	RP11-34P13.13					1.28	1.23	1.46	0.00	0.00	0.00	97	94	95	3	6	5
ENSG00000270972	RP11-326C3.15					1.87	1.37		0.00	0.00		91	89		9	11	
ENSG00000270157	RP5-894A10.6					1.03	1.06	0.53	0.00	0.00	0.00	97	97	86	3	3	14
ENSG00000271843	RP11-245J9.5					1.52	1.41	-0.22	0.00	0.00	0.00	94	92	35	6	8	65
ENSG00000269444	CTB-180A7.6					2.21	2.54	1.34	0.00	0.00	0.00	100	97	95	0	3	5
ENSG00000251323	RP11-452H21.4	LOC101928865	uncharacterized LOC101928865	Other	other	1.34			0.00			100			0		
ENSG00000244459	RP11-1398P2.1					-1.65			0.00			6			94		
ENSG00000227486	RP13-188A5.1					-0.97	-1.30	0.29	0.00	0.00	0.27	17	8	68	83	92	32
ENSG00000273192	CITF22-1A6.3					1.44	1.38	0.93	0.00	0.00	0.00	97	100	84	3	0	16
ENSG00000267532	MIR497HG					1.25			0.00			100			0		
ENSG00000239002	SCARNA10	SCARNA10	small Cajal body-specific RNA 10	Other	other	1.89			0.00			89			11		
ENSG00000227518	MIR1302-2	mir-1302	microRNA 1302-5	Cytoplasm	microRNA	1.14	1.04	0.63	0.00	0.00	0.00	97	92	81	3	8	19
ENSG00000237940	AC093642.3	LINC01238	long intergenic non-protein coding RNA 1238	Other	other	1.31	0.80	0.60	0.00	0.00	0.00	100	89	89	0	11	11
ENSG00000271975	RP11-383J24.6					-0.54	-1.14	-0.05	0.00	0.00	0.00	9	0	43	91	100	57
ENSG00000264112	RP11-159D12.2	SRSF1	serine and arginine rich splicing factor 1	Nucleus	other	1.17	1.33	0.08	0.00	0.00	0.04	97	97	54	3	3	46
ENSG00000260539	GLG1					1.27	0.66		0.00	0.00		100	83		0	17	
ENSG00000229227	RP11-38L15.2					1.38	1.10	0.74	0.00	0.00	0.00	97	94	89	3	6	11
ENSG00000222375	RN7SKP127	RN7SKP127		Other	other	2.88	2.68		0.00	0.00		100	92		0	3	
ENSG00000261574	RP1-168P16.2					-1.20	-0.49	0.66	0.00	0.00	0.00	0	33	84	100	67	16
ENSG00000152487	ARL5B-AS1					1.94	1.62		0.00	0.00		97	97		3	3	
ENSG00000212464	SNORA12	SNORA12	small nucleolar RNA, H/ACA box 12	Other	other	4.84			0.00			91			6		
ENSG00000268802	NA					-0.57	-1.10	0.64	0.00	0.00	0.00	20	3	84	80	97	16
ENSG00000269086	CTC-523E23.5					1.24	1.20		0.00	0.00		100	100		0	0	
ENSG00000270066	SCARNA2	SCARNA2	small Cajal body-specific RNA 2	Other	other	1.54	1.15		0.00	0.00		97	86		3	14	
ENSG00000261685	RP11-401P9.4					1.14	-0.20	-1.20	0.00	0.00	0.00	94	47	3	6	53	97
ENSG00000238039	AF011889.2					2.54			0.00			94			6		
ENSG00000273033	RP11-67L2.2	LINC02035	long intergenic non-protein coding RNA 2035	Other	other	-0.57	-0.99	0.40	0.00	0.00	0.00	3	0	89	97	100	11
ENSG00000272894	RP5-1159O4.1					1.32		2.25	0.00		0.00	94		100	6		0
ENSG00000100181	TPTEP1	TPTEP1	transmembrane phosphatase with tensin homology pseu	Other	other	-0.61	0.12	-0.07	0.00	0.12	0.00	11	64	35	89	36	65
ENSG00000204261	PSMB8-AS1	PSMB8-AS1	PSMB8 antisense RNA 1 (head to head)	Other	other	-0.57	-0.52	-0.33	0.00	0.00	0.00	6	0	22	94	100	78
ENSG00000260591	RP11-817O13.6					3.68			0.00			91			6		
ENSG00000272462	U91328.19					-0.56	-0.29	-0.05	0.00	0.00	0.01	3	11	41	97	89	59
ENSG00000273015	LINC00938					-0.56	-0.47	-0.38	0.00	0.00	0.00	0	8	3	100	92	97
ENSG00000202198	RN7SK	RN7SK	RNA, 7SK small nuclear	Nucleus	other	0.93	0.70	0.95	0.00	0.00	0.00	83	75	86	17	25	14
ENSG00000249456	RP11-298I20.4					-0.63	-0.37	-0.13	0.00	0.00	0.00	11	28	35	89	72	65
ENSG00000227946	AC007383.3					-0.59	-0.04	0.33	0.00	0.02	0.14	6	44	81	94	56	19
ENSG00000261526	CTB-31O20.2					1.22	1.02	0.00	0.00	0.00	0.01	100	97	51	0	3	49
ENSG00000270659	RP11-105N14.1					-0.58	-0.61	-0.87	0.00	0.00	0.00	3	6	3	97	94	97
ENSG00000174365	SNHG11	SNHG11	small nucleolar RNA host gene 11	Other	other	1.09	0.47	0.11	0.00	0.12	0.40	100	89	59	0	11	41
ENSG00000230002	ALMS1-IT1	ALMS1-IT1	ALMS1 intronic transcript 1	Other	other	1.09	1.12	-0.02	0.00	0.00	0.08	100	97	49	0	3	51
ENSG00000228327	RP11-206L10.2					1.18	1.24	0.70	0.00	0.00	0.00	97	94	84	3	6	16
ENSG00000259652	RP11-797A18.3					3.32			0.00			94			6		
ENSG00000229512	AC068580.5					-2.37	"-INF"	0.78	0.00	0.00	0.01	6	8	78	91	89	22
ENSG00000237491	RP11-206L10.9					1.07	1.15	0.43	0.00	0.00	0.00	94	97	81	6	3	19
ENSG00000256576	RP13-977J11.2	LOC100996246	uncharacterized LOC100996246	Other	other	1.09	0.02	-1.47	0.00	0.00	0.00	100	53	0	0	47	100
ENSG00000260261	RP11-480A16.1					1.22			0.00			91			9		
ENSG00000269906	RP11-248J18.2					-1.06		0.93	0.00		0.00	9		97	91		3
ENSG00000245156	RP11-867G23.3	RAB1B	RAB1B, member RAS oncogene family	Cytoplasm	other	1.07	1.66	1.39	0.00	0.00	0.00	97	100	97	3	0	3
ENSG00000266236	NARF-IT1	NARF-IT1	NARF intronic transcript 1	Other	other	1.01	1.74	1.64	0.00	0.00	0.00	97	100	97	3	0	3
ENSG00000267096	CTD-2537I9.13					1.42	1.49	1.27	0.00	0.00	0.00	94	94	81	6	6	19
ENSG00000250889	LINC01336	LINC01336		Other	other	1.36	0.67		0.00	0.09		100	78		0	22	
ENSG00000270704	SNORD64					1.66	1.76	0.22	0.00	0.00	0.29	91	94	57	9	6	43
ENSG00000269942	NA					1.99	1.71		0.00	0.00		94	89		6	11	
ENSG00000267364	RP11-47L3.1					-1.09	0.24	-1.73	0.00	0.50	0.00	9	58	19	91	42	81
ENSG00000240143	RP4-753P9.3					-0.91	-0.84	1.06	0.00	0.00	0.00	20	22	89	80	78	11
ENSG00000271869	RP11-51J9.5					1.00	1.00	-0.31	0.00	0.00	0.00	100	100	14	0	0	86
ENSG00000265975	CTB-41I6.2					-1.07	-1.03	1.15	0.00	0.00	0.00	20	11	95	80	89	5
ENSG00000271725	RP11-76I14.4					-0.59	-0.67	0.10	0.00	0.00	0.89	11	19	59	89	81	41
ENSG00000259865	RP11-488L18.10					0.85	0.41	0.45	0.00	0.35	0.69	91	64	62	9	36	38
ENSG00000267481	CTC-559E9.5					0.97	0.58	-0.44	0.00	0.00	0.00	100	92	19	0	8	81
ENSG00000239884	RN7SL608P	RN7SL608P		Other	other	1.20	1.62	0.31	0.00	0.00	0.02	89	94	68	11	6	32
ENSG00000238164	RP3-395M20.8	LOC115110	uncharacterized LOC115110	Other	other	0.87	0.92	0.95	0.00	0.00	0.00	97	100	97	3	0	3
ENSG00000225978	HAR1A	HAR1A	highly accelerated region 1A (non-protein coding)	Other	other	0.91	0.43	-1.25	0.00	0.22	0.00	97	86	3	3	14	97
ENSG00000260336	RP11-395B7.7					0.85	0.52	0.42	0.00	0.00	0.07	97	81	62	3	19	38
ENSG00000225948	RP11-554I8.1					1.84			0.00			94			6		
ENSG00000270419	CAHM	CAHM	colon adenocarcinoma hypermethylated (non-protein co	Other	other	-0.60	-1.24	0.50	0.00	0.00	0.08	11	6	78	89	94	22
ENSG00000268205	CTC-444N24.11					0.86	0.56	0.07	0.00	0.00	0.23	94	81	57	6	19	43
ENSG00000222414	RNU2-59P	RNU2-59P		Other	other	-2.02	-0.66	0.41	0.00	0.00	0.03	20	28	76	80	72	24
ENSG00000232412	RP1-315G1.3	LOC101928402	uncharacterized LOC101928402	Other	other	-0.93	-0.74	0.03	0.00	0.00	0.36	23	22	54	77	78	46
ENSG00000246084	CTD-2506J14.1	LOC101929241	uncharacterized LOC101929241	Other	other	0.97	0.43	-1.69	0.00	0.53	0.00	97	75	5	3	25	95
ENSG00000271347	RP11-701H24.7					1.68	1.53		0.00	0.00		89	92		11	8	
ENSG00000269900	RMRP	RMRP	RNA component of mitochondrial RNA processing endori	Cytoplasm	other	0.60	0.85	-0.05	0.00	0.00	0.54	77	78	49	23	22	51
ENSG00000250950	RP11-33B1.3					1.16	1.47	0.73	0.00	0.00	0.00	91	89	81	9	11	19
ENSG00000267475	CTD-2538C1.2					-0.66	0.69	0.10	0.00	0.09	0.15	26	72	54	74	28	46
ENSG00000261101	RP4-545K15.5					1.56	1.19	0.98	0.00	0.00	0.00	94	81	78	6	19	22
ENSG00000215447	BX322557.10					0.94	0.10		0.00	0.42		100	67		0	33	
ENSG00000266389	CTB-41I6.1					-0.86	-2.05	1.21	0.00	0.00	0.00	20	8	95	80	92	5
ENSG00000228485	GRK5-IT1	GRK5-IT1	GRK5 intronic transcript 1	Other	other	-0.62	-0.71	-0.05	0.00	0.00	0.24	20	22	49	80	78	51
ENSG00000243339	RN7SL738P	RN7SL738P		Other	other	-0.57	-0.80	-0.01	0.00	0.00	0.08	11	19	49	89	81	51
ENSG00000271849	CTC-332L22.1					-0.66	-0.93	-1.40	0.00	0.00	0.00	20	17	3	80	83	97
ENSG00000196559	LINC00610					0.89	0.78	0.48	0.00	0.00	0.00	97	94	78	3	6	22
ENSG00000272140	RP11-574K11.29					1.11			0.00			91			9		
ENSG00000273290	NA					0.84	0.45	0.36	0.00	0.01	0.29	97	81	76	3	19	24
ENSG00000263990	CTC-542B22.2					1.47	1.49		0.00	0.00		94	92		6	8	
ENSG00000273056	RP11-77E14.2					1.58			0.00			97			3		
ENSG00000241217	RN7SL809P	RN7SL809P	RNA, 7SL, cytoplasmic 809, pseudogene	Other	other	1.47	1.78	0.59	0.00	0.00	0.01	89	94	73	11	6	27
ENSG00000251791	SCARNA6	SCARNA6	small Cajal body-specific RNA 6	Other	other	1.71	1.62	0.95	0.00	0.00	0.00	86	94	76	14	6	24
ENSG00000272994	RP11-332H14.2	LOC100506473	uncharacterized LOC100506473	Other	other	0.84	0.83	-0.01	0.00	0.00	0.04	97	100	46	3	0	54
ENSG00000242086	LINC00969	SDHAP2	succinate dehydrogenase complex flavoprotein subunit A	Other	other	0.98	0.99	0.82	0.00	0.00	0.00	100	100	97	0	0	3
ENSG00000261596	CTB-31N19.3					-0.56	-0.42	0.24	0.00	0.00	0.24	26	17	76	74	83	24
ENSG00000260534	RP11-1006G14.4					0.91	0.93	0.19	0.00	0.00	1.00	97	100	65	3	0	35
ENSG00000272645	RP11-504P24.8	GTF2IP20	general transcription factor Ii pseudogene 20	Other	other	0.86	1.08	0.71	0.00	0.00	0.00	97	100	97	3	0	3
ENSG00000272048	NA					1.18	0.84	-0.55	0.00	0.00	0.00	97	78	24	3	22	76
ENSG00000273190	RP11-255C15.4					-0.55	-0.30	-0.64	0.00	0.00	0.00	23	31	8	77	69	92
ENSG00000214837	LINC01347	001 (includes	long intergenic non-protein coding RNA 1347	Other	other	1.06	0.94	0.61	0.00	0.00	0.00	97	92	81	3	8	19
ENSG00000272574	RP11-359K18.4					1.57	2.25	1.21	0.00	0.00	0.00	89	97	92	11	3	5
ENSG00000255455	RP11-890B15.3	LOC103611081	uncharacterized LOC103611081	Other	other	0.77	0.11	0.15	0.00	0.41	0.18	100	61	62	0	39	38
ENSG00000257900	RP11-454K7.1					0.92	1.06	0.82	0.00	0.00	0.00	89	92	92	11	8	8
ENSG00000236255	AC009404.2					0.96	0.97	0.81	0.00	0.00	0.00	89	94	89	11	6	11
ENSG00000272432	RP3-465N24.6					-0.68	-0.67	0.00	0.00	0.00	0.32	23	31	51	77	69	49
ENSG00000270022	RNU12	RNU12	RNA, U12 small nuclear	Nucleus	other	0.93	0.86	0.97	0.00	0.00	0.00	89	94	84	11	6	16
ENSG00000269044	CTC-429P9.3					0.69	0.85	0.28	0.00	0.00	0.43	100	100	70	0	0	30
ENSG00000269913	NA					1.11	0.49		0.00	0.70		89	67		11	33	
ENSG00000260404	RP11-384K6.6	LOC729218	uncharacterized LOC729218	Other	other	0.81	0.93	0.22	0.00	0.00	0.26	97	97	73	3	3	27
ENSG00000269958	RP11-73M18.8					0.76	0.66	0.29	0.00	0.00	0.03	97	97	86	3	3	14
ENSG00000255933	RP11-495K9.5					0.92	1.11	0.58	0.00	0.00	0.00	89	97	78	11	3	22
ENSG00000228107	AP000692.9					0.90	0.87		0.00	0.00		100	89		0	11	
ENSG00000230590	FTX	FTX	FTX transcript, XIST regulator (non-protein coding)	Other	other	0.75	0.46	0.30	0.00	0.03	0.09	97	83	76	3	17	24
ENSG00000257151	PWAR6	PWAR6	Prader Willi/Angelman region RNA 6	Other	other	0.79			0.00			91			9		
ENSG00000249614	RP11-703G6.1					0.85	0.80	0.69	0.00	0.00	0.00	94	92	86	6	8	14
ENSG00000270195	RP11-572O17.1					1.02	0.89	0.72	0.00	0.00	0.00	94	94	84	6	6	16
ENSG00000273142	RP11-458F8.4					0.85	0.72	0.07	0.00	0.00	0.26	91	97	57	9	3	43
ENSG00000272365	RP11-389C8.3					1.22			0.00			97			3		
ENSG00000270015	RP11-540B6.6	FAN1	FANCD2 and FANCI associated nuclease 1	Nucleus	enzyme	0.79	0.45	0.18	0.00	0.02	0.72	97	97	84	3	3	16
ENSG00000262251	RP11-199F11.2					0.90	0.65	0.74	0.00	0.00	0.00	97	92	81	3	8	19
ENSG00000262879	RP11-156P1.3					0.85	0.36	0.13	0.00	0.68	0.94	94	78	59	6	22	41
ENSG00000265625	RP11-68I3.11					0.84	0.25		0.00	0.64		89	69		11	31	
ENSG00000272812	RP5-855D21.3					1.26	0.99	0.89	0.00	0.00	0.00	89	86	86	11	14	14
ENSG00000236337	FMR1-IT1	FMR1-IT1	FMR1 intronic transcript 1	Other	other	1.70	1.14		0.00	0.00		91	86		9	14	
ENSG00000258441	LINC00641	LINC00641	long intergenic non-protein coding RNA 641	Other	other	0.69	0.26	-0.41	0.00	0.46	0.00	100	72	14	0	28	86
ENSG00000231560	AC091814.3	LOC400002	uncharacterized LOC400002	Other	other	0.86	1.14		0.00	0.00		94	94		6	6	
ENSG00000223473	GS1-124K5.3					0.89	1.14	0.63	0.00	0.00	0.01	94	86	76	6	14	24
ENSG00000237943	PRKCQ-AS1	PRKCQ-AS1	PRKCQ antisense RNA 1	Other	other	0.79	0.54	-1.37	0.00	0.00	0.00	100	94	0	0	6	100
ENSG00000225975	AC074138.3	LINC01534	long intergenic non-protein coding RNA 1534	Other	other	0.84	1.03		0.00	0.00		94	97		6	3	
ENSG00000268568	AC007228.9					0.91	1.37	0.78	0.00	0.00	0.00	86	83	89	14	17	11
ENSG00000200087	SNORA73B	SNORA73B	small nucleolar RNA, H/ACA box 73B	Other	other	1.02	1.03	0.62	0.00	0.00	0.03	66	81	73	34	19	27
ENSG00000270108	RP11-73M18.6					0.88	0.70	0.34	0.00	0.00	0.59	86	81	65	14	19	35
ENSG00000242853	RN7SL749P	RN7SL749P		Other	other	-0.57	-0.66	0.14	0.00	0.00	0.59	26	22	54	74	78	46
ENSG00000225880	LINC00115	LINC00115	long intergenic non-protein coding RNA 115	Other	other	0.88	0.85	1.06	0.00	0.00	0.00	91	97	97	9	3	3
ENSG00000252464	RN7SKP70	RN7SKP70	RNA, 7SK small nuclear pseudogene 70	Other	other	1.39	1.31	0.79	0.00	0.00	0.08	86	81	65	14	19	35
ENSG00000207445	SNORD15B	SNORD15B	small nucleolar RNA, C/D box 15B	Other	other	2.18	1.05		0.00	0.00		89	75		11	22	
ENSG00000268087	CTC-429P9.2					0.97	1.00	0.39	0.00	0.00	0.56	97	92	68	3	8	32
ENSG00000264573	RN7SL15P	RN7SL15P		Other	other	1.27	2.13	1.09	0.00	0.00	0.00	83	94	84	17	6	16
ENSG00000224078	SNHG14	SNHG14		Other	other	0.86	0.72	-0.46	0.00	0.00	0.00	97	97	8	3	3	92
ENSG00000267798	NA					1.03	1.41	0.82	0.00	0.00	0.00	89	97	95	11	3	5
ENSG00000269688	AC008982.2					0.77	1.28	0.74	0.00	0.00	0.00	94	94	89	6	6	11
ENSG00000252010	SCARNA5	SCARNA5	small Cajal body-specific RNA 5	Other	other	0.98	1.14		0.00	0.00		74	81		26	19	
ENSG00000243015	RN7SL737P	RN7SL737P		Other	other	1.34			0.00			91			9		
ENSG00000265802	RN7SL49P	RN7SL49P		Other	other	1.74	1.02		0.00	0.02		91	78		9	22	
ENSG00000260257	RP5-1085F17.3					0.67	0.65	-0.02	0.00	0.00	0.02	91	89	43	9	11	57
ENSG00000252481	SCARNA13	SCARNA13	small Cajal body-specific RNA 13	Other	other	1.54			0.00			86			11		
ENSG00000272799	RP11-474N24.6					1.03	0.60		0.00	0.30		97	72		3	28	
ENSG00000264608	RP11-192H23.8					1.10	0.66	0.36	0.00	0.02	0.14	91	75	65	9	25	35
ENSG00000272947	RP11-71H17.9					0.84	0.12	-0.41	0.00	0.16	0.00	94	58	27	6	42	73
ENSG00000271862	RP11-343L5.2					0.83	0.75	0.02	0.00	0.00	0.17	97	81	51	3	19	49
ENSG00000262652	RP13-638C3.2					0.97	1.35	1.17	0.00	0.00	0.00	89	92	84	11	8	16
ENSG00000223768	LINC00205	LINC00205	long intergenic non-protein coding RNA 205	Other	other	0.91			0.00			89			11		
ENSG00000223525	RABGAP1L-IT1	RABGAP1L-IT1	RABGAP1L intronic transcript 1	Other	other	0.87	0.49	0.59	0.00	0.04	0.00	83	72	81	17	28	19
ENSG00000224975	INE1	INE1	inactivation escape 1 (non-protein coding)	Other	other	0.70	0.86	0.69	0.00	0.00	0.00	94	97	84	6	3	16
ENSG00000268027	AC006129.2					0.68	0.16	-0.80	0.00	0.48	0.00	100	69	3	0	31	97

ENSG00000259321	RP11-468E2.5					1.03	0.89		0.00	0.00		91	81		9	19	
ENSG00000232300	FAM215B	FAM215B	family with sequence similarity 215 member B (non-prot	Other	other	0.69	0.66	0.42	0.00	0.00	0.00	86	83	92	14	17	8
ENSG00000235314	LINC00957	LINC00957	long intergenic non-protein coding RNA 957	Other	other	0.70	-0.40	-0.92	0.00	0.00	0.00	100	22	3	0	78	97
ENSG00000262202	SNORD3D					-0.68	-0.85	0.60	0.00	0.00	0.00	31	17	81	69	83	19
ENSG00000263621	NA					0.78	0.80	0.21	0.00	0.00	0.31	86	89	76	14	11	24
ENSG00000269893	SNHG8	SNHG8	small nucleolar RNA host gene 8	Other	other	0.53	0.32	-0.12	0.00	0.37	0.00	100	86	41	0	14	59
ENSG00000245164	LINC00861	LINC00861	long intergenic non-protein coding RNA 861	Other	other	0.62	-0.21	-1.52	0.00	0.00	0.00	100	36	3	0	64	97
ENSG00000245954	RP11-18H21.1	LOC100996286	uncharacterized LOC100996286	Other	other	0.71	-0.26	-2.00	0.00	0.00	0.00	94	42	5	6	58	95
ENSG00000246898	LINC00920	LINC00920	long intergenic non-protein coding RNA 920	Other	other	0.63	-0.16	-1.81	0.00	0.00	0.00	91	39	0	9	61	100
ENSG00000188185	LINC00265	LINC00265	long intergenic non-protein coding RNA 265	Other	other	0.69	0.66	1.02	0.00	0.00	0.00	97	97	97	3	3	3
ENSG00000262074	SNORD3B-2	SNORD3B-2	small nucleolar RNA, C/D box 3B-2	Other	other	-0.72	-0.99	0.64	0.00	0.00	0.00	31	22	89	69	78	11
ENSG00000272382	CTD-2035E11.4					0.89			0.00			91			9		
ENSG00000259834	KCNA3					0.63	-0.23	-1.40	0.00	0.00	0.00	94	22	0	6	78	100
ENSG00000269963	NA					0.69	0.72	0.55	0.00	0.00	0.00	91	89	73	9	11	27
ENSG00000273156	RP11-127B20.2					0.80	-0.04		0.00	0.14		83	47		17	53	
ENSG00000259380	RP11-346D14.1					0.54	0.62	0.44	0.00	0.00	0.00	86	92	84	14	8	16
ENSG00000273284	RP11-888D10.4					0.74	1.06	0.62	0.00	0.00	0.00	83	94	78	17	6	22
ENSG00000202538	RNU4-2	RNU4-2	RNA, U4 small nuclear 2	Other	other	1.40	1.13	0.27	0.00	0.00	0.75	69	69	54	31	31	46
ENSG00000265206	MIR142	mir-142	microRNA 142	Cytoplasm	microRNA	0.68	1.05	1.47	0.00	0.00	0.00	83	86	89	17	14	11
ENSG00000263164	RP11-333E1.2					0.89	0.46		0.00	0.20		80	75		20	25	
ENSG00000261716	RP11-196G18.22					0.63	0.35	-0.03	0.00	0.05	0.00	97	83	49	3	17	51
ENSG00000273353	CTA-268H5.12					1.09			0.00			86			14		
ENSG00000226029	RP4-798A10.2	LINC01772		Other	other	0.66	-0.14	-0.73	0.00	0.00	0.00	97	39	3	3	61	97
ENSG00000262194	CTD-3195I5.5					0.62	1.12	0.99	0.00	0.00	0.00	89	89	89	11	11	11
ENSG00000254911	SCARNA9	SCARNA9	small Cajal body-specific RNA 9	Other	other	0.72	0.31	0.95	0.00	0.97	0.00	77	69	95	23	31	5
ENSG00000267904	CTC-429P9.5					0.54	0.70	0.26	0.00	0.00	0.26	94	81	68	6	19	32
ENSG00000268471	MIR4453					0.67			0.00			97			3		
ENSG00000267834	RP11-167N5.5					0.74	0.85	0.74	0.00	0.00	0.00	94	83	84	6	17	16
ENSG00000270083	RP1-257I20.14					0.59	1.18	0.60	0.00	0.00	0.00	86	97	78	14	3	22
ENSG00000232164	AC092669.3	LINC01873	long intergenic non-protein coding RNA 1873	Other	other	0.58	0.54	0.42	0.00	0.00	0.00	91	78	78	9	22	22
ENSG00000268544	NA					0.65	0.55	-1.23	0.00	0.00	0.00	94	92	0	6	8	100
ENSG00000231125	AF129075.5					0.80			0.00			80			20		
ENSG00000272065	U91328.20					0.69	0.34	0.07	0.00	0.97	0.23	83	69	51	17	31	49
ENSG00000225528	RP3-370M22.8					0.81	1.30		0.00	0.00		80	100		20	0	
ENSG00000267093	NA					0.69	1.54	1.04	0.00	0.00	0.00	89	94	92	11	6	8
ENSG00000233016	SNHG7	SNHG7	small nucleolar RNA host gene 7	Other	other	0.56	0.50	0.56	0.00	0.01	0.00	100	97	100	0	3	0
ENSG00000249731	RP11-259O2.3					0.57	0.55	0.55	0.00	0.00	0.00	86	89	89	14	11	11
ENSG00000264442	NA					1.19	1.21	1.48	0.00	0.00	0.00	89	83	92	11	17	8
ENSG00000269952	RP11-324I22.3					1.06	1.47	0.31	0.00	0.00	0.60	77	86	62	23	14	38
ENSG00000273437	RP11-434H6.7					1.04	0.74	-0.90	0.00	0.08	0.00	80	64	27	20	36	73
ENSG00000232686	NA					0.70	0.89	0.01	0.00	0.00	0.12	80	86	51	20	14	49
ENSG00000267074	RP11-1094M14.5					0.73	0.95		0.00	0.00		74	89		26	11	
ENSG00000270012	LL0XNC01-7P3.1	PPP1R3F	protein phosphatase 1 regulatory subunit 3F	Other	other	0.55	0.15	-0.10	0.00	0.31	0.00	97	67	35	3	33	65
ENSG00000166770	ZNF667-AS1	ZNF667-AS1	ZNF667 antisense RNA 1 (head to head)	Other	other	0.64	1.40	0.48	0.00	0.00	0.00	100	97	84	0	3	16
ENSG00000226328	NUP50-AS1	NUP50-AS1	NUP50 antisense RNA 1 (head to head)	Other	other	0.52	0.46	0.33	0.00	0.08	0.26	94	83	73	6	17	27
ENSG00000234663	AC104820.2	LINC01934	long intergenic non-protein coding RNA 1934	Other	other	0.56			0.00			97			3		
ENSG00000233411	RP11-104L21.2					1.09			0.00			80			20		
ENSG00000272777	RP11-571L19.8					0.62	0.10	-0.36	0.00	0.97	0.00	86	58	22	14	42	78
ENSG00000239569	KMT2E-AS1	KMT2E-AS1	KMT2E antisense RNA 1 (head to head)	Other	other	0.54	0.47	0.93	0.00	0.48	0.00	86	78	97	14	22	3
ENSG00000263607	NA					0.78	1.31		0.01	0.00		86	86		14	14	
ENSG00000244625	CTA-211A9.5	MIATNB	MIAT neighbor (non-protein coding)	Other	other	0.54	-0.06	-0.36	0.01	0.01	0.00	97	44	11	3	56	89
ENSG00000257410	RP11-2H8.2					0.59	0.06	-0.52	0.01	0.79	0.00	89	56	16	11	44	84
ENSG00000260808	CTD-2007L18.5					0.62	1.05		0.01	0.00		89	86		11	14	
ENSG00000271927	CTD-2541M15.4					0.53			0.01			89			11		
ENSG00000269867	CTD-2583A14.8					0.74	0.74		0.01	0.01		89	81		11	19	
ENSG00000213971	RP11-15H20.6					0.57	0.71	0.52	0.01	0.00	0.00	91	97	89	9	3	11
ENSG00000237989	AP001046.5	LINC01679	long intergenic non-protein coding RNA 1679	Other	other	0.53	0.07	-0.34	0.01	0.41	0.00	80	58	19	20	42	81
ENSG00000208772	SNORD94	SNORD94	small nucleolar RNA, C/D box 94	Other	other	0.86			0.01			66			26		
ENSG00000272093	CTC-365E16.1					0.55	0.19		0.01	0.44		89	72		11	28	
ENSG00000269940	RP11-73M18.7					0.63	0.74	0.48	0.02	0.00	0.07	77	83	78	23	17	22
ENSG00000256582	RP11-75L1.1					0.59	0.50	-0.43	0.02	0.02	0.00	94	92	19	6	8	81
ENSG00000214293	APTR	APTR	Alu-mediated CDKN1A/p21 transcriptional regulator (nor	Other	other	0.59	0.51	0.36	0.02	0.02	0.20	91	97	81	9	3	19
ENSG00000212443	SNORA53	SNORA53	small nucleolar RNA, H/ACA box 53	Other	other	0.98	1.09	0.83	0.03	0.00	0.15	71	67	62	29	33	38
ENSG00000178440	LINC00843	LINC00843	long intergenic non-protein coding RNA 843	Other	other	0.54	0.73	0.59	0.03	0.01	0.07	83	78	76	17	22	24
ENSG00000227403	AC009299.3	LINC01806	long intergenic non-protein coding RNA 1806	Other	other	0.53	0.22	-0.70	0.04	0.48	0.00	94	58	11	6	42	89
ENSG00000272054	RP11-423P10.2	CEBPZ	CCAAT/enhancer binding protein zeta	Nucleus	iption regulator	0.51	0.85		0.04	0.00		80	86		20	14	
ENSG00000257499	NA					0.63	0.84		0.04	0.00		86	94		14	6	
ENSG00000230732	AC127904.2					0.61	0.49	0.35	0.04	0.00	0.02	69	72	68	31	28	32
ENSG00000269246	CTC-246B18.10					0.72	0.16	0.10	0.05	0.60	0.18	71	53	57	29	44	43
ENSG00000272933	RP11-47A8.5					-0.27	-1.06	0.08	0.00	0.00	0.26	31	3	54	69	97	46
ENSG00000271856	LINC01215	LINC01215	long intergenic non-protein coding RNA 1215	Other	other	-0.25	-0.87	0.09	0.00	0.00	0.24	23	0	62	77	100	38
ENSG00000270069	MIR222HG	MIR222HG		Other	other		-1.47	2.27		0.00	0.00		0	97		100	3
ENSG00000229645	NA					0.15	-0.80	0.27	0.08	0.00	0.36	60	0	76	40	100	24
ENSG00000265150	NA					0.13	-0.59	0.28	0.07	0.00	0.64	54	25	59	46	75	41
ENSG00000266088	RP5-1028K7.2					-0.40	-1.25	-0.77	0.00	0.00	0.00	17	3	8	83	97	92
ENSG00000238121	LINC00426	LINC00426	long intergenic non-protein coding RNA 426	Other	other	-0.42	-0.86	-0.29	0.00	0.00	0.00	20	3	30	80	97	70
ENSG00000260979	RP11-77H9.8					-0.44	-0.90	0.13	0.00	0.00	0.97	20	6	62	80	94	38
ENSG00000272005	RP11-91J19.4					0.07	-0.76	-1.22	0.01	0.00	0.00	60	11	3	40	89	97
ENSG00000268573	RP11-158H5.7	ZSCAN30	zinc finger and SCAN domain containing 30	Other	other	-0.46	-0.70	-1.12	0.00	0.00	0.00	14	6	3	86	94	97
ENSG00000267440	CTC-501O10.1						2.01			0.00			100			0	
ENSG00000272091	RP4-758J24.5					-0.23	-0.77	-1.13	0.00	0.00	0.00	14	6	0	86	94	100
ENSG00000261662	RP5-1042I8.7					-0.36	-0.81	0.01	0.00	0.00	0.20	26	3	51	74	97	49
ENSG00000268355	AC006129.1					0.26	-0.72	0.27	0.02	0.00	0.88	57	22	54	43	78	46
ENSG00000233721	RP11-205K6.1	LOC105376276		Other	other		2.06			0.00			100			0	
ENSG00000272449	RP3-395M20.12					0.04	-0.57	0.25	0.00	0.00	0.41	54	19	68	46	81	32
ENSG00000268947	AD000684.2						1.82			0.00			97			3	
ENSG00000235728	AC007349.5						2.14			0.00			94			6	
ENSG00000247134	RP11-11N9.4					-0.47	-0.79	-0.44	0.00	0.00	0.00	40	11	32	60	89	68
ENSG00000272384	RP11-44N11.2						1.53			0.00			94			6	
ENSG00000245060	LINC00847	LINC00847	long intergenic non-protein coding RNA 847	Other	other	-0.35	-0.51	0.12	0.00	0.00	0.45	11	6	59	89	94	41
ENSG00000272871	RP11-408A13.4					-0.30	-0.76	0.36	0.00	0.00	0.27	20	14	68	80	86	32
ENSG00000232233	RP11-573D15.2	LINC02043	long intergenic non-protein coding RNA 2043	Other	other		1.23			0.00			97			3	
ENSG00000229807	XIST	XIST	X inactive specific transcript (non-protein coding)	Nucleus	other	0.48	0.52	0.00	0.00	0.00	0.00	54	75	49	17	3	16
ENSG00000249667	LINC01259	LINC01259	long intergenic non-protein coding RNA 1259	Other	other	0.25	-0.97	-2.00	0.60	0.00	0.00	71	11	5	29	89	95
ENSG00000267519	CTD-3252C9.4					-0.31	0.70	2.60	0.00	0.00	0.00	34	89	100	66	11	0
ENSG00000273344	PAXIP1-AS1	PAXIP1-AS1	PAXIP1 antisense RNA 1 (head to head)	Other	other	0.02	-0.50	-0.29	0.00	0.00	0.00	54	17	14	46	83	86
ENSG00000262663	RP11-497H17.1						2.01			0.00			78			22	
ENSG00000260260	SNHG19	SNHG19	small nucleolar RNA host gene 19	Other	other	0.38	0.73	-0.36	0.97	0.00	0.00	77	100	14	23	0	86
ENSG00000267002	RP11-242D8.1					0.28	0.95	0.23	0.74	0.00	0.62	71	97	68	29	3	32
ENSG00000260368	RP11-521I2.3						1.32			0.00			78			22	
ENSG00000272583	RP11-344P13.6					-0.50	-0.97	-1.01	0.00	0.00	0.00	29	22	14	71	78	86
ENSG00000271359	RP11-84C13.1					-0.50	-0.61	-0.06	0.00	0.00	0.08	17	19	49	83	81	51
ENSG00000267143	RP11-677O4.6					0.39	0.95	0.43	0.03	0.00	0.01	74	86	78	26	14	22
ENSG00000232545	KB-318B8.7						1.45			0.00			83			17	
ENSG00000264352	RN7SL602P	RN7SL602P	RNA, 7SL, cytoplasmic 602, pseudogene	Other	other	0.63	1.27	0.67	0.17	0.00	0.01	74	86	78	26	14	22
ENSG00000203620	RP11-84A19.2						0.71			0.00			92			8	
ENSG00000238035	AC138035.2						0.77			0.00			92			8	
ENSG00000245532	NEAT1					0.37	0.71	1.93	0.01	0.00	0.00	69	81	97	31	19	3
ENSG00000272556	RP11-638I8.1	GTF2IP13	general transcription factor IIi pseudogene 13	Other	other		1.16			0.00			83			17	
ENSG00000251194	RP1-68D18.2					0.22	0.86	0.79	0.83	0.00	0.00	60	89	81	40	11	19
ENSG00000263874	LINC00672	LINC00672	long intergenic non-protein coding RNA 672	Other	other	0.56	0.76	-0.09	0.06	0.00	0.00	83	92	43	17	8	57
ENSG00000258199	RP11-977G19.5					0.69	0.88	0.42	0.05	0.00	0.03	86	89	70	14	11	30
ENSG00000269399	CTD-3222D19.12					0.47	0.73		0.03	0.00		91	94		9	6	
ENSG00000244357	RN7SL145P	RN7SL145P		Other	other		1.42			0.00			81			17	
ENSG00000264756	NA						1.32			0.00			86			14	
ENSG00000262380	CTB-193M12.3					0.73	1.12	0.63	0.08	0.00	0.01	77	81	76	23	19	24
ENSG00000206612	SNORA2A	SNORA2A	small nucleolar RNA, H/ACA box 2A	Other	other		1.79			0.00			81			17	
ENSG00000231865	SIK3-IT1						0.59			0.00			83			17	
ENSG00000270640	RP11-373D23.2					-0.14	0.91	1.48	0.04	0.00	0.00	43	78	95	57	22	5
ENSG00000226067	LINC00869	LINC00623	long intergenic non-protein coding RNA 623	Other	other	-0.34	-0.51	-1.10	0.00	0.00	0.00	31	28	16	69	72	84
ENSG00000226091	LINC00937	LINC00937	long intergenic non-protein coding RNA 937	Other	other	0.05	0.80	1.03	0.04	0.00	0.00	54	78	97	46	22	3
ENSG00000269925	RP3-467L1.6					0.47	0.83	0.66	0.05	0.00	0.00	77	78	78	23	22	22
ENSG00000262758	CTD-3195I5.1					0.39	0.62	0.21	0.37	0.00	0.54	86	89	70	14	11	30
ENSG00000232956	SNHG15	SNHG15	small nucleolar RNA host gene 15	Other	other	0.18	0.61	0.68	0.09	0.00	0.00	77	100	100	23	0	0
ENSG00000212607	SNORA45B	SNORA38B	small nucleolar RNA, H/ACA box 38B	Other	other		1.36			0.00			75			19	
ENSG00000231611	AP006216.11					0.39	0.65	0.38	0.29	0.00	0.12	91	97	78	9	3	22
ENSG00000245694	CRNDE	LOC101927480	uncharacterized LOC101927480	Other	other		0.83	0.81		0.00	0.00		86	84		14	16
ENSG00000239868	RN7SL34P	RN7SL34P		Other	other		0.92	0.69		0.00	0.01		81	76		19	24
ENSG00000232098	CTD-2619J13.14					0.46	0.61	0.19	0.04	0.00	0.72	80	86	59	20	14	41
ENSG00000260023	NA					0.27	0.62	-0.12	0.97	0.00	0.02	66	89	46	34	11	54
ENSG00000256092	MIR8072					0.51	0.68	0.38	0.11	0.00	0.02	86	86	81	14	14	19
ENSG00000254676	RP11-727A23.4					0.24	0.55	-0.03	0.98	0.01	0.13	57	83	49	43	17	51
ENSG00000261061	RP11-303E16.2						0.79	0.62		0.01	0.01		83	81		17	19
ENSG00000264469	RP11-173M1.8					0.22	0.70	0.72	0.10	0.01	0.00	63	83	95	37	17	5
ENSG00000259623	RP11-156E6.1	KLHL11	kelch like family member 11	Other	other	0.42	0.56	-0.22	0.52	0.01	0.00	83	92	22	17	8	78
ENSG00000243745	NA						0.78	0.97		0.01	0.00		81	73		19	27
ENSG00000248360	LINC00504	LINC00504		Other	other	0.43	0.51	0.62	0.04	0.01	0.00	91	86	86	9	14	14
ENSG00000261468	RP11-1024P17.1					0.44	0.58	-0.81	0.03	0.01	0.00	94	92	0	6	8	100
ENSG00000223692	DIP2A-IT1	DIP2A-IT1	DIP2A intronic transcript 1	Other	other	0.19	0.70	-0.35	0.31	0.01	0.01	60	78	43	40	22	57
ENSG00000245556	SCAMP1-AS1	SCAMP1-AS1	SCAMP1 antisense RNA 1	Other	other	0.26	0.51	-0.37	0.73	0.02	0.00	83	97	8	17	3	92
ENSG00000248323	LUCAT1	LUCAT1	lung cancer associated transcript 1 (non-protein coding)	Other	other			2.43			0.00			100			0
ENSG00000241657	TRBV11-2	TRBV11-2	T cell receptor beta variable 11-2	Other	other	0.20	-0.03	-2.20	0.29	0.01	0.00	71	44	0	29	56	100
ENSG00000247774	PCED1B-AS1	PCED1B-AS1	PCED1B antisense RNA 1	Other	other	0.31	0.27	-1.48	0.58	0.81	0.00	89	78	0	11	22	100
ENSG00000271109	CTC-523E23.11	LOC102723540	uncharacterized LOC102723540	Other	other	0.51	0.43	-1.38	0.06	0.06	0.00	94	94	0	6	6	100
ENSG00000260822	GS1-358P8.4					0.07	-0.38	-1.28	0.01	0.00	0.00	57	22	0	43	78	100
ENSG00000175061	LRRC75A-AS1	LRRC75A-AS1	LRRC75A antisense RNA 1	Other	other	-0.09	-0.16	-0.56	0.00	0.00	0.00	34	31	0	66	69	100
ENSG00000273443	RP11-54O7.18							2.38			0.00			100			0
ENSG00000261888	AC144831.1							2.04			0.00			97			3
ENSG00000260966	RP11-690D19.3					0.21	-0.23	-1.12	0.16	0.00	0.00	74	28	0	26	72	100
ENSG00000235999	NA					-0.33	-0.49	-1.19	0.00	0.00	0.00	20	17	0	80	83	100

ENSG00000241014	RP11-244H3.1	LOC653160	uncharacterized LOC653160	Other	other	0.46	0.18	-1.19	0.12	0.79	0.00	86	75	0	14	25	100
ENSG00000226380	MIR29B1							1.33			0.00			100			0
ENSG00000273148	RP5-1068E13.7					0.02	-0.22	-1.01	0.00	0.00	0.00	51	22	0	49	78	100
ENSG00000182165	TP53TG1	TP53TG1	TP53 target 1 (non-protein coding)	Other	other	-0.22	-0.36	-0.90	0.00	0.00	0.00	31	22	0	69	78	100
ENSG00000234389	AC007278.3							2.27			0.00			95			5
ENSG00000231133	HAR1B	HAR1B	highly accelerated region 1B (non-protein coding)	Other	other	0.38	0.38	-1.89	0.30	0.25	0.00	80	78	3	20	22	97
ENSG00000247556	OIP5-AS1	OIP5-AS1	OIP5 antisense RNA 1	Other	other	0.21	-0.38	-0.77	0.03	0.00	0.00	71	14	0	29	86	100
ENSG00000260940	RP4-575N6.5					0.13	-0.31	-1.17	0.01	0.00	0.00	54	36	3	46	64	97
ENSG00000245937	LINC01184	LINC01184	long intergenic non-protein coding RNA 1184	Other	other	-0.13	-0.45	-0.91	0.00	0.00	0.00	31	8	3	69	92	97
ENSG00000235437	LINC01278	LINC01278	long intergenic non-protein coding RNA 1278	Other	other	0.14	0.00	-0.83	0.08	0.01	0.00	77	50	3	23	50	97
ENSG00000261512	RP11-46D6.1					0.38	0.23	-0.91	0.13	0.65	0.00	91	64	3	9	36	97
ENSG00000251230	RP11-701P16.5	MIR3945HG	MIR3945 host gene	Other	other			1.93			0.00			100			0
ENSG00000232324	AC008440.10							2.80			0.00			97			3
ENSG00000258929	RP11-58E21.3							1.46			0.00			100			0
ENSG00000270346	HTATSF1P2							1.40			0.00			95			5
ENSG00000259976	RP11-553L6.5	mir-568	microRNA 568	Cytoplasm	microRNA	0.47	0.04	-0.92	0.05	0.10	0.00	80	58	3	20	42	97
ENSG00000264290	RP11-68I3.4							1.81			0.00			95			5
ENSG00000261222	CTD-2006K23.1	LOC101928343	uncharacterized LOC101928343	Other	other			1.18			0.00			97			3
ENSG00000267350	RP1-178F10.3					-0.04	-0.44	-0.68	0.00	0.00	0.00	43	11	3	57	89	97
ENSG00000268713	CTC-444N24.8					-0.41	-0.16	-0.70	0.00	0.00	0.00	17	33	3	83	67	97
ENSG00000263941	RN7SL32P	RN7SL32P	RNA, 7SL, cytoplasmic 32, pseudogene	Other	other	0.12	0.50	1.40	0.03	0.05	0.00	51	72	97	49	28	3
ENSG00000260805	RP11-61J19.5							1.31			0.00			97			3
ENSG00000257742	RP11-350F4.2					0.35	-0.12	-0.72	0.72	0.00	0.00	91	33	0	9	67	100
ENSG00000273008	RP11-351D16.3							1.30			0.00			95			5
ENSG00000270018	RP3-462E2.5					0.25	0.05	-1.01	1.00	0.21	0.00	74	56	8	26	44	92
ENSG00000255135	RP11-111M22.3					-0.30	0.08	-1.08	0.00	0.22	0.00	29	61	3	71	39	97
ENSG00000261026	CTD-3247F14.2	LOC286058	uncharacterized LOC286058	Other	other			1.22			0.00			97			3
ENSG00000175701	LINC00116	LINC00116	long intergenic non-protein coding RNA 116	Other	other	-0.01	-0.21	-0.83	0.00	0.00	0.00	46	19	0	54	81	100
ENSG00000262477	AC021224.1					0.19	-0.28	-0.72	0.23	0.00	0.00	63	42	22	37	58	78
ENSG00000258733	CTD-2341M24.1					-0.25	-0.04	-0.93	0.00	0.00	0.00	34	42	5	66	58	95
ENSG00000272899	RP11-309L24.9	LOC100130705	uncharacterized LOC100130705	Other	other			1.36			0.00			100			0
ENSG00000270101	NA					0.09	-0.11	-0.53	0.03	0.00	0.00	60	44	8	40	56	92
ENSG00000271948	RP11-242F4.2					0.16	-0.13	-0.92	0.52	0.00	0.00	71	44	11	29	56	89
ENSG00000260563	RP13-516M14.1					0.06	-0.26	-0.66	0.00	0.00	0.00	51	25	11	49	75	89
ENSG00000248476	BACH1-IT1							1.56			0.00			95			5
ENSG00000271020	RP11-10C24.1							2.29			0.00			84			16
ENSG00000269220	LINC00528	LINC00528	long intergenic non-protein coding RNA 528	Other	other	-0.17	0.28	0.86	0.00	0.75	0.00	37	94	100	63	6	0
ENSG00000273356	RP11-804H8.6					-0.39	-0.50	1.03	0.00	0.00	0.00	34	17	100	66	83	0
ENSG00000272931	RP5-943J3.2					-0.40	-0.41	-0.95	0.00	0.00	0.00	17	14	5	83	86	95
ENSG00000244567	AC096772.6					-0.33	-0.19	-0.71	0.00	0.00	0.00	20	36	0	80	64	100
ENSG00000204272	LINC01420	NBDY	negative regulator of P-body association	Other	other	-0.31	-0.21	-0.55	0.00	0.00	0.00	29	36	3	71	64	97
ENSG00000264885	RP11-815I9.4					-0.07	-0.07	-0.65	0.00	0.00	0.00	43	44	0	57	56	100
ENSG00000215417	MIR17HG							1.09			0.00			89			11
ENSG00000226950	DANCR	DANCR	differentiation antagonizing non-protein coding RNA	Other	other	-0.04	-0.15	-0.61	0.00	0.00	0.00	43	39	0	57	61	100
ENSG00000273265	RP11-353K11.1					0.04	-0.43	-1.29	0.02	0.00	0.00	57	33	11	43	67	89
ENSG00000263753	LINC00667	LINC00667	long intergenic non-protein coding RNA 667	Other	other	0.17	-0.44	-0.56	0.08	0.00	0.00	71	3	0	29	97	100
ENSG00000224914	LINC00863	LINC00863	long intergenic non-protein coding RNA 863	Other	other	0.27	-0.24	-0.56	0.23	0.00	0.00	74	28	3	26	72	97
ENSG00000261799	RP11-283I3.6	LOC283357	uncharacterized LOC283357	Other	other	0.25	0.11	-0.62	0.89	0.22	0.00	74	56	5	26	44	95
ENSG00000260317	RP11-488I3.4					-0.08	-0.03	-0.66	0.01	0.00	0.00	46	50	8	54	50	92
ENSG00000255328	RP11-326C3.12					0.62	0.17	-0.76	0.06	0.44	0.00	80	58	8	20	42	92
ENSG00000253948	RP11-410L14.2	LOC105375666		Other	other	0.11	-0.20	-1.06	0.05	0.00	0.00	54	42	11	46	58	89
ENSG00000170846	AC093323.3	LOC93622	Morf4 family associated protein 1 like 1 pseudogene	Other	other	0.09	-0.40	-0.55	0.03	0.00	0.00	66	11	5	34	89	95
ENSG00000273216	AC002059.10							1.57			0.00			92			8
ENSG00000231507	LINC01353	LINC01353	long intergenic non-protein coding RNA 1353	Other	other			1.10			0.00			100			0
ENSG00000237310	GS1-124K5.4	GS1-124K5.4	uncharacterized LOC100289098	Other	other	0.18	0.01	-0.95	0.20	0.05	0.00	60	53	11	40	47	89
ENSG00000259863	SH3RF3-AS1	SH3RF3-AS1	SH3RF3 antisense RNA 1	Other	other	0.06	-0.31	-0.66	0.00	0.00	0.00	60	28	11	40	72	89
ENSG00000263004	RP11-166P13.3					-0.02	-0.06	-0.88	0.11	0.03	0.00	46	42	3	54	58	97
ENSG00000267521	RP11-87G24.6							1.40			0.00			97			3
ENSG00000230555	RP11-517P14.2					-0.16	-0.13	-0.76	0.00	0.00	0.00	40	33	5	60	67	95
ENSG00000229152	ANKRD10-IT1	ANKRD10-IT1	ANKRD10 intronic transcript 1	Other	other	0.44	0.48	1.13	0.11	0.11	0.00	74	75	86	26	25	14
ENSG00000264456	RP11-848P1.2							0.98			0.00			95			5
ENSG00000237772	AC092620.3					-0.31		1.02	0.00		0.00	34		95	66		5
ENSG00000260997	RP4-647J21.1	LOC285957	uncharacterized LOC285957	Other	other	-0.46	-0.06	0.83	0.00	0.00	0.00	17	44	100	83	56	0
ENSG00000273456	RP11-686O6.2					-0.04	-0.03	-0.83	0.00	0.05	0.00	49	50	16	51	50	84
ENSG00000272452	RP11-391M1.4					0.38	-0.04	-0.57	0.57	0.00	0.00	80	47	14	20	53	86
ENSG00000273245	RP11-434P11.2					0.48	0.31	-0.98	0.20	0.97	0.00	77	72	14	23	28	86
ENSG00000272565	RP11-485G4.2					-0.12	0.22	0.67	0.00	0.70	0.00	46	64	100	54	36	0
ENSG00000224959	AC017002.2							1.22			0.00			84			16
ENSG00000273038	RP11-479G22.8					0.32	0.09	0.58	0.13	0.06	0.00	83	56	92	17	44	8
ENSG00000207501	RNVU1-14	RNVU1-14	RNA, variant U1 small nuclear 14	Other	other	-0.33	-0.46	0.99	0.16	0.00	0.00	49	39	97	51	61	3
ENSG00000257613	RP11-320P7.1	LINC01481	long intergenic non-protein coding RNA 1481	Other	other	0.27	-0.26	-0.70	0.79	0.00	0.00	83	33	22	17	67	78
ENSG00000224376	AC017104.6	ARMC9	armadillo repeat containing 9	Cytoplasm	other			0.73			0.00			97			3
ENSG00000241732	RP11-38P22.2							0.74			0.00			76			24
ENSG00000198106	SNX29P2					-0.13	0.14	0.59	0.00	0.03	0.00	43	56	97	57	44	3
ENSG00000269951	RP11-797A18.6					-0.08	0.07	0.61	0.00	0.01	0.00	43	58	100	57	42	0
ENSG00000226644	RP11-128M1.1							1.60			0.00			86			14
ENSG00000273272	CTA-384D8.34							1.61			0.00			97			3
ENSG00000273160	RP11-104L21.3					0.39	0.03	-1.11	0.41	0.42	0.00	71	50	14	29	47	86
ENSG00000271855	RP11-214N9.1						0.39	0.94		0.99	0.00		64	92		36	8
ENSG00000199568	RNU5A-1	RNU5A-1	RNA, U5A small nuclear 1	Other	other			2.61			0.00			78			11
ENSG00000223336	RNU2-6P	RNU2-6P	RNA, U2 small nuclear 6, pseudogene	Other	other	-0.19	-0.16	1.16	0.08	0.01	0.00	46	42	86	54	58	14
ENSG00000251580	RP11-539L10.3	LOC105374366		Other	other	0.36	0.30	-1.08	0.73	0.86	0.00	66	67	19	34	33	81
ENSG00000273175	RP11-11N7.4					-0.34	-0.45	-0.69	0.00	0.00	0.00	26	14	22	74	86	78
ENSG00000272716	RP11-563N4.1					0.01	0.24	-0.77	0.01	0.84	0.00	54	67	11	46	33	89
ENSG00000269553	U62631.5							1.02			0.00			84			16
ENSG00000273117	AC144652.1					-0.08	0.15	0.69	0.00	0.24	0.00	43	67	89	57	33	11
ENSG00000207205	RNVU1-15	RNVU1-15	RNA, variant U1 small nuclear 15	Other	other			2.27			0.00			73			24
ENSG00000237892	KLF7-IT1	KLF7-IT1	KLF7 intronic transcript 1	Other	other	0.18	0.35	0.72	0.13	0.70	0.00	69	72	84	31	28	16
ENSG00000272666	CTA-384D8.35	LOC105373098	uncharacterized LOC105373098	Other	other			0.82			0.00			84			16
ENSG00000236901	MIR600HG							0.65			0.00			84			16
ENSG00000229989	MIR181A1HG	MIR181A1HG	MIR181A1 host gene	Other	other			0.64			0.00			95			5
ENSG00000223401	RP11-211G3.2							1.26			0.00			78			22
ENSG00000229801	NA							1.37			0.00			70			30
ENSG00000235908	RHOA-IT1	RHOA-IT1		Other	other			0.83			0.00			81			19
ENSG00000269930	RP11-932O9.9					0.27	0.00	0.73	0.18	0.01	0.00	69	50	84	31	50	16
ENSG00000269919	RP1-134E15.3							0.96			0.00			76			24
ENSG00000230138	RP11-117D22.2							0.70			0.00			81			19
ENSG00000178977	LINC00324	LINC00324	long intergenic non-protein coding RNA 324	Other	other	-0.35	-0.45	0.58	0.00	0.00	0.00	29	28	81	71	72	19
ENSG00000197813	CTC-301O7.4					-0.02	-0.37	0.65	0.02	0.00	0.00	43	25	84	57	75	16
ENSG00000212456	NA					0.51		1.01	0.43		0.00	60		76	40		24
ENSG00000235621	LINC00494	LINC00494	long intergenic non-protein coding RNA 494	Other	other			0.61			0.00			78			22
ENSG00000263050	RP11-667K14.3							0.78			0.00			70			30
ENSG00000240160	RN7SL263P	RN7SL263P		Other	other			0.85			0.02			70			30
ENSG00000271914	RP4-789D17.5					0.16	0.14	0.56	0.29	0.51	0.04	60	58	73	40	42	27

Supplementary Table 3C: Overlap of genes DE in CD4+ and CD8+ fractions as compared to unfractionated PBMC samples.

Genes up-regulated in CD4+ and down-regulated in CD8+

	CD4+ vs PBMC Results									CD8+ vs PBMC Results								
EnsemblGeneIds	**GeneNames**	**logFC**	**logCPM**	**LR**	**Pvalue**	**FDR**	**MedianLogF(**	**PercentDowr**	**PercentUp**	**GeneNames**	**logFC**	**logCPM**	**LR**	**Pvalue**	**FDR**	**MedianLogF(**	**PercentDowı**	**PercentUp**
ENSG00000186815	TPCN1	0.57010976	4.62939163	74.3038222	6.70E-18	1.44E-17	0.63636169	2.85714286	97.1428571	TPCN1	-0.4822395	4.01170591	38.6181773	5.15E-10	1.02E-09	-0.5664693	88.8888889	11.1111111
ENSG00000100055	CYTH4	0.40385086	6.82564425	43.4555976	4.34E-11	7.68E-11	0.50967264	14.2857143	85.7142857	CYTH4	-0.573059	6.36477092	70.5017825	4.60E-17	1.16E-16	-0.571028	88.8888889	11.1111111

Genes down-regulated in CD4+ and up-regulated in CD8+

	CD4+ vs PBMC Results									CD8+ vs PBMC Results								
EnsemblGeneIds	**GeneNames**	**logFC**	**logCPM**	**LR**	**Pvalue**	**FDR**	**MedianLogF(**	**PercentDowr**	**PercentUp**	**GeneNames**	**logFC**	**logCPM**	**LR**	**Pvalue**	**FDR**	**MedianLogF(**	**PercentDowı**	**PercentUp**
ENSG00000073861	TBX21	-2.5831174	3.64262614	1038.40435	8.07E-228	1.16E-226	-2.5910849	100	0	TBX21	0.84101475	4.84947155	136.357887	1.67E-31	6.09E-31	0.81396416	5.55555556	94.4444444
ENSG00000007264	MATK	-2.2797468	4.40821692	1010.42844	9.72E-222	1.36E-220	-2.2020995	100	0	MATK	0.67034716	5.37041189	93.8698258	3.37E-22	9.83E-22	0.55910148	8.33333333	91.6666667
ENSG00000101082	SLA2	-1.7391343	4.33823297	610.133926	1.05E-134	9.37E-134	-1.6008776	100	0	SLA2	0.72442627	5.32868166	108.449767	2.14E-25	6.82E-25	0.66066898	11.1111111	88.8888889
ENSG00000100302	RASD2	-1.3415626	3.55928138	295.87142	2.61E-66	1.27E-65	-1.3294818	100	0	RASD2	1.24865364	4.69863195	289.111355	7.77E-65	4.92E-64	1.08310416	0	100
ENSG00000111537	IFNG	-1.9045296	1.61416643	292.557632	1.38E-65	6.62E-65	-1.9909315	94.2857143	5.71428571	IFNG	0.5061156	2.63627694	24.6825224	6.76E-07	1.16E-06	0.57772804	30.5555556	69.4444444
ENSG00000145220	LYAR	-1.0568571	3.22881949	175.203622	5.40E-40	1.80E-39	-1.030111	100	0	LYAR	0.60434701	3.93729181	60.1030942	9.00E-15	2.12E-14	0.51916139	2.77777778	97.2222222
ENSG00000030419	IKZF2	-0.7364122	4.62260595	123.331515	1.18E-28	3.20E-28	-0.6102724	94.2857143	5.71428571	IKZF2	0.44749396	5.13001686	40.4324091	2.04E-10	4.10E-10	0.50647936	19.4444444	80.5555556
ENSG00000123146	CD97	-0.5525341	7.67921764	79.6516961	4.47E-19	9.83E-19	-0.5077599	77.1428571	22.8571429	CD97	0.67602885	8.17339963	94.3230962	2.68E-22	7.85E-22	0.6355205	5.55555556	94.4444444
ENSG00000179588	ZFPM1	-0.603066	3.91550539	69.216991	8.82E-17	1.84E-16	-0.598581	80	20	ZFPM1	1.31566417	5.04389481	331.105399	5.52E-74	3.93E-73	1.20356161	2.77777778	97.2222222
ENSG00000188483	IER5L	-0.5943439	3.16728197	53.0334736	3.28E-13	6.20E-13	-0.5217895	80	20	IER5L	0.61053988	3.74100042	54.9319498	1.25E-13	2.83E-13	0.59562147	19.4444444	80.5555556

Genes Regulated in the same direction

	CD4+ vs PBMC Results									CD8+ vs PBMC Results								
EnsemblGeneIds	**GeneNames**	**logFC**	**logCPM**	**LR**	**Pvalue**	**FDR**	**MedianLogF(**	**PercentDowr**	**PercentUp**	**GeneNames**	**logFC**	**logCPM**	**LR**	**Pvalue**	**FDR**	**MedianLogF(**	**PercentDowı**	**PercentUp**
ENSG00000002933	TMEM176A	-4.6157092	3.28432572	2182.51922	0	0	-4.5776051	100	0	TMEM176A	-6.0494878	3.12752998	2393.35763	0	0	-6.3426531	100	0
ENSG00000007237	GAS7	-4.3189257	5.71935075	3534.12118	0	0	-4.2820207	100	0	GAS7	-3.0769767	5.81424142	1702.85624	0	0	-2.9850081	100	0
ENSG00000007312	CD79B	-5.1383115	5.0160411	4303.88978	0	0	-5.0033355	100	0	CD79B	-4.518447	4.9612892	2983.08862	0	0	-4.5638882	100	0
ENSG00000010671	BTK	-5.1197631	2.89600191	2320.3947	0	0	-5.1512944	100	0	BTK	-4.9921357	2.81410099	1831.56681	0	0	-5.1994175	100	0
ENSG00000011422	PLAUR	-3.8273961	6.90900637	2937.01915	0	0	-3.6890158	100	0	PLAUR	-5.362708	6.75250322	4197.84359	0	0	-5.335006	100	0
ENSG00000011600	TYROBP	-4.6188508	6.45320108	3913.07392	0	0	-4.4759645	100	0	TYROBP	-5.4830473	6.40434251	4341.5325	0	0	-5.6377018	100	0
ENSG00000019582	CD74	-4.0674413	10.4900897	3421.96946	0	0	-3.9721205	100	0	CD74	-3.7007971	10.455096	1918.20758	0	0	-3.7935346	100	0
ENSG00000025708	TYMP	-3.6476381	4.9832763	2479.93319	0	0	-3.3998281	100	0	TYMP	-4.4369081	4.99894981	2803.42119	0	0	-4.5023336	100	0
ENSG00000028137	TNFRSF1B	-2.6883568	7.4919964	1710.81304	0	0	-2.6256617	100	0	TNFRSF1B	-1.9938727	7.65750881	741.113528	3.43E-163	4.71E-162	-1.9490992	97.2222222	2.77777778
ENSG00000030582	GRN	-4.4511915	6.57268341	3827.6768	0	0	-4.4742581	100	0	GRN	-5.2528573	6.60148026	4084.12747	0	0	-5.1102897	100	0
ENSG00000038427	VCAN	-4.6996941	6.06444454	3910.25304	0	0	-4.5253754	100	0	VCAN	-6.2262528	6.04687211	4971.04903	0	0	-6.531513	100	0
ENSG00000042493	CAPG	-3.5006817	4.40574773	2135.79931	0	0	-3.3794208	100	0	CAPG	-4.5335832	4.32883541	2612.90579	0	0	-4.4101095	100	0
ENSG00000044115	CTNNA1	-3.880545	3.66313468	2051.08884	0	0	-3.8945177	100	0	CTNNA1	-4.0440641	3.67469446	1784.85673	0	0	-4.2546973	100	0
ENSG00000057704	TMCC3	-4.351095	3.39698704	2219.11949	0	0	-4.3605667	100	0	TMCC3	-2.3466202	3.59109726	660.160894	1.38E-145	1.76E-144	-2.6206668	100	0
ENSG00000066336	SPI1	-4.3790688	6.26229317	3577.98563	0	0	-4.2570218	100	0	SPI1	-5.9465206	6.23401088	4780.93412	0	0	-6.0902494	100	0
ENSG00000075826	SEC31B	3.01839719	4.21305248	1520.14726	0	0	3.06382107	0	100	SEC31B	2.79374708	4.02087402	1070.97891	6.71E-235	1.26E-233	2.68070956	0	100
ENSG00000084234	APLP2	-3.4835884	7.64621438	2687.04074	0	0	-3.2920222	100	0	APLP2	-3.6074437	7.62716468	2250.18267	0	0	-3.7044757	100	0
ENSG00000085265	FCN1	-5.0924371	8.05962372	4600.07678	0	0	-4.7373043	100	0	FCN1	-6.8298993	8.05303582	5641.8771	0	0	-6.8576671	100	0
ENSG00000086730	LAT2	-3.5532801	3.63753083	1784.48856	0	0	-3.5907553	100	0	LAT2	-3.1490575	3.65356385	1251.60606	3.72E-274	8.05E-273	-3.2401306	100	0
ENSG00000088826	SMOX	-3.4888212	4.47965152	2109.5326	0	0	-3.5352756	100	0	SMOX	-3.7568168	4.41453738	1986.17888	0	0	-3.8580394	100	0
ENSG00000095303	PTGS1	-4.5812445	3.43727938	2403.96362	0	0	-4.7564977	100	0	PTGS1	-5.2515763	3.33083421	2381.31936	0	0	-5.4665883	100	0
ENSG00000099985	OSM	-3.5864681	4.50262775	2233.21707	0	0	-3.4496356	100	0	OSM	-3.6953916	4.42760796	1945.99438	0	0	-3.8187767	100	0
ENSG00000100079	LGALS2	-4.2960423	3.00052779	1776.65534	0	0	-4.3605145	100	0	LGALS2	-6.042898	3.07351181	2386.88447	0	0	-6.1227397	100	0

ENSG00000100097	LGALS1	-3.30741	5.93073237	2335.73846	0	0	-3.2729629	100	0	LGALS1	-3.1910265	5.98850798	1759.57402	0	0	-3.1096589	100	0
ENSG00000100292	HMOX1	-4.4713384	6.12084599	3680.03652	0	0	-4.3607943	100	0	HMOX1	-5.2236728	6.02370924	3974.91278	0	0	-5.1881408	100	0
ENSG00000100300	TSPO	-2.6696029	5.31473511	1556.26749	0	0	-2.5349352	100	0	TSPO	-2.9768844	5.27205723	1559.52331	0	0	-2.876872	100	0
ENSG00000100453	GZMB	-4.411399	3.95886811	2629.4526	0	0	-4.2741169	100	0	GZMB	-1.1585836	4.65493712	205.520107	1.30E-46	6.37E-46	-1.1319203	66.6666667	33.3333333
ENSG00000100721	TCL1A	-6.2386888	1.79107689	2010.36803	0	0	-6.6974113	100	0	TCL1A	-4.6699522	1.71312441	1148.53693	9.33E-252	1.84E-250	-4.6772239	100	0
ENSG00000101057	MYBL2	-3.7489304	4.16475426	2197.78628	0	0	-3.7838832	100	0	MYBL2	-2.5216153	4.15879847	916.138883	3.04E-201	4.95E-200	-2.4837302	100	0
ENSG00000101160	CTSZ	-3.8854383	5.4100884	2915.70222	0	0	-3.8345332	100	0	CTSZ	-4.5957576	5.36617891	3189.69175	0	0	-4.6039543	100	0
ENSG00000101439	CST3	-4.339237	6.47127228	3597.0651	0	0	-4.1577047	100	0	CST3	-5.9255497	6.45520371	4751.42114	0	0	-5.9188171	100	0
ENSG00000101916	TLR8	-4.9050554	2.93122585	2242.64064	0	0	-4.8742291	100	0	TLR8	-6.7963648	2.99022251	2805.71476	0	0	-7.4129336	100	0
ENSG00000102007	PLP2	-2.6004319	5.66872403	1547.33789	0	0	-2.5815503	100	0	PLP2	-2.2303805	5.71948365	977.727154	1.25E-214	2.15E-213	-2.2404557	100	0
ENSG00000102265	TIMP1	-2.9468418	6.35356799	1925.99939	0	0	-2.776529	100	0	TIMP1	-4.0440395	6.26969579	2703.29211	0	0	-4.0474944	100	0
ENSG00000103187	COTL1	-2.6994407	8.35003244	1734.93263	0	0	-2.6025778	100	0	COTL1	-2.5170263	8.38427232	1133.35403	1.86E-248	3.64E-247	-2.5682517	100	0
ENSG00000103811	CTSH	-3.5431989	5.10356182	2472.90792	0	0	-3.4288216	100	0	CTSH	-4.6944134	5.0580527	3176.63189	0	0	-4.7496831	100	0
ENSG00000104312	RIPK2	-2.9223508	5.59426817	1870.21955	0	0	-2.6557911	100	0	RIPK2	-2.6263202	5.58584317	1301.35659	5.73E-285	1.29E-283	-2.6933214	100	0
ENSG00000105369	CD79A	-6.3594762	7.81174121	6785.74848	0	0	-6.4413839	100	0	CD79A	-4.4714707	7.7253101	3180.80037	0	0	-4.3775154	100	0
ENSG00000106066	CPVL	-5.0972943	5.78803748	4427.92723	0	0	-5.2658804	100	0	CPVL	-6.6659407	5.73431635	5374.47356	0	0	-6.7568828	100	0
ENSG00000106565	TMEM176B	-4.7380758	3.44144046	2349.1902	0	0	-4.4869257	100	0	TMEM176B	-6.1857838	3.28161532	2546.68132	0	0	-6.6478396	100	0
ENSG00000107438	PDLIM1	-4.2823556	3.88397682	2584.30133	0	0	-4.1806385	100	0	PDLIM1	-3.132899	3.8472057	1315.23794	5.52E-288	1.25E-286	-3.1654479	100	0
ENSG00000107738	C10orf54	-2.6944442	6.93634323	1708.7049	0	0	-2.535117	100	0	C10orf54	-2.5173299	6.97583517	1219.02933	4.46E-267	9.35E-266	-2.43626	100	0
ENSG00000108691	CCL2	-4.5581882	4.19580169	2536.63906	0	0	-4.5334286	100	0	CCL2	-6.3152975	4.19929903	3179.95809	0	0	-6.6095052	100	0
ENSG00000110042	DTX4	-5.2295651	5.77780448	4758.71411	0	0	-5.2319253	100	0	DTX4	-4.3870165	5.71025314	3067.39761	0	0	-4.546714	100	0
ENSG00000110077	MS4A6A	-4.5617287	3.68280926	2524.41628	0	0	-4.6543719	100	0	MS4A6A	-6.2410651	3.65188586	3214.30024	0	0	-6.4044596	100	0
ENSG00000110446	SLC15A3	-3.4038243	5.22967458	2341.43395	0	0	-3.294524	100	0	SLC15A3	-4.4910274	5.14445875	3053.4624	0	0	-4.5623276	100	0
ENSG00000110777	POU2AF1	-5.195318	3.19205088	2690.0318	0	0	-5.1995949	100	0	POU2AF1	-4.3207063	3.13174199	1722.76039	0	0	-4.2826317	100	0
ENSG00000110880	CORO1C	-2.8078553	5.08042223	1669.52376	0	0	-2.7487811	100	0	CORO1C	-2.7344257	5.07888147	1324.44676	5.50E-290	1.26E-288	-2.804274	100	0
ENSG00000111321	LTBR	-4.0406526	2.72767497	1590.26448	0	0	-4.1912191	100	0	LTBR	-5.3765605	2.72760235	1991.75389	0	0	-5.6948998	100	0
ENSG00000111666	CHPT1	-3.1012678	5.60802717	2072.62904	0	0	-3.0388111	100	0	CHPT1	-1.8546461	5.71032026	682.829458	1.62E-150	2.10E-149	-1.9021402	100	0
ENSG00000112799	LY86	-4.3798955	3.68825853	2466.59057	0	0	-4.3110538	100	0	LY86	-4.8158136	3.60695751	2349.29944	0	0	-4.896577	100	0
ENSG00000113269	RNF130	-3.1144666	5.1545903	2003.99849	0	0	-2.9660858	100	0	RNF130	-3.0441037	5.15939019	1614.87807	0	0	-3.0165605	100	0
ENSG00000114013	CD86	-4.1458321	4.99941215	3018.70654	0	0	-3.985042	100	0	CD86	-5.7699358	5.0008114	4145.07808	0	0	-5.7378972	100	0
ENSG00000114450	GNB4	-4.2930321	3.40478661	2228.31817	0	0	-4.3340417	100	0	GNB4	-4.6338661	3.34035585	2049.73477	0	0	-4.6105721	100	0
ENSG00000115956	PLEK	-4.4850637	7.41051439	3832.43748	0	0	-4.1760174	100	0	PLEK	-4.5996848	7.38692731	3247.43509	0	0	-4.4555316	100	0
ENSG00000116574	RHOU	-3.5262315	3.71159908	1775.44562	0	0	-3.4924518	100	0	RHOU	-4.2286718	3.677791	1992.43631	0	0	-4.3197466	100	0
ENSG00000116701	NCF2	-4.0792696	4.86360606	2903.6948	0	0	-3.9608907	100	0	NCF2	-5.4391991	4.8035547	3729.84071	0	0	-5.6990073	100	0
ENSG00000117984	CTSD	-3.2659199	6.86956962	2361.21707	0	0	-3.1165516	100	0	CTSD	-3.3843619	6.89557164	2011.54122	0	0	-3.4108364	100	0
ENSG00000119655	NPC2	-2.798472	6.03894148	1773.7683	0	0	-2.6638036	100	0	NPC2	-3.3737981	5.9948929	2031.41918	0	0	-3.3749265	100	0
ENSG00000120708	TGFBI	-4.7180946	5.63742387	3882.1399	0	0	-4.6095805	100	0	TGFBI	-6.1367459	5.61897875	4741.36694	0	0	-6.3013252	100	0
ENSG00000121064	SCPEP1	-2.7970259	5.05460727	1649.80324	0	0	-2.6636559	100	0	SCPEP1	-2.6583607	5.10980842	1263.89857	7.92E-277	1.74E-275	-2.6441696	100	0
ENSG00000121316	PLBD1	-5.1415	4.38021023	3662.84351	0	0	-5.1578093	100	0	PLBD1	-6.6949804	4.38820476	4336.56378	0	0	-7.132773	100	0
ENSG00000121552	CSTA	-4.5014977	3.97310946	2715.80037	0	0	-4.3862561	100	0	CSTA	-6.2854952	3.9236133	3598.2967	0	0	-6.4205715	100	0
ENSG00000123384	LRP1	-3.5861052	6.13377226	2625.44108	0	0	-3.4592486	100	0	LRP1	-4.7606223	6.07473281	3466.91478	0	0	-4.8453366	100	0
ENSG00000123689	G0S2	-4.7230788	7.60976584	4115.42484	0	0	-4.523553	100	0	G0S2	-6.5951731	7.5769061	5479.35349	0	0	-6.4538761	100	0
ENSG00000124145	SDC4	-3.5780521	3.33245925	1610.36376	0	0	-3.4834844	100	0	SDC4	-4.446691	3.293692	1829.18484	0	0	-4.6774305	100	0
ENSG00000125124	BBS2	2.70633163	4.90608514	1511.03031	0	0	2.84860099	0	100	BBS2	2.11941558	4.36532413	743.770031	9.08E-164	1.25E-162	2.00849502	0	100
ENSG00000126759	CFP	-2.6422581	5.30559208	1523.92306	0	0	-2.4464092	100	0	CFP	-3.9929189	5.21702656	2508.46346	0	0	-4.041528	100	0
ENSG00000127951	FGL2	-4.2533832	3.55065954	2160.93684	0	0	-4.0769357	100	0	FGL2	-5.4843786	3.67146127	2693.72755	0	0	-5.68742	100	0
ENSG00000128383	APOBEC3A	-4.5759645	4.96229936	3194.61714	0	0	-4.4872246	100	0	APOBEC3A	-6.123336	5.00833119	4088.85064	0	0	-6.3316709	100	0
ENSG00000130202	PVRL2	-4.2700222	2.7037846	1732.81435	0	0	-4.4337513	100	0	PVRL2	-4.4602951	2.69182628	1551.26305	0	0	-4.5346694	100	0
ENSG00000131042	LILRB2	-4.1071422	4.64725311	2787.85583	0	0	-4.0961087	100	0	LILRB2	-5.8479082	4.59525897	3878.5205	0	0	-6.2199775	100	0
ENSG00000131401	NAPSB	-4.1320035	4.35578943	2708.51072	0	0	-3.9792932	100	0	NAPSB	-5.4185456	4.31733953	3280.89062	0	0	-5.8285116	100	0
ENSG00000131724	IL13RA1	-5.2358507	2.96592344	2485.70632	0	0	-5.2653224	100	0	IL13RA1	-5.5120323	2.92065457	2200.66929	0	0	-5.4985559	100	0
ENSG00000133789	SWAP70	-2.9287854	5.63547599	1883.33525	0	0	-2.8439876	100	0	SWAP70	-3.1041637	5.53955202	1737.36081	0	0	-3.1247569	100	0
ENSG00000135218	CD36	-4.6546919	3.34816666	2267.24809	0	0	-4.4822188	100	0	CD36	-6.1043124	3.3110364	2637.52181	0	0	-6.7019896	100	0

ENSG00000135363	LMO2	-4.3034024	3.49270952	2237.60058	0	0	-4.2270263	100	0	LMO2	-5.9748528	3.47293722	2920.66736	0	0	-6.2398194	100	0
ENSG00000135404	CD63	-3.710913	6.31007184	2820.53003	0	0	-3.6541088	100	0	CD63	-3.4678971	6.32776715	2137.96573	0	0	-3.5118053	100	0
ENSG00000136630	HLX	-4.8188179	3.10266242	2263.15335	0	0	-5.0653685	100	0	HLX	-6.1185974	3.10713994	2601.71477	0	0	-6.4449701	100	0
ENSG00000136869	TLR4	-4.5468911	5.09204622	3409.54211	0	0	-4.2847766	100	0	TLR4	-6.2321926	5.05346008	4588.98334	0	0	-6.5991547	100	0
ENSG00000139832	RAB20	-4.5410996	4.2995796	3065.96999	0	0	-4.4828008	100	0	RAB20	-6.0348653	4.24340316	3807.432	0	0	-6.1375889	100	0
ENSG00000140044	JDP2	-4.6957113	4.37773659	3259.00436	0	0	-4.5620082	100	0	JDP2	-6.1399405	4.34935683	3964.78114	0	0	-6.3668952	100	0
ENSG00000140379	BCL2A1	-2.6155408	5.3721965	1489.79435	0	0	-2.524805	100	0	BCL2A1	-3.4561247	5.24745097	2013.32183	0	0	-3.4843256	100	0
ENSG00000141574	SECTM1	-3.1720754	3.96179711	1601.97827	0	0	-2.9480053	100	0	SECTM1	-4.4820851	3.92760923	2263.79546	0	0	-4.7872442	100	0
ENSG00000142512	SIGLEC10	-4.8460797	2.71908658	2073.48162	0	0	-4.8649128	100	0	SIGLEC10	-4.5389623	2.68129634	1569.46223	0	0	-4.5979935	100	0
ENSG00000143878	RHOB	-3.1248683	5.76877786	2086.94691	0	0	-2.9596921	100	0	RHOB	-1.7914263	5.92333565	620.9071	4.75E-137	5.69E-136	-1.8542063	100	0
ENSG00000146072	TNFRSF21	-3.4311061	4.87327449	2234.13414	0	0	-3.3542981	100	0	TNFRSF21	-3.2688581	4.87628596	1736.80512	0	0	-3.337885	100	0
ENSG00000150457	LATS2	-3.9673838	4.13630152	2413.63161	0	0	-4.0761419	100	0	LATS2	-1.9318146	4.37070458	609.701335	1.30E-134	1.53E-133	-1.7118199	100	0
ENSG00000151948	GLT1D1	-4.1516001	2.56069336	1587.95837	0	0	-3.9761135	100	0	GLT1D1	-5.9054996	2.56826394	2078.48718	0	0	-6.0596101	100	0
ENSG00000153064	BANK1	-6.2344267	4.07571716	4302.5668	0	0	-6.0891458	100	0	BANK1	-4.7633565	3.94601075	2496.76828	0	0	-4.8597245	100	0
ENSG00000155130	NA	-4.5370806	6.71618472	3893.46714	0	0	-4.275207	100	0	NA	-5.7322905	6.66979124	4676.32351	0	0	-5.6417652	100	0
ENSG00000155465	SLC7A7	-4.5777241	5.15124987	3620.88974	0	0	-4.4587986	100	0	SLC7A7	-5.8477522	5.17678996	4362.00789	0	0	-6.0295355	100	0
ENSG00000155629	PIK3AP1	-4.2955145	4.91567933	3214.72616	0	0	-4.3706362	100	0	PIK3AP1	-1.6525281	5.26182797	515.519611	3.99E-114	4.18E-113	-1.4783289	100	0
ENSG00000156966	B3GNT7	-6.229367	4.26883004	4654.06579	0	0	-6.4960281	100	0	B3GNT7	-1.6466044	4.49509025	467.359128	1.20E-103	1.16E-102	-1.666821	100	0
ENSG00000158457	TSPAN33	-5.2511245	5.35994928	4605.82297	0	0	-4.9956841	100	0	TSPAN33	-4.0048169	5.27838409	2580.74704	0	0	-4.0086914	100	0
ENSG00000158825	CDA	-4.7225288	2.41686158	1785.50444	0	0	-4.6582444	100	0	CDA	-6.5213953	2.37078584	2145.01813	0	0	-7.1451154	100	0
ENSG00000158869	FCER1G	-4.4265612	5.08107254	3345.12583	0	0	-4.386564	100	0	FCER1G	-5.3298947	5.09054667	3815.02085	0	0	-5.2714181	100	0
ENSG00000160991	ORAI2	-2.7667837	5.77694248	1735.13484	0	0	-2.6962876	100	0	ORAI2	-1.7824895	5.89065287	650.351093	1.87E-143	2.37E-142	-1.8599992	100	0
ENSG00000161921	CXCL16	-2.9322946	6.69525006	1930.52387	0	0	-2.8026268	100	0	CXCL16	-3.0993087	6.70818421	1716.32735	0	0	-2.9332992	100	0
ENSG00000162444	RBP7	-4.8182409	1.82644643	1522.17359	0	0	-5.1065461	100	0	RBP7	-6.3944107	1.79344425	1694.30445	0	0	-7.0055165	100	0
ENSG00000162734	PEA15	-3.1037953	5.03081859	1991.85368	0	0	-2.9820459	100	0	PEA15	-2.7324542	5.0179432	1328.9523	5.77E-291	1.33E-289	-2.7475084	100	0
ENSG00000163131	CTSS	-3.3384352	7.79721377	2496.00074	0	0	-3.0549498	100	0	CTSS	-3.2769837	7.78264924	1894.9666	0	0	-3.2445121	100	0
ENSG00000163220	S100A9	-5.2609068	7.85195291	4850.76056	0	0	-5.1143898	100	0	S100A9	-6.901556	7.86563382	5723.50158	0	0	-6.961067	100	0
ENSG00000163221	S100A12	-4.6669755	4.02968835	2878.96107	0	0	-4.5329815	100	0	S100A12	-6.4974692	4.00817229	3757.85917	0	0	-6.8865052	100	0
ENSG00000163534	FCRL1	-6.4069375	4.03665082	4231.69559	0	0	-6.4200116	100	0	FCRL1	-4.230346	3.91557202	2038.86582	0	0	-4.1447586	100	0
ENSG00000163563	MNDA	-4.9346449	3.44688484	2644.14722	0	0	-5.2535766	100	0	MNDA	-6.6341862	3.46477902	3263.284	0	0	-7.3056619	100	0
ENSG00000163694	RBM47	-4.2312358	4.0705048	2584.98335	0	0	-4.1906169	100	0	RBM47	-5.8858245	4.06722075	3474.57273	0	0	-6.1003861	100	0
ENSG00000163823	CCR1	-5.1013947	5.17526486	4153.14982	0	0	-5.0616303	100	0	CCR1	-6.6925824	5.10576574	5048.40711	0	0	-7.0237088	100	0
ENSG00000165025	SYK	-4.6700227	4.87087243	3593.48409	0	0	-4.7161266	100	0	SYK	-5.0311479	4.82399155	3393.50589	0	0	-5.102915	100	0
ENSG00000165030	NFIL3	-2.9975548	5.25427912	1877.39772	0	0	-2.7267562	100	0	NFIL3	-2.4088491	5.3117596	1057.81801	4.86E-232	8.96E-231	-2.39954	100	0
ENSG00000165140	FBP1	-3.6362522	3.6744019	1828.7263	0	0	-3.6435342	100	0	FBP1	-4.7723932	3.65411025	2316.48463	0	0	-4.9879741	100	0
ENSG00000165168	CYBB	-4.9418555	5.18030302	4030.45181	0	0	-4.822201	100	0	CYBB	-5.5464137	5.13388115	4068.74403	0	0	-5.6231666	100	0
ENSG00000165178	NCF1C	-4.454762	1.99814313	1483.02511	0	0	-4.4446965	100	0	NCF1C	-4.5943809	1.98237677	1242.3928	3.74E-272	8.00E-271	-4.6724053	100	0
ENSG00000168081	PNOC	-5.4574685	1.3742072	1520.77704	0	0	-5.7777662	100	0	PNOC	-4.7007958	1.29785612	996.135003	1.24E-218	2.19E-217	-4.9725571	100	0
ENSG00000168461	RAB31	-5.1193129	4.01108695	3341.40772	0	0	-4.9947255	100	0	RAB31	-5.897663	4.0035239	3436.86092	0	0	-6.0019566	100	0
ENSG00000168792	ABHD15	-3.6794945	3.63678685	1901.48026	0	0	-3.7736405	100	0	ABHD15	-2.6262895	3.63588021	913.718037	1.02E-200	1.66E-199	-2.6292758	100	0
ENSG00000169504	CLIC4	-4.6166447	5.76534448	3983.31818	0	0	-4.5519935	100	0	CLIC4	-4.4969602	5.66441043	3205.31023	0	0	-4.5563744	100	0
ENSG00000169896	ITGAM	-4.4614764	5.22758248	3606.02231	0	0	-4.4864187	100	0	ITGAM	-1.8039744	5.49607307	631.365039	2.52E-139	3.10E-138	-1.8354157	100	0
ENSG00000170458	CD14	-4.9072307	6.13493239	4192.7027	0	0	-4.6540953	100	0	CD14	-6.3180041	6.16484645	5168.7963	0	0	-6.4163477	100	0
ENSG00000170866	NA	-4.6281127	3.25489678	1903.0959	0	0	-4.1360599	88.5714286	0	NA	-6.568015	3.35360776	2558.10137	0	0	-7.0720471	88.8888889	2.77777778
ENSG00000171051	FPR1	-4.9727281	4.81506732	3783.86275	0	0	-5.1731573	100	0	FPR1	-6.6642002	4.76633572	4671.29197	0	0	-6.9020934	100	0
ENSG00000171604	CXXC5	-4.6931696	5.89987466	4087.74526	0	0	-4.6660803	100	0	CXXC5	-3.6964745	5.88208985	2375.58207	0	0	-3.7073177	100	0
ENSG00000171777	RASGRP4	-3.9658681	2.79293586	1600.49703	0	0	-3.8670802	100	0	RASGRP4	-5.8344344	2.76055652	2203.07069	0	0	-6.4780324	100	0
ENSG00000173801	JUP	-3.0894523	4.10928875	1591.84555	0	0	-2.9985034	100	0	JUP	-3.0665024	4.05644328	1293.69589	2.65E-283	5.93E-282	-3.0934293	100	0
ENSG00000175489	LRRC25	-5.0026983	4.66609695	3806.2395	0	0	-4.9979925	100	0	LRRC25	-6.5408434	4.6867854	4573.56913	0	0	-6.8162167	100	0
ENSG00000176597	B3GNT5	-4.1996043	4.74495577	2965.82091	0	0	-4.1906971	100	0	B3GNT5	-5.0298209	4.66526327	3280.80576	0	0	-5.052696	100	0
ENSG00000178789	CD300LB	-4.3045277	3.68390033	2321.13535	0	0	-4.2312094	100	0	CD300LB	-6.0321381	3.59852519	3060.92754	0	0	-6.1993766	100	0
ENSG00000179344	HLA-DQB1	-5.1114991	6.14924697	4305.32713	0	0	-4.8669317	100	0	HLA-DQB1	-4.5673983	6.17004636	3126.66109	0	0	-4.5864298	100	0
ENSG00000180739	S1PR5	-5.3637183	3.92204503	3428.89975	0	0	-5.4138488	100	0	S1PR5	-1.4685661	4.46652573	319.436526	1.92E-71	1.33E-70	-1.302892	83.3333333	16.6666667

ENSG00000181467	RAP2B	-2.5810845	6.37412377	1562.29673	0	0	-2.4762072	100	0	RAP2B	-1.9786534	6.41988727	797.045165	2.37E-175	3.43E-174	-2.0690891	100	0
ENSG00000182718	ANXA2	-3.1516213	5.98236079	2169.94305	0	0	-3.116357	100	0	ANXA2	-3.0892247	5.9944183	1685.62244	0	0	-3.0794503	100	0
ENSG00000183779	ZNF703	-3.5082117	4.86745548	2318.91824	0	0	-3.2939926	100	0	ZNF703	-2.7729123	4.88150529	1276.55861	1.40E-279	3.13E-278	-2.8209948	100	0
ENSG00000184060	ADAP2	-4.3113898	3.00787821	1898.3865	0	0	-4.4526215	100	0	ADAP2	-5.633789	3.01797782	2320.44	0	0	-5.764227	100	0
ENSG00000185033	SEMA4B	-3.0532879	4.538995	1766.09436	0	0	-2.9278143	100	0	SEMA4B	-2.5089555	4.5437995	1046.07998	1.73E-229	3.17E-228	-2.5614291	100	0
ENSG00000185101	ANO9	3.13128413	5.00444859	1902.11336	0	0	3.10201664	0	100	ANO9	2.49705916	4.38581026	954.417861	1.45E-209	2.44E-208	2.44209772	0	100
ENSG00000185339	TCN2	-4.7339936	2.1746479	1642.1631	0	0	-4.8616745	100	0	TCN2	-6.1053422	2.25468536	1861.48778	0	0	-6.5880478	100	0
ENSG00000185432	METTL7A	-4.7762706	2.8607045	2176.20378	0	0	-4.6881017	100	0	METTL7A	-3.4412868	2.91202273	1140.97765	4.10E-250	8.04E-249	-3.4846035	100	0
ENSG00000186074	CD300LF	-4.1075058	3.23351474	1903.26916	0	0	-4.1644279	100	0	CD300LF	-5.8277177	3.16674892	2567.63829	0	0	-6.3373508	100	0
ENSG00000187116	LILRA5	-4.7092309	4.0388959	2940.79235	0	0	-4.5158621	100	0	LILRA5	-6.2420411	4.02401388	3630.87661	0	0	-6.6948146	100	0
ENSG00000188536	HBA2	-6.2436497	2.92889787	2052.16827	0	0	-7.3488101	100	0	HBA2	-4.3971771	2.98771689	953.264766	2.59E-209	4.31E-208	-5.5089479	94.4444444	5.55555556
ENSG00000189057	FAM111B	-4.7417664	3.01039414	2244.10538	0	0	-4.8483822	100	0	FAM111B	-4.1579601	2.87570514	1482.8859	0	0	-4.2444235	100	0
ENSG00000189060	H1F0	-2.9239996	4.49006256	1579.45173	0	0	-3.0089909	100	0	H1F0	-4.3893886	4.37863828	2525.86987	0	0	-4.4551958	100	0
ENSG00000196092	PAX5	-7.3427543	6.35579805	7644.6211	0	0	-7.232435	100	0	PAX5	-4.9998848	6.26315455	3809.9434	0	0	-5.147243	100	0
ENSG00000196126	HLA-DRB1	-4.9296305	7.74261978	4568.83287	0	0	-4.8633628	100	0	HLA-DRB1	-4.6308866	7.6998504	3320.88675	0	0	-4.527916	100	0
ENSG00000196154	S100A4	-2.9721744	7.26148482	2031.58466	0	0	-2.9319783	100	0	S100A4	-2.9284964	7.26754701	1571.06126	0	0	-2.9164528	100	0
ENSG00000196562	SULF2	-3.6782758	4.63309403	2394.41189	0	0	-3.4862118	100	0	SULF2	-4.9102841	4.53914214	2994.57211	0	0	-5.2916885	100	0
ENSG00000196743	GM2A	-3.5055542	4.3498763	2135.86947	0	0	-3.3466322	100	0	GM2A	-3.9495501	4.3490832	2163.69074	0	0	-3.9934122	100	0
ENSG00000197249	SERPINA1	-5.1411408	7.02898864	4629.02012	0	0	-4.8327214	100	0	SERPINA1	-6.4679172	7.05889565	5366.78194	0	0	-6.515477	100	0
ENSG00000197405	C5AR1	-4.7864819	6.91347196	4156.6725	0	0	-4.6088165	100	0	C5AR1	-6.3909168	6.8352739	5362.1829	0	0	-6.3729999	100	0
ENSG00000197629	MPEG1	-4.944025	6.5210254	4357.8346	0	0	-4.7910018	100	0	MPEG1	-6.3238065	6.45437189	5243.61009	0	0	-6.5306904	100	0
ENSG00000197746	PSAP	-3.0489418	10.0686571	2103.94174	0	0	-2.8570252	100	0	PSAP	-3.4088541	10.0575187	1718.77568	0	0	-3.3378781	100	0
ENSG00000197766	CFD	-4.653133	4.27038758	3095.48541	0	0	-4.5410466	100	0	CFD	-6.3082252	4.24175798	3926.73225	0	0	-6.3192704	100	0
ENSG00000198053	SIRPA	-4.6099694	5.65895512	3753.72036	0	0	-4.5036932	100	0	SIRPA	-6.1633359	5.62656451	4877.54681	0	0	-6.2429327	100	0
ENSG00000198502	HLA-DRB5	-6.0837695	5.52868953	5273.6727	0	0	-6.2672649	100	0	HLA-DRB5	-6.1010334	5.46345156	4499.27801	0	0	-6.231919	100	0
ENSG00000198848	CES1	-4.639146	2.3255197	1576.03084	0	0	-4.8006046	100	0	CES1	-6.0901451	2.56667534	1941.5047	0	0	-6.5707707	100	0
ENSG00000204103	MAFB	-4.7824457	7.0605996	4177.07752	0	0	-4.6002526	100	0	MAFB	-6.0962931	6.98492844	4997.26362	0	0	-6.2246188	100	0
ENSG00000204252	HLA-DOA	-4.0555294	3.93214117	2391.27063	0	0	-4.0078184	100	0	HLA-DOA	-1.4334484	4.16091915	332.926544	2.22E-74	1.58E-73	-1.4278891	97.2222222	2.77777778
ENSG00000204257	HLA-DMA	-3.8744227	6.59514787	3152.76557	0	0	-3.7706358	100	0	HLA-DMA	-3.5272368	6.55796944	2234.26494	0	0	-3.4873932	100	0
ENSG00000204287	HLA-DRA	-5.2173304	9.74489869	4943.33191	0	0	-5.0784816	100	0	HLA-DRA	-5.0460578	9.67009566	3332.26792	0	0	-4.8625458	100	0
ENSG00000204482	LST1	-3.7749205	5.24484717	2742.23936	0	0	-3.6644565	100	0	LST1	-4.2700862	5.19509106	2815.69424	0	0	-4.3080783	100	0
ENSG00000211598	IGKV4-1	-7.7911488	3.46684251	4376.19862	0	0	-9.3150613	100	0	IGKV4-1	-6.6548056	3.29166798	3116.62041	0	0	-7.0312837	100	0
ENSG00000211648	IGLV1-47	-6.9634855	1.89655154	2244.93446	0	0	-9.6329653	100	0	IGLV1-47	-6.1341434	1.84960578	1654.63352	0	0	-6.4488005	100	0
ENSG00000211649	IGLV7-46	-7.2481913	0.68776352	1492.65382	0	0	-10000	100	0	IGLV7-46	-5.7224904	0.65397545	977.949079	1.12E-214	1.92E-213	-6.2907406	100	0
ENSG00000211651	IGLV1-44	-8.0529669	2.11356698	2720.83174	0	0	-8.6291364	100	0	IGLV1-44	-5.7030936	2.06941245	1647.97895	0	0	-6.3592425	100	0
ENSG00000211653	IGLV1-40	-6.9691907	2.54905941	2910.04971	0	0	-7.6538457	100	0	IGLV1-40	-5.5560822	2.46399373	1905.26285	0	0	-5.7815477	100	0
ENSG00000211660	IGLV2-23	-7.9262171	2.11906667	2655.94997	0	0	-10000	100	0	IGLV2-23	-6.3981224	2.1052319	1865.71409	0	0	-7.3963739	100	0
ENSG00000211662	IGLV3-21	-7.6086407	2.67390184	3174.50302	0	0	-8.4822508	100	0	IGLV3-21	-7.8204071	2.60897606	2688.66119	0	0	-8.2486336	100	0
ENSG00000211663	IGLV3-19	-7.5634089	2.37407184	2910.43336	0	0	-8.4182559	100	0	IGLV3-19	-6.3592337	2.25537278	2015.99837	0	0	-6.4975539	100	0
ENSG00000211666	IGLV2-14	-7.2007245	4.04068092	4963.54486	0	0	-7.6063428	100	0	IGLV2-14	-5.2100288	3.96090776	2887.09183	0	0	-5.2635439	100	0
ENSG00000211668	IGLV2-11	-7.3655404	2.34383318	2744.43095	0	0	-8.0841068	100	0	IGLV2-11	-5.5879455	2.244158	1714.23486	0	0	-5.4880337	100	0
ENSG00000211671	NA	-7.4972125	1.96219219	2429.46159	0	0	-8.4113698	100	0	NA	-6.4324792	1.93796475	1780.31501	0	0	-7.0029139	100	0
ENSG00000211673	IGLV3-1	-7.2897996	3.0536284	3490.24964	0	0	-7.8095481	100	0	IGLV3-1	-6.8335602	2.96058498	2733.47539	0	0	-7.2301266	100	0
ENSG00000211677	IGLC2	-7.0431384	4.32542491	4494.379	0	0	-7.037561	88.5714286	0	IGLC2	-5.9386209	4.32532541	3191.8797	0	0	-5.733966	88.8888889	0
ENSG00000211679	IGLC3	-7.1685688	4.24413216	5295.49761	0	0	-7.3145422	100	0	IGLC3	-5.8976029	4.13771028	3556.7416	0	0	-5.7877776	100	0
ENSG00000211893	IGHG2	-7.7087566	3.31020407	3796.16706	0	0	-9.0065849	100	0	IGHG2	-7.6488646	3.18045998	3131.62586	0	0	-8.2522484	100	0
ENSG00000211896	IGHG1	-7.4753869	6.14713091	7098.54057	0	0	-7.8921394	100	0	IGHG1	-7.4179873	6.04347129	6072.68106	0	0	-7.8009828	100	0
ENSG00000211897	IGHG3	-6.6286815	3.48991934	3542.85329	0	0	-7.4379156	100	0	IGHG3	-5.6930083	3.38071425	2532.65755	0	0	-5.8251971	100	0
ENSG00000211898	IGHD	-7.0867255	6.46670146	7328.22957	0	0	-7.2175308	100	0	IGHD	-4.580132	6.42967796	3341.01718	0	0	-4.6051084	100	0
ENSG00000211899	IGHM	-7.2272283	9.18422568	8072.31217	0	0	-7.2579073	100	0	IGHM	-4.8605318	9.10065227	3315.06483	0	0	-4.8810891	100	0
ENSG00000211933	IGHV6-1	-7.0621975	0.7814254	1551.38484	0	0	-10000	100	0	IGHV6-1	-5.5931436	0.70273303	993.696857	4.21E-218	7.42E-217	-5.7782628	100	0
ENSG00000211934	IGHV1-2	-7.5490701	2.74592174	3234.06116	0	0	-7.9001168	100	0	IGHV1-2	-5.910515	2.67335719	2157.07954	0	0	-5.9831704	100	0
ENSG00000211937	IGHV2-5	-8.0484423	1.44206466	2149.69969	0	0	-10000	100	0	IGHV2-5	-7.1739226	1.33033726	1566.77067	0	0	-5004.1154	100	0

ENSG00000211938	IGHV3-7	-7.4774906	2.5428963	3084.43637	0	0	-8.5194744	100	0	IGHV3-7	-5.6844236	2.47796746	1963.49172	0	0	-5.9575492	100	0
ENSG00000211940	NA	-8.5925638	1.61940188	1740.57118	0	0	-9.6349024	74.2857143	0	NA	-7.0529763	1.59528136	1243.71516	1.93E-272	4.15E-271	-7.1180832	75	2.77777778
ENSG00000211941	IGHV3-11	-7.2874562	2.10062595	2552.71055	0	0	-8.3330467	100	0	IGHV3-11	-5.8150061	2.03233602	1680.35583	0	0	-5.9954244	100	0
ENSG00000211943	IGHV3-15	-7.0521741	2.07207635	2471.02933	0	0	-8.3782093	100	0	IGHV3-15	-6.3159489	1.98643094	1804.33532	0	0	-6.4432663	100	0
ENSG00000211945	IGHV1-18	-6.9423918	2.40545871	2729.70102	0	0	-7.5101532	100	0	IGHV1-18	-5.0821182	2.35030175	1614.6918	0	0	-5.2396555	100	0
ENSG00000211947	IGHV3-21	-7.2795173	2.66277462	3119.80667	0	0	-7.8764464	100	0	IGHV3-21	-5.2830739	2.61913949	1873.44526	0	0	-5.4591125	100	0
ENSG00000211949	IGHV3-23	-7.4711664	3.96472475	5059.9829	0	0	-7.8136548	100	0	IGHV3-23	-6.182075	3.87582708	3496.07054	0	0	-6.1890746	100	0
ENSG00000211953	NA	-7.1803428	2.31180657	2637.48553	0	0	-7.6877402	100	0	NA	-5.173147	2.2562857	1549.18146	0	0	-5.4410674	100	0
ENSG00000211956	IGHV4-34	-6.4848717	2.95606032	3111.38975	0	0	-6.4578529	100	0	IGHV4-34	-5.6996535	2.86347514	2251.17548	0	0	-5.7840391	100	0
ENSG00000211962	IGHV1-46	-6.9166541	1.50165431	1990.65644	0	0	-7.3345607	100	0	IGHV1-46	-5.7747518	1.40439664	1316.43696	3.03E-288	6.85E-287	-5.7685334	100	0
ENSG00000211964	IGHV3-48	-7.4761462	2.29917504	2816.53541	0	0	-8.2538134	100	0	IGHV3-48	-5.6452667	2.20385658	1744.28852	0	0	-6.0795688	100	0
ENSG00000211965	IGHV3-49	-7.0481736	0.83243956	1528.93979	0	0	-10000	100	0	IGHV3-49	-5.4333921	0.76678773	954.131445	1.68E-209	2.81E-208	-6.1456446	100	0
ENSG00000211966	IGHV5-51	-7.561271	3.126885	3776.65694	0	0	-8.2753605	100	0	IGHV5-51	-6.4187055	3.01132761	2671.71359	0	0	-6.4724018	100	0
ENSG00000211967	IGHV3-53	-6.6236952	1.36798525	1850.42241	0	0	-6.7454465	100	0	IGHV3-53	-5.4058512	1.28092116	1191.01486	5.47E-261	1.12E-259	-5.5547852	100	0
ENSG00000211973	IGHV1-69	-7.3926021	3.85027868	4892.83358	0	0	-7.551125	100	0	IGHV1-69	-4.9744365	3.82282648	2627.30014	0	0	-4.9950351	100	0
ENSG00000213719	CLIC1	-3.0461132	6.68740364	2089.15194	0	0	-2.8904555	100	0	CLIC1	-2.7040771	6.73207341	1395.21654	2.30E-305	5.45E-304	-2.6159673	100	0
ENSG00000214212	C19orf38	-3.6765343	4.41384518	2312.71578	0	0	-3.4544577	100	0	C19orf38	-5.2235382	4.35009725	3232.71907	0	0	-5.0916757	100	0
ENSG00000221869	CEBPD	-4.2368529	5.95328679	3337.73489	0	0	-4.3229442	100	0	CEBPD	-5.3020646	5.89175368	4016.56306	0	0	-5.0699034	100	0
ENSG00000223865	HLA-DPB1	-4.8134354	8.06981538	4494.00012	0	0	-4.8170557	100	0	HLA-DPB1	-3.8866825	8.01895965	2496.05399	0	0	-3.8380637	100	0
ENSG00000224650	IGHV3-74	-6.8048376	1.23565235	1738.8508	0	0	-7.8741533	100	0	IGHV3-74	-5.7255914	1.12803714	1163.97857	4.11E-255	8.25E-254	-5.8795739	100	0
ENSG00000229391	HLA-DRB6	-4.8473794	3.11872415	2281.90674	0	0	-4.9118312	100	0	HLA-DRB6	-4.6188546	3.14892672	1840.1411	0	0	-4.3848255	100	0
ENSG00000231389	HLA-DPA1	-4.8584757	8.18150458	4529.54941	0	0	-4.644834	100	0	HLA-DPA1	-4.6896488	8.14675137	3315.13683	0	0	-4.6009386	100	0
ENSG00000231475	IGHV4-31	-6.9598773	1.38758413	1900.04675	0	0	-7.4261246	100	0	IGHV4-31	-4.6656228	1.34467273	1002.22668	5.89E-220	1.05E-218	-4.8057964	100	0
ENSG00000231486	NA	-5.5859428	5.06926473	4857.59594	0	0	-5.567605	100	0	NA	-5.1612825	4.97718807	3624.48549	0	0	-5.0860326	100	0
ENSG00000232629	HLA-DQB2	-5.0754922	3.28778376	2656.37789	0	0	-5.0491686	100	0	HLA-DQB2	-4.5615241	3.21283662	1914.5946	0	0	-4.6041908	100	0
ENSG00000233276	GPX1	-2.986444	5.92516354	1971.71022	0	0	-2.8773461	100	0	GPX1	-2.9274504	5.91061836	1589.92613	0	0	-2.9299518	100	0
ENSG00000235568	NFAM1	-4.3867266	3.40276464	2180.49875	0	0	-4.5131471	100	0	NFAM1	-6.1227668	3.35694758	2854.16156	0	0	-6.8172449	100	0
ENSG00000237541	HLA-DQA2	-4.3876754	3.47646646	2315.14717	0	0	-4.3640834	100	0	HLA-DQA2	-4.3097158	3.36697833	1847.24263	0	0	-4.2649472	100	0
ENSG00000239951	IGKV3-20	-7.4053646	4.09141278	5244.78624	0	0	-7.7734797	100	0	IGKV3-20	-5.1316594	4.02543177	2892.49498	0	0	-5.0906967	100	0
ENSG00000239998	LILRA2	-4.7914776	3.68218971	2725.43964	0	0	-4.7159109	100	0	LILRA2	-6.5366084	3.6884095	3435.07577	0	0	-7.2440622	100	0
ENSG00000240671	IGKV1-8	-7.3081332	0.76396608	1587.15677	0	0	-8.1017741	100	0	IGKV1-8	-5.3688837	0.71628703	956.368062	5.48E-210	9.26E-209	-5.4787013	100	0
ENSG00000240864	IGKV1-16	-7.0512204	1.056412	1688.96877	0	0	-10000	100	0	IGKV1-16	-5.604137	1.02003845	1108.98806	3.68E-243	7.04E-242	-5.810118	100	0
ENSG00000241294	IGKV2-24	-7.7383575	1.30792025	1816.4053	0	0	-10000	100	0	IGKV2-24	-6.4297888	1.23648152	1275.03813	3.00E-279	6.68E-278	-6.9567322	100	0
ENSG00000241351	IGKV3-11	-7.4202088	3.43020924	4185.84928	0	0	-8.0842643	100	0	IGKV3-11	-5.4126452	3.34083081	2504.44499	0	0	-5.3827155	100	0
ENSG00000241839	PLEKHO2	-3.4973396	5.72541113	2530.78411	0	0	-3.3257143	100	0	PLEKHO2	-3.2659548	5.75171051	1860.14851	0	0	-3.2411737	100	0
ENSG00000243466	IGKV1-5	-7.6311309	3.32833214	4058.53015	0	0	-8.5913765	100	0	IGKV1-5	-6.2787887	3.22528274	2818.9747	0	0	-6.2964442	100	0
ENSG00000244437	IGKV3-15	-6.9225786	2.35143725	2699.43982	0	0	-7.7286592	100	0	IGKV3-15	-5.3209004	2.25892108	1661.93266	0	0	-5.5515525	100	0
ENSG00000244575	IGKV1-27	-7.1168868	1.42633608	2007.3855	0	0	-8.0054371	100	0	IGKV1-27	-5.1456024	1.35755904	1156.44989	1.78E-253	3.55E-252	-5.411938	100	0
ENSG00000244734	HBB	-6.6334449	5.78001334	4635.01612	0	0	-6.9452619	100	0	HBB	-5.2346566	5.73725631	2449.04824	0	0	-5.2299241	94.4444444	5.55555556
ENSG00000254709	IGLL5	-6.8583023	3.034072	3427.71156	0	0	-7.5120638	100	0	IGLL5	-5.0601566	2.96356408	2019.51653	0	0	-4.9420517	100	0
ENSG00000115902	SLC1A4	-2.8894123	4.09334084	1413.32458	0.00E+00	5.37E-308	-2.8125916	100	0	SLC1A4	-1.5669356	4.30778784	396.152219	3.79E-88	3.17E-87	-1.4219178	97.2222222	2.77777778
ENSG00000119900	OGFRL1	-2.4546942	5.90338473	1403.12549	4.40E-307	8.76E-306	-2.3383725	100	0	OGFRL1	-1.6442227	6.01110125	561.796508	3.42E-124	3.81E-123	-1.6204332	100	0
ENSG00000169413	RNASE6	-3.9099932	2.44271473	1400.96863	1.29E-306	2.57E-305	-3.7198161	100	0	RNASE6	-5.5159613	2.33557562	1774.91707	0	0	-5.870038	100	0
ENSG00000172216	CEBPB	-2.4362218	6.07465393	1380.21318	4.19E-302	8.22E-301	-2.3236255	100	0	CEBPB	-2.0535036	6.10253802	833.383852	2.98E-183	4.47E-182	-2.0060425	100	0
ENSG00000161929	SCIMP	-4.1262456	2.15980459	1374.6622	6.74E-301	1.32E-299	-4.1328367	100	0	SCIMP	-4.4571969	2.15095466	1257.25892	2.20E-275	4.78E-274	-4.522873	100	0
ENSG00000158106	RHPN1	2.76842576	4.22510068	1358.63887	2.04E-297	3.93E-296	2.86587581	0	100	RHPN1	2.2085345	3.68282393	654.483664	2.37E-144	3.01E-143	2.23372377	0	100
ENSG00000167851	CD300A	-3.301682	3.12542813	1355.39242	1.04E-296	1.98E-295	-3.2163668	100	0	CD300A	-0.9328543	3.57288924	121.490792	2.98E-28	1.01E-27	-0.9163276	91.6666667	8.33333333
ENSG00000128245	YWHAH	-2.7092628	4.26896879	1354.26493	1.82E-296	3.48E-295	-2.7447072	100	0	YWHAH	-2.4019278	4.24839078	905.107551	7.61E-199	1.22E-197	-2.4368473	100	0
ENSG00000067182	TNFRSF1A	-2.4828717	5.30265915	1345.12565	1.77E-294	3.36E-293	-2.5179648	100	0	TNFRSF1A	-2.6960405	5.27169777	1321.06235	2.99E-289	6.83E-288	-2.7832826	100	0
ENSG00000206172	HBA1	-6.3638104	1.79888269	1342.05607	8.20E-294	1.55E-292	-8.5101988	100	0	HBA1	-3.4670361	1.91000128	419.727895	2.80E-93	2.43E-92	-4.3203473	86.1111111	11.1111111
ENSG00000211936	NA	-6.0464003	1.01075149	1341.09437	1.33E-293	2.51E-292	-6.2609182	100	0	NA	-5.0968724	0.87823436	855.423992	4.81E-188	7.36E-187	-5.2168521	100	0
ENSG00000189319	FAM53B	-2.3517318	6.9214198	1335.64766	2.03E-292	3.80E-291	-2.1691075	100	0	FAM53B	-1.2308409	7.2194044	304.027735	4.37E-68	2.92E-67	-1.4493146	94.4444444	5.55555556
ENSG00000165175	MID1IP1	-2.4621918	5.11853096	1331.37286	1.72E-291	3.21E-290	-2.3612766	100	0	MID1IP1	-2.9936789	4.9863489	1551.37829	0	0	-3.0042019	100	0

ENSG00000205269	TMEM170B	-2.4273385	5.34328524	1322.13276	1.75E-289	3.26E-288	-2.4054131	100	0	TMEM170B	-2.9595139	5.22923835	1562.71537	0	0	-2.8769353	100	0
ENSG00000163453	IGFBP7	-4.2629084	1.83648017	1321.04348	3.02E-289	5.62E-288	-4.475984	100	0	IGFBP7	-4.5707734	1.7607928	1151.25932	2.39E-252	4.73E-251	-4.5515228	100	0
ENSG00000239855	IGKV1-6	-7.8719001	0.25178684	1320.07594	4.90E-289	9.09E-288	-10000	100	0	IGKV1-6	-6.8274383	0.13092716	919.779231	4.92E-202	8.06E-201	-10000	100	0
ENSG00000102034	ELF4	-2.3607764	6.17980689	1319.61724	6.17E-289	1.14E-287	-2.2219983	100	0	ELF4	-2.2023124	6.20090712	951.100986	7.65E-209	1.27E-207	-2.0353417	100	0
ENSG00000213722	DDAH2	-2.962895	3.59767157	1314.19828	9.28E-288	1.70E-286	-2.9361217	100	0	DDAH2	-2.9981597	3.59497753	1122.32668	4.64E-246	9.00E-245	-3.0616081	100	0
ENSG00000122694	GLIPR2	-2.9098306	3.75908635	1312.38815	2.30E-287	4.20E-286	-2.7509378	100	0	GLIPR2	-2.4899127	3.81516527	852.003062	2.67E-187	4.06E-186	-2.4925294	100	0
ENSG00000187446	CHP1	-2.3970073	5.33885511	1311.73483	3.18E-287	5.81E-286	-2.3307433	100	0	CHP1	-1.4494131	5.50127488	428.851659	2.89E-95	2.56E-94	-1.4183895	100	0
ENSG00000197956	S100A6	-2.3164217	7.63079463	1311.54318	3.51E-287	6.38E-286	-2.1717893	100	0	S100A6	-2.2813087	7.64610868	1002.05273	6.43E-220	1.14E-218	-2.280579	100	0
ENSG00000115828	QPCT	-3.9994204	2.17839903	1310.3541	6.36E-287	1.15E-285	-3.8891859	100	0	QPCT	-5.2640171	2.15466294	1555.74132	0	0	-5.3239846	100	0
ENSG00000181481	RNF135	-3.4681649	2.73680775	1310.23957	6.73E-287	1.22E-285	-3.3138366	100	0	RNF135	-3.4204126	2.76416183	1065.90955	8.48E-234	1.58E-232	-3.3343667	100	0
ENSG00000104903	LYL1	-3.7565714	2.32317326	1306.70561	3.94E-286	7.11E-285	-3.7430157	100	0	LYL1	-4.050482	2.25279276	1165.83967	1.62E-255	3.27E-254	-4.2035188	100	0
ENSG00000015475	BID	-2.4652907	4.93431679	1306.0606	5.45E-286	9.78E-285	-2.3970979	100	0	BID	-2.4169828	4.9451666	1058.44253	3.56E-232	6.57E-231	-2.4403691	100	0
ENSG00000019169	MARCO	-4.5236498	1.70120997	1290.59652	1.25E-282	2.23E-281	-4.8074146	100	0	MARCO	-6.2522989	1.74065562	1507.75698	0	0	-6.9016621	100	0
ENSG00000211974	IGHV2-70	-6.6421222	0.46550883	1290.37821	1.39E-282	2.48E-281	-10000	100	0	IGHV2-70	-7.1936178	0.39022648	1064.87026	1.43E-233	2.65E-232	-10000	100	0
ENSG00000211939	NA	-5.7400193	1.45845908	1283.25356	4.93E-281	8.72E-280	-6.0287674	94.2857143	5.71428571	NA	-5.4315017	1.42577465	980.791038	2.69E-215	4.65E-214	-5.9303803	97.2222222	2.77777778
ENSG00000172322	CLEC12A	-4.3728588	1.91703062	1280.91682	1.59E-280	2.80E-279	-4.0786412	100	0	CLEC12A	-6.2017633	1.86585201	1554.64335	0	0	-6.3662806	100	0
ENSG00000130775	THEMIS2	-2.3192939	6.29958344	1276.57869	1.39E-279	2.45E-278	-2.229273	100	0	THEMIS2	-3.304792	6.21772936	1907.49781	0	0	-3.5465751	100	0
ENSG00000125505	MBOAT7	-2.5688188	4.41565309	1273.33918	7.03E-279	1.24E-277	-2.4606141	100	0	MBOAT7	-2.9855613	4.38389445	1365.77579	5.75E-299	1.34E-297	-2.9780413	100	0
ENSG00000158481	CD1C	-4.7000824	1.4943985	1269.66555	4.42E-278	7.75E-277	-4.7982865	100	0	CD1C	-5.5220326	1.37215872	1161.31749	1.56E-254	3.12E-253	-6.173355	100	0
ENSG00000073849	ST6GAL1	-2.3281125	5.91440337	1267.91404	1.06E-277	1.86E-276	-2.2686357	100	0	ST6GAL1	-2.4022017	5.78674859	1124.58513	1.50E-246	2.91E-245	-2.5131016	100	0
ENSG00000211950	IGHV1-24	-5.0983366	1.00644822	1267.63747	1.22E-277	2.13E-276	-5.1663512	100	0	IGHV1-24	-5.578538	0.89412687	1066.20773	7.30E-234	1.37E-232	-5.6407132	100	0
ENSG00000178719	GRINA	-2.3209554	5.81401763	1266.53272	2.12E-277	3.69E-276	-2.1968131	100	0	GRINA	-2.5074349	5.80298586	1200.23067	5.43E-263	1.12E-261	-2.5874106	100	0
ENSG00000185112	FAM43A	-3.1007867	3.29180007	1264.43904	6.04E-277	1.05E-275	-2.9354395	100	0	FAM43A	-0.6117813	3.82600836	55.7548285	8.21E-14	1.87E-13	-0.5015452	77.7777778	22.2222222
ENSG00000161944	ASGR2	-4.2295929	1.81304772	1263.10459	1.18E-276	2.04E-275	-4.2830274	100	0	ASGR2	-6.0550993	1.78239754	1575.60882	0	0	-6.4632258	100	0
ENSG00000158470	B4GALT5	-2.3945377	5.1097461	1259.76389	6.27E-276	1.08E-274	-2.1995508	100	0	B4GALT5	-1.0571496	5.4018913	228.099319	1.55E-51	8.18E-51	-1.017949	100	0
ENSG00000167173	C15orf39	-2.2863676	6.69332083	1256.07462	3.97E-275	6.84E-274	-2.0738365	100	0	C15orf39	-2.2403037	6.68791966	989.496871	3.45E-217	6.04E-216	-2.1819163	100	0
ENSG00000211650	IGLV5-45	-7.665599	0.14230738	1247.61779	2.73E-273	4.69E-272	-10000	100	0	IGLV5-45	-6.6439164	0.07951099	896.980856	4.45E-197	7.05E-196	-10000	100	0
ENSG00000164687	FABP5	-2.6908919	4.0854703	1247.21513	3.34E-273	5.72E-272	-2.6925461	100	0	FABP5	-1.2952234	4.34852522	277.789362	2.28E-62	1.38E-61	-1.246255	94.4444444	5.55555556
ENSG00000167703	SLC43A2	-2.2682573	6.84026005	1244.19255	1.52E-272	2.59E-271	-2.2469943	100	0	SLC43A2	-2.5263224	6.76475594	1232.30349	5.82E-270	1.23E-268	-2.5855899	100	0
ENSG00000175040	CHST2	-2.404529	5.10367684	1243.87597	1.78E-272	3.02E-271	-2.2859575	100	0	CHST2	-2.4937986	5.02512179	1117.92118	4.21E-245	8.12E-244	-2.5321211	100	0
ENSG00000114315	HES1	-3.3104703	2.83088694	1239.43713	1.64E-271	2.77E-270	-3.2706203	100	0	HES1	-3.4899041	2.68699801	1063.6594	2.61E-233	4.84E-232	-3.5106281	100	0
ENSG00000144228	SPOPL	-2.303501	5.57073871	1239.20304	1.84E-271	3.11E-270	-2.3232432	100	0	SPOPL	-2.0874742	5.55538476	851.759593	3.01E-187	4.58E-186	-2.1960736	100	0
ENSG00000161381	PLXDC1	2.54513856	4.69261932	1238.45079	2.69E-271	4.52E-270	2.27362244	0	100	PLXDC1	2.04031205	4.12646812	621.465973	3.59E-137	4.31E-136	1.76148751	0	100
ENSG00000146535	GNA12	-2.2500818	6.81625306	1237.42035	4.50E-271	7.55E-270	-2.1691592	100	0	GNA12	-1.9612546	6.80025977	783.324024	2.28E-172	3.26E-171	-1.9333666	100	0
ENSG00000175274	TP53I11	-3.0980408	3.133098	1230.37322	1.53E-269	2.56E-268	-2.9948614	100	0	TP53I11	-2.8456921	3.15752122	885.033285	1.76E-194	2.75E-193	-2.7657071	100	0
ENSG00000136158	SPRY2	-3.5462701	2.45999388	1227.39335	6.79E-269	1.14E-267	-3.3733406	100	0	SPRY2	-0.7998757	2.9894848	71.9952151	2.16E-17	5.47E-17	-0.6922587	77.7777778	22.2222222
ENSG00000211976	IGHV3-73	-7.0471396	0.25297677	1225.87804	1.45E-268	2.42E-267	-10000	100	0	IGHV3-73	-6.2894346	0.19738289	860.944232	3.04E-189	4.67E-188	-7.281722	100	0
ENSG00000155366	RHOC	-2.8313316	3.61220434	1224.18257	3.39E-268	5.64E-267	-2.7110809	100	0	RHOC	-1.9795358	3.74187707	550.453641	1.00E-121	1.09E-120	-2.0007932	100	0
ENSG00000163545	NUAK2	-2.2878767	5.67072172	1222.9962	6.13E-268	1.02E-266	-2.192086	100	0	NUAK2	-2.0144255	5.65508296	810.757938	2.47E-178	3.63E-177	-2.0551723	100	0
ENSG00000143870	PDIA6	-2.3207653	5.23284855	1217.46225	9.78E-267	1.61E-265	-2.2913275	100	0	PDIA6	-1.8276837	5.26845512	655.465306	1.45E-144	1.84E-143	-1.8352158	100	0
ENSG00000104763	ASAH1	-2.2655539	6.02671129	1217.25435	1.09E-266	1.79E-265	-2.148141	100	0	ASAH1	-2.4170946	5.98754829	1143.70242	1.05E-250	2.07E-249	-2.4803648	100	0
ENSG00000140406	MESDC1	-2.2903436	5.56063203	1208.97718	6.83E-265	1.12E-263	-2.2367811	100	0	MESDC1	-2.3638225	5.47993544	1074.06214	1.43E-235	2.71E-234	-2.3386347	100	0
ENSG00000059377	TBXAS1	-3.1420607	3.07850416	1205.11608	4.71E-264	7.70E-263	-3.1383673	100	0	TBXAS1	-5.158386	2.93473891	2018.17133	0	0	-5.2350864	100	0
ENSG00000211951	IGHV2-26	-7.3976983	0.01282831	1204.125	7.74E-264	1.26E-262	-10000	100	0	IGHV2-26	-5.9032877	-0.0416333	801.887017	2.10E-176	3.07E-175	-6.170188	100	0
ENSG00000033327	GAB2	-2.217093	6.94668897	1194.2067	1.11E-261	1.79E-260	-2.3240921	100	0	GAB2	-2.0592807	6.94950708	849.633576	8.73E-187	1.32E-185	-2.0839094	100	0
ENSG00000188677	PARVB	-2.7951671	3.55918943	1182.13364	4.66E-259	7.51E-258	-2.6724833	100	0	PARVB	-2.7755275	3.52444209	975.461932	3.87E-214	6.62E-213	-2.8220721	100	0
ENSG00000146112	PPP1R18	-2.2355941	6.05610259	1175.90537	1.05E-257	1.69E-256	-2.1043509	100	0	PPP1R18	-2.085121	6.08275539	864.319795	5.60E-190	8.63E-189	-2.1005972	100	0
ENSG00000122877	EGR2	-2.5996551	4.14867641	1174.39478	2.24E-257	3.59E-256	-2.313559	100	0	EGR2	-2.7098479	4.19061595	1031.83164	2.16E-226	3.93E-225	-2.8451942	100	0
ENSG00000156273	BACH1	-2.1727404	7.55793362	1171.35945	1.02E-256	1.64E-255	-1.9966086	100	0	BACH1	-1.9612749	7.5448805	769.194127	2.69E-169	3.83E-168	-1.966433	100	0
ENSG00000148158	SNX30	-2.2658717	5.24861576	1163.1979	6.07E-255	9.66E-254	-2.1054792	100	0	SNX30	-1.5998246	5.402761	508.755907	1.18E-112	1.22E-111	-1.5502132	97.2222222	2.77777778
ENSG00000243264	IGKV2D-29	-7.1388625	0.0368816	1160.20537	2.72E-254	4.31E-253	-10000	100	0	IGKV2D-29	-6.3069466	-0.044887	816.6697	1.28E-179	1.89E-178	-10000	100	0
ENSG00000137166	FOXP4	-2.2403813	5.46512243	1156.13701	2.08E-253	3.29E-252	-2.0819801	100	0	FOXP4	-1.7696585	5.48934649	622.857034	1.79E-137	2.16E-136	-1.7668045	100	0
ENSG00000119729	RHOQ	-2.490149	4.19144439	1153.54944	7.59E-253	1.20E-251	-2.4551542	100	0	RHOQ	-2.3046217	4.2042	847.709594	2.29E-186	3.45E-185	-2.3290524	100	0

ENSG00000159399	HK2	-2.2206107	5.86575429	1139.72733	7.67E-250	1.20E-248	-2.1073086	100	0	HK2	-2.2718195	5.71365152	942.708576	5.10E-207	8.42E-206	-2.265009	100	0
ENSG00000127838	PNKD	-2.4564459	4.28648146	1129.84175	1.08E-247	1.67E-246	-2.3225215	100	0	PNKD	-2.863336	4.30860364	1245.1149	9.57E-273	2.07E-271	-2.958291	100	0
ENSG00000184730	APOBR	-2.4519414	4.22428035	1124.86532	1.30E-246	2.02E-245	-2.41524	100	0	APOBR	-1.9520181	4.28454064	626.990557	2.26E-138	2.76E-137	-1.8656748	100	0
ENSG00000126709	IFI6	-2.2606172	5.22508021	1123.51452	2.56E-246	3.96E-245	-2.1506718	100	0	IFI6	-2.2466087	5.33642471	922.600094	1.20E-202	1.97E-201	-2.2036148	100	0
ENSG00000087086	FTL	-2.1520899	10.3269411	1121.9873	5.50E-246	8.46E-245	-1.9882094	100	0	FTL	-2.0994724	10.3366723	703.413964	5.41E-155	7.15E-154	-2.1332337	100	0
ENSG00000137507	LRRC32	-2.71144	3.60823767	1120.55206	1.13E-245	1.73E-244	-2.6082574	100	0	LRRC32	-3.8230522	3.41070577	1566.29857	0	0	-3.8428056	100	0
ENSG00000177989	ODF3B	-2.853315	3.33633237	1117.59225	4.96E-245	7.60E-244	-2.8322982	100	0	ODF3B	-3.2654995	3.30124416	1154.71819	4.23E-253	8.43E-252	-3.2121088	100	0
ENSG00000131873	CHSY1	-2.2116098	5.27540788	1115.46789	1.44E-244	2.20E-243	-2.2440173	100	0	CHSY1	-1.0633407	5.52131632	235.631917	3.53E-53	1.90E-52	-1.0643255	100	0
ENSG00000177374	HIC1	-3.3551736	2.48773722	1103.44534	5.89E-242	8.98E-241	-3.2189505	100	0	HIC1	-2.3214255	2.67132626	493.959747	1.96E-109	1.98E-108	-2.5066914	100	0
ENSG00000179388	EGR3	-2.652111	3.92806368	1102.27509	1.06E-241	1.61E-240	-2.6478439	97.1428571	2.85714286	EGR3	-1.9541431	4.00273288	548.239619	3.04E-121	3.30E-120	-1.9986179	100	0
ENSG00000186350	RXRA	-2.4640786	4.15149936	1098.41554	7.30E-241	1.11E-239	-2.4095086	100	0	RXRA	-2.0973826	4.22607851	684.304376	7.74E-151	1.01E-149	-2.3490876	100	0
ENSG00000111669	TPI1	-2.1330086	5.89156095	1087.99974	1.34E-238	2.02E-237	-2.1210067	100	0	TPI1	-1.4588107	6.00753063	442.29409	3.43E-98	3.15E-97	-1.3992339	100	0
ENSG00000211638	IGLV8-61	-7.8665403	-0.0546704	1084.84889	6.49E-238	9.73E-237	-10000	100	0	IGLV8-61	-5.1813725	-0.1524849	616.271849	4.84E-136	5.77E-135	-6.1702063	100	0
ENSG00000198932	GPRASP1	2.14596771	6.02392108	1084.69287	7.01E-238	1.05E-236	2.24194618	0	100	GPRASP1	1.40458613	5.42372915	395.833786	4.45E-88	3.71E-87	1.38224891	0	100
ENSG00000148834	GSTO1	-2.3253079	4.48326438	1081.00207	4.45E-237	6.63E-236	-2.1079369	100	0	GSTO1	-2.5225873	4.41606599	1026.28446	3.48E-225	6.27E-224	-2.6155803	100	0
ENSG00000104870	FCGRT	-2.1541767	5.73609798	1080.72298	5.11E-237	7.61E-236	-2.1059001	100	0	FCGRT	-2.9213789	5.59968875	1543.15784	0	0	-2.9444996	100	0
ENSG00000143162	CREG1	-2.2941797	4.62406156	1079.52602	9.31E-237	1.38E-235	-2.2321778	100	0	CREG1	-2.7187184	4.59574723	1212.93885	9.40E-266	1.97E-264	-2.938845	100	0
ENSG00000253276	CCDC71L	-2.6821097	3.50069125	1070.88021	7.05E-235	1.04E-233	-2.5561469	100	0	CCDC71L	-2.4394978	3.51012486	764.920237	2.29E-168	3.24E-167	-2.3796054	100	0
ENSG00000139631	CSAD	2.84393624	3.3651276	1070.71227	7.66E-235	1.13E-233	2.73246779	0	100	CSAD	1.80389477	2.46383616	292.955299	1.13E-65	7.24E-65	1.65957559	2.77777778	97.2222222
ENSG00000086062	B4GALT1	-2.0489496	7.80166088	1065.34041	1.13E-233	1.65E-232	-1.9187737	100	0	B4GALT1	-0.9078373	8.03607592	171.711559	3.13E-39	1.34E-38	-0.9064827	100	0
ENSG00000140105	WARS	-2.1062832	6.14373723	1058.34318	3.74E-232	5.45E-231	-1.9775935	100	0	WARS	-2.0721439	6.24607075	857.236034	1.94E-188	2.98E-187	-2.0433954	100	0
ENSG00000175505	CLCF1	-3.7059396	1.74329151	1057.19503	6.64E-232	9.64E-231	-3.5704785	100	0	CLCF1	-1.4183139	2.13803144	165.008956	9.11E-38	3.79E-37	-1.5286532	91.6666667	8.33333333
ENSG00000168961	LGALS9	-2.1003445	5.86134805	1056.89798	7.71E-232	1.12E-230	-2.0050355	100	0	LGALS9	-2.4804064	5.76524251	1186.30173	5.79E-260	1.18E-258	-2.5523516	100	0
ENSG00000178996	SNX18	-2.1076926	5.7580151	1054.46573	2.60E-231	3.76E-230	-2.0596794	100	0	SNX18	-1.969129	5.7576515	770.124377	1.69E-169	2.41E-168	-1.926704	100	0
ENSG00000111729	CLEC4A	-3.2235714	2.44446612	1052.23603	7.95E-231	1.15E-229	-3.0544376	100	0	CLEC4A	-3.8720082	2.37635681	1116.04618	1.07E-244	2.07E-243	-3.9826992	100	0
ENSG00000188820	FAM26F	-3.02537	2.92111327	1034.58036	5.47E-227	7.80E-226	-2.9229007	100	0	FAM26F	-3.8292081	2.70508663	1208.38724	9.17E-265	1.91E-263	-3.9580507	100	0
ENSG00000171700	RGS19	-2.4535987	3.88841467	1030.63941	3.93E-226	5.59E-225	-2.2995303	100	0	RGS19	-2.4663442	3.90717472	872.703236	8.43E-192	1.30E-190	-2.4706224	100	0
ENSG00000114738	MAPKAPK3	-2.0916255	5.43571073	1021.62644	3.58E-224	5.05E-223	-2.0113046	100	0	MAPKAPK3	-2.3256966	5.41016242	1027.36401	2.02E-225	3.66E-224	-2.3980493	100	0
ENSG00000142657	PGD	-2.0921294	5.31661727	1014.26502	1.42E-222	2.00E-221	-2.0733595	100	0	PGD	-1.9564339	5.35470845	745.36441	4.09E-164	5.65E-163	-2.0954734	100	0
ENSG00000124181	PLCG1	2.01924185	7.1845552	1013.72878	1.86E-222	2.61E-221	2.06742517	0	100	PLCG1	1.80451413	6.95044633	664.53819	1.54E-146	1.98E-145	1.69643982	0	100
ENSG00000136250	AOAH	-2.2925749	4.42922373	1013.58623	2.00E-222	2.80E-221	-2.2724342	100	0	AOAH	-1.741859	4.50771625	507.963664	1.76E-112	1.82E-111	-1.8996759	97.2222222	2.77777778
ENSG00000187091	PLCD1	2.13750843	4.87573393	1004.86643	1.57E-220	2.19E-219	2.24251725	0	100	PLCD1	1.63484761	4.46352717	473.742606	4.91E-105	4.80E-104	1.62825721	0	100
ENSG00000103381	CPPED1	-3.1828923	2.4581609	999.998315	1.80E-219	2.50E-218	-2.9284744	100	0	CPPED1	-2.9723066	2.4683745	726.657278	4.78E-160	6.41E-159	-3.0297507	100	0
ENSG00000182287	AP1S2	-2.0841235	5.16614631	992.516591	7.60E-218	1.05E-216	-1.9211015	100	0	AP1S2	-2.2006927	5.11270205	909.015532	1.08E-199	1.74E-198	-2.0947899	100	0
ENSG00000126247	CAPNS1	-2.0101281	6.36459917	991.371226	1.35E-217	1.87E-216	-1.9081002	100	0	CAPNS1	-1.5247843	6.44768565	484.833799	1.90E-107	1.89E-106	-1.556962	100	0
ENSG00000233429	HOTAIRM1	-2.9895647	2.67911603	984.860785	3.51E-216	4.84E-215	-2.8651783	100	0	HOTAIRM1	-2.4992841	2.85818941	632.018006	1.82E-139	2.24E-138	-2.6083772	100	0
ENSG00000187840	EIF4EBP1	-3.2433077	2.16773492	980.588104	2.98E-215	4.09E-214	-3.225473	100	0	EIF4EBP1	-1.7464183	2.37160456	280.936295	4.69E-63	2.88E-62	-1.7265323	100	0
ENSG00000125753	VASP	-2.0285571	6.05107363	976.204968	2.67E-214	3.65E-213	-2.0604578	100	0	VASP	-1.4325717	6.15980346	423.495309	4.23E-94	3.70E-93	-1.547224	100	0
ENSG00000197582	GPX1P1	-3.0444031	2.48300557	974.236395	7.15E-214	9.76E-213	-2.9117573	100	0	GPX1P1	-3.0744585	2.45498552	806.445574	2.14E-177	3.14E-176	-3.1405094	100	0
ENSG00000130489	SCO2	-2.5180479	3.57912493	973.683221	9.43E-214	1.28E-212	-2.5171699	100	0	SCO2	-2.7596319	3.63792114	964.9515	7.46E-212	1.27E-210	-2.8177685	100	0
ENSG00000130592	LSP1	-1.9617624	7.5489895	973.650057	9.59E-214	1.30E-212	-1.9464812	100	0	LSP1	-1.8542218	7.53680571	685.474407	4.31E-151	5.63E-150	-1.9685898	100	0
ENSG00000211829	TRDC	-3.2810002	2.12521624	970.795297	4.00E-213	5.43E-212	-3.2937953	100	0	TRDC	-2.6147249	2.10533236	528.55439	5.83E-117	6.21E-116	-2.5697657	100	0
ENSG00000143537	ADAM15	-2.2796821	4.13010545	967.381404	2.21E-212	2.99E-211	-2.1630972	100	0	ADAM15	-2.5952284	4.10135666	984.633763	3.93E-216	6.83E-215	-2.4996931	100	0
ENSG00000166340	TPP1	-2.0239284	5.761538	959.634352	1.07E-210	1.43E-209	-1.9458554	100	0	TPP1	-2.173143	5.72822135	908.065566	1.73E-199	2.79E-198	-2.2565997	100	0
ENSG00000102218	RP2	-2.0790928	4.80260833	948.919428	2.28E-208	3.02E-207	-2.0000142	100	0	RP2	-1.7157324	4.8448203	556.744598	4.29E-123	4.73E-122	-1.7097244	100	0
ENSG00000127947	PTPN12	-2.039059	5.14854699	947.835901	3.92E-208	5.18E-207	-1.9098445	100	0	PTPN12	-1.2983997	5.29142817	338.218379	1.56E-75	1.12E-74	-1.3874342	100	0
ENSG00000142669	SH3BGRL3	-1.9355845	7.48607592	944.809612	1.78E-207	2.35E-206	-1.7685537	100	0	SH3BGRL3	-1.4341318	7.59620077	415.060908	2.90E-92	2.50E-91	-1.4380244	100	0
ENSG00000104918	RETN	-4.1949178	0.89922051	938.607134	3.97E-206	5.23E-205	-4.0900526	100	0	RETN	-4.8708927	0.94455675	901.442498	4.77E-198	7.57E-197	-4.9206544	100	0
ENSG00000136167	LCP1	-1.9187529	8.75870932	931.666833	1.28E-204	1.67E-203	-1.8057376	100	0	LCP1	-1.599268	8.81425691	480.667614	1.53E-106	1.51E-105	-1.5754183	100	0
ENSG00000189068	VSTM1	-4.5957486	0.81028379	930.732853	2.05E-204	2.67E-203	-4.8427889	100	0	VSTM1	-6.2688302	0.77535257	1018.98731	1.34E-223	2.40E-222	-10000	100	0
ENSG00000115526	CHST10	-2.5806521	3.23225268	927.26491	1.16E-203	1.51E-202	-2.4013529	100	0	CHST10	-0.7800726	3.57061244	88.8408221	4.28E-21	1.22E-20	-0.8409345	94.4444444	5.55555556
ENSG00000085514	PILRA	-2.561171	3.37203302	925.279702	3.14E-203	4.07E-202	-2.5125806	100	0	PILRA	-3.0924011	3.3216625	1044.20299	4.43E-229	8.10E-228	-3.1965185	100	0
ENSG00000159840	ZYX	-1.9274122	7.16040117	925.123574	3.39E-203	4.39E-202	-1.7609355	100	0	ZYX	-1.4595304	7.31912514	430.750792	1.12E-95	9.90E-95	-1.4097227	97.2222222	2.77777778

ENSG00000211670	IGLV3-9	-6.3789046	-0.3820574	923.868697	6.36E-203	8.22E-202	-10000	100	0	IGLV3-9	-5.0141314	-0.3712476	590.482706	1.97E-130	2.27E-129	-5.6679177	100	0
ENSG00000057657	PRDM1	-2.0114874	5.23370347	914.980195	5.44E-201	7.02E-200	-1.8600731	100	0	PRDM1	-2.7223326	5.20405403	1235.39644	1.24E-270	2.62E-269	-2.445149	100	0
ENSG00000170275	CRTAP	-1.9537289	5.53880224	910.900198	4.19E-200	5.40E-199	-1.8242067	100	0	CRTAP	-2.5095462	5.42647547	1190.81062	6.06E-261	1.24E-259	-2.4334525	100	0
ENSG00000138166	DUSP5	-1.9236688	6.39374184	909.638935	7.88E-200	1.01E-198	-1.8543064	100	0	DUSP5	-1.8287768	6.33248192	680.660812	4.80E-150	6.19E-149	-1.8802379	100	0
ENSG00000164733	CTSB	-1.9313467	6.6244001	907.387836	2.43E-199	3.12E-198	-1.7006972	100	0	CTSB	-3.2649099	6.50631878	1915.32552	0	0	-3.4205807	100	0
ENSG00000211445	GPX3	-3.377137	1.8303502	902.289576	3.12E-198	3.99E-197	-3.2417037	100	0	GPX3	-3.795052	1.7938737	841.468324	5.20E-185	7.83E-184	-3.8489111	100	0
ENSG00000111796	KLRB1	-1.9757	5.34251761	900.253101	8.65E-198	1.10E-196	-1.894887	100	0	KLRB1	-1.4918594	5.36283627	440.955023	6.71E-98	6.13E-97	-1.490272	100	0
ENSG00000211935	IGHV1-3	-4.2854256	0.90539311	897.2417	3.90E-197	4.95E-196	-4.4858303	97.1428571	2.85714286	IGHV1-3	-3.5740636	0.81269804	504.450234	1.02E-111	1.05E-110	-4.1008091	91.6666667	8.33333333
ENSG00000105639	JAK3	1.88980477	7.22264416	896.029904	7.16E-197	9.07E-196	1.87900757	0	100	JAK3	1.17053599	6.69224292	291.730687	2.09E-65	1.33E-64	1.14612751	2.77777778	97.2222222
ENSG00000035862	TIMP2	-1.9586807	5.33550383	891.185358	8.09E-196	1.02E-194	-1.885918	100	0	TIMP2	-1.9722785	5.35106006	757.655558	8.69E-167	1.22E-165	-1.9910667	100	0
ENSG00000172059	KLF11	-1.9313698	5.57773084	890.050163	1.43E-195	1.79E-194	-1.857716	100	0	KLF11	-1.8562643	5.5454865	684.589313	6.71E-151	8.74E-150	-1.8109421	100	0
ENSG00000169692	AGPAT2	-2.7992967	2.61488771	882.563514	6.06E-194	7.54E-193	-2.6909387	100	0	AGPAT2	-2.4891731	2.68682055	599.481592	2.17E-132	2.54E-131	-2.4163025	100	0
ENSG00000159128	IFNGR2	-1.9034518	6.03123476	882.214226	7.22E-194	8.94E-193	-1.7875291	100	0	IFNGR2	-2.9863294	5.79608512	1655.61465	0	0	-3.0649072	100	0
ENSG00000162511	LAPTM5	-1.8854842	11.0238722	878.63847	4.32E-193	5.34E-192	-1.8275737	100	0	LAPTM5	-2.0128322	10.9266037	633.477889	8.76E-140	1.08E-138	-2.0582532	100	0
ENSG00000174125	TLR1	-2.1844517	4.0585791	875.996665	1.62E-192	2.00E-191	-2.1360667	100	0	TLR1	-2.8248357	3.91416328	1120.77589	1.01E-245	1.95E-244	-2.8313486	100	0
ENSG00000154978	VOPP1	-1.8722879	6.95171739	875.859949	1.74E-192	2.14E-191	-1.7909889	100	0	VOPP1	-1.8929348	6.86257557	736.34669	3.73E-162	5.09E-161	-1.9456134	100	0
ENSG00000091490	SEL1L3	-1.9467262	5.27616444	870.874946	2.11E-191	2.58E-190	-1.7564424	100	0	SEL1L3	-1.7213314	5.20192248	584.735887	3.50E-129	4.00E-128	-1.8454909	100	0
ENSG00000088992	TESC	-2.8528469	2.42959855	863.721702	7.56E-190	9.21E-189	-2.7660779	100	0	TESC	-1.9039651	2.59455327	355.832831	2.28E-79	1.70E-78	-1.9047653	100	0
ENSG00000075426	FOSL2	-1.8367068	8.68635513	863.054894	1.06E-189	1.28E-188	-1.7875945	100	0	FOSL2	-0.5111493	9.01735702	50.7944411	1.03E-12	2.26E-12	-0.508462	91.6666667	8.33333333
ENSG00000213366	GSTM2	2.30701717	3.83737394	859.459343	6.38E-189	7.71E-188	2.14450794	0	100	GSTM2	1.10665608	2.78868186	127.74114	1.28E-29	4.49E-29	0.94778309	19.4444444	80.5555556
ENSG00000169385	RNASE2	-4.9338647	0.32180955	857.575546	1.64E-188	1.97E-187	-5.7341684	100	0	RNASE2	-6.4485937	0.37634242	886.479462	8.53E-195	1.34E-193	-10000	100	0
ENSG00000232216	IGHV3-43	-6.1587434	-0.2988754	852.322638	2.27E-187	2.72E-186	-10000	100	0	IGHV3-43	-6.2228027	-0.3887244	647.714307	7.02E-143	8.85E-142	-10000	100	0
ENSG00000100365	NCF4	-2.737752	2.65201114	852.125853	2.51E-187	3.00E-186	-2.7423353	100	0	NCF4	-4.6651095	2.46705636	1502.20143	0	0	-4.6390466	100	0
ENSG00000142409	ZNF787	-2.0866585	4.27849102	850.964012	4.49E-187	5.34E-186	-2.113325	100	0	ZNF787	-1.9909961	4.25726897	651.898973	8.63E-144	1.10E-142	-2.0115345	100	0
ENSG00000244509	APOBEC3C	-2.2399935	3.79377967	845.568287	6.68E-186	7.94E-185	-2.1531126	100	0	APOBEC3C	-0.9086103	4.11654827	137.875429	7.76E-32	2.86E-31	-0.9755444	100	0
ENSG00000174021	GNG5	-1.9704931	4.67557118	837.596591	3.62E-184	4.26E-183	-1.9138507	100	0	GNG5	-1.729705	4.70604493	550.262681	1.10E-121	1.20E-120	-1.7746898	100	0
ENSG00000181444	ZNF467	-2.5524113	2.98723905	834.573825	1.64E-183	1.93E-182	-2.3701141	100	0	ZNF467	-3.2096507	2.92167543	988.66456	5.23E-217	9.14E-216	-3.2237736	100	0
ENSG00000111640	GAPDH	-1.8074571	9.33584652	829.70727	1.88E-182	2.19E-181	-1.7039819	100	0	GAPDH	-1.3122152	9.43848203	313.310201	4.15E-70	2.83E-69	-1.3222431	100	0
ENSG00000171867	PRNP	-1.7974171	7.36955149	828.383344	3.64E-182	4.24E-181	-1.6848595	100	0	PRNP	-1.1248018	7.46393128	267.566637	3.85E-60	2.27E-59	-1.0333156	100	0
ENSG00000106991	ENG	-2.2209094	3.86203408	824.837492	2.15E-181	2.49E-180	-2.1145737	100	0	ENG	-2.4643048	3.85635344	821.288629	1.27E-180	1.88E-179	-2.5021905	100	0
ENSG00000108932	SLC16A6	-2.1837695	3.81144623	819.634588	2.91E-180	3.35E-179	-2.0869387	100	0	SLC16A6	-1.5560208	3.94773835	373.002075	4.15E-83	3.26E-82	-1.5768383	100	0
ENSG00000065882	TBC1D1	-1.8227195	5.89520007	818.323313	5.60E-180	6.45E-179	-1.6868041	100	0	TBC1D1	-1.1902136	5.98828704	304.157507	4.09E-68	2.74E-67	-1.2510562	100	0
ENSG00000148429	USP6NL	-1.9706497	4.55988028	817.500907	8.45E-180	9.71E-179	-1.8644625	100	0	USP6NL	-1.5557319	4.58815751	440.028538	1.07E-97	9.74E-97	-1.5607566	100	0
ENSG00000128203	ASPHD2	-2.6479333	2.60604812	809.741607	4.11E-178	4.70E-177	-2.6038409	100	0	ASPHD2	-2.1469339	2.64123886	461.576419	2.18E-102	2.07E-101	-2.1094045	100	0
ENSG00000105963	ADAP1	-2.6626957	2.59163235	807.281161	1.41E-177	1.60E-176	-2.5004123	100	0	ADAP1	-1.5298276	2.85436611	248.9586	4.38E-56	2.46E-55	-1.564306	97.2222222	2.77777778
ENSG00000170677	SOCS6	-2.2717678	3.53917332	802.654775	1.43E-176	1.62E-175	-2.2651375	100	0	SOCS6	-2.7982423	3.42825874	954.675238	1.28E-209	2.15E-208	-2.7257569	100	0
ENSG00000169756	LIMS1	-2.0748207	4.08961335	800.615467	3.97E-176	4.49E-175	-2.0375564	100	0	LIMS1	-1.9781715	4.07901218	613.355908	2.08E-135	2.47E-134	-2.0270011	100	0
ENSG00000177105	RHOG	-1.7798743	6.82459667	799.659569	6.40E-176	7.22E-175	-1.7043002	100	0	RHOG	-1.3761861	6.88548517	399.75206	6.24E-89	5.26E-88	-1.4320135	100	0
ENSG00000140030	GPR65	-2.0419788	4.14027592	790.906464	5.12E-174	5.75E-173	-1.8735856	100	0	GPR65	-1.3910091	4.24679609	328.895111	1.67E-73	1.18E-72	-1.3458771	100	0
ENSG00000196187	TMEM63A	1.8093388	5.81974213	790.574877	6.04E-174	6.77E-173	1.83948455	0	100	TMEM63A	1.21000639	5.30345943	295.647261	2.92E-66	1.89E-65	1.1217112	2.77777778	97.2222222
ENSG00000146540	C7orf50	-1.9760005	4.3693004	783.024152	2.65E-172	2.95E-171	-1.7341468	100	0	C7orf50	-1.883234	4.33260518	595.866315	1.33E-131	1.54E-130	-1.8469591	100	0
ENSG00000165527	ARF6	-1.7447768	7.53892301	778.759561	2.24E-171	2.49E-170	-1.6763342	100	0	ARF6	-1.3375595	7.58222853	373.331496	3.52E-83	2.77E-82	-1.3764979	100	0
ENSG00000198833	UBE2J1	-1.7481491	7.22562736	777.021715	5.35E-171	5.91E-170	-1.7201174	100	0	UBE2J1	-1.4627407	7.20927021	449.21261	1.07E-99	9.98E-99	-1.4813324	100	0
ENSG00000170296	GABARAP	-1.8440591	5.08001412	775.418319	1.19E-170	1.31E-169	-1.6917727	100	0	GABARAP	-1.9751196	5.04022477	739.762524	6.75E-163	9.25E-162	-1.9858145	100	0
ENSG00000133246	PRAM1	-2.4504186	3.0785769	774.554435	1.84E-170	2.02E-169	-2.5011652	100	0	PRAM1	-2.8682432	3.04648235	824.959462	2.02E-181	3.01E-180	-3.1134821	100	0
ENSG00000130402	ACTN4	-1.7908134	5.45913666	768.145688	4.55E-169	4.98E-168	-1.7213221	100	0	ACTN4	-0.6870127	5.8199634	96.2476836	1.01E-22	3.01E-22	-0.654874	86.1111111	13.8888889
ENSG00000142227	EMP3	-1.7319678	7.08306149	764.923596	2.28E-168	2.49E-167	-1.6685883	100	0	EMP3	-1.6900983	7.04412734	589.937398	2.59E-130	2.97E-129	-1.8087626	100	0
ENSG00000177697	CD151	-2.2538839	3.42378479	764.709292	2.54E-168	2.77E-167	-2.169411	100	0	CD151	-1.8881641	3.46887069	460.417284	3.90E-102	3.70E-101	-1.9894034	100	0
ENSG00000223350	IGLV9-49	-6.2118837	-0.4859033	761.425047	1.32E-167	1.43E-166	-10000	100	0	IGLV9-49	-6.3243425	-0.4869072	637.390552	1.23E-140	1.53E-139	-10000	100	0
ENSG00000178695	KCTD12	-1.8276224	5.05773434	756.166075	1.83E-166	1.99E-165	-1.8774749	100	0	KCTD12	-2.9995298	4.85604232	1499.68698	0	0	-3.1314168	100	0
ENSG00000128524	ATP6V1F	-1.7503088	5.84043507	749.073216	6.38E-165	6.88E-164	-1.7880296	100	0	ATP6V1F	-1.4304838	5.87188202	424.014144	3.26E-94	2.86E-93	-1.5179587	100	0
ENSG00000074800	ENO1	-1.6997947	8.01733781	748.416519	8.87E-165	9.55E-164	-1.5793957	100	0	ENO1	-1.6176745	7.9990363	526.287643	1.81E-116	1.92E-115	-1.6771766	100	0
ENSG00000103490	PYCARD	-2.6240584	2.48132305	745.685696	3.48E-164	3.73E-163	-2.575912	100	0	PYCARD	-2.6727339	2.46352963	624.422432	8.16E-138	9.90E-137	-2.5800786	100	0

ENSG00000122862	SRGN	-1.7232266	9.27312084	743.831829	8.80E-164	9.42E-163	-1.6219228	100	0	SRGN	-1.2820519	9.3828439	295.395733	3.32E-66	2.14E-65	-1.2465234	100	0
ENSG00000160685	ZBTB7B	-1.9051611	4.42770003	739.542929	7.54E-163	8.03E-162	-1.8266659	100	0	ZBTB7B	-3.5269249	4.25100404	1683.15886	0	0	-3.4222016	100	0
ENSG00000237499	RP11-356I2.4	1.87442159	4.57595727	736.973346	2.73E-162	2.90E-161	2.02291349	0	100	RP11-356I2.4	2.04707433	4.65096434	728.01484	2.42E-160	3.26E-159	2.00088737	2.77777778	97.2222222
ENSG00000254470	AP5B1	-1.979263	4.09053511	735.995465	4.45E-162	4.72E-161	-1.8290882	100	0	AP5B1	-1.7337777	4.14936732	486.703724	7.43E-108	7.43E-107	-1.6210371	100	0
ENSG00000132680	KIAA0907	2.10867782	3.72291775	727.392854	3.30E-160	3.48E-159	2.12722776	0	100	KIAA0907	1.95730058	3.52000305	506.455929	3.74E-112	3.84E-111	1.89738599	2.77777778	97.2222222
ENSG00000162419	GMEB1	-1.8221145	4.6365489	723.225446	2.66E-159	2.79E-158	-1.7614737	100	0	GMEB1	-0.9313179	4.81033157	170.774915	5.01E-39	2.14E-38	-0.9578082	100	0
ENSG00000136213	CHST12	-2.4985854	2.61672107	722.303022	4.23E-159	4.41E-158	-2.4210974	100	0	CHST12	-0.5716209	3.1628334	40.3949629	2.07E-10	4.18E-10	-0.6798374	75	25
ENSG00000177156	TALDO1	-1.8951558	4.39767017	721.733497	5.62E-159	5.86E-158	-1.8257327	100	0	TALDO1	-1.7946796	4.39802134	542.67649	4.93E-120	5.32E-119	-1.8383899	100	0
ENSG00000066739	ATG2B	1.74566876	5.43082588	719.497523	1.72E-158	1.79E-157	1.80842415	0	100	ATG2B	1.51889644	5.27264134	457.064475	2.09E-101	1.98E-100	1.44783943	0	100
ENSG00000130714	POMT1	2.01173877	3.90205238	706.831124	9.78E-156	1.01E-154	1.96920781	0	100	POMT1	1.60397793	3.51385798	345.596114	3.86E-77	2.83E-76	1.68084971	0	100
ENSG00000185201	IFITM2	-1.7199967	5.47683701	704.681027	2.87E-155	2.96E-154	-1.5853788	100	0	IFITM2	-1.7110662	5.47340436	576.521917	2.14E-127	2.40E-126	-1.7145537	100	0
ENSG00000084207	GSTP1	-1.7166178	5.35504797	703.406204	5.43E-155	5.59E-154	-1.6150502	100	0	GSTP1	-1.4647781	5.40695021	433.154749	3.34E-96	2.99E-95	-1.5357269	100	0
ENSG00000129757	CDKN1C	-2.4671973	2.70089452	700.670607	2.14E-154	2.19E-153	-2.355029	100	0	CDKN1C	-1.8082947	2.84226098	330.219179	8.61E-74	6.10E-73	-2.0104386	97.2222222	2.77777778
ENSG00000123684	LPGAT1	-1.7812666	4.71950838	700.397577	2.45E-154	2.50E-153	-1.6380308	100	0	LPGAT1	-0.7318536	4.96836002	107.662966	3.19E-25	1.01E-24	-0.7079067	100	0
ENSG00000265666	RARA-AS1	-2.7237553	1.98139602	700.143767	2.78E-154	2.84E-153	-2.6076048	100	0	RARA-AS1	-2.0309593	2.03131935	336.283925	4.11E-75	2.95E-74	-1.9467173	100	0
ENSG00000248124	RRN3P1	1.863547	4.34439326	698.279207	7.08E-154	7.17E-153	1.89825926	0	100	RRN3P1	1.40787109	3.89689603	309.655384	2.60E-69	1.76E-68	1.37635452	0	100
ENSG00000102524	TNFSF13B	-2.5551719	2.62731573	697.534808	1.03E-153	1.04E-152	-2.6364679	100	0	TNFSF13B	-4.3983681	2.50610149	1370.10601	6.58E-300	1.55E-298	-4.4763625	100	0
ENSG00000172757	CFL1	-1.6378115	8.33116091	696.356389	1.85E-153	1.87E-152	-1.5613236	100	0	CFL1	-1.0179765	8.47786876	207.481135	4.87E-47	2.40E-46	-1.0561031	100	0
ENSG00000141682	PMAIP1	-1.6652401	6.34650403	695.116699	3.45E-153	3.47E-152	-1.6094108	100	0	PMAIP1	-0.9839963	6.4598733	206.620666	7.50E-47	3.68E-46	-1.0480068	100	0
ENSG00000198723	C19orf45	2.62056204	2.33512298	691.376613	2.24E-152	2.26E-151	2.66149798	0	100	C19orf45	1.98817749	1.72469594	281.502979	3.53E-63	2.17E-62	1.99663816	0	100
ENSG00000001036	FUCA2	-2.5250853	2.39067681	690.695882	3.15E-152	3.17E-151	-2.3978463	100	0	FUCA2	-2.8197277	2.35741369	674.805593	9.01E-149	1.16E-147	-2.80589	100	0
ENSG00000100605	ITPK1	-1.6965671	5.29653667	689.813624	4.91E-152	4.92E-151	-1.6072058	100	0	ITPK1	-1.027753	5.44505692	219.733994	1.03E-49	5.31E-49	-1.088934	97.2222222	2.77777778
ENSG00000108828	VAT1	-1.9686697	3.94617598	683.741227	1.03E-150	1.03E-149	-1.8530555	100	0	VAT1	-2.5486335	3.85775867	876.97895	9.92E-193	1.54E-191	-2.7666352	100	0
ENSG00000034152	MAP2K3	-1.6574109	6.24475062	682.846042	1.61E-150	1.60E-149	-1.5672346	100	0	MAP2K3	-0.9324747	6.38564946	187.031187	1.41E-42	6.43E-42	-0.9419847	100	0
ENSG00000198804	MT-CO1	-1.6718649	12.6907177	682.845814	1.61E-150	1.60E-149	-1.556349	100	0	MT-CO1	-1.0873559	12.8151788	165.786498	6.16E-38	2.57E-37	-1.1535689	100	0
ENSG00000090013	BLVRB	-2.7307935	1.98129116	680.886233	4.29E-150	4.27E-149	-2.476886	100	0	BLVRB	-1.8581652	2.10800127	278.870945	1.32E-62	8.08E-62	-2.0048094	100	0
ENSG00000170385	SLC30A1	-1.7765135	4.63041949	677.707746	2.11E-149	2.09E-148	-1.7443852	100	0	SLC30A1	-0.8594187	4.88899283	143.730932	4.07E-33	1.54E-32	-0.8162489	100	0
ENSG00000111252	SH2B3	-1.6196887	7.57022002	676.864314	3.21E-149	3.19E-148	-1.4709618	100	0	SH2B3	-1.7316885	7.47963848	613.750349	1.71E-135	2.03E-134	-1.6606198	100	0
ENSG00000109113	RAB34	-2.3300474	2.82729312	676.79944	3.32E-149	3.29E-148	-2.2024717	100	0	RAB34	-3.696272	2.69984712	1169.32949	2.82E-256	5.71E-255	-3.7935524	100	0
ENSG00000183386	FHL3	-2.4294465	2.544161	676.711488	3.47E-149	3.43E-148	-2.311795	100	0	FHL3	-1.8525444	2.605239	343.686612	1.00E-76	7.32E-76	-1.8461884	100	0
ENSG00000108819	PPP1R9B	-1.6321526	6.4961653	676.577177	3.71E-149	3.67E-148	-1.516068	100	0	PPP1R9B	-1.1461509	6.57117789	279.466924	9.81E-63	6.01E-62	-1.1776976	97.2222222	2.77777778
ENSG00000125657	TNFSF9	-2.7948315	1.78970946	675.768151	5.56E-149	5.49E-148	-2.6992246	100	0	TNFSF9	-1.3948181	2.10805478	157.683552	3.63E-36	1.46E-35	-1.3101112	94.4444444	5.55555556
ENSG00000171310	CHST11	-1.6660919	5.43574178	673.344852	1.87E-148	1.84E-147	-1.6174455	100	0	CHST11	-1.3797342	5.4775365	393.432493	1.48E-87	1.23E-86	-1.4263146	100	0
ENSG00000177879	AP3S1	-1.6986214	5.06534489	671.87098	3.91E-148	3.84E-147	-1.6801534	100	0	AP3S1	-1.2427126	5.14798614	311.522361	1.02E-69	6.92E-69	-1.3013038	100	0
ENSG00000005893	LAMP2	-1.6651177	5.47111481	667.492113	3.51E-147	3.42E-146	-1.5892304	100	0	LAMP2	-1.6397824	5.46460647	547.208986	5.10E-121	5.53E-120	-1.6215108	100	0
ENSG00000142634	EFHD2	-1.6108102	7.28342576	665.540791	9.32E-147	9.06E-146	-1.6387966	100	0	EFHD2	-0.6898398	7.51689244	99.8390133	1.65E-23	5.00E-23	-0.7839614	91.6666667	8.33333333
ENSG00000105738	SIPA1L3	-1.7095959	4.97490665	664.410171	1.64E-146	1.59E-145	-1.5947399	100	0	SIPA1L3	-1.5633251	4.87675647	463.222851	9.56E-103	9.12E-102	-1.6560044	100	0
ENSG00000150403	TMCO3	-1.9971242	3.62470782	663.345726	2.80E-146	2.71E-145	-1.9382639	100	0	TMCO3	-1.7297569	3.65257485	428.937397	2.77E-95	2.45E-94	-1.7076829	100	0
ENSG00000110987	BCL7A	-1.7018496	5.07706743	661.831068	5.97E-146	5.78E-145	-1.612688	100	0	BCL7A	-1.4347793	5.02521678	401.088339	3.19E-89	2.69E-88	-1.471094	100	0
ENSG00000140749	IGSF6	-2.9053929	1.51566013	660.939832	9.33E-146	9.02E-145	-2.6631439	100	0	IGSF6	-3.3341934	1.45763958	634.729285	4.68E-140	5.79E-139	-3.3627927	100	0
ENSG00000188313	PLSCR1	-1.8911815	4.04807113	659.627944	1.80E-145	1.74E-144	-1.7308978	100	0	PLSCR1	-1.9664268	4.09867888	609.690171	1.31E-134	1.54E-133	-1.893248	100	0
ENSG00000165516	KLHDC2	1.62389925	6.02552856	657.13532	6.27E-145	6.03E-144	1.65850992	0	100	KLHDC2	0.99050277	5.52233661	205.728237	1.17E-46	5.74E-46	0.99801408	2.77777778	97.2222222
ENSG00000172270	BSG	-1.6390314	5.67505951	656.817935	7.35E-145	7.05E-144	-1.5866051	100	0	BSG	-1.0798646	5.81320219	242.864319	9.34E-55	5.14E-54	-1.1564655	97.2222222	2.77777778
ENSG00000135334	AKIRIN2	-1.6224628	5.99414955	656.634963	8.06E-145	7.72E-144	-1.5301213	100	0	AKIRIN2	-1.3741166	5.99818649	399.18747	8.28E-89	6.94E-88	-1.367188	100	0
ENSG00000185825	BCAP31	-1.658025	5.24674267	654.153383	2.79E-144	2.67E-143	-1.5839072	100	0	BCAP31	-1.2402121	5.35641966	315.116487	1.68E-70	1.15E-69	-1.2841449	100	0
ENSG00000085117	CD82	-1.6674654	5.37951023	651.899642	8.63E-144	8.25E-143	-1.5144974	100	0	CD82	-2.7984065	5.13970932	1393.86717	4.52E-305	1.07E-303	-2.6937764	100	0
ENSG00000259261	IGHV4OR15-8	-4.9083217	-0.4831849	650.571766	1.68E-143	1.60E-142	-5.5477346	97.1428571	2.85714286	IGHV4OR15-8	-4.6988652	-0.5856953	450.532149	5.52E-100	5.18E-99	-5.3840672	91.6666667	8.33333333
ENSG00000072135	PTPN18	-1.6825737	4.96671983	650.159296	2.06E-143	1.96E-142	-1.5768146	100	0	PTPN18	-1.6569608	4.960013	515.040993	5.08E-114	5.30E-113	-1.7779205	100	0
ENSG00000124570	SERPINB6	-2.1552201	3.21178492	648.965487	3.75E-143	3.56E-142	-2.0652497	100	0	SERPINB6	-0.6275902	3.60620242	56.9335383	4.51E-14	1.04E-13	-0.730678	88.8888889	11.1111111
ENSG00000166484	MAPK7	-1.787776	4.34219926	648.819226	4.04E-143	3.83E-142	-1.7288855	100	0	MAPK7	-2.175312	4.25184346	759.013395	4.40E-167	6.18E-166	-2.2335898	100	0
ENSG00000141140	NA	1.8747583	4.03441122	646.382465	1.37E-142	1.29E-141	1.87509352	0	100	NA	1.70037871	3.85911899	432.382758	4.92E-96	4.39E-95	1.56983969	0	100
ENSG00000173457	PPP1R14B	-1.7813686	4.31789009	642.674873	8.75E-142	8.27E-141	-1.7161489	100	0	PPP1R14B	-1.514516	4.29756785	394.35516	9.33E-88	7.75E-87	-1.6370314	100	0
ENSG00000136840	ST6GALNAC4	-1.9256896	3.77679839	639.452985	4.39E-141	4.13E-140	-1.7931662	100	0	ST6GALNAC4	-1.1878637	3.87662832	220.798233	6.06E-50	3.13E-49	-1.2551755	100	0

ENSG00000182606	TRAK1	-1.6019731	5.82715779	635.025196	4.04E-140	3.77E-139	-1.5451241	100	0	TRAK1	-1.2315938	5.85801948	322.357297	4.44E-72	3.10E-71	-1.2834715	100	0
ENSG00000136026	CKAP4	-1.6167282	5.52307016	633.573147	8.35E-140	7.78E-139	-1.4381001	100	0	CKAP4	-1.335532	5.5369635	368.716709	3.56E-82	2.76E-81	-1.3598985	100	0
ENSG00000151176	PLBD2	-1.9740012	3.57841478	633.337824	9.39E-140	8.74E-139	-1.8648109	100	0	PLBD2	-2.5092768	3.50597589	787.940409	2.26E-173	3.25E-172	-2.5919568	100	0
ENSG00000106799	TGFBR1	-1.6040449	5.79857246	632.071525	1.77E-139	1.64E-138	-1.4952113	100	0	TGFBR1	-1.0621157	5.87072915	238.359615	8.96E-54	4.88E-53	-0.9824006	100	0
ENSG00000026950	BTN3A1	1.65763257	5.58540037	630.519803	3.85E-139	3.57E-138	1.57895556	0	100	BTN3A1	1.63802895	5.42436846	515.599179	3.84E-114	4.02E-113	1.45359406	0	100
ENSG00000100612	DHRS7	-1.7906099	4.1669224	629.552155	6.25E-139	5.79E-138	-1.7139507	100	0	DHRS7	-0.9067829	4.4055012	149.890211	1.83E-34	7.16E-34	-0.9508502	100	0
ENSG00000163931	TKT	-1.5656333	7.581347	628.057419	1.32E-138	1.22E-137	-1.4370511	100	0	TKT	-1.7143767	7.5318804	592.156461	8.51E-131	9.83E-130	-1.6816596	100	0
ENSG00000122223	CD244	-2.2643244	2.71838	624.970058	6.21E-138	5.71E-137	-2.1432434	100	0	CD244	-1.6420404	2.80022282	291.38342	2.48E-65	1.58E-64	-1.6951244	100	0
ENSG00000172531	PPP1CA	-1.6065506	5.47797704	622.687918	1.95E-137	1.79E-136	-1.4917023	100	0	PPP1CA	-0.9240174	5.66246819	180.480169	3.81E-41	1.70E-40	-1.0405935	100	0
ENSG00000164713	BRI3	-1.587704	5.75567068	622.563593	2.07E-137	1.90E-136	-1.5153013	100	0	BRI3	-1.4778646	5.74290868	448.548748	1.49E-99	1.39E-98	-1.5562402	100	0
ENSG00000155229	MMS19	1.64257778	4.98781567	621.748868	3.11E-137	2.85E-136	1.60884912	0	100	MMS19	1.14937284	4.58325872	245.603211	2.36E-55	1.31E-54	1.05706776	2.77777778	97.2222222
ENSG00000011132	APBA3	1.69402544	4.60499448	620.893795	4.78E-137	4.36E-136	1.76093958	0	100	APBA3	1.26937486	4.25394682	277.252201	2.98E-62	1.81E-61	1.22679722	2.77777778	97.2222222
ENSG00000169230	PRELID1	-1.7043554	4.57117557	619.18044	1.13E-136	1.03E-135	-1.6460346	100	0	PRELID1	-1.8993862	4.51938353	626.424588	3.00E-138	3.65E-137	-1.912715	100	0
ENSG00000171314	PGAM1	-1.5647218	6.25002059	615.972852	5.62E-136	5.08E-135	-1.5027922	100	0	PGAM1	-1.2759087	6.30063549	344.915499	5.42E-77	3.96E-76	-1.3138917	100	0
ENSG00000176531	PHLDB3	1.70307881	4.63099018	615.313619	7.82E-136	7.06E-135	1.66621998	0	100	PHLDB3	2.08980915	4.78714842	793.03652	1.76E-174	2.54E-173	1.96359311	0	100
ENSG00000198435	NRARP	-2.3112173	2.67266601	614.973874	9.27E-136	8.36E-135	-2.2691765	100	0	NRARP	-2.5305499	2.54540366	576.594633	2.06E-127	2.32E-126	-2.4298022	100	0
ENSG00000218422	NA	2.14558819	2.99921156	611.505236	5.26E-135	4.72E-134	2.15069663	0	100	NA	1.91214629	2.76370345	381.432184	6.07E-85	4.88E-84	1.86563418	0	100
ENSG00000067560	RHOA	-1.5189022	8.424185	604.956486	1.40E-133	1.25E-132	-1.508108	100	0	RHOA	-1.1244684	8.49111651	253.790107	3.87E-57	2.21E-56	-1.1931605	100	0
ENSG00000182487	NCF1B	-2.3939685	2.30358779	603.793544	2.50E-133	2.23E-132	-2.2336988	100	0	NCF1B	-2.6696103	2.22105137	580.297229	3.23E-128	3.66E-127	-2.5732728	100	0
ENSG00000085491	SLC25A24	-1.8774837	3.69448741	602.263215	5.39E-133	4.79E-132	-1.8328577	100	0	SLC25A24	-2.0965742	3.62619997	599.057212	2.68E-132	3.13E-131	-1.977622	100	0
ENSG00000140403	DNAJA4	1.60661151	5.04231818	601.590645	7.55E-133	6.70E-132	1.69585411	0	100	DNAJA4	1.16751222	4.66529646	257.970691	4.75E-58	2.74E-57	1.14428065	0	100
ENSG00000102316	MAGED2	1.58813682	5.43891044	600.400534	1.37E-132	1.21E-131	1.63284675	0	100	MAGED2	1.47000418	5.18911406	430.255867	1.43E-95	1.27E-94	1.41203863	0	100
ENSG00000213930	GALT	1.88972923	3.72528816	599.13477	2.58E-132	2.28E-131	1.89988175	0	100	GALT	1.09529943	3.06127934	145.422626	1.74E-33	6.63E-33	0.92047144	0	100
ENSG00000112242	E2F3	-1.8806434	3.69674658	598.920965	2.87E-132	2.54E-131	-1.8488076	100	0	E2F3	-1.0988999	3.86748302	188.262972	7.61E-43	3.48E-42	-1.1386881	97.2222222	2.77777778
ENSG00000238105	GOLGA2P5	1.78645952	4.09243846	597.265498	6.59E-132	5.78E-131	1.70100893	0	100	GOLGA2P5	1.58069651	3.87058949	380.631211	9.07E-85	7.25E-84	1.5064684	0	100
ENSG00000140941	MAP1LC3B	-1.5145145	7.42225073	597.123676	7.07E-132	6.19E-131	-1.4611686	100	0	MAP1LC3B	-0.9427738	7.51116899	188.882394	5.58E-43	2.56E-42	-0.9212633	100	0
ENSG00000104894	CD37	-1.5094425	8.06888522	595.620908	1.50E-131	1.31E-130	-1.4109248	100	0	CD37	-1.5578792	7.96816456	490.549126	1.08E-108	1.09E-107	-1.5710781	100	0
ENSG00000126456	IRF3	1.59150655	5.20611808	595.001087	2.05E-131	1.78E-130	1.69805974	0	100	IRF3	1.1213144	4.8105615	239.355951	5.43E-54	2.96E-53	0.92465653	2.77777778	97.2222222
ENSG00000141753	IGFBP4	-2.4025801	2.20643299	594.870362	2.19E-131	1.90E-130	-2.2607222	100	0	IGFBP4	-2.3884195	2.12182996	460.848451	3.14E-102	2.98E-101	-2.3988822	100	0
ENSG00000149925	ALDOA	-1.5066796	8.02555497	593.819449	3.70E-131	3.21E-130	-1.423845	100	0	ALDOA	-1.1982979	8.09856725	292.113941	1.72E-65	1.10E-64	-1.1843309	100	0
ENSG00000116191	RALGPS2	-1.6648645	4.71003396	582.423212	1.11E-128	9.58E-128	-1.4617499	100	0	RALGPS2	-1.7983609	4.5732212	554.461467	1.35E-122	1.48E-121	-1.6563057	100	0
ENSG00000174171	RP11-23P13.6	2.20163922	2.7395332	577.256162	1.48E-127	1.27E-126	2.19188939	0	100	RP11-23P13.6	2.16496657	2.70314761	446.24002	4.75E-99	4.40E-98	2.13567232	0	100
ENSG00000101307	SIRPB1	-2.2238406	2.83156571	576.541655	2.12E-127	1.81E-126	-2.2318921	94.2857143	5.71428571	SIRPB1	-2.7636173	2.84747646	705.987617	1.49E-155	1.98E-154	-3.0527797	100	0
ENSG00000148175	STOM	-1.5973405	4.92638675	575.584113	3.42E-127	2.92E-126	-1.6141493	100	0	STOM	-0.7323504	5.185013	108.288451	2.32E-25	7.39E-25	-0.6426165	97.2222222	2.77777778
ENSG00000111674	ENO2	1.89569777	3.54639009	572.239676	1.83E-126	1.55E-125	1.79249766	0	100	ENO2	1.5167959	3.19578288	284.096913	9.61E-64	5.97E-63	1.44477231	0	100
ENSG00000127124	HIVEP3	-1.6117777	4.65289902	571.731924	2.36E-126	1.99E-125	-1.5361385	100	0	HIVEP3	-1.895643	4.54342115	626.298536	3.19E-138	3.88E-137	-1.8651003	100	0
ENSG00000153094	BCL2L11	-1.482272	7.37726063	568.400514	1.25E-125	1.05E-124	-1.3743404	100	0	BCL2L11	-1.2735082	7.3307872	344.033617	8.44E-77	6.16E-76	-1.3083074	100	0
ENSG00000130479	MAP1S	-1.5865332	4.82486792	567.092213	2.41E-125	2.02E-124	-1.5152479	100	0	MAP1S	-1.1578852	4.89303455	258.817062	3.11E-58	1.80E-57	-1.3435071	97.2222222	2.77777778
ENSG00000137802	MAPKBP1	1.66588572	4.3103679	565.282353	5.96E-125	4.97E-124	1.65648365	0	100	MAPKBP1	1.52694474	4.14855856	385.233098	9.03E-86	7.31E-85	1.44405078	0	100
ENSG00000110324	IL10RA	-1.4659714	8.06527535	562.55826	2.33E-124	1.94E-123	-1.3511249	100	0	IL10RA	-1.3939158	8.08709367	389.745433	9.40E-87	7.70E-86	-1.3482058	100	0
ENSG00000112561	TFEB	-1.7510454	3.93989749	561.863849	3.30E-124	2.74E-123	-1.6964342	100	0	TFEB	-1.5309834	3.9915194	368.405922	4.16E-82	3.22E-81	-1.6420194	97.2222222	2.77777778
ENSG00000147872	PLIN2	-1.5039937	6.23766301	559.818009	9.21E-124	7.63E-123	-1.3796254	100	0	PLIN2	-1.9480429	6.06366962	759.761214	3.03E-167	4.26E-166	-1.9212682	100	0
ENSG00000140332	TLE3	-1.4628337	8.09209958	558.23167	2.04E-123	1.68E-122	-1.3566954	100	0	TLE3	-0.8071703	8.23978196	132.879737	9.61E-31	3.46E-30	-0.8546698	97.2222222	2.77777778
ENSG00000166949	SMAD3	-1.4850187	6.14503924	557.09214	3.61E-123	2.97E-122	-1.4304018	100	0	SMAD3	-2.1139174	5.95638455	902.127796	3.38E-198	5.40E-197	-2.0945874	100	0
ENSG00000162144	CYB561A3	-1.5497062	4.95127377	556.912537	3.95E-123	3.24E-122	-1.4613492	100	0	CYB561A3	-1.2839284	4.9363001	322.592165	3.95E-72	2.75E-71	-1.3290807	100	0
ENSG00000184232	OAF	-2.1022572	2.79760658	556.704209	4.38E-123	3.59E-122	-2.0442356	100	0	OAF	-1.9190667	2.83634122	389.308015	1.17E-86	9.58E-86	-1.9526097	100	0
ENSG00000132600	PRMT7	1.76808615	3.84544949	556.316893	5.32E-123	4.36E-122	1.81916704	0	100	PRMT7	1.42199774	3.52626526	281.210691	4.09E-63	2.52E-62	1.3499686	2.77777778	97.2222222
ENSG00000122122	SASH3	-1.464978	7.2377127	553.437491	2.25E-122	1.83E-121	-1.3650379	100	0	SASH3	-1.1726268	7.24498659	292.592028	1.35E-65	8.67E-65	-1.2754826	100	0
ENSG00000175348	TMEM9B	-1.4962228	5.61085007	552.18953	4.20E-122	3.41E-121	-1.3927796	100	0	TMEM9B	-0.8145181	5.76396317	142.564063	7.32E-33	2.76E-32	-0.816372	100	0
ENSG00000072062	PRKACA	-1.5421393	5.01341075	552.075737	4.45E-122	3.61E-121	-1.4792994	100	0	PRKACA	-1.3202443	5.05901962	341.663809	2.77E-76	2.01E-75	-1.330173	100	0
ENSG00000002834	LASP1	-1.4607541	7.06333043	552.038792	4.53E-122	3.67E-121	-1.4267208	100	0	LASP1	-0.5905621	7.31660224	74.7315838	5.39E-18	1.39E-17	-0.5364662	91.6666667	8.33333333
ENSG00000104324	CPQ	-1.9886214	3.05824879	549.745978	1.43E-121	1.16E-120	-1.937543	100	0	CPQ	-1.8165566	3.0842844	387.208266	3.35E-86	2.73E-85	-1.7535126	100	0
ENSG00000100445	SDR39U1	1.98551431	3.13519355	547.751233	3.88E-121	3.13E-120	1.84709082	0	100	SDR39U1	1.63763357	2.80937911	282.848	1.80E-63	1.11E-62	1.48770871	2.77777778	97.2222222

ENSG00000168758	SEMA4C	1.59787074	4.54547154	546.845935	6.11E-121	4.92E-120	1.68342715	0	100	SEMA4C	0.98969074	4.06171313	161.000703	6.84E-37	2.79E-36	0.86967601	5.55555556	94.4444444
ENSG00000124783	SSR1	-1.463323	6.27652768	544.272615	2.22E-120	1.78E-119	-1.4246795	100	0	SSR1	-1.1311989	6.33443659	275.762383	6.30E-62	3.80E-61	-1.1783604	100	0
ENSG00000143622	RIT1	-1.4587683	6.40386586	544.100154	2.42E-120	1.94E-119	-1.3826351	100	0	RIT1	-1.1357253	6.45300333	278.049583	2.00E-62	1.22E-61	-1.1457752	100	0
ENSG00000147119	CHST7	-2.1124682	2.65563373	541.378317	9.45E-120	7.54E-119	-2.119108	100	0	CHST7	-1.2707123	2.82621836	176.575291	2.71E-40	1.19E-39	-1.2529625	100	0
ENSG00000165312	OTUD1	-1.4666276	6.66445211	540.128494	1.77E-119	1.41E-118	-1.1517444	100	0	OTUD1	-1.7757322	6.54863198	646.49446	1.29E-142	1.62E-141	-1.8257405	100	0
ENSG00000185650	ZFP36L1	-1.4391874	8.18024508	538.513608	3.97E-119	3.16E-118	-1.4082388	100	0	ZFP36L1	-1.3637137	8.15002228	368.542005	3.89E-82	3.01E-81	-1.3201425	100	0
ENSG00000110911	SLC11A2	1.60121271	4.41360752	537.116621	7.99E-119	6.34E-118	1.64825988	0	100	SLC11A2	1.02613089	3.99558169	172.315331	2.31E-39	9.96E-39	1.02073249	2.77777778	97.2222222
ENSG00000113971	NPHP3	1.57446846	4.54380702	535.753353	1.58E-118	1.25E-117	1.62612239	0	100	NPHP3	1.21352927	4.26078892	254.789883	2.35E-57	1.34E-56	1.16429354	0	100
ENSG00000213658	LAT	2.01060758	2.98462247	534.892492	2.44E-118	1.93E-117	2.03957131	0	100	LAT	1.97904575	2.9078865	424.699331	2.32E-94	2.03E-93	1.9390286	0	100
ENSG00000056558	TRAF1	1.47583121	5.88961306	533.165361	5.79E-118	4.56E-117	1.45599495	0	100	TRAF1	0.7367484	5.34199886	112.269005	3.12E-26	1.01E-25	0.66734292	5.55555556	94.4444444
ENSG00000106683	LIMK1	-1.5886292	4.45063287	532.187278	9.44E-118	7.42E-117	-1.4677313	100	0	LIMK1	-1.0831507	4.56789915	218.031494	2.43E-49	1.24E-48	-1.0765384	100	0
ENSG00000196700	ZNF512B	1.480133	5.33179486	529.4917	3.64E-117	2.86E-116	1.53477637	0	100	ZNF512B	0.70604314	4.76827861	97.1909111	6.30E-23	1.88E-22	0.64260528	5.55555556	94.4444444
ENSG00000177239	MAN1B1	1.46957117	5.55654603	528.986462	4.69E-117	3.67E-116	1.49452628	0	100	MAN1B1	1.30489792	5.42261375	344.695473	6.06E-77	4.42E-76	1.32404339	0	100
ENSG00000119922	IFIT2	-1.7933811	3.63264286	525.855167	2.25E-116	1.76E-115	-1.6873369	100	0	IFIT2	-1.5647124	3.7603885	347.91851	1.20E-77	8.85E-77	-1.7318594	97.2222222	2.77777778
ENSG00000135127	CCDC64	1.46442177	5.43148434	525.463848	2.74E-116	2.14E-115	1.51941544	0	100	CCDC64	1.42268843	5.33115969	413.600778	6.03E-92	5.18E-91	1.39611507	0	100
ENSG00000178467	P4HTM	1.73317342	3.76867583	524.400293	4.67E-116	3.63E-115	1.72116366	0	100	P4HTM	1.39182511	3.47928584	266.17109	7.75E-60	4.56E-59	1.28196356	0	100
ENSG00000214022	REPIN1	-1.4532738	5.55847961	523.014967	9.35E-116	7.26E-115	-1.3862106	100	0	REPIN1	-1.4025418	5.51251639	406.79409	1.83E-90	1.55E-89	-1.4799751	100	0
ENSG00000155252	PI4K2A	-1.4417995	5.79411464	522.275273	1.35E-115	1.05E-114	-1.3752733	100	0	PI4K2A	-0.8740704	5.91114335	164.575726	1.13E-37	4.70E-37	-0.8858587	100	0
ENSG00000149311	ATM	1.41785484	7.40806929	519.469295	5.52E-115	4.27E-114	1.41897306	0	100	ATM	1.05734271	7.08497298	235.292648	4.18E-53	2.25E-52	0.93999501	11.1111111	88.8888889
ENSG00000105519	CAPS	1.64968742	4.06866734	519.379702	5.77E-115	4.47E-114	1.69586011	0	100	CAPS	1.29007998	3.74963185	247.378888	9.68E-56	5.42E-55	1.06580223	2.77777778	97.2222222
ENSG00000180530	NRIP1	-1.4166933	7.29619115	518.928822	7.24E-115	5.59E-114	-1.2577117	100	0	NRIP1	-1.3462492	7.24794843	377.080168	5.38E-84	4.26E-83	-1.3412617	100	0
ENSG00000058600	POLR3E	1.42759483	6.53836801	518.677493	8.21E-115	6.34E-114	1.6036884	0	100	POLR3E	1.30869054	6.34099086	364.88328	2.43E-81	1.86E-80	1.19408608	0	100
ENSG00000163754	GYG1	-1.6910846	3.85658377	518.662225	8.27E-115	6.38E-114	-1.5706072	100	0	GYG1	-0.9936719	4.03260469	162.51204	3.20E-37	1.31E-36	-0.9428228	100	0
ENSG00000215041	NEURL4	1.65943503	3.98739874	517.131751	1.78E-114	1.37E-113	1.73113977	0	100	NEURL4	1.44666229	3.78167062	314.054085	2.86E-70	1.96E-69	1.37412715	2.77777778	97.2222222
ENSG00000168159	RNF187	-1.4938223	4.90234802	515.236784	4.60E-114	3.52E-113	-1.4768747	100	0	RNF187	-1.2147844	4.97076059	288.784902	9.15E-65	5.78E-64	-1.302288	100	0
ENSG00000105355	PLIN3	-1.4595531	5.3495126	513.955089	8.74E-114	6.67E-113	-1.4348843	100	0	PLIN3	-1.7857903	5.27439897	627.60537	1.66E-138	2.03E-137	-1.8973946	100	0
ENSG00000151748	SAV1	-1.6606028	3.95705948	513.841387	9.26E-114	7.05E-113	-1.6000453	100	0	SAV1	-1.7039725	3.86715157	437.137272	4.54E-97	4.10E-96	-1.7660931	97.2222222	2.77777778
ENSG00000105717	PBX4	1.88631075	3.1861708	512.841547	1.53E-113	1.16E-112	1.91470386	0	100	PBX4	1.45798244	2.8483108	240.522189	3.03E-54	1.66E-53	1.38778261	0	100
ENSG00000223509	RP11-632K20.7	1.4737378	5.04654152	512.551952	1.77E-113	1.34E-112	1.54955553	0	100	RP11-632K20.	1.18097673	4.79630542	266.673551	6.02E-60	3.55E-59	1.1635527	2.77777778	97.2222222
ENSG00000100092	SH3BP1	-1.4793792	5.03177688	512.007019	2.32E-113	1.76E-112	-1.4418377	100	0	SH3BP1	-1.0645251	5.16687802	225.489785	5.74E-51	3.01E-50	-1.0786455	97.2222222	2.77777778
ENSG00000135956	TMEM127	-1.3959987	7.13652121	508.455797	1.37E-112	1.03E-111	-1.3667276	100	0	TMEM127	-1.1782164	7.15032204	297.055265	1.44E-66	9.36E-66	-1.24937	100	0
ENSG00000002919	SNX11	-1.5505761	4.39055084	507.918277	1.80E-112	1.35E-111	-1.4296089	100	0	SNX11	-0.8252764	4.56341549	129.273675	5.91E-30	2.09E-29	-0.8578553	100	0
ENSG00000101421	CHMP4B	-1.3939644	7.14499865	504.008893	1.28E-111	9.54E-111	-1.3402797	100	0	CHMP4B	-1.1038262	7.18066254	259.899217	1.81E-58	1.05E-57	-1.1932909	100	0
ENSG00000066322	ELOVL1	-1.5613783	4.30173624	503.715312	1.48E-111	1.10E-110	-1.4611344	100	0	ELOVL1	-0.8373381	4.49639367	131.092929	2.36E-30	8.40E-30	-0.8786324	100	0
ENSG00000175463	TBC1D10C	1.41057174	6.62199208	503.064333	2.05E-111	1.53E-110	1.44942674	0	100	TBC1D10C	0.93667028	6.21555245	186.356716	1.98E-42	9.00E-42	0.81042135	0	100
ENSG00000082153	BZW1	-1.3784225	8.08332461	501.991542	3.50E-111	2.61E-110	-1.2524511	100	0	BZW1	-0.7267148	8.22586206	108.582318	2.00E-25	6.39E-25	-0.7049773	100	0
ENSG00000134574	DDB2	1.67611823	3.81421645	501.12119	5.42E-111	4.03E-110	1.77581069	0	100	DDB2	1.04715898	3.33329005	148.150376	4.40E-34	1.70E-33	0.99593828	0	100
ENSG00000215302	CTD-3092A11.1	1.81023134	3.32337799	500.486433	7.45E-111	5.54E-110	1.96609438	0	100	CTD-3092A11.	1.20203917	2.89160558	167.564411	2.52E-38	1.06E-37	1.11476066	0	100
ENSG00000181852	RNF41	-1.4492623	5.12808429	500.329536	8.06E-111	5.98E-110	-1.3194771	100	0	RNF41	-0.9495396	5.20925812	186.274289	2.07E-42	9.37E-42	-0.9466207	100	0
ENSG00000157350	ST3GAL2	-1.6849521	3.76718534	499.895433	1.00E-110	7.42E-110	-1.5714884	100	0	ST3GAL2	-1.7063396	3.74414883	427.008735	7.28E-95	6.42E-94	-1.7008813	100	0
ENSG00000111229	ARPC3	-1.3914273	7.01581782	499.341376	1.32E-110	9.79E-110	-1.3321226	100	0	ARPC3	-1.0762195	7.05258629	246.99074	1.18E-55	6.58E-55	-1.1486092	100	0
ENSG00000106665	CLIP2	-1.7347437	3.59759947	498.842748	1.70E-110	1.26E-109	-1.7298115	100	0	CLIP2	-1.5870466	3.61069536	359.265743	4.07E-80	3.07E-79	-1.6751845	100	0
ENSG00000134899	ERCC5	1.4431481	5.12322142	498.100456	2.46E-110	1.82E-109	1.52329507	0	100	ERCC5	1.1566601	4.89117092	263.637423	2.76E-59	1.61E-58	1.09524783	0	100
ENSG00000180376	CCDC66	1.46540721	4.85396992	495.244418	1.03E-109	7.57E-109	1.53072359	0	100	CCDC66	1.0147191	4.47805058	189.105294	4.98E-43	2.29E-42	0.92448841	2.77777778	97.2222222
ENSG00000162241	SLC25A45	1.5472124	4.40408461	493.661635	2.28E-109	1.67E-108	1.61454431	0	100	SLC25A45	1.11477675	4.02563055	201.51949	9.73E-46	4.65E-45	0.96361221	2.77777778	97.2222222
ENSG00000079616	KIF22	1.39585199	6.03544032	493.648748	2.29E-109	1.68E-108	1.47540531	0	100	KIF22	1.43456053	6.0014604	434.65501	1.58E-96	1.41E-95	1.29496404	0	100
ENSG00000137161	CNPY3	-1.4015576	5.85661109	491.092958	8.24E-109	6.03E-108	-1.3304898	100	0	CNPY3	-1.2136168	5.88965577	308.488964	4.66E-69	3.14E-68	-1.3163462	100	0
ENSG00000143862	ARL8A	-1.4062322	5.59766581	490.652537	1.03E-108	7.50E-108	-1.3469422	100	0	ARL8A	-1.147795	5.62469883	277.10233	3.21E-62	1.95E-61	-1.1619859	100	0
ENSG00000137404	NRM	-2.1831893	2.08510568	489.003906	2.35E-108	1.71E-107	-2.1039324	100	0	NRM	-2.3197282	2.02507787	427.823815	4.84E-95	4.27E-94	-2.414174	100	0
ENSG00000162408	NOL9	1.39139196	6.27820796	488.995387	2.36E-108	1.71E-107	1.45244604	0	100	NOL9	1.15252234	6.02744053	282.792615	1.85E-63	1.14E-62	1.02636837	0	100
ENSG00000160305	DIP2A	1.40201522	5.80140431	487.118443	6.04E-108	4.37E-107	1.3753231	0	100	DIP2A	1.5783803	5.91573087	509.680598	7.44E-113	7.71E-112	1.44678201	0	100
ENSG00000137486	ARRB1	-1.5558438	4.24864632	485.240535	1.55E-107	1.12E-106	-1.3802865	100	0	ARRB1	-2.2716707	4.09954737	795.983923	4.03E-175	5.83E-174	-2.2176475	100	0
ENSG00000126264	HCST	-1.4629029	4.77488444	483.992043	2.89E-107	2.08E-106	-1.3237388	100	0	HCST	-0.4434976	5.08338952	40.1007745	2.41E-10	4.84E-10	-0.546344	86.1111111	13.8888889

ENSG00000177885	GRB2	-1.3573431	7.2444786	483.289267	4.11E-107	2.96E-106	-1.3413363	100	0	GRB2	-1.1826289	7.23970086	299.171753	4.99E-67	3.26E-66	-1.2154304	100	0
ENSG00000134324	LPIN1	1.38389796	5.84905116	479.876568	2.27E-106	1.63E-105	1.47267587	0	100	LPIN1	1.12228882	5.60705365	265.487859	1.09E-59	6.41E-59	1.11602447	0	100
ENSG00000184939	ZFP90	1.53577969	4.28338778	479.662074	2.53E-106	1.81E-105	1.56535561	0	100	ZFP90	0.78036778	3.78956321	94.6272453	2.30E-22	6.74E-22	0.65991471	5.55555556	94.4444444
ENSG00000111412	C12orf49	-1.4509185	4.80957835	479.232777	3.14E-106	2.24E-105	-1.344752	100	0	C12orf49	-0.8374158	4.90627129	140.009627	2.65E-32	9.89E-32	-0.812503	100	0
ENSG00000177595	PIDD1	1.44366629	4.79451272	476.124451	1.49E-105	1.06E-104	1.48258725	0	100	PIDD1	1.20720432	4.57348713	269.798279	1.26E-60	7.45E-60	1.07058686	0	100
ENSG00000120063	GNA13	-1.3366083	8.63622656	473.952455	4.42E-105	3.14E-104	-1.2325449	100	0	GNA13	-0.6613966	8.77796087	87.3390535	9.14E-21	2.58E-20	-0.6005009	100	0
ENSG00000176155	CCDC57	1.39733379	5.39877818	473.199066	6.45E-105	4.58E-104	1.52581977	0	100	CCDC57	1.59666783	5.46064112	520.192545	3.84E-115	4.05E-114	1.46287147	0	100
ENSG00000180902	D2HGDH	1.64156054	3.81356352	471.479472	1.53E-104	1.08E-103	1.66173363	0	100	D2HGDH	1.31967327	3.55252878	241.667427	1.70E-54	9.36E-54	1.12554571	0	100
ENSG00000111144	LTA4H	-1.3728364	5.78697422	468.931334	5.47E-104	3.84E-103	-1.2526673	100	0	LTA4H	-1.2385417	5.76371015	319.639022	1.74E-71	1.20E-70	-1.2754251	100	0
ENSG00000197586	ENTPD6	1.38922301	5.29214875	465.638485	2.85E-103	2.00E-102	1.34208998	0	100	ENTPD6	0.70137208	4.77699961	95.5472972	1.44E-22	4.26E-22	0.52902308	8.33333333	91.6666667
ENSG00000090863	GLG1	1.3487561	6.42080603	465.38748	3.23E-103	2.26E-102	1.3850396	0	100	GLG1	1.02168853	6.15284891	223.689217	1.42E-50	7.36E-50	0.97997996	5.55555556	94.4444444
ENSG00000169508	GPR183	-1.3349044	7.72539044	463.741285	7.37E-103	5.15E-102	-1.2040543	100	0	GPR183	-3.0809181	7.38168032	1735.53784	0	0	-3.0339989	100	0
ENSG00000103245	NARFL	1.82443882	3.05106891	463.448884	8.54E-103	5.96E-102	1.82001205	0	100	NARFL	1.43328643	2.74546684	219.830907	9.85E-50	5.06E-49	1.41609346	0	100
ENSG00000117298	ECE1	-1.3315292	7.06273581	463.437385	8.59E-103	5.99E-102	-1.2140414	100	0	ECE1	-0.9936696	7.1291938	212.383793	4.15E-48	2.08E-47	-0.9604076	100	0
ENSG00000076554	TPD52	-1.6616462	3.59606659	463.430778	8.62E-103	6.00E-102	-1.5455469	100	0	TPD52	-1.7382946	3.47285794	409.311623	5.18E-91	4.42E-90	-1.7599235	100	0
ENSG00000131759	RARA	-1.3358071	6.93355029	462.383005	1.46E-102	1.01E-101	-1.2845643	100	0	RARA	-0.6954265	7.09728967	105.343322	1.03E-24	3.20E-24	-0.7947323	97.2222222	2.7777778
ENSG00000100401	RANGAP1	1.33317707	7.48899126	461.63968	2.11E-102	1.47E-101	1.48760054	0	100	RANGAP1	1.4716026	7.51470503	450.091269	6.89E-100	6.44E-99	1.26907408	0	100
ENSG00000065615	CYB5R4	-1.4313358	4.69158048	461.616476	2.14E-102	1.48E-101	-1.3393855	100	0	CYB5R4	-1.0774164	4.73684161	224.141104	1.13E-50	5.88E-50	-1.0765696	100	0
ENSG00000170322	NFRKB	1.35700296	5.69488714	461.144145	2.71E-102	1.88E-101	1.41274695	0	100	NFRKB	0.69628618	5.18357949	100.685988	1.08E-23	3.28E-23	0.62955305	5.55555556	94.4444444
ENSG00000103507	BCKDK	-1.957236	2.56825174	459.853829	5.17E-102	3.57E-101	-1.8537347	100	0	BCKDK	-1.3542421	2.70972521	196.233532	1.39E-44	6.47E-44	-1.3502838	100	0
ENSG00000110660	SLC35F2	-1.6805802	3.53610473	458.774316	8.88E-102	6.12E-101	-1.6243101	100	0	SLC35F2	-1.6480337	3.43288262	358.375479	6.36E-80	4.78E-79	-1.5718061	100	0
ENSG00000140931	CMTM3	-1.3465073	5.83311873	456.724549	2.48E-101	1.71E-100	-1.3674731	100	0	CMTM3	-1.2679903	5.83750746	338.685318	1.23E-75	8.90E-75	-1.2195074	100	0
ENSG00000118503	TNFAIP3	1.35241426	11.8256087	456.681212	2.54E-101	1.74E-100	1.49407573	0	100	TNFAIP3	1.70412188	12.0119239	418.515988	5.13E-93	4.46E-92	1.81816187	0	100
ENSG00000048392	RRM2B	-1.4183322	4.76401627	456.118013	3.36E-101	2.31E-100	-1.3221723	100	0	RRM2B	-1.260289	4.73523119	302.379483	9.99E-68	6.62E-67	-1.2957685	100	0
ENSG00000121579	NAA50	-1.3207934	6.86683298	453.881288	1.03E-100	7.03E-100	-1.2346967	100	0	NAA50	-0.7636218	6.97305533	126.787448	2.07E-29	7.22E-29	-0.8047138	97.2222222	2.7777778
ENSG00000002586	CD99	-1.3360731	6.22918501	453.707493	1.13E-100	7.67E-100	-1.2812376	100	0	CD99	-1.0820046	6.30598876	246.001735	1.93E-55	1.08E-54	-1.1501606	97.2222222	2.7777778
ENSG00000063245	EPN1	-1.3401997	5.83218127	451.764458	2.98E-100	2.02E-99	-1.3155398	100	0	EPN1	-1.1866322	5.8696876	296.530277	1.88E-66	1.21E-65	-1.2363787	97.2222222	2.7777778
ENSG00000169442	CD52	-1.3160424	7.24475055	451.33271	3.70E-100	2.51E-99	-1.325078	100	0	CD52	-1.3383923	7.17720438	373.428058	3.36E-83	2.64E-82	-1.3941432	100	0
ENSG00000103064	SLC7A6	1.35581794	5.42444412	451.188234	3.98E-100	2.70E-99	1.35669512	0	100	SLC7A6	0.8310957	5.02264386	139.234134	3.91E-32	1.45E-31	0.75702253	8.33333333	91.6666667
ENSG00000068697	LAPTM4A	-1.3120461	7.10242079	450.557108	5.46E-100	3.70E-99	-1.1992847	100	0	LAPTM4A	-0.998976	7.1672107	213.214769	2.73E-48	1.37E-47	-0.9609758	100	0
ENSG00000109618	SEPSECS	1.44955288	4.4872274	446.916612	3.38E-99	2.28E-98	1.50365577	0	100	SEPSECS	1.13977202	4.28331894	224.638371	8.80E-51	4.59E-50	1.06928084	2.77777778	97.2222222
ENSG00000091317	CMTM6	-1.3016692	7.72826421	446.8702	3.46E-99	2.33E-98	-1.2006179	100	0	CMTM6	-1.5078271	7.63071029	467.174123	1.32E-103	1.27E-102	-1.5336898	100	0
ENSG00000134287	ARF3	-1.3513682	5.32909475	445.433781	7.11E-99	4.77E-98	-1.2715835	100	0	ARF3	-0.7463782	5.50884688	118.357607	1.45E-27	4.85E-27	-0.7502326	100	0
ENSG00000126602	TRAP1	1.50402938	4.14880236	441.748563	4.51E-98	3.02E-97	1.51665453	0	100	TRAP1	1.05030246	3.76076583	166.637736	4.01E-38	1.68E-37	0.87909802	2.77777778	97.2222222
ENSG00000204316	MRPL38	1.49392435	4.14108138	441.557974	4.96E-98	3.32E-97	1.44369547	0	100	MRPL38	1.44721042	4.05534483	341.765235	2.63E-76	1.91E-75	1.33520557	0	100
ENSG00000163558	PRKCI	1.62264143	3.58235513	441.053723	6.38E-98	4.26E-97	1.70467299	0	100	PRKCI	1.43445534	3.38515664	276.540112	4.26E-62	2.57E-61	1.48205577	0	100
ENSG00000139370	SLC15A4	-1.3647626	5.01486048	440.98728	6.60E-98	4.40E-97	-1.3466919	100	0	SLC15A4	-0.7870721	5.1155637	126.474077	2.42E-29	8.44E-29	-0.9122286	100	0
ENSG00000111328	CDK2AP1	-1.8210843	2.8723088	438.227441	2.63E-97	1.75E-96	-1.8484806	100	0	CDK2AP1	-1.9131905	2.82997264	396.013792	4.06E-88	3.39E-87	-1.9245295	100	0
ENSG00000112977	DAP	-1.3294603	5.44050746	436.991405	4.89E-97	3.24E-96	-1.1747876	100	0	DAP	-1.1376476	5.45917695	271.088601	6.57E-61	3.92E-60	-1.2207333	100	0
ENSG00000114650	SCAP	1.32740054	5.45690166	436.754541	5.51E-97	3.65E-96	1.40235924	0	100	SCAP	1.24906908	5.36580212	322.245892	4.70E-72	3.27E-71	1.16432717	0	100
ENSG00000155926	SLA	-1.334134	5.60061987	434.635249	1.59E-96	1.05E-95	-1.3249213	100	0	SLA	-1.0395418	5.69188781	220.124712	8.50E-50	4.37E-49	-1.1155176	97.2222222	2.77777778
ENSG00000053900	ANAPC4	1.59613669	3.64814869	434.627871	1.60E-96	1.06E-95	1.67679072	0	100	ANAPC4	1.41011495	3.43269808	271.023434	6.79E-61	4.04E-60	1.35595975	0	100
ENSG00000105851	PIK3CG	-1.3105195	5.77998337	430.285315	1.41E-95	9.27E-95	-1.1977922	100	0	PIK3CG	-0.6716337	5.95866845	96.3663372	9.55E-23	2.83E-22	-0.6051852	97.2222222	2.77777778
ENSG00000180694	TMEM64	-1.5173155	3.96653619	429.964842	1.65E-95	1.09E-94	-1.4029372	100	0	TMEM64	-1.3497769	3.95147728	288.90774	8.60E-65	5.43E-64	-1.396757	100	0
ENSG00000137492	PRKRIR	-1.2854605	6.78369989	429.447392	2.14E-95	1.41E-94	-1.2519237	100	0	PRKRIR	-0.7926455	6.87071971	137.208704	1.09E-31	3.99E-31	-0.7581684	100	0
ENSG00000115687	PASK	1.292119	7.06918769	429.142272	2.50E-95	1.64E-94	1.41553178	0	100	PASK	1.71499764	7.29876805	602.88798	3.94E-133	4.62E-132	1.57310886	0	100
ENSG00000136286	MYO1G	-1.2916324	6.32516425	428.886952	2.84E-95	1.86E-94	-1.2689557	100	0	MYO1G	-0.8092913	6.45492554	139.29645	3.79E-32	1.41E-31	-0.888265	91.6666667	8.33333333
ENSG00000179833	SERTAD2	-1.2820985	6.7373765	427.975548	4.48E-95	2.93E-94	-1.2107166	100	0	SERTAD2	-0.9604708	6.77985833	199.438918	2.77E-45	1.31E-44	-0.9839998	100	0
ENSG00000168734	PKIG	-1.8428105	2.7361957	427.854453	4.76E-95	3.11E-94	-1.8982643	100	0	PKIG	-1.0083457	2.8286729	114.182874	1.19E-26	3.88E-26	-1.2218012	88.8888889	11.1111111
ENSG00000143110	C1orf162	-1.5520294	3.77910025	427.840266	4.80E-95	3.13E-94	-1.4612862	100	0	C1orf162	-2.0141841	3.68524937	570.449574	4.48E-126	5.01E-125	-2.0131521	100	0
ENSG00000254999	BRK1	-1.3272762	5.27096781	426.759622	8.24E-95	5.37E-94	-1.2627995	100	0	BRK1	-1.1246637	5.28833183	259.644289	2.05E-58	1.19E-57	-1.1809084	100	0
ENSG00000171298	GAA	-1.4050789	4.66015821	426.207133	1.09E-94	7.08E-94	-1.4934779	94.2857143	5.71428571	GAA	-1.906284	4.54445285	604.147262	2.10E-133	2.46E-132	-2.2182854	94.4444444	5.55555556
ENSG00000152256	PDK1	1.3111371	5.83751174	425.75067	1.37E-94	8.89E-94	1.44142658	0	100	PDK1	0.69208681	5.38038111	99.4191139	2.04E-23	6.16E-23	0.75755385	8.33333333	91.6666667

ENSG00000090006	LTBP4	1.47964264	4.14176714	424.538461	2.51E-94	1.63E-93	1.53273514	0	100	LTBP4	1.16234956	3.93633825	209.427506	1.83E-47	9.08E-47	1.07288966	2.77777778	97.2222222
ENSG00000198431	TXNRD1	-1.3099943	5.66248806	424.179685	3.00E-94	1.94E-93	-1.3857994	100	0	TXNRD1	-0.81296	5.77689716	139.840819	2.88E-32	1.08E-31	-0.8210589	94.4444444	5.55555556
ENSG00000139433	GLTP	-1.3130249	5.38626324	423.966	3.34E-94	2.16E-93	-1.2734193	100	0	GLTP	-0.6561295	5.5672141	92.0161336	8.60E-22	2.48E-21	-0.6587834	100	0
ENSG00000107317	PTGDS	-2.1597521	1.89445338	423.054184	5.28E-94	3.40E-93	-2.1410278	97.1428571	2.85714286	PTGDS	-1.3866478	2.24454315	144.443021	2.84E-33	1.08E-32	-1.6412423	80.5555556	19.4444444
ENSG00000137509	PRCP	-1.4712276	4.10243365	421.440767	1.19E-93	7.63E-93	-1.2807987	100	0	PRCP	-0.6691492	4.32988106	78.5100071	7.96E-19	2.12E-18	-0.7069385	88.8888889	11.1111111
ENSG00000262319	CTC-457L16.2	1.65007177	3.40934465	421.373911	1.23E-93	7.88E-93	1.64242983	0	100	CTC-457L16.2	0.74610146	2.75249251	59.7724536	1.06E-14	2.51E-14	0.73899531	13.8888889	86.1111111
ENSG00000125731	SH2D3A	1.42246106	4.33586068	419.510414	3.12E-93	2.00E-92	1.51490454	0	100	SH2D3A	1.03071502	3.9633898	172.899469	1.72E-39	7.43E-39	1.0120401	2.77777778	97.2222222
ENSG00000067225	PKM	-1.2661484	7.40935757	419.497408	3.14E-93	2.01E-92	-1.1624228	100	0	PKM	-1.8733311	7.23871685	708.43757	4.37E-156	5.81E-155	-1.8322271	100	0
ENSG00000117500	TMED5	-1.2885398	5.73397164	419.225437	3.60E-93	2.30E-92	-1.1929699	100	0	TMED5	-0.9721908	5.78342889	201.250496	1.11E-45	5.32E-45	-0.8975613	100	0
ENSG00000173991	TCAP	1.79485029	2.8162283	417.564005	8.27E-93	5.26E-92	1.76861392	0	100	TCAP	1.43719004	2.50603299	204.979735	1.71E-46	8.33E-46	1.44542168	0	100
ENSG00000104904	OAZ1	-1.2716795	7.29958874	416.010048	1.80E-92	1.15E-91	-1.327834	100	0	OAZ1	-1.3057968	7.27618991	348.119573	1.09E-77	8.01E-77	-1.4642622	100	0
ENSG00000023892	DEF6	1.27407194	6.30771899	413.792491	5.48E-92	3.47E-91	1.33002172	0	100	DEF6	1.19269047	6.20413979	300.379316	2.72E-67	1.79E-66	1.04238082	2.77777778	97.2222222
ENSG00000122986	HVCN1	-1.671055	3.27207366	413.623474	5.96E-92	3.77E-91	-1.5027652	100	0	HVCN1	-2.1311739	3.07198633	524.62573	4.17E-116	4.42E-115	-2.1786083	100	0
ENSG00000162909	CAPN2	-1.2678702	6.20816323	412.000081	1.35E-91	8.48E-91	-1.2329246	100	0	CAPN2	-1.1219027	6.24912369	267.07374	4.93E-60	2.91E-59	-1.1440504	100	0
ENSG00000215908	CROCCP2	1.36951461	4.54720214	410.139369	3.42E-91	2.15E-90	1.35838431	0	100	CROCCP2	1.45663323	4.52746087	384.228983	1.49E-85	1.21E-84	1.39444905	0	100
ENSG00000215908	CROCCP2	1.36951461	4.54720214	410.139369	3.42E-91	2.15E-90	1.35838431	0	100	CROCCP2	1.13487923	4.45627587	203.913016	2.92E-46	2.87E-45	1.39444905	0	100
ENSG00000242372	EIF6	-1.3229723	4.90571402	410.125208	3.44E-91	2.16E-90	-1.3073026	100	0	EIF6	-0.8256708	5.01537208	138.509618	5.64E-32	2.09E-31	-0.9214182	100	0
ENSG00000136193	SCRN1	-1.4489937	4.13483319	408.879527	6.43E-91	4.02E-90	-1.2860878	100	0	SCRN1	-0.8652455	4.26834529	131.84353	1.62E-30	5.79E-30	-0.855041	97.2222222	2.77777778
ENSG00000165806	CASP7	-1.4542701	4.00207461	407.060031	1.60E-90	9.99E-90	-1.3408262	100	0	CASP7	-0.9267586	4.09242284	145.97584	1.31E-33	5.04E-33	-0.9521663	100	0
ENSG00000160404	TOR2A	-1.5757455	3.4928807	405.725167	3.12E-90	1.94E-89	-1.4470027	100	0	TOR2A	-0.9821414	3.65447888	142.735625	6.71E-33	2.53E-32	-1.0168051	100	0
ENSG00000112335	SNX3	-1.2619066	6.06925047	404.684103	5.26E-90	3.26E-89	-1.2433538	100	0	SNX3	-1.1885335	6.02728507	301.618848	1.46E-67	9.64E-67	-1.2448839	100	0
ENSG00000144218	AFF3	-1.3145681	5.01043156	404.245099	6.56E-90	4.05E-89	-1.1604951	100	0	AFF3	-2.5057007	4.61729811	1071.38805	5.47E-235	1.03E-233	-2.4936975	100	0
ENSG00000104774	MAN2B1	-1.2487487	6.61140286	403.85396	7.98E-90	4.93E-89	-1.176694	100	0	MAN2B1	-1.3906656	6.55315428	407.213865	1.48E-90	1.26E-89	-1.4310731	100	0
ENSG00000100307	CBX7	1.32349007	4.88401232	403.740056	8.45E-90	5.21E-89	1.33649593	0	100	CBX7	0.69558903	4.45153048	88.467436	5.17E-21	1.47E-20	0.63303611	5.55555556	94.4444444
ENSG00000011275	RNF216	1.24174987	6.7731983	402.003461	2.02E-89	1.24E-88	1.29772671	0	100	RNF216	1.28147928	6.76156279	351.354834	2.15E-78	1.59E-77	1.19681372	0	100
ENSG00000197321	SVIL	1.30738067	4.96550192	401.181786	3.05E-89	1.87E-88	1.39178345	0	100	SVIL	0.71949434	4.51233232	96.4003127	9.39E-23	2.79E-22	0.6914597	8.33333333	91.6666667
ENSG00000068831	RASGRP2	1.23025874	8.23844427	398.851163	9.80E-89	5.99E-88	1.27686705	0	100	RASGRP2	0.74990789	7.84013556	118.211984	1.56E-27	5.21E-27	0.59502214	0	100
ENSG00000114626	ABTB1	1.25999398	5.76427211	398.403279	1.23E-88	7.49E-88	1.32919883	0	100	ABTB1	0.83689328	5.44157659	145.465243	1.70E-33	6.50E-33	0.74583607	8.33333333	91.6666667
ENSG00000182158	CREB3L2	-1.3848294	4.27911963	397.715107	1.73E-88	1.06E-87	-1.3064813	100	0	CREB3L2	-1.44913	4.22017168	355.93437	2.16E-79	1.61E-78	-1.4217445	100	0
ENSG00000112079	STK38	1.27766869	5.35223806	396.738745	2.82E-88	1.72E-87	1.27943694	0	100	STK38	0.84534734	4.97354469	141.651571	1.16E-32	4.35E-32	0.72690302	2.77777778	97.2222222
ENSG00000100647	KIAA0247	-1.2280907	6.88383404	395.035754	6.63E-88	4.02E-87	-1.1216465	100	0	KIAA0247	-0.8564261	6.92889406	159.856944	1.22E-36	4.95E-36	-0.8197555	100	0
ENSG00000158941	CCAR2	1.23442651	6.72826084	394.887669	7.14E-88	4.33E-87	1.21533247	0	100	CCAR2	1.22760833	6.7018848	320.739759	9.99E-72	6.95E-71	1.0905944	0	100
ENSG00000090104	RGS1	1.24792258	9.70485761	393.930476	1.15E-87	6.98E-87	1.35763971	0	100	RGS1	0.91374544	9.41942573	151.73699	7.23E-35	2.85E-34	0.7226664	11.1111111	88.8888889
ENSG00000116663	FBXO6	-2.0386879	1.78925736	393.854918	1.20E-87	7.25E-87	-1.9576968	100	0	FBXO6	-1.1824501	1.9918536	118.673591	1.23E-27	4.15E-27	-1.1979345	100	0
ENSG00000140474	ULK3	1.29623238	4.99599881	393.432623	1.48E-87	8.95E-87	1.28099907	0	100	ULK3	1.0531101	4.7255173	211.03721	8.16E-48	4.06E-47	0.90451542	0	100
ENSG00000239779	WBP1	1.49871978	3.71234003	392.863068	1.97E-87	1.19E-86	1.5198912	0	100	WBP1	0.90757965	3.25286389	108.752053	1.84E-25	5.87E-25	0.7883306	0	100
ENSG00000106868	SUSD1	-1.7671019	2.6604022	391.748975	3.44E-87	2.08E-86	-1.6212929	100	0	SUSD1	-1.0490008	2.84715885	122.629791	1.68E-28	5.74E-28	-1.0578335	97.2222222	2.77777778
ENSG00000134590	FAM127A	-2.1089753	1.55971449	388.920208	1.42E-86	8.55E-86	-2.0764591	100	0	FAM127A	-1.4722197	1.6701146	159.679643	1.33E-36	5.39E-36	-1.4599402	100	0
ENSG00000058453	CROCC	1.32579659	4.65137977	388.332403	1.91E-86	1.15E-85	1.35702436	0	100	CROCC	1.27552063	4.51927447	292.294431	1.57E-65	1.01E-64	1.190363	2.77777778	97.2222222
ENSG00000084072	PPIE	1.32637365	4.66590852	387.662336	2.67E-86	1.60E-85	1.39408649	0	100	PPIE	1.28462106	4.59262093	302.23148	1.08E-67	7.10E-67	1.27278049	0	100
ENSG00000132965	ALOX5AP	-1.4940742	3.67644549	387.480222	2.93E-86	1.75E-85	-1.3770913	100	0	ALOX5AP	-2.2205795	3.47940326	638.945366	5.67E-141	7.05E-140	-2.141418	100	0
ENSG00000139055	ERP27	1.6243877	3.14704388	387.227339	3.32E-86	1.98E-85	1.67591033	0	100	ERP27	1.19049803	2.75684293	157.841907	3.35E-36	1.35E-35	1.08567198	0	100
ENSG00000150093	ITGB1	-1.2213479	6.44779139	386.237342	5.46E-86	3.26E-85	-1.1492372	100	0	ITGB1	-1.105299	6.41020357	260.232845	1.53E-58	8.86E-58	-1.0666477	100	0
ENSG00000178498	DTX3	1.40241341	4.09751868	385.213663	9.12E-86	5.43E-85	1.40648012	0	100	DTX3	1.73830355	4.28368811	511.068979	3.71E-113	3.86E-112	1.72947782	0	100
ENSG00000051523	CYBA	-1.2239912	6.54853326	384.126699	1.57E-85	9.34E-85	-1.1520192	100	0	CYBA	-0.4595487	6.80462007	44.1933369	2.97E-11	6.18E-11	-0.6940834	72.2222222	27.7777778
ENSG00000142687	KIAA0319L	1.29687307	4.79233541	383.819623	1.83E-85	1.09E-84	1.3717067	0	100	KIAA0319L	0.78524642	4.40086958	111.990808	3.59E-26	1.16E-25	0.75061175	2.77777778	97.2222222
ENSG00000180448	HMHA1	1.20527282	8.99779156	383.678067	1.97E-85	1.17E-84	1.28456416	0	100	HMHA1	1.02127874	8.83062119	203.831384	3.05E-46	1.47E-45	0.98638359	2.77777778	97.2222222
ENSG00000171606	ZNF274	1.2266248	5.95423386	383.624958	2.02E-85	1.20E-84	1.21196823	0	100	ZNF274	0.71363396	5.57490465	109.095416	1.55E-25	4.95E-25	0.64257587	5.55555556	94.4444444
ENSG00000135905	DOCK10	1.20295947	7.34458466	383.549604	2.10E-85	1.24E-84	1.19045725	0	100	DOCK10	0.76060321	7.0014966	125.747366	3.49E-29	1.21E-28	0.73163028	5.55555556	94.4444444
ENSG00000120129	DUSP1	-1.2347549	9.90484179	381.544042	5.74E-85	3.39E-84	-1.2692707	94.2857143	5.71428571	DUSP1	-0.7142347	10.0796048	85.7500265	2.04E-20	5.70E-20	-0.888569	83.3333333	16.6666667
ENSG00000116954	RRAGC	-1.2479865	5.30611198	380.975746	7.63E-85	4.51E-84	-1.0761202	100	0	RRAGC	-1.0336948	5.30307235	220.323592	7.69E-50	3.96E-49	-1.0234865	100	0
ENSG00000069956	MAPK6	-1.2180011	6.17439058	380.630281	9.07E-85	5.35E-84	-1.1163971	100	0	MAPK6	-1.3335633	6.08232226	376.016482	9.17E-84	7.24E-83	-1.3256088	100	0
ENSG00000069849	ATP1B3	-1.3185972	4.6256554	380.161806	1.15E-84	6.75E-84	-1.3321898	97.1428571	2.85714286	ATP1B3	-0.3516515	4.93862725	24.3906512	7.86E-07	1.34E-06	-0.5039639	77.7777778	22.2222222

ENSG00000154845	PPP4R1	-1.2476359	5.17828979	378.972112	2.08E-84	1.22E-83	-1.1901144	100	0	PPP4R1	-0.7950807	5.26723337	132.581586	1.12E-30	4.01E-30	-0.7828684	100	0
ENSG00000137076	TLN1	-1.2010647	7.13414186	377.810038	3.73E-84	2.19E-83	-1.0574214	100	0	TLN1	-1.0065422	7.16304435	215.956704	6.89E-49	3.50E-48	-1.0396366	100	0
ENSG00000130023	ERMARD	1.64920644	2.96846173	374.721557	1.75E-83	1.03E-82	1.68271497	0	100	ERMARD	1.44546412	2.75347706	226.66668	3.18E-51	1.67E-50	1.41149408	0	100
ENSG00000106348	IMPDH1	-1.2824334	4.75894672	374.47675	1.98E-83	1.16E-82	-1.1615853	100	0	IMPDH1	-1.5503204	4.66758568	439.315236	1.53E-97	1.39E-96	-1.5292158	100	0
ENSG00000164039	BDH2	1.48996301	3.54352315	372.864627	4.45E-83	2.60E-82	1.48723158	0	100	BDH2	1.32577231	3.32991349	233.968096	8.13E-53	4.38E-52	1.27627871	2.77777778	97.2222222
ENSG00000166685	COG1	1.24603511	5.04082992	371.730079	7.86E-83	4.58E-82	1.30667686	0	100	COG1	1.16866821	4.95942508	272.533693	3.18E-61	1.90E-60	1.09848555	0	100
ENSG00000100439	ABHD4	-1.7891382	2.37164587	371.073785	1.09E-82	6.35E-82	-1.6813255	100	0	ABHD4	-0.5750613	2.70511461	36.9521646	1.21E-09	2.36E-09	-0.5328534	94.4444444	5.55555556
ENSG00000155640	C10orf12	-1.4444065	3.76862282	370.18842	1.70E-82	9.90E-82	-1.4038519	100	0	C10orf12	-0.8626555	3.90816442	118.507088	1.34E-27	4.50E-27	-0.8645993	97.2222222	2.77777778
ENSG00000099821	POLRMT	1.2775596	4.72909788	369.592896	2.30E-82	1.33E-81	1.29009216	0	100	POLRMT	1.02946431	4.49701983	193.793483	4.72E-44	2.19E-43	0.89082662	2.77777778	97.2222222
ENSG00000204371	EHMT2	1.24081295	5.0715193	369.236038	2.74E-82	1.59E-81	1.34269009	0	100	EHMT2	1.26891361	5.02083148	319.076706	2.30E-71	1.59E-70	1.18957392	2.77777778	97.2222222
ENSG00000099991	CABIN1	1.20556437	5.77148677	368.493792	3.98E-82	2.30E-81	1.33358424	0	100	CABIN1	1.30660791	5.79667804	360.221993	2.52E-80	1.90E-79	1.22063854	0	100
ENSG00000232533	AC093673.5	-2.1871138	1.13379707	368.364549	4.25E-82	2.45E-81	-2.0965804	100	0	AC093673.5	-1.3149813	1.26797998	113.971519	1.32E-26	4.31E-26	-1.3228422	100	0
ENSG00000164896	FASTK	1.25026359	4.92129317	368.186402	4.65E-82	2.68E-81	1.27946904	0	100	FASTK	0.9339783	4.66248594	166.93057	3.46E-38	1.45E-37	0.84918565	0	100
ENSG00000136238	RAC1	-1.1879367	6.59262472	366.334834	1.18E-81	6.75E-81	-1.1937466	100	0	RAC1	-1.0485134	6.59139534	238.343835	9.03E-54	4.91E-53	-1.088647	100	0
ENSG00000103966	EHD4	-1.2064423	5.97337831	365.49081	1.79E-81	1.03E-80	-1.2244064	100	0	EHD4	-1.0842844	5.96413835	245.87013	2.06E-55	1.15E-54	-1.1682708	97.2222222	2.77777778
ENSG00000169718	DUS1L	1.20251499	6.01183795	365.05594	2.23E-81	1.28E-80	1.18547395	0	100	DUS1L	1.0058274	5.83340974	212.092997	4.80E-48	2.40E-47	0.89659804	5.55555556	94.4444444
ENSG00000105486	LIG1	1.34667728	4.32348014	364.695091	2.67E-81	1.53E-80	1.30888524	0	100	LIG1	0.94441723	4.00345383	142.657956	6.98E-33	2.63E-32	0.89118924	2.77777778	97.2222222
ENSG00000133961	NUMB	-1.2362716	5.0620159	364.59112	2.82E-81	1.61E-80	-1.2091504	100	0	NUMB	-1.6237882	4.93284794	508.523257	1.33E-112	1.37E-111	-1.6643541	100	0
ENSG00000230989	HSBP1	-1.2484711	4.93346141	364.265881	3.32E-81	1.89E-80	-1.2136153	100	0	HSBP1	-1.534986	4.84928716	445.689078	6.26E-99	5.80E-98	-1.5417294	100	0
ENSG00000057608	GDI2	-1.2012774	5.81794718	364.1019	3.60E-81	2.04E-80	-1.0487057	100	0	GDI2	-1.2242719	5.75710551	315.143981	1.65E-70	1.14E-69	-1.2315145	100	0
ENSG00000131067	GGT7	1.43011764	3.76211875	363.741035	4.32E-81	2.45E-80	1.48397057	0	100	GGT7	0.64704294	3.18620253	54.3351111	1.69E-13	3.82E-13	0.57587659	11.1111111	88.8888889
ENSG00000162704	ARPC5	-1.2644961	4.79577686	362.963807	6.37E-81	3.61E-80	-1.1675861	100	0	ARPC5	-1.2463441	4.7961106	297.072674	1.43E-66	9.29E-66	-1.2184245	100	0
ENSG00000159335	PTMS	-1.9417871	1.88314562	362.295677	8.91E-81	5.03E-80	-1.9024523	100	0	PTMS	-1.6964576	2.05071662	219.183522	1.36E-49	6.99E-49	-1.4420604	91.6666667	8.33333333
ENSG00000185187	SIGIRR	1.19617729	6.08395867	362.004159	1.03E-80	5.82E-80	1.18655337	0	100	SIGIRR	0.82237314	5.8169085	143.200666	5.31E-33	2.01E-32	0.64656415	0	100
ENSG00000129968	ABHD17A	1.18432799	6.75341847	360.434438	2.26E-80	1.28E-79	1.2139384	0	100	ABHD17A	1.57055364	6.98509773	507.109062	2.70E-112	2.78E-111	1.47864549	0	100
ENSG00000171161	ZNF672	-1.4217022	3.72171305	359.865477	3.01E-80	1.70E-79	-1.3971168	100	0	ZNF672	-1.0215287	3.78391295	162.448891	3.30E-37	1.35E-36	-1.102945	100	0
ENSG00000163050	ADCK3	1.17775319	6.54165744	359.368229	3.87E-80	2.17E-79	1.15281367	0	100	ADCK3	0.97191896	6.37431155	202.700824	5.38E-46	2.59E-45	0.92454844	0	100
ENSG00000140511	HAPLN3	1.20092806	5.64724916	358.284002	6.66E-80	3.74E-79	1.1917342	0	100	HAPLN3	0.76855541	5.30138144	123.391895	1.14E-28	3.92E-28	0.81388461	5.55555556	94.4444444
ENSG00000167996	FTH1	-1.1750166	10.0084805	358.138828	7.16E-80	4.02E-79	-1.0976393	100	0	FTH1	-0.8958038	10.0568492	140.890661	1.70E-32	6.38E-32	-0.9625466	97.2222222	2.77777778
ENSG00000167202	TBC1D2B	1.20399779	5.36784408	356.971943	1.29E-79	7.20E-79	1.16840906	0	100	TBC1D2B	1.02663397	5.20849158	213.364095	2.53E-48	1.27E-47	1.02485356	2.77777778	97.2222222
ENSG00000158863	FAM160B2	1.22832296	4.95849987	356.285409	1.81E-79	1.01E-78	1.29628501	0	100	FAM160B2	0.95814876	4.71971083	176.952155	2.24E-40	9.89E-40	0.87615961	0	100
ENSG00000134996	OSTF1	-1.5286533	3.25845341	355.605842	2.55E-79	1.42E-78	-1.4754053	100	0	OSTF1	-0.9735215	3.37303048	128.443613	8.98E-30	3.16E-29	-1.0867242	100	0
ENSG00000118515	SGK1	-1.1662469	8.07605382	354.554917	4.32E-79	2.41E-78	-0.9938254	100	0	SGK1	-1.7044323	7.88700998	555.168028	9.46E-123	1.04E-121	-1.7921392	100	0
ENSG00000130299	GTPBP3	1.51390687	3.29529338	354.325969	4.84E-79	2.70E-78	1.500279	0	100	GTPBP3	1.29098184	3.0802501	204.990562	1.70E-46	8.29E-46	1.16861431	0	100
ENSG00000123131	PRDX4	-1.740511	2.39536434	353.052445	9.17E-79	5.09E-78	-1.6581975	100	0	PRDX4	-1.7918478	2.32543571	296.94011	1.53E-66	9.90E-66	-1.9665419	100	0
ENSG00000247596	TWF2	-1.4136808	3.70873231	352.928683	9.76E-79	5.41E-78	-1.3958911	100	0	TWF2	-0.6578541	3.96375745	70.191935	5.38E-17	1.35E-16	-0.7372732	91.6666667	8.33333333
ENSG00000213281	NRAS	-1.1526138	7.25555266	351.571997	1.93E-78	1.07E-77	-1.1370569	100	0	NRAS	-0.6492083	7.3436859	91.1259345	1.35E-21	3.88E-21	-0.6364057	100	0
ENSG00000008282	SYPL1	-1.1841919	5.4868062	351.094734	2.45E-78	1.36E-77	-1.1022633	100	0	SYPL1	-1.0833883	5.45236951	244.514061	4.08E-55	2.26E-54	-1.0210551	100	0
ENSG00000162302	RPS6KA4	-1.3945274	3.79036421	350.934408	2.65E-78	1.47E-77	-1.3732819	100	0	RPS6KA4	-1.4777979	3.76304304	321.758514	6.00E-72	4.17E-71	-1.5928393	100	0
ENSG00000160213	CSTB	-1.3550032	4.00823229	350.251066	3.74E-78	2.07E-77	-1.3512442	100	0	CSTB	-1.5248949	3.91173732	357.514565	9.79E-80	7.33E-79	-1.5467949	100	0
ENSG00000172671	ZFAND4	1.24209132	4.70713901	350.196539	3.84E-78	2.12E-77	1.2712629	0	100	ZFAND4	1.01252975	4.50512529	188.67438	6.19E-43	2.84E-42	0.96426293	5.55555556	94.4444444
ENSG00000131797	CLUHP3	1.2087334	5.13693349	348.456227	9.19E-78	5.06E-77	1.16928186	0	100	CLUHP3	1.04176139	4.87086534	211.849473	5.42E-48	2.71E-47	1.00058786	2.77777778	97.2222222
ENSG00000174227	PIGG	1.2180416	4.90285832	348.279685	1.00E-77	5.52E-77	1.37021676	0	100	PIGG	1.01366974	4.72823714	199.089281	3.30E-45	1.56E-44	0.94662946	0	100
ENSG00000182541	LIMK2	1.14724641	7.1048261	346.934867	1.97E-77	1.08E-76	1.17732602	0	100	LIMK2	0.91851932	6.93449257	182.836624	1.16E-41	5.23E-41	0.83575479	0	100
ENSG00000176871	WSB2	-1.2764971	4.38757681	346.607232	2.32E-77	1.27E-76	-1.1489043	100	0	WSB2	-0.9697818	4.46096422	172.973395	1.66E-39	7.17E-39	-0.983996	100	0
ENSG00000159461	AMFR	-1.1430585	7.14686139	345.685503	3.69E-77	2.02E-76	-1.0864339	100	0	AMFR	-0.9766104	7.13923952	205.993245	1.03E-46	5.03E-46	-1.0388822	100	0
ENSG00000197150	ABCB8	1.44070761	3.56499848	345.641251	3.77E-77	2.06E-76	1.50948652	0	100	ABCB8	1.32799397	3.40745537	236.338743	2.47E-53	1.34E-52	1.18258829	2.77777778	97.2222222
ENSG00000140612	SEC11A	-1.1680207	5.78185035	344.891039	5.49E-77	3.00E-76	-1.1417933	100	0	SEC11A	-1.1275749	5.76239054	270.927038	7.13E-61	4.24E-60	-1.2033137	100	0
ENSG00000187742	SECISBP2	1.14893765	6.58080239	344.680752	6.10E-77	3.32E-76	1.1652253	0	100	SECISBP2	0.74605947	6.25728236	122.137823	2.15E-28	7.34E-28	0.65105126	0	100
ENSG00000114353	GNAI2	-1.1421408	7.72081645	343.82482	9.37E-77	5.10E-76	-1.0251978	100	0	GNAI2	-0.9769614	7.75956893	198.586718	4.25E-45	2.01E-44	-1.0188545	100	0
ENSG00000182199	SHMT2	-1.2627817	4.44538074	343.746309	9.75E-77	5.30E-76	-1.1340621	100	0	SHMT2	-1.3040758	4.35320765	299.819212	3.61E-67	2.36E-66	-1.3728789	100	0
ENSG00000120992	LYPLA1	-1.2096745	4.86263067	342.158281	2.16E-76	1.17E-75	-1.0177125	100	0	LYPLA1	-1.183218	4.81584228	273.201401	2.28E-61	1.36E-60	-1.2342867	100	0
ENSG00000168118	RAB4A	-1.3170445	4.05491088	341.112233	3.65E-76	1.98E-75	-1.2146085	100	0	RAB4A	-0.7192173	4.20732802	90.4265423	1.92E-21	5.50E-21	-0.7951161	97.2222222	2.77777778

ENSG00000075624	ACTB	-1.1480486	10.4322473	340.537675	4.87E-76	2.64E-75	-1.0519563	100	0	ACTB	-0.6408921	10.5759797	69.7442688	6.75E-17	1.69E-16	-0.6700234	94.4444444	5.55555556
ENSG00000198624	CCDC69	-1.1311051	7.39449554	340.062266	6.18E-76	3.34E-75	-1.0584481	100	0	CCDC69	-0.5082992	7.58900026	55.820406	7.94E-14	1.81E-13	-0.5573053	97.2222222	2.77777778
ENSG00000197694	SPTAN1	1.13120418	7.28851939	339.569072	7.92E-76	4.28E-75	1.1734927	0	100	SPTAN1	1.17577815	7.25107669	294.664717	4.79E-66	3.08E-65	1.15337953	0	100
ENSG00000110274	CEP164	1.34912162	3.93085895	338.822671	1.15E-75	6.22E-75	1.36349534	0	100	CEP164	1.10159187	3.68832467	178.627028	9.67E-41	4.28E-40	1.04230173	2.77777778	97.2222222
ENSG00000136068	FLNB	1.13833465	7.13719989	338.182725	1.59E-75	8.56E-75	1.21901756	0	100	FLNB	1.33171633	7.28927132	371.596736	8.40E-83	6.56E-82	1.26895341	0	100
ENSG00000227500	SCAMP4	-1.4059613	3.58395735	338.11581	1.64E-75	8.85E-75	-1.3873758	100	0	SCAMP4	-0.9543143	3.72332791	138.006598	7.26E-32	2.68E-31	-0.9605898	97.2222222	2.77777778
ENSG00000012232	EXTL3	-1.2875279	4.20771798	336.086247	4.54E-75	2.44E-74	-1.2330705	100	0	EXTL3	-0.5825085	4.43083466	62.6847916	2.43E-15	5.82E-15	-0.6330445	97.2222222	2.77777778
ENSG00000113916	BCL6	-1.1402581	6.47159049	335.656232	5.63E-75	3.02E-74	-1.0763625	100	0	BCL6	-1.1500884	6.35841074	282.054119	2.68E-63	1.65E-62	-1.0820269	100	0
ENSG00000042753	AP2S1	-1.2846034	4.23821424	335.482668	6.15E-75	3.30E-74	-1.1872204	100	0	AP2S1	-0.8756976	4.34528855	136.101597	1.90E-31	6.92E-31	-0.9157741	97.2222222	2.77777778
ENSG00000104142	VPS18	-1.1660497	5.29366017	334.900063	8.23E-75	4.41E-74	-1.1075975	100	0	VPS18	-0.8886162	5.32780316	165.5127	7.07E-38	2.95E-37	-0.9459826	100	0
ENSG00000171552	BCL2L1	-1.2705646	4.29793947	334.786341	8.72E-75	4.66E-74	-1.2347663	100	0	BCL2L1	-1.0747414	4.32449313	204.881796	1.80E-46	8.74E-46	-1.1053408	100	0
ENSG00000162980	ARL5A	-1.1546077	5.58361298	334.552965	9.80E-75	5.23E-74	-1.1586022	100	0	ARL5A	-1.0118862	5.56128036	216.148988	6.26E-49	3.18E-48	-1.0079414	100	0
ENSG00000160948	VPS28	1.144716	6.06708509	334.519062	9.97E-75	5.32E-74	1.18038625	0	100	VPS28	0.92470096	5.83619251	180.494828	3.78E-41	1.69E-40	0.92348757	2.77777778	97.2222222
ENSG00000119723	COQ6	1.46515669	3.28031405	334.47582	1.02E-74	5.43E-74	1.50793302	0	100	COQ6	1.2693172	3.09534948	200.766401	1.42E-45	6.77E-45	1.23689666	0	100
ENSG00000185883	ATP6V0C	-1.1719455	5.19826672	334.262524	1.13E-74	6.04E-74	-1.0931612	100	0	ATP6V0C	-0.9119273	5.24763529	171.098607	4.26E-39	1.82E-38	-0.9398048	100	0
ENSG00000241106	HLA-DOB	-1.7185619	2.49297403	333.874637	1.38E-74	7.34E-74	-1.5930351	94.2857143	5.71428571	HLA-DOB	-1.7748435	2.36609973	273.795905	1.69E-61	1.01E-60	-1.9281322	97.2222222	2.77777778
ENSG00000197969	VPS13A	1.16667393	5.36522607	333.741844	1.47E-74	7.84E-74	1.26991982	0	100	VPS13A	1.32490917	5.405364	356.657166	1.50E-79	1.13E-78	1.18579232	0	100
ENSG00000133318	RTN3	-1.2105862	4.7647847	333.67966	1.52E-74	8.08E-74	-1.1079081	100	0	RTN3	-1.3919202	4.69406394	361.008487	1.70E-80	1.29E-79	-1.4252726	100	0
ENSG00000185591	SP1	-1.1425211	6.00402569	333.507107	1.66E-74	8.80E-74	-1.0743276	100	0	SP1	-1.0292541	5.98023229	227.989103	1.64E-51	8.64E-51	-1.0822413	100	0
ENSG00000136720	HS6ST1	-1.2597572	4.35364412	333.277868	1.86E-74	9.87E-74	-1.2386483	100	0	HS6ST1	-1.3379641	4.29151353	307.429522	7.93E-69	5.34E-68	-1.4002836	100	0
ENSG00000185158	LRRC37B	1.14179756	5.83194388	332.550751	2.67E-74	1.42E-73	1.24327961	0	100	LRRC37B	0.8870512	5.60313062	168.211096	1.82E-38	7.68E-38	0.80659522	0	100
ENSG00000198899	MT-ATP6	-1.1380042	11.2899034	332.102506	3.35E-74	1.77E-73	-1.0827802	100	0	MT-ATP6	-0.6553584	11.432162	67.7528808	1.85E-16	4.60E-16	-0.7330409	94.4444444	5.55555556
ENSG00000170088	TMEM192	-1.3177136	3.94160357	330.596003	7.13E-74	3.76E-73	-1.2018418	100	0	TMEM192	-1.0754117	3.94751515	187.786962	9.67E-43	4.41E-42	-1.0866171	100	0
ENSG00000116406	EDEM3	1.23135585	4.48284264	329.762301	1.08E-73	5.70E-73	1.30595088	0	100	EDEM3	0.7130777	4.14704317	87.2977903	9.34E-21	2.63E-20	0.68729777	13.8888889	86.1111111
ENSG00000169710	FASN	1.13326787	7.31141873	329.661422	1.14E-73	5.99E-73	1.04448813	0	100	FASN	2.19237761	7.99645594	917.694674	1.40E-201	2.28E-200	2.12577161	0	100
ENSG00000103091	WDR59	1.29770732	4.06270508	329.159848	1.46E-73	7.70E-73	1.43838439	0	100	WDR59	1.0617621	3.79922151	174.23538	8.79E-40	3.82E-39	1.07872802	2.77777778	97.2222222
ENSG00000115271	GCA	-1.624431	2.58850021	328.783144	1.77E-73	9.28E-73	-1.647737	100	0	GCA	-2.4815324	2.44363938	559.536069	1.06E-123	1.17E-122	-2.5307749	100	0
ENSG00000159720	ATP6V0D1	-1.1319967	5.98899556	328.307224	2.25E-73	1.18E-72	-1.0063832	100	0	ATP6V0D1	-0.7647416	6.08946951	126.84128	2.01E-29	7.03E-29	-0.8470332	100	0
ENSG00000168297	PXK	-1.2278986	4.47470752	327.983492	2.64E-73	1.38E-72	-1.1441475	100	0	PXK	-0.5873607	4.66467414	66.7209958	3.13E-16	7.70E-16	-0.7138414	94.4444444	5.55555556
ENSG00000140853	NLRC5	1.10983594	7.78413125	327.94326	2.70E-73	1.41E-72	1.19689166	0	100	NLRC5	1.39730036	7.95158454	398.709878	1.05E-88	8.81E-88	1.34859041	0	100
ENSG00000108771	DHX58	1.3638414	3.6828541	327.190558	3.93E-73	2.06E-72	1.45426347	0	100	DHX58	0.7496616	3.24266893	74.4603243	6.19E-18	1.59E-17	0.6985661	8.33333333	91.6666667
ENSG00000131378	RFTN1	-1.1325862	5.88677338	327.100013	4.12E-73	2.15E-72	-1.062917	100	0	RFTN1	-0.5909877	6.03104937	76.3886448	2.33E-18	6.09E-18	-0.5920317	100	0
ENSG00000070814	TCOF1	1.15476864	5.42898497	327.006428	4.31E-73	2.25E-72	1.27116547	2.85714286	97.1428571	TCOF1	1.13865894	5.36402638	265.374589	1.16E-59	6.77E-59	1.13338878	2.77777778	97.2222222
ENSG00000197535	MYO5A	-1.1366585	5.6664114	326.964033	4.41E-73	2.30E-72	-1.0266045	100	0	MYO5A	-0.6031424	5.81572711	78.4410328	8.24E-19	2.19E-18	-0.5955393	100	0
ENSG00000023902	PLEKHO1	-1.1197572	6.85946871	326.823293	4.73E-73	2.47E-72	-0.9435749	100	0	PLEKHO1	-1.0857516	6.85744637	252.848171	6.22E-57	3.52E-56	-1.0545712	100	0
ENSG00000163386	NA	-1.1449991	5.4850573	326.08887	6.83E-73	3.56E-72	-1.1125961	100	0	NA	-1.3416323	5.34097746	370.913768	1.18E-82	9.22E-82	-1.4663164	100	0
ENSG00000166508	MCM7	1.1168997	6.51158229	325.975633	7.23E-73	3.77E-72	1.20263962	0	100	MCM7	0.88281229	6.29899406	168.752289	1.39E-38	5.86E-38	0.79934384	2.77777778	97.2222222
ENSG00000137309	HMGA1	-1.1103102	7.50737464	324.633245	1.42E-72	7.37E-72	-0.9781066	100	0	HMGA1	-1.0425059	7.45978988	228.639426	1.18E-51	6.26E-51	-1.0718464	100	0
ENSG00000110090	CPT1A	-1.2977547	4.01165449	324.547507	1.48E-72	7.69E-72	-1.2569722	100	0	CPT1A	-0.8208904	4.1526612	112.718441	2.49E-26	8.07E-26	-0.9029872	97.2222222	2.77777778
ENSG00000174606	ANGEL2	1.160805	5.12083413	323.816313	2.14E-72	1.11E-71	1.25349354	0	100	ANGEL2	1.17527021	5.10357517	277.941998	2.11E-62	1.28E-61	1.14202666	0	100
ENSG00000131748	STARD3	1.12829792	5.94161256	323.589594	2.39E-72	1.24E-71	1.20180859	0	100	STARD3	0.9100325	5.76128592	176.139651	3.38E-40	1.48E-39	0.86724598	2.77777778	97.2222222
ENSG00000022976	ZNF839	1.25630224	4.21493154	323.229731	2.87E-72	1.48E-71	1.27776969	0	100	ZNF839	0.93429172	3.97002402	142.884297	6.23E-33	2.35E-32	0.83467603	0	100
ENSG00000169410	PTPN9	-1.4745054	3.12441348	321.904044	5.57E-72	2.88E-71	-1.3119262	100	0	PTPN9	-1.3298105	3.16464981	221.993608	3.32E-50	1.72E-49	-1.3197377	100	0
ENSG00000183283	DAZAP2	-1.0986702	9.16337564	321.125272	8.24E-72	4.24E-71	-1.0386922	100	0	DAZAP2	-0.771811	9.23070495	114.801812	8.70E-27	2.86E-26	-0.7849336	100	0
ENSG00000177700	POLR2L	-1.3221458	3.82581877	319.758809	1.63E-71	8.40E-71	-1.2631671	100	0	POLR2L	-0.7295456	4.00014802	87.5663223	8.15E-21	2.30E-20	-0.7879425	91.6666667	8.33333333
ENSG00000130725	UBE2M	-1.2307943	4.32753992	319.621195	1.75E-71	8.98E-71	-1.2076352	100	0	UBE2M	-0.4771798	4.55374502	43.2748214	4.76E-11	9.78E-11	-0.5332651	97.2222222	2.77777778
ENSG00000165699	TSC1	1.13259813	5.38929826	318.797513	2.65E-71	1.35E-70	1.15800476	0	100	TSC1	0.93194144	5.20601899	179.186754	7.29E-41	3.24E-40	0.885273	2.77777778	97.2222222
ENSG00000224531	SMIM13	-1.3989215	3.41188388	318.694681	2.79E-71	1.43E-70	-1.3350879	100	0	SMIM13	-0.740002	3.53172139	79.6965652	4.37E-19	1.17E-18	-0.7669154	97.2222222	2.77777778
ENSG00000167004	PDIA3	-1.0910887	7.93900532	318.541332	3.01E-71	1.54E-70	-1.0499856	100	0	PDIA3	-0.8626166	7.96140313	156.055964	8.23E-36	3.30E-35	-0.8459358	100	0
ENSG00000155368	DBI	-1.1714396	4.79784448	317.957124	4.04E-71	2.06E-70	-1.1362494	100	0	DBI	-0.5480839	4.97009205	60.8120426	6.28E-15	1.49E-14	-0.5830043	88.8888889	11.1111111
ENSG00000090432	MUL1	-1.1560389	4.9759825	317.718247	4.55E-71	2.32E-70	-1.0993271	100	0	MUL1	-0.8397254	5.02890114	143.591314	4.36E-33	1.66E-32	-0.9202165	100	0
ENSG00000122417	ODF2L	1.20020026	4.51415703	316.215077	9.67E-71	4.92E-70	1.26033096	0	100	ODF2L	1.29373265	4.50110189	304.682483	3.15E-68	2.11E-67	1.26062124	2.77777778	97.2222222
ENSG00000239911	PRKAG2-AS1	-2.0253829	1.07327983	314.925756	1.85E-70	9.36E-70	-1.9252991	100	0	PRKAG2-AS1	-2.0882363	0.99716145	245.438651	2.56E-55	1.43E-54	-2.1452531	100	0

ENSG00000132824	SERINC3	1.10342253	6.21043474	314.177399	2.69E-70	1.36E-69	1.17849494	0	100	SERINC3	0.8617855	5.98295754	161.038406	6.71E-37	2.74E-36	0.84450588	5.55555556	94.4444444
ENSG00000051825	MPHOSPH9	1.12963004	5.20102814	312.530394	6.14E-70	3.10E-69	1.17962566	0	100	MPHOSPH9	1.10850038	5.12190088	250.026457	2.56E-56	1.44E-55	1.03224601	0	100
ENSG00000110429	FBXO3	1.10389985	6.19863475	312.308989	6.86E-70	3.46E-69	1.13389311	0	100	FBXO3	0.98882958	6.06979859	208.813164	2.49E-47	1.23E-46	0.91035333	2.77777778	97.2222222
ENSG00000241058	NSUN6	1.55591155	2.7052192	311.357991	1.11E-69	5.55E-69	1.53890695	0	100	NSUN6	1.20043144	2.37343215	140.226488	2.38E-32	8.88E-32	1.11658529	0	100
ENSG00000040199	PHLPP2	-1.1602527	4.77099598	310.129786	2.05E-69	1.03E-68	-1.0220629	100	0	PHLPP2	-0.7278843	4.80322111	104.211217	1.82E-24	5.62E-24	-0.7531989	97.2222222	2.77777778
ENSG00000138814	PPP3CA	-1.1669117	4.67981485	310.058877	2.12E-69	1.06E-68	-1.0895394	100	0	PPP3CA	-0.5824599	4.80538489	67.3887496	2.23E-16	5.52E-16	-0.6193049	100	0
ENSG00000156639	ZFAND3	-1.0988436	5.82330247	309.042306	3.53E-69	1.77E-68	-0.9952247	100	0	ZFAND3	-0.7336628	5.93551665	116.921878	2.99E-27	9.90E-27	-0.7509829	100	0
ENSG00000178741	COX5A	-1.1624844	4.70350908	308.880035	3.83E-69	1.91E-68	-1.0443205	100	0	COX5A	-0.6925932	4.8203158	94.9533851	1.95E-22	5.74E-22	-0.8130767	97.2222222	2.77777778
ENSG00000225828	FAM229A	1.31647686	3.7249336	308.219061	5.34E-69	2.66E-68	1.40478269	0	100	FAM229A	0.82379434	3.37121631	93.62781	3.81E-22	1.11E-21	0.75368204	0	100
ENSG00000105656	ELL	-1.1010304	5.55224309	304.762438	3.02E-68	1.50E-67	-1.0539166	100	0	ELL	-0.5019767	5.70520803	54.0815965	1.92E-13	4.33E-13	-0.6563352	88.8888889	11.1111111
ENSG00000171791	BCL2	-1.1044023	5.64685996	304.671041	3.16E-68	1.57E-67	-0.9896708	100	0	BCL2	-1.4760333	5.43298412	441.39247	5.39E-98	4.94E-97	-1.541815	100	0
ENSG00000184678	HIST2H2BE	-1.3623143	3.49981213	303.917084	4.62E-68	2.28E-67	-1.3006991	97.1428571	2.85714286	HIST2H2BE	-0.7109864	3.58468594	73.3311568	1.10E-17	2.80E-17	-0.7708101	94.4444444	5.55555556
ENSG00000152492	CCDC50	-1.0952001	6.15679525	303.878175	4.71E-68	2.33E-67	-1.0158212	100	0	CCDC50	-1.2668421	6.03458884	335.719498	5.46E-75	3.90E-74	-1.2784614	100	0
ENSG00000185989	RASA3	1.06895684	7.71641114	303.84322	4.79E-68	2.37E-67	1.07598961	0	100	RASA3	0.85906772	7.53223163	157.153533	4.74E-36	1.91E-35	0.71358196	2.77777778	97.2222222
ENSG00000123607	TTC21B	1.29953719	3.74451199	303.320971	6.23E-68	3.07E-67	1.2935835	0	100	TTC21B	1.25455085	3.67921937	233.275882	1.15E-52	6.16E-52	1.18823515	2.77777778	97.2222222
ENSG00000143549	TPM3	-1.0634093	8.4265238	303.124	6.87E-68	3.39E-67	-1.0720023	100	0	TPM3	-0.7247386	8.50200577	106.851871	4.80E-25	1.51E-24	-0.7041496	100	0
ENSG00000153310	FAM49B	-1.0792778	6.2862833	303.027158	7.22E-68	3.56E-67	-0.9768868	100	0	FAM49B	-0.674443	6.39801574	99.7988932	1.69E-23	5.10E-23	-0.6651564	100	0
ENSG00000182220	ATP6AP2	-1.0800275	6.47270874	302.654695	8.70E-68	4.29E-67	-0.9384396	100	0	ATP6AP2	-1.1413588	6.43025857	279.334629	1.05E-62	6.42E-62	-1.1290208	100	0
ENSG00000132879	FBXO44	1.34337672	3.57262012	301.890879	1.28E-67	6.28E-67	1.32407187	0	100	FBXO44	0.76639953	3.12693574	73.1763067	1.19E-17	3.03E-17	0.57551157	11.1111111	88.8888889
ENSG00000164941	INTS8	1.13114802	4.86783039	301.423084	1.61E-67	7.93E-67	1.17382447	0	100	INTS8	0.68977436	4.51770713	89.5474504	2.99E-21	8.56E-21	0.59611456	2.77777778	97.2222222
ENSG00000160712	IL6R	-1.1416015	4.95532057	300.839987	2.16E-67	1.06E-66	-1.0844786	100	0	IL6R	-3.4967655	4.58042046	1796.49369	0	0	-3.4324156	100	0
ENSG00000164327	RICTOR	1.06144301	8.09344564	299.20707	4.90E-67	2.40E-66	1.07091327	0	100	RICTOR	1.00930516	8.02798514	207.636714	4.50E-47	2.22E-46	1.00144058	5.55555556	94.4444444
ENSG00000095059	DHPS	1.16925499	4.57524601	298.993631	5.46E-67	2.67E-66	1.24349188	0	100	DHPS	0.92990269	4.34463562	151.862082	6.79E-35	2.68E-34	0.76736909	5.55555556	94.4444444
ENSG00000180304	OAZ2	-1.0991557	5.35559796	298.633083	6.54E-67	3.20E-66	-1.044038	100	0	OAZ2	-0.8285837	5.4244476	144.739934	2.45E-33	9.33E-33	-0.8508398	100	0
ENSG00000100429	HDAC10	1.49127139	2.83865704	298.061534	8.71E-67	4.26E-66	1.54986265	0	100	HDAC10	1.2402647	2.58398794	157.969209	3.14E-36	1.27E-35	1.02819822	2.77777778	97.2222222
ENSG00000118689	FOXO3	-1.0710145	6.48863253	297.043549	1.45E-66	7.09E-66	-0.9547959	100	0	FOXO3	-1.2986284	6.34118063	360.742369	1.94E-80	1.47E-79	-1.2325755	100	0
ENSG00000143753	DEGS1	-1.0858171	5.49682888	296.834805	1.61E-66	7.87E-66	-0.9827786	100	0	DEGS1	-0.9117834	5.49102368	176.00235	3.62E-40	1.58E-39	-0.8556394	100	0
ENSG00000213995	CARKD	1.1341532	4.72830323	295.624025	2.96E-66	1.44E-65	1.15769369	0	100	CARKD	0.88549224	4.5149683	146.188804	1.18E-33	4.53E-33	0.84523794	0	100
ENSG00000153107	ANAPC1	1.12353302	4.83694791	295.515977	3.12E-66	1.52E-65	1.10332097	0	100	ANAPC1	1.02778659	4.73270617	204.415532	2.27E-46	1.10E-45	0.92257706	0	100
ENSG00000266777	SH3GL1P1	1.63679764	2.27965812	295.484729	3.17E-66	1.54E-65	1.69478685	0	100	SH3GL1P1	1.83205103	2.35184929	309.114537	3.41E-69	2.30E-68	1.80771323	0	100
ENSG00000067836	ROGDI	-1.4689704	2.89509774	295.274151	3.53E-66	1.71E-65	-1.4137242	100	0	ROGDI	-1.853635	2.79743316	360.797948	1.89E-80	1.43E-79	-2.0046286	97.2222222	2.77777778
ENSG00000102897	LYRM1	-1.4244274	3.03682364	294.951596	4.15E-66	2.01E-65	-1.3486027	100	0	LYRM1	-0.8324025	3.1707987	90.4990691	1.85E-21	5.31E-21	-0.881712	100	0
ENSG00000187667	NA	1.1191648	4.88728003	294.642981	4.84E-66	2.34E-65	1.16513491	0	100	NA	1.24855999	4.93476324	306.359823	1.36E-68	9.12E-68	1.12237003	0	100
ENSG00000188522	FAM83G	-1.3032587	3.68891266	294.063459	6.47E-66	3.13E-65	-1.2415701	100	0	FAM83G	-0.7733761	3.80146429	91.4501121	1.14E-21	3.30E-21	-0.8070373	91.6666667	8.33333333
ENSG00000132781	MUTYH	1.35486812	3.34345659	293.927009	6.93E-66	3.35E-65	1.3764478	0	100	MUTYH	1.06051376	3.08410837	141.879392	1.03E-32	3.89E-32	1.03228729	0	100
ENSG00000013810	TACC3	1.06782566	6.01962837	293.903851	7.01E-66	3.38E-65	1.15764347	0	100	TACC3	0.73266247	5.74048846	116.065346	4.60E-27	1.52E-26	0.6564707	0	100
ENSG00000263826	RP11-573D15.9	1.38690091	3.23480755	293.721812	7.68E-66	3.70E-65	1.43608455	0	100	RP11-573D15.	1.29598508	3.1006689	205.795595	1.14E-46	5.56E-46	1.26993375	2.77777778	97.2222222
ENSG00000164823	OSGIN2	-1.1375366	4.65587823	293.509828	8.55E-66	4.12E-65	-1.0681489	100	0	OSGIN2	-1.0572286	4.62849342	211.10833	7.87E-48	3.92E-47	-1.0542656	100	0
ENSG00000151498	ACAD8	1.31829684	3.56788868	292.921601	1.15E-65	5.52E-65	1.40795264	0	100	ACAD8	1.41217758	3.59587797	282.526709	2.11E-63	1.31E-62	1.31565658	0	100
ENSG00000249115	HAUS5	1.29419149	3.68434601	292.309214	1.56E-65	7.49E-65	1.41080134	0	100	HAUS5	1.10497202	3.45575655	168.696585	1.43E-38	6.03E-38	0.97464188	2.77777778	97.2222222
ENSG00000095209	TMEM38B	-1.385753	3.18742304	292.115811	1.72E-65	8.24E-65	-1.2578704	100	0	TMEM38B	-1.3354891	3.13918643	224.727923	8.42E-51	4.39E-50	-1.41331	100	0
ENSG00000198721	ECI2	1.36688795	3.27279245	291.690862	2.13E-65	1.02E-64	1.39455297	0	100	ECI2	1.24183923	3.14025612	194.495892	3.32E-44	1.54E-43	1.19829046	0	100
ENSG00000198728	LDB1	1.06659431	5.87633217	291.081672	2.89E-65	1.38E-64	1.11708643	0	100	LDB1	0.93357211	5.73707032	185.603049	2.90E-42	1.31E-41	0.84009292	2.77777778	97.2222222
ENSG00000148384	INPP5E	1.30842664	3.58333589	290.882073	3.19E-65	1.53E-64	1.36624402	0	100	INPP5E	0.77960451	3.14529391	78.1590446	9.51E-19	2.52E-18	0.69147243	2.77777778	97.2222222
ENSG00000142188	TMEM50B	1.15123858	4.56771947	290.4615	3.94E-65	1.88E-64	1.09846013	0	100	TMEM50B	0.92479086	4.34345351	152.097593	6.03E-35	2.38E-34	0.85453354	2.77777778	97.2222222
ENSG00000102580	DNAJC3	-1.0577363	6.17353294	290.366809	4.14E-65	1.97E-64	-0.9735319	100	0	DNAJC3	-0.4959978	6.30920303	54.1526318	1.86E-13	4.18E-13	-0.5071632	97.2222222	2.77777778
ENSG00000108773	KAT2A	1.21061607	4.22435456	290.29688	4.28E-65	2.04E-64	1.11950007	0	100	KAT2A	0.92921504	3.92209409	133.38552	7.45E-31	2.68E-30	0.73936739	2.77777778	97.2222222
ENSG00000136490	LIMD2	1.04214145	8.98286067	290.239662	4.41E-65	2.10E-64	1.10561071	0	100	LIMD2	0.84105513	8.80732385	140.041878	2.61E-32	9.74E-32	0.76041206	2.77777778	97.2222222
ENSG00000131669	NINJ1	-1.0473586	7.5178197	289.990885	5.00E-65	2.37E-64	-0.8969077	100	0	NINJ1	-0.8659032	7.53309717	157.77946	3.46E-36	1.39E-35	-1.0204326	100	0
ENSG00000158805	ZNF276	1.06031243	6.02640589	289.774091	5.57E-65	2.64E-64	1.11410326	0	100	ZNF276	1.18760653	6.09263804	302.000186	1.21E-67	7.97E-67	1.17862539	0	100
ENSG00000137501	SYTL2	1.27995126	3.72489587	289.429041	6.62E-65	3.14E-64	1.34285147	0	100	SYTL2	1.86854435	4.14526235	559.38261	1.15E-123	1.27E-122	1.73646017	0	100
ENSG00000119632	IFI27L2	-1.5445461	2.49204727	288.526077	1.04E-64	4.93E-64	-1.4716642	100	0	IFI27L2	-1.0303102	2.62133871	111.166577	5.44E-26	1.75E-25	-0.9985406	97.2222222	2.77777778
ENSG00000149781	FERMT3	-1.061278	5.83258048	286.243278	3.27E-64	1.54E-63	-1.042619	100	0	FERMT3	-1.2585112	5.77713449	323.771487	2.18E-72	1.53E-71	-1.3396708	97.2222222	2.77777778

ENSG00000091527	CDV3	-1.0321111	8.33009233	286.200609	3.35E-64	1.58E-63	-0.9609476	100	0	CDV3	-0.5710786	8.42880447	67.1667891	2.49E-16	6.16E-16	-0.5681671	100	0
ENSG00000185624	P4HB	-1.0374894	7.17046538	286.184544	3.37E-64	1.59E-63	-0.9835277	100	0	P4HB	-0.6283559	7.29048859	85.4259669	2.41E-20	6.70E-20	-0.6765166	97.2222222	2.77777778
ENSG00000164338	UTP15	1.11702996	4.6911816	284.842747	6.61E-64	3.10E-63	1.17913245	0	100	UTP15	0.86274646	4.4345288	136.442242	1.60E-31	5.84E-31	0.76812486	0	100
ENSG00000173281	PPP1R3B	-1.1793558	4.25071437	284.586057	7.52E-64	3.52E-63	-1.0031404	100	0	PPP1R3B	-1.6906837	4.06943814	456.78018	2.41E-101	2.28E-100	-1.6728569	100	0
ENSG00000123358	NR4A1	-1.0743677	6.45922856	283.758973	1.14E-63	5.33E-63	-0.8948646	88.5714286	11.4285714	NR4A1	-0.9017029	6.3829689	170.324479	6.28E-39	2.68E-38	-0.9194443	91.6666667	8.33333333
ENSG00000084112	SSH1	-1.0429788	6.46356108	282.810853	1.83E-63	8.55E-63	-0.9731236	100	0	SSH1	-0.805795	6.49202379	139.700348	3.10E-32	1.15E-31	-0.7334738	100	0
ENSG00000141456	PELP1	1.09063035	4.90663303	281.501657	3.53E-63	1.64E-62	1.11830314	0	100	PELP1	0.94972005	4.80527923	176.343634	3.05E-40	1.34E-39	0.85340255	2.77777778	97.2222222
ENSG00000157600	TMEM164	-1.1680466	4.23951686	280.887035	4.81E-63	2.23E-62	-1.0698885	100	0	TMEM164	-1.2001918	4.18553437	245.953848	1.98E-55	1.10E-54	-1.2287581	100	0
ENSG00000137642	SORL1	1.02408394	8.03160906	280.59625	5.57E-63	2.58E-62	1.11045777	0	100	SORL1	0.66620553	7.76654999	94.0736486	3.04E-22	8.89E-22	0.57336331	8.33333333	91.6666667
ENSG00000122490	PQLC1	-1.0493636	5.73916485	280.211391	6.75E-63	3.13E-62	-0.9688259	100	0	PQLC1	-0.783689	5.81709641	131.665882	1.77E-30	6.32E-30	-0.9392348	97.2222222	2.77777778
ENSG00000024048	UBR2	1.05065094	5.57607042	279.413392	1.01E-62	4.66E-62	1.03040647	0	100	UBR2	0.87110042	5.46633862	160.949132	7.02E-37	2.86E-36	0.79733234	0	100
ENSG00000078674	PCM1	1.02691523	7.10762411	279.254958	1.09E-62	5.05E-62	1.08106646	0	100	PCM1	0.94919905	7.00244708	194.360341	3.55E-44	1.65E-43	0.95967912	5.55555556	94.4444444
ENSG00000007047	MARK4	-1.2299997	3.805926	279.165879	1.14E-62	5.28E-62	-1.2000082	100	0	MARK4	-0.7142132	3.96336015	82.9233076	8.53E-20	2.34E-19	-0.7213368	97.2222222	2.77777778
ENSG00000156931	VPS8	1.09774278	4.72313529	277.367145	2.81E-62	1.30E-61	1.14188027	0	100	VPS8	0.70062858	4.37178074	89.0829091	3.79E-21	1.08E-20	0.60246529	8.33333333	91.6666667
ENSG00000035403	VCL	-1.2377623	3.84417614	277.169098	3.11E-62	1.43E-61	-1.1223127	100	0	VCL	-1.4492266	3.73705583	299.114367	5.14E-67	3.36E-66	-1.5504243	100	0
ENSG00000140264	SERF2	-1.0241506	6.83170503	275.7784	6.25E-62	2.87E-61	-0.9662161	100	0	SERF2	-0.9612049	6.79796698	198.168181	5.24E-45	2.47E-44	-1.0493833	97.2222222	2.77777778
ENSG00000198736	MSRB1	-1.7130555	1.69775104	275.734618	6.38E-62	2.93E-61	-1.480843	100	0	MSRB1	-1.8128523	1.71690697	242.480102	1.13E-54	6.23E-54	-1.7651515	100	0
ENSG00000125746	EML2	1.34138976	3.30016955	275.166481	8.49E-62	3.90E-61	1.48571391	0	100	EML2	0.96537165	2.96802943	107.765182	3.03E-25	9.58E-25	0.96964004	8.33333333	91.6666667
ENSG00000136044	APPL2	1.03592043	5.75075319	274.670933	1.09E-61	4.99E-61	1.09137176	0	100	APPL2	0.94205062	5.62422126	189.619866	3.85E-43	1.77E-42	0.84574342	0	100
ENSG00000157500	APPL1	-1.0488855	5.29430419	274.207367	1.37E-61	6.29E-61	-0.9891075	100	0	APPL1	-0.9233722	5.27155846	177.790061	1.47E-40	6.51E-40	-0.9422305	100	0
ENSG00000100151	PICK1	1.43939092	2.743737	273.532123	1.93E-61	8.81E-61	1.45510024	0	100	PICK1	1.39366352	2.62583622	201.907105	8.01E-46	3.84E-45	1.32996654	0	100
ENSG00000113719	ERGIC1	-1.0260521	6.15447828	273.153691	2.33E-61	1.06E-60	-0.9934342	100	0	ERGIC1	-0.6560524	6.2469932	94.7067209	2.21E-22	6.48E-22	-0.6711252	100	0
ENSG00000188725	SMIM15	-1.1455914	4.24855384	273.02741	2.48E-61	1.13E-60	-1.06932	100	0	SMIM15	-1.1287415	4.19098751	219.515502	1.15E-49	5.92E-49	-1.104339	100	0
ENSG00000164808	SPIDR	-1.1961295	3.95267848	272.966165	2.56E-61	1.17E-60	-1.1740113	100	0	SPIDR	-1.278002	3.87232972	256.121109	1.20E-57	6.90E-57	-1.285689	100	0
ENSG00000108518	PFN1	-1.0083222	8.38636456	272.207359	3.75E-61	1.71E-60	-0.9526975	100	0	PFN1	-0.7587387	8.42487737	117.365802	2.39E-27	7.93E-27	-0.8338977	97.2222222	2.77777778
ENSG00000140545	MFGE8	1.24296272	3.64932377	269.788208	1.26E-60	5.71E-60	1.2708296	0	100	MFGE8	1.49249726	3.73026409	330.261792	8.43E-74	5.97E-73	1.36265614	0	100
ENSG00000186660	ZFP91	-1.00651	7.17855248	269.445354	1.50E-60	6.78E-60	-0.9373357	100	0	ZFP91	-0.755691	7.1848717	124.156287	7.79E-29	2.68E-28	-0.7850387	100	0
ENSG00000025156	HSF2	1.03605816	5.43090002	268.641722	2.24E-60	1.01E-59	1.05921644	0	100	HSF2	1.00556101	5.33096791	207.953157	3.84E-47	1.90E-46	1.03173188	2.77777778	97.2222222
ENSG00000125827	TMX4	-1.0102665	6.71582184	268.099974	2.94E-60	1.33E-59	-0.9034241	100	0	TMX4	-0.6104274	6.78844125	81.5527595	1.71E-19	4.63E-19	-0.6398927	97.2222222	2.77777778
ENSG00000144535	DIS3L2	1.06615664	4.83973711	267.926919	3.21E-60	1.45E-59	1.10689122	0	100	DIS3L2	0.93318634	4.68405965	168.516597	1.56E-38	6.59E-38	0.89726949	0	100
ENSG00000101224	CDC25B	1.02253285	6.25825924	267.131557	4.79E-60	2.15E-59	1.15048549	2.85714286	97.1428571	CDC25B	1.2231151	6.29366551	314.119587	2.77E-70	1.90E-69	1.16752974	2.77777778	97.2222222
ENSG00000162695	SLC30A7	1.07470586	4.77336251	266.604101	6.24E-60	2.80E-59	1.12110196	0	100	SLC30A7	0.64246441	4.48152918	76.6376036	2.05E-18	5.38E-18	0.57681275	5.55555556	94.4444444
ENSG00000114978	MOB1A	-0.9886979	8.21917518	263.482565	2.99E-59	1.33E-58	-0.9161638	100	0	MOB1A	-0.616033	8.27492431	78.7517244	7.04E-19	1.88E-18	-0.6210581	100	0
ENSG00000129292	PHF20L1	1.00747407	6.01727874	262.580385	4.70E-59	2.09E-58	1.14258777	0	100	PHF20L1	0.80011973	5.85744031	138.605925	5.37E-32	1.99E-31	0.77796369	2.77777778	97.2222222
ENSG00000167325	RRM1	1.04285188	5.03787047	262.064247	6.09E-59	2.71E-58	1.15033568	0	100	RRM1	1.10283311	4.99293888	243.147574	8.10E-55	4.47E-54	1.00408258	2.77777778	97.2222222
ENSG00000108515	ENO3	1.4851498	2.41541724	261.773517	7.05E-59	3.13E-58	1.51019886	0	100	ENO3	1.15931037	2.08172178	119.250307	9.23E-28	3.11E-27	1.04166785	0	100
ENSG00000011258	MBTD1	1.01225793	5.76243265	261.726635	7.21E-59	3.20E-58	1.05456446	0	100	MBTD1	0.87350998	5.6208948	162.565294	3.11E-37	1.28E-36	0.8518903	0	100
ENSG00000158710	TAGLN2	-0.9872459	8.3891546	260.950323	1.07E-58	4.71E-58	-0.888173	100	0	TAGLN2	-0.8054601	8.37634741	131.456624	1.97E-30	7.02E-30	-0.8392002	100	0
ENSG00000112679	DUSP22	-1.130622	4.19663158	260.343982	1.44E-58	6.38E-58	-1.0746767	100	0	DUSP22	-0.8947388	4.19273068	136.957135	1.23E-31	4.52E-31	-0.9987395	97.2222222	2.77777778
ENSG00000100034	PPM1F	-1.0570596	4.85715435	259.640344	2.06E-58	9.05E-58	-1.0656199	100	0	PPM1F	-1.4726958	4.74016752	406.656047	1.96E-90	1.66E-89	-1.52777	100	0
ENSG00000159082	SYNJ1	1.04962976	4.88053851	259.622925	2.07E-58	9.12E-58	1.07472205	0	100	SYNJ1	0.74287999	4.67003065	106.116023	6.95E-25	2.18E-24	0.68077865	2.77777778	97.2222222
ENSG00000165915	SLC39A13	1.03776663	4.97392246	258.221252	4.19E-58	1.84E-57	1.08650039	0	100	SLC39A13	0.68062826	4.70847499	90.4356879	1.91E-21	5.48E-21	0.64643307	2.77777778	97.2222222
ENSG00000254912	RP11-632K20.2	1.63389974	1.81547454	257.643274	5.60E-58	2.45E-57	1.68007392	0	100	RP11-632K20.	1.21614361	1.57846953	107.318388	3.79E-25	1.20E-24	1.16514383	0	100
ENSG00000138293	NA	-0.984349	7.05532177	257.57899	5.78E-58	2.53E-57	-0.9627052	100	0	NA	-0.8072432	7.07155874	141.946687	9.99E-33	3.76E-32	-0.8210351	100	0
ENSG00000028528	SNX1	1.03623445	5.06214349	257.137486	7.22E-58	3.16E-57	1.08873795	0	100	SNX1	0.79066805	4.83377778	123.285365	1.21E-28	4.13E-28	0.69130322	2.77777778	97.2222222
ENSG00000136810	TXN	-1.1059201	4.29670704	256.822955	8.45E-58	3.69E-57	-1.1546776	100	0	TXN	-1.3258862	4.19397232	298.293835	7.75E-67	5.05E-66	-1.3879994	100	0
ENSG00000196757	ZNF700	1.34710645	2.98130404	255.495083	1.65E-57	7.15E-57	1.39969249	2.85714286	97.1428571	ZNF700	1.08658102	2.77391093	129.406015	5.53E-30	1.96E-29	1.16743852	5.55555556	94.4444444
ENSG00000172301	COPRS	-1.6948593	1.44849776	254.794478	2.34E-57	1.01E-56	-1.6313013	100	0	COPRS	-1.5894576	1.38374217	172.302871	2.32E-39	1.00E-38	-1.5737131	100	0
ENSG00000167785	ZNF558	1.25357946	3.45801767	254.73406	2.41E-57	1.05E-56	1.16445207	0	100	ZNF558	0.770171	3.0828414	74.0054165	7.79E-18	2.00E-17	0.67960143	8.33333333	91.6666667
ENSG00000196839	ADA	1.09056121	4.41291474	254.501531	2.71E-57	1.17E-56	1.12745381	2.85714286	97.1428571	ADA	0.73707097	4.12463526	91.8876476	9.17E-22	2.65E-21	0.65059581	8.33333333	91.6666667
ENSG00000166887	VPS39	0.98253171	6.68787787	254.095624	3.32E-57	1.44E-56	1.05060713	0	100	VPS39	0.90630866	6.6188502	179.003609	8.00E-41	3.55E-40	0.86886335	0	100
ENSG00000107341	UBE2R2	-0.9934108	5.9292875	253.85408	3.75E-57	1.62E-56	-0.9169522	100	0	UBE2R2	-1.0302787	5.88627825	227.772781	1.82E-51	9.63E-51	-1.0986365	100	0
ENSG00000073921	PICALM	-0.984908	6.43755139	253.460685	4.57E-57	1.97E-56	-0.9547687	100	0	PICALM	-1.0788087	6.39990466	252.386806	7.84E-57	4.44E-56	-1.0654848	100	0

ENSG00000100994	PYGB	0.99722291	5.73444602	253.387313	4.74E-57	2.05E-56	0.97856286	0	100	PYGB	0.72520511	5.53863313	111.880781	3.79E-26	1.23E-25	0.68411971	0	100
ENSG00000141560	FN3KRP	1.13521053	4.04824482	253.386348	4.74E-57	2.05E-56	1.16702261	0	100	FN3KRP	1.01917467	3.9072448	165.937525	5.71E-38	2.39E-37	0.86318638	0	100
ENSG00000173442	EHBP1L1	-0.9932402	6.08475019	253.246102	5.09E-57	2.19E-56	-0.9192531	100	0	EHBP1L1	-1.3671046	5.91944552	390.26068	7.26E-87	5.96E-86	-1.3467895	100	0
ENSG00000151503	NCAPD3	1.11371575	4.17332526	252.349006	7.99E-57	3.44E-56	1.0915822	0	100	NCAPD3	1.28354905	4.25125253	284.303405	8.67E-64	5.40E-63	1.23754908	0	100
ENSG00000107263	RAPGEF1	-0.9653938	8.23234113	251.281883	1.36E-56	5.85E-56	-0.9455725	100	0	RAPGEF1	-0.9257918	8.20100914	175.885583	3.84E-40	1.68E-39	-0.9051809	100	0
ENSG00000181061	HIGD1A	-1.114958	4.14873938	251.041924	1.54E-56	6.59E-56	-1.0584078	100	0	HIGD1A	-0.8832041	4.19077228	135.106013	3.13E-31	1.14E-30	-0.9265623	100	0
ENSG00000170540	ARL6IP1	-0.9764819	6.71710195	250.952271	1.61E-56	6.89E-56	-0.978231	100	0	ARL6IP1	-0.6314033	6.76375428	87.4343266	8.71E-21	2.46E-20	-0.6620958	100	0
ENSG00000128928	IVD	1.24570381	3.36780017	249.499866	3.34E-56	1.42E-55	1.23715695	0	100	IVD	1.57884182	3.53637311	348.966457	7.12E-78	5.25E-77	1.51006913	0	100
ENSG00000065978	YBX1	-0.9650137	9.20005798	249.247362	3.79E-56	1.61E-55	-0.9181957	100	0	YBX1	-0.5453957	9.29048199	57.313728	3.72E-14	8.60E-14	-0.585251	100	0
ENSG00000250479	CHCHD10	-1.3049703	3.04117388	249.109717	4.06E-56	1.73E-55	-1.2653921	100	0	CHCHD10	-0.9324858	3.1334184	109.041183	1.59E-25	5.08E-25	-1.0766938	97.2222222	2.77777778
ENSG00000169241	SLC50A1	-1.1849039	3.65474649	248.772285	4.81E-56	2.04E-55	-1.0715748	100	0	SLC50A1	-0.8461787	3.67801602	109.071108	1.57E-25	5.01E-25	-0.8942774	100	0
ENSG00000029993	HMGB3	-1.2113288	3.52698444	248.704841	4.98E-56	2.11E-55	-1.1370041	100	0	HMGB3	-0.7601665	3.59833053	85.5994204	2.20E-20	6.14E-20	-0.8125394	94.4444444	5.55555556
ENSG00000204149	AGAP6	1.33784848	2.88951239	248.513954	5.48E-56	2.32E-55	1.51076309	0	100	AGAP6	1.23838949	2.78026872	172.105999	2.57E-39	1.10E-38	1.19185074	0	100
ENSG00000140157	NIPA2	-0.9894904	5.4570129	246.687181	1.37E-55	5.80E-55	-0.9342507	100	0	NIPA2	-0.7419184	5.45013176	117.191789	2.61E-27	8.65E-27	-0.7987432	100	0
ENSG00000087338	GMCL1	0.9914859	5.38473061	245.584686	2.38E-55	1.00E-54	1.02018042	0	100	GMCL1	1.31916089	5.54499133	361.258083	1.50E-80	1.14E-79	1.26822652	0	100
ENSG00000104472	CHRAC1	-0.9773434	5.98626864	245.297425	2.75E-55	1.16E-54	-0.8676212	100	0	CHRAC1	-0.5828381	6.02123276	74.113256	7.38E-18	1.90E-17	-0.5928675	100	0
ENSG00000198712	MT-CO2	-0.9784502	11.9445114	245.095238	3.05E-55	1.28E-54	-0.8956604	100	0	MT-CO2	-0.4381475	12.1255659	28.9840264	7.30E-08	1.31E-07	-0.5081612	88.8888889	11.1111111
ENSG00000183918	SH2D1A	1.00507839	5.11804407	244.976134	3.23E-55	1.36E-54	0.97462658	0	100	SH2D1A	0.87818637	4.9817123	153.896885	2.44E-35	9.68E-35	0.85849571	2.77777778	97.2222222
ENSG00000140526	ABHD2	-0.9874402	5.55978092	244.948702	3.28E-55	1.38E-54	-0.8461017	100	0	ABHD2	-1.0114781	5.58480485	213.82096	2.02E-48	1.01E-47	-1.0538467	100	0
ENSG00000227218	RP11-203J24.8	1.44172631	2.38135381	244.837643	3.47E-55	1.45E-54	1.42146054	0	100	RP11-203J24.8	1.11531313	2.12291395	110.655156	7.04E-26	2.27E-25	1.07739829	2.77777778	97.2222222
ENSG00000149187	CELF1	0.96575342	6.84101528	244.789684	3.55E-55	1.49E-54	1.02900157	0	100	CELF1	0.83785771	6.6717619	151.565949	7.88E-35	3.10E-34	0.74486759	5.55555556	94.4444444
ENSG00000106803	SEC61B	-0.9942546	5.22479746	244.701294	3.71E-55	1.55E-54	-0.9251843	100	0	SEC61B	-0.4755188	5.34223024	47.9968695	4.27E-12	9.17E-12	-0.5413043	94.4444444	5.55555556
ENSG00000174943	KCTD13	1.18041061	3.63566358	244.206813	4.76E-55	1.99E-54	1.26873712	0	100	KCTD13	1.07775304	3.5391665	167.678334	2.38E-38	1.00E-37	0.9824007	0	100
ENSG00000112531	QKI	-0.9587386	6.92786607	244.076056	5.08E-55	2.12E-54	-0.8746718	100	0	QKI	-0.7698098	6.94017347	129.292717	5.85E-30	2.07E-29	-0.749647	100	0
ENSG00000089902	RCOR1	-0.97706	5.7877509	243.639541	6.33E-55	2.64E-54	-0.9077504	97.1428571	2.85714286	RCOR1	-0.5369737	5.86018082	62.6366587	2.49E-15	5.96E-15	-0.59429	94.4444444	5.55555556
ENSG00000143119	CD53	-0.9685519	6.25806019	243.42059	7.06E-55	2.94E-54	-0.818124	100	0	CD53	-0.7450549	6.29377144	119.990724	6.36E-28	2.15E-27	-0.7482975	100	0
ENSG00000008838	MED24	1.00720822	5.08320379	243.148725	8.09E-55	3.37E-54	1.1227879	0	100	MED24	1.04017676	5.09962925	218.135974	2.31E-49	1.18E-48	0.9318265	2.77777778	97.2222222
ENSG00000175334	BANF1	-1.1150978	4.00030422	242.828052	9.51E-55	3.96E-54	-1.1368918	100	0	BANF1	-0.5135232	4.14598514	45.8656522	1.27E-11	2.67E-11	-0.6080165	91.6666667	8.33333333
ENSG00000106605	BLVRA	-1.2675402	3.18797185	242.786765	9.71E-55	4.04E-54	-1.1460474	100	0	BLVRA	-1.59487	3.09275389	305.321916	2.28E-68	1.53E-67	-1.5497035	100	0
ENSG00000103353	UBFD1	1.01634926	4.8229815	241.543868	1.81E-54	7.53E-54	1.12306015	0	100	UBFD1	0.82565233	4.63990955	130.45174	3.26E-30	1.16E-29	0.75927015	0	100
ENSG00000105520	LPPR2	-1.2547024	3.36258077	241.468019	1.88E-54	7.82E-54	-1.282318	88.5714286	11.4285714	LPPR2	-2.0983669	3.19326984	499.37094	1.30E-110	1.33E-109	-2.2512157	94.4444444	5.55555556
ENSG00000117362	APH1A	-0.9511876	7.20194163	241.45024	1.90E-54	7.88E-54	-0.8574797	100	0	APH1A	-0.6671235	7.26297117	96.7757046	7.76E-23	2.31E-22	-0.7313942	97.2222222	2.77777778
ENSG00000108294	NA	-1.0086414	4.94343629	241.366901	1.98E-54	8.22E-54	-1.0235851	100	0	NA	-0.6783755	5.04318142	93.5523868	3.96E-22	1.15E-21	-0.8068782	94.4444444	5.55555556
ENSG00000176340	COX8A	-0.9781842	5.48642657	240.223123	3.52E-54	1.45E-53	-0.9888457	100	0	COX8A	-0.701191	5.5630325	104.742003	1.39E-24	4.32E-24	-0.7545266	94.4444444	5.55555556
ENSG00000182796	TMEM198B	1.19540507	3.52036985	240.1843	3.59E-54	1.48E-53	1.22813803	0	100	TMEM198B	0.87535293	3.21109484	100.621667	1.11E-23	3.39E-23	0.81617318	0	100
ENSG00000217555	CKLF	-1.5199763	1.95825428	238.941289	6.69E-54	2.75E-53	-1.3990163	100	0	CKLF	-1.8091284	1.88376923	259.015964	2.81E-58	1.63E-57	-1.8715937	100	0
ENSG00000141429	GALNT1	-0.9592316	6.30446747	238.887763	6.87E-54	2.82E-53	-0.862065	100	0	GALNT1	-0.5029363	6.42008742	55.2865449	1.04E-13	2.37E-13	-0.5406084	94.4444444	5.55555556
ENSG00000102172	SMS	-1.0630386	4.31004392	238.684079	7.61E-54	3.13E-53	-1.0154718	100	0	SMS	-1.2361827	4.2352886	263.884107	2.44E-59	1.42E-58	-1.313011	100	0
ENSG00000148803	FUOM	-1.7332201	1.08476736	236.994507	1.78E-53	7.29E-53	-1.6501477	100	0	FUOM	-1.9831872	1.01272651	226.748826	3.05E-51	1.60E-50	-2.0158132	100	0
ENSG00000166401	SERPINB8	-1.046386	4.42745288	236.568082	2.20E-53	9.03E-53	-0.998637	100	0	SERPINB8	-1.1533329	4.33849639	234.039428	7.84E-53	4.22E-52	-1.1216351	100	0
ENSG00000223705	NSUN5P1	1.04376352	4.48032239	236.427146	2.36E-53	9.69E-53	1.01236388	0	100	NSUN5P1	0.69084485	4.17219441	82.3547773	1.14E-19	3.10E-19	0.6082312	5.55555556	94.4444444
ENSG00000132635	PCED1A	1.08089264	4.24723292	236.338187	2.47E-53	1.01E-52	1.01526029	0	100	PCED1A	0.90252095	4.06723158	133.701312	6.35E-31	2.29E-30	0.73882082	2.77777778	97.2222222
ENSG00000184182	UBE2F	-1.0279358	4.57125325	235.98348	2.95E-53	1.21E-52	-0.9901654	100	0	UBE2F	-1.3110217	4.44250247	309.0656	3.49E-69	2.36E-68	-1.2845639	100	0
ENSG00000125245	GPR18	-1.0999277	4.04718816	235.921569	3.05E-53	1.25E-52	-0.9629107	97.1428571	2.85714286	GPR18	-0.5855835	4.11586454	57.7939655	2.91E-14	6.76E-14	-0.5456174	94.4444444	5.55555556
ENSG00000120306	CYSTM1	-1.5932228	1.68148022	234.954445	4.95E-53	2.02E-52	-1.5717811	100	0	CYSTM1	-1.174926	1.74411134	105.353614	1.02E-24	3.19E-24	-1.1163964	94.4444444	5.55555556
ENSG00000113532	ST8SIA4	-1.0055877	4.76313123	234.241975	7.08E-53	2.89E-52	-0.9582829	100	0	ST8SIA4	-1.1192714	4.71764082	240.696791	2.77E-54	1.52E-53	-1.1715518	100	0
ENSG00000176946	THAP4	-1.0536829	4.30388243	233.949222	8.21E-53	3.34E-52	-0.9488741	100	0	THAP4	-0.8003265	4.34587746	114.182589	1.19E-26	3.88E-26	-0.7995353	97.2222222	2.77777778
ENSG00000119917	IFIT3	-1.234549	3.38923502	233.702952	9.29E-53	3.77E-52	-1.1488051	94.2857143	5.71428571	IFIT3	-1.3058161	3.4750575	217.713954	2.85E-49	1.45E-48	-1.3887857	86.1111111	13.8888889
ENSG00000105122	RASAL3	0.96482554	5.53611842	232.773114	1.48E-52	6.01E-52	0.99632847	2.85714286	97.1428571	RASAL3	1.18224767	5.60882884	287.862055	1.45E-64	9.14E-64	1.16983556	2.77777778	97.2222222
ENSG00000106615	RHEB	-0.9706857	5.24632053	232.475635	1.72E-52	6.97E-52	-0.989527	97.1428571	2.85714286	RHEB	-0.6055937	5.28523971	77.1492033	1.59E-18	4.17E-18	-0.6934036	100	0
ENSG00000124224	PPP4R1L	0.96781832	5.24831576	232.320604	1.86E-52	7.53E-52	1.04406363	0	100	PPP4R1L	0.56032588	4.91515828	63.6552014	1.48E-15	3.58E-15	0.5345422	2.77777778	97.2222222
ENSG00000188295	ZNF669	-1.191857	3.38651481	232.043904	2.14E-52	8.64E-52	-1.1499879	100	0	ZNF669	-1.1592464	3.32696194	180.89589	3.09E-41	1.38E-40	-1.1679151	100	0
ENSG00000187650	VMAC	1.27552154	2.92257056	229.806934	6.57E-52	2.65E-51	1.21824754	0	100	VMAC	0.83602847	2.57101181	74.3949473	6.40E-18	1.65E-17	0.74403256	5.55555556	94.4444444

ENSG00000176624	MEX3C	-0.9273303	7.17783945	229.666911	7.05E-52	2.84E-51	-0.8232212	100	0	MEX3C	-0.63497	7.18127308	88.2604441	5.74E-21	1.63E-20	-0.667225	100	0
ENSG00000140943	MBTPS1	0.92795662	6.95407429	229.585672	7.34E-52	2.95E-51	1.00751377	0	100	MBTPS1	0.80345008	6.81887674	141.450974	1.28E-32	4.81E-32	0.78443289	0	100
ENSG00000100099	HPS4	0.95041533	5.56907731	229.538354	7.52E-52	3.02E-51	0.9968479	0	100	HPS4	0.85695679	5.45885097	155.870623	9.04E-36	3.61E-35	0.7506516	0	100
ENSG0000064601	CTSA	-0.9876803	5.01159401	228.593279	1.21E-51	4.85E-51	-0.9552313	91.4285714	8.57142857	CTSA	-0.6226071	5.15196643	76.9506276	1.75E-18	4.60E-18	-0.8394418	75	25
ENSG00000101452	DHX35	1.00941381	4.56071458	228.465761	1.29E-51	5.17E-51	1.06040432	0	100	DHX35	1.0861564	4.52947169	219.616402	1.10E-49	5.63E-49	0.92341901	0	100
ENSG00000166479	TMX3	1.0024187	4.64059677	228.373821	1.35E-51	5.41E-51	1.06063642	0	100	TMX3	0.88440072	4.50012344	144.612145	2.61E-33	9.95E-33	0.765806	2.77777778	97.2222222
ENSG00000204120	GIGYF2	0.94526689	5.61487713	227.8688	1.74E-51	6.96E-51	0.93956336	0	100	GIGYF2	0.70666051	5.42923398	105.974477	7.47E-25	2.34E-24	0.66258303	2.77777778	97.2222222
ENSG00000131374	TBC1D5	-1.0011862	4.67489481	227.506381	2.09E-51	8.33E-51	-0.8136261	100	0	TBC1D5	-1.204971	4.52907304	266.92468	5.31E-60	3.13E-59	-1.220931	100	0
ENSG00000244038	DDOST	-0.936821	6.06961793	227.235446	2.39E-51	9.54E-51	-0.8375209	100	0	DDOST	-0.6521024	6.13373361	92.8832272	5.55E-22	1.61E-21	-0.7289204	97.2222222	2.77777778
ENSG00000181666	HKR1	1.00246733	4.63263813	227.166849	2.47E-51	9.87E-51	0.99880961	0	100	HKR1	1.13226662	4.65865526	243.111509	8.25E-55	4.54E-54	1.09528147	0	100
ENSG00000131236	CAP1	-0.926705	7.01877914	226.975175	2.72E-51	1.09E-50	-0.7784789	100	0	CAP1	-0.7508501	7.05758167	122.75636	1.58E-28	5.39E-28	-0.8090483	100	0
ENSG00000163346	PBXIP1	0.9178039	7.72451379	226.380047	3.67E-51	1.46E-50	0.97577709	0	100	PBXIP1	0.82907365	7.59430867	146.371935	1.08E-33	4.13E-33	0.72983498	0	100
ENSG00000166341	DCHS1	0.94761171	5.55522242	225.972068	4.51E-51	1.79E-50	0.96007127	0	100	DCHS1	1.22628846	5.69598851	314.402182	2.40E-70	1.65E-69	1.11083252	2.77777778	97.2222222
ENSG00000242861	RP11-285F7.2	1.82285142	0.58522012	225.883118	4.71E-51	1.87E-50	1.92003849	0	100	RP11-285F7.2	1.16257691	0.03880343	61.6277187	4.15E-15	9.88E-15	0.97901238	5.55555556	94.4444444
ENSG00000189159	HN1	-1.1130408	3.78591602	225.821403	4.86E-51	1.93E-50	-1.0673026	97.1428571	2.85714286	HN1	-0.5480765	3.94982733	49.129957	2.40E-12	5.18E-12	-0.6879355	88.8888889	11.1111111
ENSG00000162971	TYW5	0.97742656	4.92667298	225.370245	6.10E-51	2.42E-50	0.97238921	2.85714286	97.1428571	TYW5	0.95094369	4.85451234	177.099371	2.08E-40	9.19E-40	0.89365017	5.55555556	94.4444444
ENSG00000184886	NA	-1.2911949	2.80334715	224.86035	7.88E-51	3.12E-50	-1.2552981	100	0	NA	-0.5632917	2.90961866	38.0043179	7.06E-10	1.39E-09	-0.640194	88.8888889	11.1111111
ENSG0000086300	SNX10	-1.1076878	3.88831512	224.605182	8.95E-51	3.54E-50	-1.0602844	94.2857143	5.71428571	SNX10	-1.4451846	3.7509824	308.919804	3.75E-69	2.53E-68	-1.4308383	100	0
ENSG00000138069	RAB1A	-0.9239202	6.5953533	224.381533	1.00E-50	3.96E-50	-0.8614102	100	0	RAB1A	-0.8262541	6.56646033	148.951825	2.94E-34	1.14E-33	-0.8622492	100	0
ENSG00000187189	TSPYL4	0.93388965	5.82971957	224.378304	1.00E-50	3.96E-50	0.98154964	0	100	TSPYL4	1.1304097	5.88430351	274.313918	1.30E-61	7.82E-61	1.09189783	0	100
ENSG00000168092	PAFAH1B2	-0.9305759	5.9640819	224.217934	1.09E-50	4.29E-50	-0.9309513	100	0	PAFAH1B2	-0.6719058	5.98819992	98.6957401	2.94E-23	8.85E-23	-0.7191134	100	0
ENSG00000119041	GTF3C3	1.02789432	4.31118902	223.846642	1.31E-50	5.16E-50	1.10827782	0	100	GTF3C3	0.87336904	4.21258902	133.921785	5.68E-31	2.05E-30	0.81750516	2.77777778	97.2222222
ENSG00000171608	PIK3CD	0.91040444	8.14002712	223.82164	1.33E-50	5.22E-50	0.94799397	0	100	PIK3CD	0.61024447	7.92670729	78.9539144	6.36E-19	1.70E-18	0.54780486	2.77777778	97.2222222
ENSG00000170619	COMMD5	-1.1389803	3.5737939	223.725771	1.39E-50	5.48E-50	-1.005337	100	0	COMMD5	-0.7095373	3.65932065	76.5720602	2.12E-18	5.56E-18	-0.7528527	100	0
ENSG00000138867	GUCD1	-0.9195036	6.64675763	223.654957	1.44E-50	5.68E-50	-0.8633881	100	0	GUCD1	-0.8041019	6.61195108	141.580885	1.20E-32	4.51E-32	-0.9237756	100	0
ENSG00000235655	H3F3AP4	-1.011468	4.47097866	223.525147	1.54E-50	6.05E-50	-0.9911011	100	0	H3F3AP4	-0.6419875	4.54728936	77.0860998	1.64E-18	4.31E-18	-0.708792	97.2222222	2.77777778
ENSG00000100376	FAM118A	0.93989078	5.55583734	223.502656	1.56E-50	6.12E-50	0.97638454	0	100	FAM118A	0.87828991	5.43192026	162.020272	4.10E-37	1.68E-36	0.8658728	0	100
ENSG00000141580	WDR45B	-0.9268131	6.12801437	222.781465	2.24E-50	8.78E-50	-0.8118652	100	0	WDR45B	-0.4699628	6.25647589	48.3262119	3.61E-12	7.76E-12	-0.5728079	91.6666667	8.33333333
ENSG00000169221	TBC1D10B	-1.041003	4.19237438	221.997385	3.32E-50	1.30E-49	-0.9419395	100	0	TBC1D10B	-0.4993085	4.41037513	45.4588573	1.56E-11	3.27E-11	-0.525205	94.4444444	5.55555556
ENSG00000119986	AVPI1	-1.3137209	2.69151113	221.664828	3.92E-50	1.54E-49	-1.2779432	97.1428571	2.85714286	AVPI1	-0.7240743	2.8546851	59.9734955	9.61E-15	2.27E-14	-0.7840705	88.8888889	11.1111111
ENSG00000146425	DYNLT1	0.97589883	4.77697805	221.455329	4.35E-50	1.71E-49	1.01320133	0	100	DYNLT1	0.64969027	4.54890782	79.4013862	5.07E-19	1.36E-18	0.70826599	13.8888889	86.1111111
ENSG0000021574	SPAST	-1.020595	4.32674212	221.240712	4.85E-50	1.90E-49	-0.8157973	100	0	SPAST	-0.6656294	4.42356678	81.6868603	1.59E-19	4.33E-19	-0.7251777	94.4444444	5.55555556
ENSG00000119522	DENND1A	-0.9676624	4.89446094	221.220212	4.90E-50	1.91E-49	-0.8321548	100	0	DENND1A	-0.9774196	4.87151665	187.973163	8.81E-43	4.02E-42	-1.0030283	100	0
ENSG0000085978	ATG16L1	0.9212464	6.15625523	221.121163	5.15E-50	2.01E-49	0.96996593	0	100	ATG16L1	1.02415536	6.12782561	226.960098	2.74E-51	1.45E-50	0.9357809	0	100
ENSG00000135926	TMBIM1	-0.9207173	6.27057339	220.753989	6.19E-50	2.42E-49	-0.8385814	100	0	TMBIM1	-1.1127786	6.17959205	263.959007	2.35E-59	1.37E-58	-1.1051468	100	0
ENSG00000184602	SNN	-0.9171823	6.90610512	220.750687	6.20E-50	2.42E-49	-0.7360965	100	0	SNN	-0.7374688	6.92433369	117.82158	1.90E-27	6.33E-27	-0.8292792	100	0
ENSG00000103342	GSPT1	0.90632705	7.44290175	220.271729	7.89E-50	3.07E-49	0.94054609	0	100	GSPT1	1.14458932	7.51100434	277.019099	3.35E-62	2.03E-61	1.03470348	2.77777778	97.2222222
ENSG00000115977	AAK1	0.93733659	5.41646747	220.136153	8.45E-50	3.29E-49	1.01355298	0	100	AAK1	0.64194509	5.20086509	85.2996035	2.56E-20	7.13E-20	0.50959129	2.77777778	97.2222222
ENSG00000169032	MAP2K1	-0.9462511	5.12152747	219.93332	9.35E-50	3.64E-49	-0.8884452	100	0	MAP2K1	-0.5713276	5.21103342	68.4016706	1.33E-16	3.32E-16	-0.5874134	100	0
ENSG00000256525	POLG2	1.36491333	2.39803255	219.469004	1.18E-49	4.59E-49	1.17711244	0	100	POLG2	1.08294798	2.15495411	106.110286	6.97E-25	2.19E-24	0.93898959	2.77777778	97.2222222
ENSG00000185324	CDK10	1.12466447	3.64932729	218.46433	1.96E-49	7.58E-49	1.10190686	0	100	CDK10	0.97199885	3.34638581	126.950092	1.91E-29	6.66E-29	0.90587013	0	100
ENSG0000023041	ZDHHC6	0.9945873	4.46581601	217.768799	2.77E-49	1.07E-48	1.02726383	0	100	ZDHHC6	0.87850812	4.32605874	139.027723	4.34E-32	1.61E-31	0.84464701	0	100
ENSG00000134250	NOTCH2	-0.9066431	6.87891428	217.005691	4.07E-49	1.57E-48	-0.790789	97.1428571	2.85714286	NOTCH2	-1.1276707	6.79410391	271.727288	4.77E-61	2.85E-60	-1.1559027	100	0
ENSG00000170242	USP47	0.89937787	7.3139436	216.888789	4.32E-49	1.66E-48	0.96178669	0	100	USP47	0.83294209	7.20746537	149.700501	2.02E-34	7.87E-34	0.7553918	2.77777778	97.2222222
ENSG00000205302	SNX2	-0.9180419	5.867956	216.860265	4.38E-49	1.69E-48	-0.843577	100	0	SNX2	-0.6561351	5.89652647	93.5764841	3.91E-22	1.14E-21	-0.6558142	100	0
ENSG00000182952	HMGN4	-1.0411338	4.0439774	215.432727	8.97E-49	3.43E-48	-0.9694841	100	0	HMGN4	-0.6725726	4.15540076	78.5808929	7.68E-19	2.05E-18	-0.6806919	100	0
ENSG0000014123	UFL1	0.93094677	5.30228462	214.338795	1.55E-48	5.93E-48	0.93365257	0	100	UFL1	0.67051095	5.10237036	91.8827258	9.20E-22	2.65E-21	0.63318133	11.1111111	88.8888889
ENSG00000172936	MYD88	-0.9150672	5.79673381	214.074723	1.77E-48	6.76E-48	-0.8237352	100	0	MYD88	-0.6328383	5.87696229	86.7151846	1.25E-20	3.52E-20	-0.6471413	97.2222222	2.77777778
ENSG0000003509	NDUFAF7	1.18509569	3.15396405	213.782811	2.05E-48	7.82E-48	1.26612019	0	100	NDUFAF7	0.86041874	2.91898941	88.9874355	3.97E-21	1.13E-20	0.77312576	0	100
ENSG00000130559	CAMSAP1	-0.9429127	5.05277684	213.582854	2.27E-48	8.64E-48	-0.8047964	100	0	CAMSAP1	-0.9608104	4.98631375	183.200716	9.70E-42	4.36E-41	-0.8520876	100	0
ENSG00000189077	TMEM120A	-1.3498645	2.36000873	213.344555	2.56E-48	9.73E-48	-1.3789058	97.1428571	2.85714286	TMEM120A	-1.7034215	2.24440919	255.917038	1.33E-57	7.64E-57	-1.6514014	97.2222222	2.77777778
ENSG00000185946	RNPC3	1.00945908	4.29841407	212.936023	3.14E-48	1.19E-47	1.03019281	0	100	RNPC3	0.7121624	4.06179226	84.9741308	3.02E-20	8.37E-20	0.55566291	8.33333333	91.6666667
ENSG00000163041	H3F3A	-0.8867021	8.05722853	211.677334	5.91E-48	2.24E-47	-0.8631726	100	0	H3F3A	-0.5607686	8.11731232	65.7574211	5.10E-16	1.25E-15	-0.6008785	100	0

ENSG00000130024	PHF10	0.8916886	6.91821733	211.645131	6.01E-48	2.27E-47	0.95366787	0	100	PHF10	0.58089913	6.64102478	73.7604712	8.82E-18	2.26E-17	0.57499183	11.1111111	88.8888889
ENSG00000104219	ZDHHC2	-1.0223064	4.11110716	211.385502	6.85E-48	2.59E-47	-0.9086521	100	0	ZDHHC2	-0.8428251	4.16622606	121.748133	2.62E-28	8.90E-28	-0.7977141	100	0
ENSG00000177565	TBL1XR1	0.91022344	5.78115607	211.188774	7.56E-48	2.85E-47	0.94374118	0	100	TBL1XR1	1.02404583	5.83047679	221.677301	3.90E-50	2.01E-49	0.90328083	2.77777778	97.2222222
ENSG00000162702	ZNF281	-0.9142969	5.52092245	210.842877	8.99E-48	3.39E-47	-0.8746829	100	0	ZNF281	-0.8114419	5.49216433	140.029092	2.62E-32	9.80E-32	-0.8191697	100	0
ENSG00000102910	LONP2	0.90624333	5.73005579	210.833282	9.04E-48	3.41E-47	0.92152252	0	100	LONP2	0.57661205	5.45818013	71.0196813	3.54E-17	8.94E-17	0.52989695	5.55555556	94.4444444
ENSG00000108091	CCDC6	-0.8982172	6.21245986	210.741702	9.46E-48	3.56E-47	-0.8681963	100	0	CCDC6	-0.7578143	6.19107651	125.748822	3.49E-29	1.21E-28	-0.8344879	100	0
ENSG00000167566	NCKAP5L	-1.0411357	4.04546855	210.630596	1.00E-47	3.77E-47	-1.014265	100	0	NCKAP5L	-0.9322909	4.07431742	143.617531	4.31E-33	1.63E-32	-0.8994712	97.2222222	2.77777778
ENSG00000196954	CASP4	-0.9077864	5.62207045	210.622028	1.00E-47	3.78E-47	-0.7945656	100	0	CASP4	-0.4661429	5.75740506	47.2667392	6.20E-12	1.32E-11	-0.5193032	97.2222222	2.77777778
ENSG00000094880	CDC23	0.99386888	4.32085329	210.384896	1.13E-47	4.26E-47	1.01867851	0	100	CDC23	0.88702529	4.21344385	137.06521	1.17E-31	4.28E-31	0.83623551	2.77777778	97.2222222
ENSG00000165233	C9orf89	-0.9164756	5.51258885	210.337257	1.16E-47	4.36E-47	-0.7940537	97.1428571	2.85714286	C9orf89	-0.805851	5.55351814	136.502144	1.55E-31	5.67E-31	-0.892407	97.2222222	2.77777778
ENSG00000134970	TMED7	-0.9029143	5.78211868	209.648809	1.64E-47	6.15E-47	-0.8381183	100	0	TMED7	-0.7777974	5.79125774	128.869986	7.24E-30	2.55E-29	-0.711057	100	0
ENSG00000144579	CTDSP1	-0.9250452	5.14319077	209.31664	1.94E-47	7.26E-47	-0.8642611	100	0	CTDSP1	-1.0314236	5.07002006	212.96444	3.10E-48	1.55E-47	-1.1289472	97.2222222	2.77777778
ENSG00000069399	BCL3	-0.8894937	6.58132755	208.862726	2.43E-47	9.10E-47	-0.8384494	100	0	BCL3	-0.8992312	6.54063386	175.133722	5.60E-40	2.44E-39	-0.8933188	97.2222222	2.77777778
ENSG00000118454	ANKRD13C	0.90911494	5.40037591	208.77356	2.54E-47	9.52E-47	0.98287297	0	100	ANKRD13C	0.83909553	5.30801312	148.17817	4.34E-34	1.68E-33	0.71750654	0	100
ENSG00000258738	RP11-73E17.2	-1.1843995	3.05433175	208.437461	3.01E-47	1.13E-46	-1.0693017	100	0	RP11-73E17.2	-1.0319678	3.02909782	131.367292	2.06E-30	7.34E-30	-0.9805997	100	0
ENSG00000164430	MB21D1	-1.1556693	3.20575903	207.71853	4.32E-47	1.61E-46	-1.0626838	100	0	MB21D1	-1.1998088	3.18259037	181.825239	1.94E-41	8.68E-41	-1.2654569	100	0
ENSG00000154102	C16orf74	-1.4874949	1.60829625	207.641642	4.49E-47	1.68E-46	-1.3631419	100	0	C16orf74	-1.5508847	1.47660854	166.459229	4.39E-38	1.84E-37	-1.6799077	100	0
ENSG00000231025	RP11-175O19.4	-1.0956004	3.55287043	207.373962	5.14E-47	1.91E-46	-1.0065737	100	0	RP11-175O19.	-0.5374273	3.70791092	44.6303752	2.38E-11	4.96E-11	-0.5417295	97.2222222	2.77777778
ENSG00000163728	TTC14	0.97479289	4.46099864	207.286765	5.37E-47	2.00E-46	1.10932209	0	100	TTC14	0.95564813	4.37623148	162.933184	2.59E-37	1.06E-36	0.93128057	5.55555556	94.4444444
ENSG00000083937	CHMP2B	-0.900197	5.65957146	207.122595	5.83E-47	2.17E-46	-0.8532367	100	0	CHMP2B	-0.7108134	5.67007758	108.088201	2.57E-25	8.17E-25	-0.7402394	100	0
ENSG00000105810	CDK6	-0.9293338	4.97654364	206.776732	6.94E-47	2.58E-46	-0.8342928	100	0	CDK6	-1.45723	4.72883973	394.153135	1.03E-87	8.56E-87	-1.4542923	100	0
ENSG00000112303	VNN2	-1.1604566	3.30327442	206.215848	9.19E-47	3.41E-46	-0.9042949	97.1428571	2.85714286	VNN2	-1.1145509	3.28761604	155.947809	8.69E-36	3.48E-35	-1.2517383	88.8888889	11.1111111
ENSG00000109861	CTSC	-0.9255242	5.06241352	205.281192	1.47E-46	5.45E-46	-0.715499	100	0	CTSC	-1.0763381	5.00916323	229.791356	6.62E-52	3.52E-51	-1.0234732	100	0
ENSG00000184014	DENND5A	-0.886682	6.59904661	204.956146	1.73E-46	6.41E-46	-0.7842062	100	0	DENND5A	-1.4884402	6.37282842	464.962085	4.00E-103	3.83E-102	-1.4438627	100	0
ENSG00000268218	AC137932.4	1.19596006	2.99964832	204.692235	1.98E-46	7.31E-46	1.21522537	0	100	AC137932.4	1.66607438	3.27111168	348.586099	8.61E-78	6.35E-77	1.74156538	0	100
ENSG00000167460	TPM4	-0.8830889	6.6297016	204.645096	2.02E-46	7.48E-46	-0.8331723	100	0	TPM4	-1.1968874	6.47941742	302.984112	7.37E-68	4.90E-67	-1.2052917	100	0
ENSG00000169914	OTUD3	0.93903594	4.7281425	204.086972	2.68E-46	9.89E-46	0.95473621	0	100	OTUD3	1.03514428	4.69490283	204.800698	1.87E-46	9.10E-46	0.87819221	0	100
ENSG00000164048	ZNF589	1.04900729	3.80826524	204.041855	2.74E-46	1.01E-45	1.03037183	0	100	ZNF589	0.76876241	3.55788345	87.1772877	9.92E-21	2.79E-20	0.69071746	0	100
ENSG00000170471	RALGAPB	0.88573889	5.9807294	203.129518	4.33E-46	1.59E-45	0.95299702	0	100	RALGAPB	1.00017189	6.01885861	215.721119	7.76E-49	3.93E-48	0.97913989	0	100
ENSG00000161920	MED11	-1.4797049	1.54523539	202.716138	5.33E-46	1.96E-45	-1.3840595	100	0	MED11	-1.2628381	1.58553111	118.788757	1.16E-27	3.91E-27	-1.3396573	100	0
ENSG00000161981	SNRNP25	-1.3263764	2.23416796	201.383591	1.04E-45	3.81E-45	-1.1712432	100	0	SNRNP25	-0.6165898	2.3767459	37.9093378	7.41E-10	1.45E-09	-0.701964	88.8888889	11.1111111
ENSG00000204397	CARD16	-1.2717008	2.55275598	201.241616	1.12E-45	4.09E-45	-1.2034557	100	0	CARD16	-1.6357414	2.45540115	258.633784	3.41E-58	1.97E-57	-1.5865224	100	0
ENSG00000131876	SNRPA1	0.87392034	6.47061953	201.180722	1.15E-45	4.21E-45	0.88840822	0	100	SNRPA1	0.70228735	6.27582775	108.369057	2.23E-25	7.10E-25	0.59471697	0	100
ENSG00000154589	LY96	-1.4241843	1.78369276	200.949536	1.30E-45	4.73E-45	-1.3799172	100	0	LY96	-2.470539	1.55807195	402.559766	1.53E-89	1.29E-88	-2.4321089	100	0
ENSG00000223547	ZNF844	-0.986909	4.21324689	200.878429	1.34E-45	4.89E-45	-0.94613	100	0	ZNF844	-1.1633583	4.0889136	224.908992	7.69E-51	4.01E-50	-1.0772526	100	0
ENSG00000140992	PDPK1	-0.891506	5.4209578	200.481412	1.64E-45	5.97E-45	-0.8134658	100	0	PDPK1	-0.7899368	5.40227028	132.118403	1.41E-30	5.05E-30	-0.7932781	100	0
ENSG00000243678	NME1-NME2	-0.9608317	4.42302404	200.460192	1.66E-45	6.03E-45	-0.8299269	100	0	NME1-NME2	-1.070853	4.35529477	204.08448	2.68E-46	1.30E-45	-1.077338	100	0
ENSG00000196455	PIK3R4	0.95986131	4.39386103	199.977975	2.11E-45	7.68E-45	0.99377417	0	100	PIK3R4	1.04014157	4.39559851	196.688517	1.10E-44	5.15E-44	0.91043401	0	100
ENSG00000089597	GANAB	0.87175847	6.7245598	199.754841	2.36E-45	8.58E-45	0.9134056	2.85714286	97.1428571	GANAB	0.78957949	6.61373157	135.154614	3.05E-31	1.11E-30	0.74727619	8.33333333	91.6666667
ENSG00000112297	AIM1	0.87965694	6.08179225	199.27775	3.00E-45	1.09E-44	0.88756022	0	100	AIM1	0.70678197	5.87273533	108.078203	2.58E-25	8.21E-25	0.67372069	8.33333333	91.6666667
ENSG00000166275	C10orf32	-0.9972655	4.07570295	199.182472	3.15E-45	1.14E-44	-0.8736583	100	0	C10orf32	-0.7637677	4.11299462	99.4992611	1.96E-23	5.93E-23	-0.7878561	100	0
ENSG00000119402	FBXW2	0.88962457	5.39355399	199.001361	3.45E-45	1.25E-44	0.9523057	0	100	FBXW2	0.59242325	5.18521536	73.2787635	1.13E-17	2.88E-17	0.54233823	5.55555556	94.4444444
ENSG00000166794	PPIB	-0.8730355	6.26867398	198.945601	3.55E-45	1.29E-44	-0.7815997	100	0	PPIB	-0.6780716	6.29856778	100.360578	1.27E-23	3.86E-23	-0.7719233	97.2222222	2.77777778
ENSG00000133895	MEN1	1.00077667	4.03867699	198.634696	4.15E-45	1.50E-44	1.10979084	0	100	MEN1	0.9985719	3.97027266	161.453431	5.45E-37	2.23E-36	0.92578545	2.77777778	97.2222222
ENSG00000080345	RIF1	0.86991016	6.47991704	198.324061	4.85E-45	1.75E-44	0.92903906	0	100	RIF1	0.81334343	6.34048981	142.838057	6.38E-33	2.41E-32	0.79651911	8.33333333	91.6666667
ENSG00000198843	SELT	-0.8593399	6.90161562	197.062226	9.14E-45	3.30E-44	-0.778109	100	0	SELT	-0.6470125	6.89886625	91.7838833	9.67E-22	2.79E-21	-0.6668099	100	0
ENSG00000132254	ARFIP2	0.89716128	5.08108406	197.012557	9.37E-45	3.38E-44	0.98026495	0	100	ARFIP2	0.81618684	4.98167197	135.452999	2.63E-31	9.57E-31	0.73169992	0	100
ENSG00000083099	LYRM2	-0.9821238	4.13707698	196.780508	1.05E-44	3.79E-44	-0.8298174	100	0	LYRM2	-0.6315702	4.21048403	70.2382959	5.26E-17	1.32E-16	-0.6678861	97.2222222	2.77777778
ENSG00000110074	FOXRED1	1.15847812	3.03166573	196.732697	1.08E-44	3.88E-44	1.25334982	0	100	FOXRED1	1.17228258	2.9974832	166.880849	3.55E-38	1.49E-37	1.10324209	0	100
ENSG00000066777	ARFGEF1	0.87311064	5.74378908	196.295077	1.34E-44	4.83E-44	0.93363985	0	100	ARFGEF1	0.86292417	5.68632279	159.913119	1.18E-36	4.81E-36	0.84471192	2.77777778	97.2222222
ENSG00000072501	SMC1A	0.8777599	5.63692383	195.898418	1.64E-44	5.89E-44	0.91482526	0	100	SMC1A	0.84518386	5.5840359	151.802228	7.00E-35	2.76E-34	0.7772379	8.33333333	91.6666667
ENSG00000106404	CLDN15	1.17656156	2.91219375	195.696708	1.82E-44	6.51E-44	1.22703078	0	100	CLDN15	0.98795807	2.66866005	106.70316	5.17E-25	1.63E-24	0.84100446	2.77777778	97.2222222
ENSG00000145349	CAMK2D	-0.8952863	5.12749459	195.470388	2.03E-44	7.29E-44	-0.7624031	100	0	CAMK2D	-1.0839673	4.95465041	233.742028	9.11E-53	4.88E-52	-1.0872771	100	0

ENSG00000112146	FBXO9	0.91469586	4.77110167	195.322424	2.19E-44	7.84E-44	1.01291885	0	100	FBXO9	0.61702151	4.55249551	71.9940334	2.16E-17	5.47E-17	0.63466597	8.33333333	91.6666667
ENSG00000060762	MPC1	-0.9971882	3.99769501	195.158386	2.38E-44	8.51E-44	-0.903878	100	0	MPC1	-0.7698558	4.03694499	100.018183	1.51E-23	4.57E-23	-0.8356968	100	0
ENSG00000139679	LPAR6	-1.0993661	3.41962941	195.137759	2.40E-44	8.59E-44	-0.9507821	97.1428571	2.85714286	LPAR6	-2.9048433	3.05677259	889.639751	1.75E-195	2.76E-194	-2.9388513	100	0
ENSG00000159388	BTG2	-0.8536639	8.50347168	194.170373	3.91E-44	1.40E-43	-0.6627179	97.1428571	2.85714286	BTG2	-0.7918467	8.47664914	125.872895	3.28E-29	1.14E-28	-0.7685296	100	0
ENSG00000213903	LTB4R	0.98481885	4.08388581	194.140433	3.97E-44	1.42E-43	0.99368983	0	100	LTB4R	0.96989164	4.04480335	155.704456	9.82E-36	3.92E-35	0.93374352	2.77777778	97.2222222
ENSG00000142192	APP	-0.864557	6.20055703	193.845952	4.60E-44	1.64E-43	-0.7781371	97.1428571	2.85714286	APP	-2.1038304	5.82407349	887.043128	6.43E-195	1.01E-193	-2.1151144	100	0
ENSG00000136003	ISCU	0.84959582	7.08783562	192.228002	1.04E-43	3.69E-43	0.84509104	0	100	ISCU	0.97851833	7.13903819	206.564888	7.72E-47	3.78E-46	0.89925027	0	100
ENSG00000161203	AP2M1	-0.862247	6.07639606	192.103708	1.10E-43	3.92E-43	-0.7708662	100	0	AP2M1	-0.5695408	6.14799242	70.8412525	3.87E-17	9.77E-17	-0.6137578	100	0
ENSG00000102317	RBM3	-0.8433703	9.06109549	191.796735	1.29E-43	4.58E-43	-0.7732121	100	0	RBM3	-0.5709527	9.09879732	63.7899161	1.38E-15	3.34E-15	-0.5972867	100	0
ENSG00000122971	ACADS	1.29342389	2.24752707	191.743364	1.32E-43	4.70E-43	1.32769669	0	100	ACADS	1.13120412	2.1244509	114.944392	8.09E-27	2.66E-26	1.11201847	2.77777778	97.2222222
ENSG00000142230	SAE1	-0.9878451	4.00254461	191.639124	1.39E-43	4.95E-43	-0.8912745	100	0	SAE1	-0.5062785	4.12212352	44.4795608	2.57E-11	5.35E-11	-0.5042273	100	0
ENSG00000119760	SUPT7L	0.86758575	5.50920571	191.508307	1.49E-43	5.28E-43	0.93864819	0	100	SUPT7L	0.8786474	5.43835355	163.988971	1.52E-37	6.30E-37	0.81959031	0	100
ENSG00000120725	SIL1	-1.1385983	3.06050202	191.071551	1.86E-43	6.57E-43	-1.0810708	100	0	SIL1	-1.1881343	3.01018512	170.06634	7.16E-39	3.04E-38	-1.3168302	100	0
ENSG00000141644	MBD1	0.85687621	6.01813681	191.016317	1.91E-43	6.74E-43	0.90943993	0	100	MBD1	0.67831993	5.89486571	100.197439	1.38E-23	4.18E-23	0.57794146	2.77777778	97.2222222
ENSG00000126088	UROD	0.95485518	4.25675284	191.001065	1.92E-43	6.79E-43	0.95752264	0	100	UROD	0.68584738	4.03297426	78.8705284	6.63E-19	1.77E-18	0.58132586	5.55555556	94.4444444
ENSG00000243646	IL10RB	-1.0206816	3.77279645	190.77067	2.16E-43	7.62E-43	-0.9365946	100	0	IL10RB	-1.3721288	3.69440362	278.567615	1.54E-62	9.40E-62	-1.452891	100	0
ENSG00000131368	MRPS25	0.93754998	4.46689607	190.684459	2.25E-43	7.95E-43	0.93900757	0	100	MRPS25	0.8589188	4.33489838	132.244917	1.32E-30	4.74E-30	0.74010905	0	100
ENSG00000101856	PGRMC1	-0.934135	4.42471211	190.604388	2.35E-43	8.27E-43	-0.8723269	100	0	PGRMC1	-0.9549159	4.36492307	164.513806	1.17E-37	4.85E-37	-1.0112447	100	0
ENSG00000128739	SNRPN	1.3019093	2.18466385	190.559637	2.40E-43	8.46E-43	1.33870151	0	100	SNRPN	1.42915353	2.23149214	189.588098	3.91E-43	1.80E-42	1.41513917	0	100
ENSG00000148399	DPH7	0.91250236	4.64184088	189.883613	3.37E-43	1.19E-42	0.97389533	0	100	DPH7	0.85578963	4.55735065	138.018544	7.22E-32	2.67E-31	0.70246683	0	100
ENSG00000167394	ZNF668	-1.1609243	2.92659488	189.843844	3.44E-43	1.21E-42	-1.2711322	100	0	ZNF668	-0.7335596	3.02351763	66.4746366	3.54E-16	8.70E-16	-0.8303295	94.4444444	5.55555556
ENSG00000104969	SGTA	-0.8629047	5.53134345	189.653304	3.78E-43	1.33E-42	-0.864006	100	0	SGTA	-0.4775623	5.64342156	49.315807	2.18E-12	4.72E-12	-0.539882	97.2222222	2.77777778
ENSG00000176953	NFATC2IP	0.87499986	5.29571627	189.279796	4.57E-43	1.60E-42	0.85999733	0	100	NFATC2IP	0.78011584	5.16631767	125.006502	5.07E-29	1.75E-28	0.71877302	2.77777778	97.2222222
ENSG00000101040	ZMYND8	0.95728895	4.19255969	188.957701	5.37E-43	1.88E-42	1.01972202	0	100	ZMYND8	0.59205852	3.85684659	56.1618245	6.67E-14	1.53E-13	0.53787275	5.55555556	94.4444444
ENSG00000031698	SARS	0.8603838	5.60801956	188.90554	5.51E-43	1.93E-42	0.96186539	0	100	SARS	0.95970246	5.63496258	195.968863	1.58E-44	7.38E-44	0.92325022	0	100
ENSG00000130313	PGLS	-0.930332	4.41691106	188.822908	5.74E-43	2.01E-42	-0.9071576	100	0	PGLS	-0.9146465	4.39009402	151.260134	9.19E-35	3.61E-34	-1.0013594	97.2222222	2.77777778
ENSG00000172354	GNB2	-0.8511337	6.27476403	188.36344	7.24E-43	2.53E-42	-0.8180882	97.1428571	2.85714286	GNB2	-0.6084352	6.34904804	80.3466596	3.14E-19	8.46E-19	-0.6274767	91.6666667	8.33333333
ENSG00000100564	PIGH	0.95645466	4.19436905	188.35488	7.27E-43	2.54E-42	1.04152315	0	100	PIGH	0.97197761	4.14098513	161.57067	5.13E-37	2.10E-36	0.89490217	0	100
ENSG00000120662	MTRF1	1.16855245	2.82855827	188.234921	7.72E-43	2.70E-42	1.19765301	0	100	MTRF1	0.82729631	2.47023625	70.6562253	4.25E-17	1.07E-16	0.73103743	2.77777778	97.2222222
ENSG00000121691	CAT	-0.9678235	4.14351422	188.225802	7.76E-43	2.71E-42	-0.9157421	97.1428571	2.85714286	CAT	-0.8465675	4.12661871	121.691142	2.70E-28	9.16E-28	-0.8782642	100	0
ENSG00000187605	TET3	-0.8421768	6.97989149	188.192894	7.88E-43	2.75E-42	-0.7742635	100	0	TET3	-0.6227424	6.99469732	84.3473608	4.15E-20	1.14E-19	-0.7011029	94.4444444	5.55555556
ENSG00000103051	COG4	1.08950818	3.30254008	187.825193	9.49E-43	3.31E-42	1.16006161	0	100	COG4	0.83033006	3.11141772	87.3579828	9.06E-21	2.55E-20	0.74895766	5.55555556	94.4444444
ENSG00000146282	RARS2	0.96031188	4.11645033	187.788299	9.66E-43	3.37E-42	1.0248067	0	100	RARS2	0.68679027	3.89787052	77.033119	1.68E-18	4.42E-18	0.63777643	0	100
ENSG00000116685	KIAA2013	-0.9455945	4.31082869	187.663831	1.03E-42	3.58E-42	-0.9920965	97.1428571	2.85714286	KIAA2013	-0.7220649	4.35461536	94.0270632	3.11E-22	9.10E-22	-0.7935304	97.2222222	2.77777778
ENSG00000165097	KDM1B	-1.0207365	3.72353701	187.301627	1.23E-42	4.30E-42	-0.8656984	100	0	KDM1B	-1.0479488	3.68036598	163.333602	2.12E-37	8.72E-37	-1.1058953	100	0
ENSG00000116497	S100PBP	1.01406058	3.72968928	187.131951	1.34E-42	4.67E-42	1.09591569	0	100	S100PBP	0.72218876	3.48671853	75.3513649	3.94E-18	1.02E-17	0.55348493	0	100
ENSG00000267244	CTB-31O20.4	0.97738035	4.04057424	186.55261	1.80E-42	6.24E-42	0.91340094	0	100	CTB-31O20.4	1.13569236	4.1014192	212.939786	3.14E-48	1.57E-47	1.14403944	2.77777778	97.2222222
ENSG00000272501	XXbac-BPG299	1.10965849	3.11942232	185.904124	2.49E-42	8.63E-42	1.13960004	0	100	XXbac-BPG29	0.75145052	2.8188319	65.0766424	7.20E-16	1.75E-15	0.76544266	5.55555556	94.4444444
ENSG00000152127	MGAT5	-0.8390345	6.45802229	185.060904	3.81E-42	1.31E-41	-0.7865191	100	0	MGAT5	-0.7656625	6.40383066	127.916665	1.17E-29	4.11E-29	-0.8292408	100	0
ENSG00000130726	TRIM28	0.83052889	7.69403402	184.870739	4.19E-42	1.45E-41	0.86623864	0	100	TRIM28	1.03324263	7.7370206	225.828423	4.84E-51	2.54E-50	0.93510714	0	100
ENSG00000048471	SNX29	-0.8403126	6.4684337	184.766973	4.41E-42	1.52E-41	-0.6663583	97.1428571	2.85714286	SNX29	-1.2584782	6.21915656	338.104996	1.65E-75	1.19E-74	-1.3133469	100	0
ENSG00000042445	RETSAT	1.14336747	2.96268344	184.712799	4.53E-42	1.56E-41	1.13793824	0	100	RETSAT	1.30091972	2.97259196	199.640265	2.50E-45	1.19E-44	1.26354709	0	100
ENSG00000160588	MPZL3	0.92772962	4.40178828	184.538221	4.95E-42	1.70E-41	0.94967227	2.85714286	97.1428571	MPZL3	1.10066307	4.47562158	216.243301	5.97E-49	3.03E-48	1.02204733	2.77777778	97.2222222
ENSG00000092010	PSME1	-0.8339058	6.84513984	184.506756	5.03E-42	1.73E-41	-0.7789526	100	0	PSME1	-0.5360447	6.9340204	62.7953598	2.29E-15	5.50E-15	-0.5716167	97.2222222	2.77777778
ENSG00000170266	GLB1	-1.1110935	3.15370634	184.480241	5.10E-42	1.75E-41	-1.0001908	100	0	GLB1	-1.9487975	2.99366825	425.306759	1.71E-94	1.50E-93	-2.0953747	100	0
ENSG00000007923	DNAJC11	0.97537826	3.9433131	184.374324	5.38E-42	1.85E-41	1.03108176	0	100	DNAJC11	0.85414463	3.85476398	116.821031	3.14E-27	1.04E-26	0.78217495	0	100
ENSG00000184900	SUMO3	-0.8311528	6.92576228	184.179832	5.93E-42	2.04E-41	-0.8298961	100	0	SUMO3	-0.6549591	6.93794241	93.910165	3.30E-22	9.63E-22	-0.6911452	100	0
ENSG00000100528	CNIH1	-0.8591609	5.24208903	183.523335	8.24E-42	2.82E-41	-0.8597432	100	0	CNIH1	-0.941735	5.15292152	181.630531	2.14E-41	9.56E-41	-0.9330935	100	0
ENSG00000129933	MAU2	0.8302427	6.84783747	183.365605	8.93E-42	3.05E-41	0.89706961	0	100	MAU2	0.83455887	6.81899151	151.936696	6.54E-35	2.58E-34	0.75091064	0	100
ENSG00000156804	FBXO32	0.87588122	4.94636734	183.33246	9.07E-42	3.10E-41	0.85301994	0	100	FBXO32	0.97392161	4.97693774	188.450285	6.93E-43	3.17E-42	0.85328451	2.77777778	97.2222222
ENSG00000163510	CWC22	0.87232655	4.94088323	183.189483	9.75E-42	3.33E-41	0.95139288	0	100	CWC22	0.77161971	4.80600234	117.743841	1.97E-27	6.59E-27	0.67175799	0	100
ENSG00000143761	ARF1	-0.8222645	8.52710798	182.836696	1.16E-41	3.97E-41	-0.8309242	100	0	ARF1	-0.4881937	8.58960672	48.6887089	3.00E-12	6.47E-12	-0.5328546	100	0
ENSG00000170260	ZNF212	0.94171414	4.2234206	182.741367	1.22E-41	4.17E-41	0.89081906	2.85714286	97.1428571	ZNF212	1.17425795	4.35195678	243.139563	8.13E-55	4.48E-54	1.07845121	0	100

ENSG00000178188	SH2B1	0.85378007	5.2953401	181.866071	1.90E-41	6.46E-41	0.93844805	0	100	SH2B1	0.69278486	5.14474814	98.9061501	2.65E-23	7.97E-23	0.59124946	2.77777778	97.2222222
ENSG00000167792	NDUFV1	0.84592227	5.78338134	181.62524	2.14E-41	7.29E-41	0.82348423	0	100	NDUFV1	0.83650847	5.72843329	147.488121	6.14E-34	2.36E-33	0.78144444	2.77777778	97.2222222
ENSG00000228253	MT-ATP8	-0.8235457	8.93973567	181.539202	2.24E-41	7.61E-41	-0.7805249	97.1428571	2.85714286	MT-ATP8	-0.756632	8.94666172	108.822773	1.77E-25	5.67E-25	-0.7772962	94.4444444	5.55555556
ENSG00000198520	C1orf228	0.88638618	4.79954987	181.236474	2.60E-41	8.85E-41	0.80985093	0	100	C1orf228	0.92210799	4.75750645	163.396876	2.05E-37	8.45E-37	0.72860979	0	100
ENSG00000139746	RBM26	0.82788944	6.48502949	180.880948	3.11E-41	1.06E-40	0.92400139	0	100	RBM26	0.58429709	6.28511645	74.9827663	4.75E-18	1.23E-17	0.51550012	8.33333333	91.6666667
ENSG00000139645	ANKRD52	0.83829309	5.79985207	180.606725	3.57E-41	1.21E-40	0.93680498	0	100	ANKRD52	0.93793329	5.79870118	187.968259	8.83E-43	4.03E-42	0.85046829	5.55555556	94.4444444
ENSG00000123374	CDK2	1.14096591	2.8725816	179.508788	6.20E-41	2.10E-40	1.1266082	0	100	CDK2	1.00321156	2.68911975	110.161911	9.03E-26	2.90E-25	0.84364664	0	100
ENSG00000146066	HIGD2A	-0.8550355	5.08544242	178.783011	8.94E-41	3.02E-40	-0.7755568	100	0	HIGD2A	-0.4840229	5.18604987	48.738472	2.92E-12	6.32E-12	-0.5764251	91.6666667	8.33333333
ENSG00000147874	HAUS6	0.8408796	5.42310163	178.765608	9.01E-41	3.05E-40	0.87603977	0	100	HAUS6	0.70606191	5.28447126	104.103009	1.92E-24	5.94E-24	0.68046608	2.77777778	97.2222222
ENSG00000105677	TMEM147	-1.0123885	3.57849952	178.754595	9.06E-41	3.06E-40	-0.95345	100	0	TMEM147	-0.5391567	3.69528996	44.4278338	2.64E-11	5.49E-11	-0.614103	91.6666667	8.33333333
ENSG00000134686	PHC2	-0.8264782	6.2982076	178.479963	1.04E-40	3.51E-40	-0.7066528	100	0	PHC2	-0.6892343	6.32133466	103.77109	2.27E-24	7.01E-24	-0.7040086	100	0
ENSG00000154889	MPPE1	0.90237036	4.42811873	178.459439	1.05E-40	3.55E-40	0.95838523	0	100	MPPE1	0.85535018	4.33812508	132.344553	1.26E-30	4.52E-30	0.81400063	0	100
ENSG00000176973	FAM89B	-1.3351388	1.78051458	178.152027	1.23E-40	4.13E-40	-1.3724921	100	0	FAM89B	-1.2880734	1.74497057	128.302106	9.64E-30	3.39E-29	-1.2686294	100	0
ENSG00000078369	GNB1	-0.8137306	7.52226723	178.148221	1.23E-40	4.14E-40	-0.6548685	100	0	GNB1	-0.7400086	7.52025805	117.741187	1.98E-27	6.59E-27	-0.8018465	100	0
ENSG00000167699	GLOD4	0.83992204	5.38746364	177.89063	1.40E-40	4.70E-40	0.89296203	0	100	GLOD4	0.66693357	5.23351404	93.0273119	5.16E-22	1.50E-21	0.56303293	0	100
ENSG00000135968	GCC2	0.813253	7.23325018	177.833568	1.44E-40	4.84E-40	0.88418237	0	100	GCC2	0.52145249	7.00279318	59.3540996	1.32E-14	3.09E-14	0.5390016	8.33333333	91.6666667
ENSG00000047932	GOPC	0.87150841	4.75654853	177.541901	1.67E-40	5.59E-40	0.90022004	0	100	GOPC	0.58567773	4.55262734	64.9022133	7.87E-16	1.91E-15	0.55955356	11.1111111	88.8888889
ENSG00000133606	MKRN1	-0.8121492	7.26682432	177.193931	1.99E-40	6.66E-40	-0.778824	100	0	MKRN1	-0.5860149	7.29556187	75.0309985	4.63E-18	1.20E-17	-0.6394143	100	0
ENSG00000121022	COPS5	0.84490202	5.20263734	177.187679	1.99E-40	6.67E-40	0.94934696	0	100	COPS5	0.74936084	5.08694611	115.954964	4.86E-27	1.60E-26	0.66402847	0	100
ENSG00000182979	MTA1	0.84506492	5.31903929	177.117985	2.06E-40	6.91E-40	0.95921608	0	100	MTA1	0.6824417	5.1505723	94.8311692	2.07E-22	6.09E-22	0.50813103	5.55555556	94.4444444
ENSG00000103197	TSC2	0.85772788	5.00886107	176.541277	2.76E-40	9.22E-40	0.94655931	0	100	TSC2	0.77569088	4.86775908	117.713613	2.00E-27	6.68E-27	0.68321635	5.55555556	94.4444444
ENSG00000149554	CHEK1	1.0236714	3.45962151	176.363207	3.02E-40	1.01E-39	1.0591546	0	100	CHEK1	1.08507778	3.42575205	163.292363	2.16E-37	8.90E-37	1.01902183	0	100
ENSG00000065911	MTHFD2	-0.9119826	4.32079742	175.998489	3.62E-40	1.21E-39	-0.9087596	91.4285714	8.57142857	MTHFD2	-0.8708546	4.2483781	132.283446	1.30E-30	4.66E-30	-0.9000678	97.2222222	2.77777778
ENSG00000166188	ZNF319	-0.973282	3.7844872	175.764412	4.08E-40	1.36E-39	-0.8686533	100	0	ZNF319	-0.7659997	3.83168404	93.4177406	4.23E-22	1.23E-21	-0.8996261	100	0
ENSG00000138801	PAPSS1	-1.1113778	2.91553486	175.438324	4.80E-40	1.60E-39	-1.0863807	100	0	PAPSS1	-1.359853	2.8324201	208.665049	2.69E-47	1.33E-46	-1.3870773	100	0
ENSG00000169100	SLC25A6	-0.8081571	9.33432306	175.031519	5.89E-40	1.96E-39	-0.7315602	100	0	SLC25A6	-0.5137415	9.40310015	50.0337721	1.51E-12	3.30E-12	-0.5464046	91.6666667	8.33333333
ENSG00000134046	MBD2	-0.818379	6.07090864	174.251153	8.72E-40	2.89E-39	-0.7832251	100	0	MBD2	-0.9377712	6.02214148	190.026171	3.14E-43	1.44E-42	-0.9250012	100	0
ENSG00000031823	RANBP3	0.81052435	6.51552061	173.95343	1.01E-39	3.36E-39	0.85386536	0	100	RANBP3	1.07688866	6.64797183	251.372928	1.30E-56	7.37E-56	0.98826032	0	100
ENSG00000113732	ATP6V0E1	-0.886003	4.50946273	173.823284	1.08E-39	3.58E-39	-0.6978166	100	0	ATP6V0E1	-0.5468427	4.61943077	56.9602218	4.45E-14	1.03E-13	-0.6156739	94.4444444	5.55555556
ENSG00000125834	STK35	0.83580306	5.26171755	173.600165	1.21E-39	4.00E-39	0.84006433	0	100	STK35	0.81096668	5.16557506	135.116252	3.11E-31	1.13E-30	0.67182377	5.55555556	94.4444444
ENSG00000122674	CCZ1	1.04948132	3.23169324	173.099671	1.56E-39	5.14E-39	1.05714429	0	100	CCZ1	1.09707855	3.1910834	155.879232	9.00E-36	3.60E-35	1.0046615	0	100
ENSG00000102158	MAGT1	-0.8267254	5.47339289	172.928919	1.70E-39	5.60E-39	-0.7436155	100	0	MAGT1	-0.6419325	5.49249646	88.052956	6.37E-21	1.81E-20	-0.6591264	100	0
ENSG00000254909	RP11-110I1.5	2.17860958	-1.1543375	172.865913	1.75E-39	5.78E-39	2.29967065	5.71428571	94.2857143	RP11-110I1.5	2.19634746	-1.2348556	129.322365	5.77E-30	2.04E-29	2.34135689	2.77777778	97.2222222
ENSG00000100580	TMED8	-0.8669578	4.6705192	172.789397	1.82E-39	6.00E-39	-0.7013707	100	0	TMED8	-0.8261997	4.67103174	131.127046	2.32E-30	8.26E-30	-0.7355268	100	0
ENSG00000100596	SPTLC2	-0.8921552	4.37945555	172.337159	2.28E-39	7.53E-39	-0.7803011	100	0	SPTLC2	-0.7866543	4.37032211	113.182592	1.97E-26	6.40E-26	-0.8420154	100	0
ENSG00000143373	ZNF687	-0.8134714	6.03059011	172.161579	2.50E-39	8.22E-39	-0.6791163	100	0	ZNF687	-0.7643784	5.99014613	127.402836	1.52E-29	5.31E-29	-0.8692494	100	0
ENSG00000040633	PHF23	-1.2132719	2.33900982	172.045541	2.64E-39	8.71E-39	-1.1278035	97.1428571	2.85714286	PHF23	-1.2060123	2.33299913	136.464902	1.58E-31	5.78E-31	-1.1698689	97.2222222	2.77777778
ENSG00000174652	ZNF266	0.81505266	5.78710418	171.300435	3.85E-39	1.26E-38	0.88810578	0	100	ZNF266	0.8985501	5.77159081	173.156778	1.51E-39	6.54E-39	0.81895038	2.77777778	97.2222222
ENSG00000142082	SIRT3	1.14184647	2.66390308	170.725821	5.14E-39	1.69E-38	1.12269884	0	100	SIRT3	1.17922666	2.65495841	148.844764	3.10E-34	1.20E-33	1.01531596	2.77777778	97.2222222
ENSG00000083535	PIBF1	1.00718977	3.45455498	170.575448	5.54E-39	1.82E-38	1.04199338	0	100	PIBF1	0.59523962	3.17888926	46.011515	1.18E-11	2.48E-11	0.56404261	8.33333333	91.6666667
ENSG00000181915	ADO	-0.8956077	4.29422365	170.440212	5.93E-39	1.94E-38	-0.8077583	97.1428571	2.85714286	ADO	-1.0893931	4.15702166	204.010195	2.78E-46	1.35E-45	-1.1447307	100	0
ENSG00000124466	LYPD3	0.84123036	5.13018682	170.209814	6.66E-39	2.18E-38	0.89542988	5.71428571	94.2857143	LYPD3	0.91890821	5.1773428	170.472493	5.83E-39	2.49E-38	0.99471589	2.77777778	97.2222222
ENSG00000076513	ANKRD13A	-0.8090886	5.88382887	170.029465	7.29E-39	2.39E-38	-0.7116433	100	0	ANKRD13A	-0.7905111	5.8609024	135.763662	2.25E-31	8.19E-31	-0.8410741	100	0
ENSG00000226479	TMEM185B	-0.9361878	3.93489308	169.965101	7.53E-39	2.46E-38	-0.8618959	100	0	TMEM185B	-0.8030086	3.91882339	105.447872	9.74E-25	3.04E-24	-0.8559278	100	0
ENSG00000149091	DGKZ	0.79470538	7.14783947	169.570634	9.18E-39	3.00E-38	0.89187662	0	100	DGKZ	0.59728744	6.98193165	78.2237775	9.20E-19	2.44E-18	0.56651187	2.77777778	97.2222222
ENSG00000099968	BCL2L13	-0.9325022	3.9702713	169.565757	9.20E-39	3.01E-38	-0.8007445	100	0	BCL2L13	-1.0813324	3.89584848	187.071752	1.39E-42	6.30E-42	-1.1155952	100	0
ENSG00000137478	FCHSD2	-0.8353956	5.12173701	169.386957	1.01E-38	3.29E-38	-0.7643791	100	0	FCHSD2	-1.0526883	4.92395069	217.352192	3.42E-49	1.74E-48	-1.1231971	100	0
ENSG00000172500	FIBP	-0.9679472	3.69940811	169.017459	1.21E-38	3.96E-38	-0.9230196	100	0	FIBP	-0.6620596	3.75706346	67.9304022	1.69E-16	4.21E-16	-0.7692966	94.4444444	5.55555556
ENSG00000131015	ULBP2	1.34093805	1.87231428	169.005008	1.22E-38	3.98E-38	1.2270599	0	100	ULBP2	1.56545509	1.78894625	179.637462	5.82E-41	2.59E-40	1.56897542	8.33333333	91.6666667
ENSG00000185262	UBALD2	-0.7898954	7.81160399	167.779879	2.26E-38	7.34E-38	-0.8390092	97.1428571	2.85714286	UBALD2	-0.7722078	7.71229973	127.087808	1.78E-29	6.22E-29	-0.838055	100	0
ENSG00000132646	PCNA	0.83420063	5.39010856	167.75919	2.28E-38	7.41E-38	0.90659668	11.4285714	88.5714286	PCNA	1.35026056	5.60915093	371.97927	6.94E-83	5.43E-82	1.27835322	5.55555556	94.4444444
ENSG00000111203	ITFG2	0.8766386	4.44896238	167.757277	2.29E-38	7.41E-38	0.89577203	0	100	ITFG2	0.77475887	4.33101595	107.694788	3.14E-25	9.92E-25	0.69824807	2.77777778	97.2222222
ENSG00000270589	RP11-348N5.7	1.28296569	1.86079259	166.737987	3.82E-38	1.24E-37	1.24295689	2.85714286	97.1428571	RP11-348N5.7	1.43788293	1.89465184	168.072068	1.95E-38	8.22E-38	1.36287857	0	100

ENSG00000005022	SLC25A5	-0.7867459	7.37467872	166.701707	3.89E-38	1.26E-37	-0.762934	100	0	SLC25A5	-0.4582877	7.43396468	45.5434585	1.49E-11	3.14E-11	-0.5179935	94.4444444	5.55555556
ENSG00000184381	PLA2G6	0.93347502	3.88011863	165.951925	5.67E-38	1.83E-37	0.97758492	0	100	PLA2G6	0.99552926	3.83225844	156.035914	8.31E-36	3.33E-35	0.93635065	2.77777778	97.2222222
ENSG00000172366	FAM195A	-1.1670317	2.44142377	165.910713	5.79E-38	1.87E-37	-1.058609	100	0	FAM195A	-1.0516592	2.44924804	111.160247	5.46E-26	1.76E-25	-1.1112675	100	0
ENSG00000125898	FAM110A	-1.0567792	3.05958111	165.890758	5.84E-38	1.88E-37	-0.929965	100	0	FAM110A	-0.763274	3.15528904	74.7199071	5.42E-18	1.40E-17	-0.8842054	97.2222222	2.77777778
ENSG00000101365	IDH3B	0.79735093	6.09162097	165.515742	7.06E-38	2.27E-37	0.79612175	0	100	IDH3B	0.72619005	6.01461361	114.744789	8.95E-27	2.94E-26	0.6477865	0	100
ENSG00000178104	PDE4DIP	0.80142318	5.70407367	165.348651	7.68E-38	2.47E-37	0.87980106	0	100	PDE4DIP	0.94776638	5.81200656	191.319748	1.64E-43	7.56E-43	0.89324568	2.77777778	97.2222222
ENSG00000102858	MGRN1	-0.7980902	5.8375453	165.242972	8.10E-38	2.60E-37	-0.779972	100	0	MGRN1	-0.6785479	5.85347571	99.8342786	1.66E-23	5.01E-23	-0.7138249	97.2222222	2.77777778
ENSG00000104946	TBC1D17	0.85387087	4.5782158	165.118206	8.62E-38	2.77E-37	0.97583658	0	100	TBC1D17	0.95074427	4.55836347	170.391755	6.08E-39	2.59E-38	0.87326907	0	100
ENSG00000175567	UCP2	-0.8053779	5.75069924	164.69561	1.07E-37	3.42E-37	-0.6757477	100	0	UCP2	-0.786921	5.67144382	131.16026	2.28E-30	8.13E-30	-0.7819962	97.2222222	2.77777778
ENSG00000090905	TNRC6A	0.79372597	6.23520654	164.572036	1.13E-37	3.64E-37	0.86256826	0	100	TNRC6A	0.74572484	6.18289088	121.008067	3.81E-28	1.29E-27	0.6899997	2.77777778	97.2222222
ENSG00000196371	FUT4	-0.9198797	3.99234048	164.539876	1.15E-37	3.69E-37	-0.8171832	100	0	FUT4	-1.0305111	3.92282116	169.754269	8.37E-39	3.55E-38	-1.0641677	100	0
ENSG00000115548	KDM3A	0.77941226	7.98424509	164.485169	1.19E-37	3.80E-37	0.8030933	0	100	KDM3A	0.944481	8.00759155	186.329162	2.01E-42	9.12E-42	0.85739341	0	100
ENSG00000138095	LRPPRC	0.79193388	6.25770434	164.457075	1.20E-37	3.85E-37	0.85026344	0	100	LRPPRC	0.68910374	6.13156797	103.768045	2.27E-24	7.02E-24	0.63068275	2.77777778	97.2222222
ENSG00000239305	RNF103	0.79563195	6.01159445	164.432611	1.22E-37	3.89E-37	0.86294732	0	100	RNF103	0.61080546	5.83290462	80.8145845	2.48E-19	6.70E-19	0.5428624	5.55555556	94.4444444
ENSG00000089053	ANAPC5	0.79621169	6.11917304	164.38229	1.25E-37	3.99E-37	0.83405148	0	100	ANAPC5	0.80159607	6.05304377	138.213155	6.55E-32	2.42E-31	0.7888399	5.55555556	94.4444444
ENSG00000137337	MDC1	0.80034565	5.67050912	164.357139	1.26E-37	4.04E-37	0.9093474	0	100	MDC1	0.70112532	5.5636539	105.314887	1.04E-24	3.25E-24	0.65861423	2.77777778	97.2222222
ENSG00000213064	SFT2D2	-0.7827575	6.96348744	164.327685	1.28E-37	4.10E-37	-0.7332713	100	0	SFT2D2	-0.4690347	7.01281811	48.4785549	3.34E-12	7.20E-12	-0.5359214	97.2222222	2.77777778
ENSG00000118640	VAMP8	-0.8533286	4.59025919	164.077664	1.45E-37	4.64E-37	-0.764644	100	0	VAMP8	-0.6644458	4.63326685	83.8420804	5.36E-20	1.47E-19	-0.7552586	97.2222222	2.77777778
ENSG00000066422	ZBTB11	0.78976458	6.34619156	163.928423	1.57E-37	5.00E-37	0.84053191	0	100	ZBTB11	0.72370493	6.20648981	113.440551	1.73E-26	5.62E-26	0.68095616	5.55555556	94.4444444
ENSG00000066557	LRRC40	0.92411823	3.90092388	163.868291	1.62E-37	5.15E-37	0.97466753	0	100	LRRC40	0.90316585	3.8069009	127.895373	1.18E-29	4.16E-29	0.85296668	5.55555556	94.4444444
ENSG00000135506	OS9	-0.7973349	6.09754671	163.846657	1.63E-37	5.21E-37	-0.749778	97.1428571	2.85714286	OS9	-0.8881362	6.04786392	166.671949	3.95E-38	1.65E-37	-1.0341091	91.6666667	8.33333333
ENSG00000100219	XBP1	-0.7904553	6.24603269	163.505896	1.94E-37	6.18E-37	-0.6819743	100	0	XBP1	-0.5205383	6.28984835	59.6067064	1.16E-14	2.73E-14	-0.5345004	100	0
ENSG00000159216	RUNX1	-0.7924737	6.07617312	162.889316	2.64E-37	8.41E-37	-0.6940828	100	0	RUNX1	-1.5559917	5.81204691	494.525151	1.48E-109	1.50E-108	-1.4905301	100	0
ENSG00000028277	POU2F2	-0.8532134	4.67749284	162.878788	2.66E-37	8.45E-37	-0.6219416	94.2857143	5.71428571	POU2F2	-1.2993034	4.48876724	301.56996	1.50E-67	9.87E-67	-1.3404407	100	0
ENSG00000167670	CHAF1A	0.91340192	3.94489094	162.484536	3.24E-37	1.03E-36	1.0306034	0	100	CHAF1A	0.83158711	3.83408703	110.079021	9.42E-26	3.02E-25	0.78120113	0	100
ENSG00000123329	ARHGAP9	0.78877104	6.22727969	162.055229	4.02E-37	1.28E-36	0.86266595	0	100	ARHGAP9	1.16639664	6.37841854	289.419822	6.65E-65	4.22E-64	1.07515568	0	100
ENSG00000152558	TMEM123	-0.7758838	9.4479303	161.262325	6.00E-37	1.90E-36	-0.6556678	100	0	TMEM123	-0.9581345	9.29825666	173.862206	1.06E-39	4.60E-39	-0.9081956	100	0
ENSG00000095002	MSH2	0.97773865	3.46387241	160.948316	7.02E-37	2.22E-36	0.998158	0	100	MSH2	0.85020746	3.30297298	98.049799	4.08E-23	1.22E-22	0.82345523	0	100
ENSG00000118564	FBXL5	-0.7822717	6.32018266	160.779785	7.64E-37	2.41E-36	-0.7217038	100	0	FBXL5	-0.7904012	6.27962989	136.632974	1.45E-31	5.31E-31	-0.8135062	100	0
ENSG00000169180	XPO6	0.76877792	7.7844766	160.670342	8.08E-37	2.55E-36	0.84979581	0	100	XPO6	0.65826969	7.6868152	93.1746179	4.79E-22	1.39E-21	0.58995563	0	100
ENSG00000136653	NA	-0.7708759	8.68864253	160.448927	9.03E-37	2.85E-36	-0.6306942	100	0	NA	-0.5467444	8.70581695	60.6300143	6.89E-15	1.63E-14	-0.6278569	100	0
ENSG00000105220	GPI	-0.785388	5.96844131	160.33389	9.57E-37	3.01E-36	-0.760406	100	0	GPI	-0.5525279	6.0275016	66.4477351	3.59E-16	8.82E-16	-0.5995126	97.2222222	2.77777778
ENSG00000180182	MED14	0.79184669	5.65857109	160.158805	1.04E-36	3.29E-36	0.8355435	0	100	MED14	0.8614815	5.62967489	158.072658	2.98E-36	1.21E-35	0.75981596	2.77777778	97.2222222
ENSG00000146676	PURB	-0.7853648	5.94223591	159.598091	1.39E-36	4.35E-36	-0.7195242	100	0	PURB	-1.0454991	5.79153665	233.89104	8.45E-53	4.54E-52	-1.0701631	100	0
ENSG00000213699	SLC35F6	-0.8930876	4.03608563	159.365535	1.56E-36	4.88E-36	-0.7480205	100	0	SLC35F6	-0.73945	4.05846422	92.4823184	6.79E-22	1.97E-21	-0.7518434	100	0
ENSG00000171103	TRMT61B	0.96612714	3.48440267	159.236267	1.66E-36	5.21E-36	1.02406289	0	100	TRMT61B	0.76030596	3.27310441	78.1900119	9.36E-19	2.48E-18	0.65739126	0	100
ENSG00000082014	SMARCD3	-1.0446106	3.09876399	159.179229	1.71E-36	5.35E-36	-1.1168141	88.5714286	11.4285714	SMARCD3	-0.352845	3.36345075	16.219618	5.64E-05	8.65E-05	-0.6251739	66.6666667	33.3333333
ENSG00000102898	NUTF2	-0.8856081	4.08416857	158.714662	2.16E-36	6.75E-36	-0.8014246	100	0	NUTF2	-0.5770481	4.12916075	57.7317251	3.00E-14	6.98E-14	-0.6175882	100	0
ENSG00000108666	C17orf75	1.15404339	2.33651857	158.592338	2.30E-36	7.17E-36	1.14221156	0	100	C17orf75	0.75112013	2.05314852	50.3082093	1.31E-12	2.88E-12	0.69292625	13.8888889	86.1111111
ENSG00000147535	PPAPDC1B	-0.9822105	3.45565106	158.56776	2.33E-36	7.26E-36	-0.9820307	100	0	PPAPDC1B	-0.6280566	3.45732461	55.4509703	9.58E-14	2.18E-13	-0.6898597	88.8888889	11.1111111
ENSG00000136518	ACTL6A	1.07644115	2.79025479	158.501699	2.40E-36	7.50E-36	1.15977705	0	100	ACTL6A	0.61768868	2.43107784	39.1677994	3.89E-10	7.74E-10	0.52674178	8.33333333	91.6666667
ENSG00000101193	GID8	-0.7818698	5.82736497	158.489137	2.42E-36	7.54E-36	-0.7066412	100	0	GID8	-0.4990322	5.85462642	54.6866015	1.41E-13	3.20E-13	-0.5888178	100	0
ENSG00000175826	CTDNEP1	-0.7801237	5.96156719	158.356166	2.59E-36	8.06E-36	-0.7255404	100	0	CTDNEP1	-0.5390206	6.00699821	63.5392943	1.57E-15	3.79E-15	-0.6137118	94.4444444	5.55555556
ENSG00000196911	KPNA5	0.81714424	4.83625404	157.96374	3.15E-36	9.81E-36	0.8704702	0	100	KPNA5	0.59255983	4.68356146	67.7960682	1.81E-16	4.50E-16	0.54580201	8.33333333	91.6666667
ENSG00000071127	WDR1	-0.7678619	7.22348097	157.749912	3.51E-36	1.09E-35	-0.6575368	100	0	WDR1	-0.5852941	7.26120607	73.5927733	9.60E-18	2.46E-17	-0.6196193	88.8888889	11.1111111
ENSG00000130305	NSUN5	0.86094979	4.28177445	157.690449	3.62E-36	1.12E-35	0.9476047	0	100	NSUN5	0.80030395	4.18428636	111.902817	3.75E-26	1.21E-25	0.74046438	0	100
ENSG00000184596	NA	1.34824301	1.34228984	157.563831	3.85E-36	1.20E-35	1.33290344	2.85714286	97.1428571	NA	1.65912995	1.53208722	192.024038	1.15E-43	5.32E-43	1.64443733	2.77777778	97.2222222
ENSG00000071894	CPSF1	0.79190408	5.60104381	157.539875	3.90E-36	1.21E-35	0.87815268	5.71428571	94.2857143	CPSF1	1.00161138	5.65862412	204.469042	2.21E-46	1.07E-45	0.81074361	5.55555556	94.4444444
ENSG00000103152	MPG	-1.105876	2.58376037	157.295776	4.41E-36	1.37E-35	-0.9542293	100	0	MPG	-1.0100704	2.57560487	106.873519	4.75E-25	1.50E-24	-1.091205	97.2222222	2.77777778
ENSG00000165733	BMS1	0.77825171	5.87155824	157.1289	4.80E-36	1.49E-35	0.78758148	0	100	BMS1	0.79679414	5.78341015	137.198837	1.09E-31	4.01E-31	0.64661799	0	100
ENSG00000136908	DPM2	0.92947079	3.7402392	157.104445	4.86E-36	1.50E-35	1.00131449	0	100	DPM2	0.75891783	3.60489346	84.8362037	3.24E-20	8.97E-20	0.66305036	5.55555556	94.4444444
ENSG00000129245	FXR2	0.85719491	4.3078221	156.750891	5.80E-36	1.80E-35	0.8834974	0	100	FXR2	0.94478642	4.29846792	159.541336	1.43E-36	5.78E-36	0.86274714	0	100
ENSG00000130939	UBE4B	0.79965953	5.05114041	156.425498	6.83E-36	2.11E-35	0.89433703	0	100	UBE4B	0.83451112	5.00875252	141.815388	1.07E-32	4.01E-32	0.82680485	0	100

ENSG00000118705	RPN2	-0.7728034	6.14352422	156.301768	7.27E-36	2.25E-35	-0.7188761	100	0	RPN2	-0.5995578	6.16551935	78.8650079	6.65E-19	1.78E-18	-0.684372	100	0
ENSG00000205138	SDHAF1	-1.2368095	1.79324928	155.754349	9.58E-36	2.96E-35	-1.162927	100	0	SDHAF1	-0.7661973	1.89054076	50.0664983	1.49E-12	3.25E-12	-0.8753626	97.2222222	2.77777778
ENSG00000148296	SURF6	0.82785561	4.5894729	155.739393	9.65E-36	2.98E-35	0.82131408	0	100	SURF6	0.89223224	4.58730579	151.053975	1.02E-34	4.00E-34	0.74902597	0	100
ENSG00000111679	PTPN6	-0.7793808	5.80413474	155.497852	1.09E-35	3.36E-35	-0.6557265	97.1428571	2.85714286	PTPN6	-1.5243002	5.58281274	469.267445	4.63E-104	4.48E-103	-1.4898945	100	0
ENSG00000122068	FYTTD1	-0.7613341	7.07501088	155.361303	1.17E-35	3.60E-35	-0.6969881	100	0	FYTTD1	-0.7594968	6.99736932	125.787201	3.42E-29	1.19E-28	-0.7728001	100	0
ENSG00000105518	TMEM205	-1.1087439	2.53537838	154.502532	1.80E-35	5.55E-35	-0.9471848	100	0	TMEM205	-1.3158031	2.42705356	169.816971	8.11E-39	3.44E-38	-1.3928273	100	0
ENSG00000243449	C4orf48	-1.3323059	1.2763562	154.371152	1.92E-35	5.92E-35	-1.34101	100	0	C4orf48	-0.8149332	1.42406913	47.3687267	5.88E-12	1.26E-11	-0.8189666	88.8888889	11.1111111
ENSG00000144909	OSBPL11	-0.8355548	4.45274414	153.705526	2.69E-35	8.25E-35	-0.7013073	100	0	OSBPL11	-0.8362496	4.41772467	127.638125	1.35E-29	4.72E-29	-0.8581473	97.2222222	2.77777778
ENSG00000099795	NDUFB7	-0.9417245	3.59378928	153.385472	3.16E-35	9.66E-35	-0.8739294	94.2857143	5.71428571	NDUFB7	-0.6984656	3.63234841	73.1945287	1.17E-17	3.00E-17	-0.8038744	91.6666667	8.33333333
ENSG00000113742	CPEB4	-0.7775961	5.69665422	153.358112	3.20E-35	9.79E-35	-0.6909706	97.1428571	2.85714286	CPEB4	-0.7170555	5.69773001	108.91159	1.70E-25	5.42E-25	-0.7322999	94.4444444	5.55555556
ENSG00000135441	BLOC1S1	-1.0297786	2.97673351	153.186016	3.49E-35	1.07E-34	-1.0013327	100	0	BLOC1S1	-0.7971694	3.03630146	78.1281607	9.66E-19	2.56E-18	-0.8937382	94.4444444	5.55555556
ENSG00000171522	PTGER4	0.76386517	8.728633	153.168666	3.52E-35	1.08E-34	0.93242876	14.2857143	85.7142857	PTGER4	0.64326196	8.59681005	81.6773799	1.60E-19	4.35E-19	0.61952098	16.6666667	83.3333333
ENSG00000155827	RNF20	0.84550309	4.31068558	153.0498	3.74E-35	1.14E-34	0.871798	0	100	RNF20	0.6168375	4.10819916	65.752716	5.11E-16	1.25E-15	0.56098764	0	100
ENSG00000119392	GLE1	0.81834548	4.59198419	152.676523	4.51E-35	1.38E-34	0.8649259	0	100	GLE1	0.64370979	4.45652834	77.342788	1.44E-18	3.79E-18	0.58069831	0	100
ENSG00000205155	PSENEN	-1.2244567	1.82772974	152.365186	5.27E-35	1.61E-34	-1.2580722	100	0	PSENEN	-0.7789226	1.94587874	51.8514788	5.99E-13	1.33E-12	-0.7828514	94.4444444	5.55555556
ENSG00000076928	ARHGEF1	0.753145	8.69494799	152.273663	5.52E-35	1.68E-34	0.79019501	0	100	ARHGEF1	0.72274911	8.58696946	103.574252	2.51E-24	7.73E-24	0.50235509	5.55555556	94.4444444
ENSG00000125871	MGME1	-1.1060945	2.45956112	152.174104	5.80E-35	1.77E-34	-1.0581481	100	0	MGME1	-0.9947716	2.44302764	100.230056	1.36E-23	4.11E-23	-1.0091802	100	0
ENSG00000065029	ZNF76	0.85089623	4.25776864	151.502103	8.14E-35	2.47E-34	0.93599673	2.85714286	97.1428571	ZNF76	0.76896528	4.12286721	100.903281	9.66E-24	2.95E-23	0.63836652	2.77777778	97.2222222
ENSG00000167685	ZNF444	0.87388768	4.01889339	151.306951	8.98E-35	2.73E-34	0.9985201	0	100	ZNF444	0.68853423	3.8675776	76.4443961	2.27E-18	5.92E-18	0.67362011	5.55555556	94.4444444
ENSG00000186480	INSIG1	-0.7570254	6.48206408	151.17603	9.59E-35	2.91E-34	-0.6289153	100	0	INSIG1	-0.8425325	6.39327498	153.102348	3.64E-35	1.44E-34	-0.8124403	100	0
ENSG00000035928	RFC1	0.75718522	6.29409836	151.119233	9.87E-35	2.99E-34	0.80759179	0	100	RFC1	0.6136345	6.11616154	82.4176733	1.10E-19	3.01E-19	0.55867181	5.55555556	94.4444444
ENSG00000117448	AKR1A1	-0.8864142	3.92036852	150.969475	1.06E-34	3.23E-34	-0.7495648	100	0	AKR1A1	-0.669937	3.93523253	72.7981787	1.44E-17	3.66E-17	-0.7100262	94.4444444	5.55555556
ENSG00000054148	PHPT1	-1.0947736	2.51870686	150.480889	1.36E-34	4.12E-34	-1.1254135	100	0	PHPT1	-0.6951291	2.62874694	51.4650647	7.29E-13	1.61E-12	-0.7470475	91.6666667	8.33333333
ENSG00000065613	SLK	-0.7581262	6.08977204	150.395493	1.42E-34	4.30E-34	-0.6422777	100	0	SLK	-0.5551639	6.11181369	67.4852159	2.12E-16	5.26E-16	-0.5700667	94.4444444	5.55555556
ENSG00000157800	SLC37A3	0.90086026	3.77785519	150.326582	1.47E-34	4.45E-34	0.95687839	0	100	SLC37A3	0.74565561	3.61181319	83.5971024	6.07E-20	1.67E-19	0.67147059	0	100
ENSG00000141985	SH3GL1	-0.7788726	5.21112941	150.294468	1.49E-34	4.52E-34	-0.7385813	100	0	SH3GL1	-0.5013077	5.26534578	52.5942679	4.10E-13	9.14E-13	-0.5945511	97.2222222	2.77777778
ENSG00000099992	TBC1D10A	0.80067463	4.73554412	150.100401	1.65E-34	4.98E-34	0.82623418	0	100	TBC1D10A	0.95302194	4.78911477	178.252511	1.17E-40	5.16E-40	0.85888318	0	100
ENSG00000196182	STK40	-0.7724187	5.44118965	149.98472	1.75E-34	5.28E-34	-0.587416	100	0	STK40	-1.0184779	5.37198055	215.387765	9.17E-49	4.64E-48	-1.0174643	100	0
ENSG00000104388	RAB2A	-0.758261	6.02589405	149.854026	1.87E-34	5.63E-34	-0.6998655	97.1428571	2.85714286	RAB2A	-0.4830437	6.05958247	51.2866401	7.98E-13	1.76E-12	-0.5632728	94.4444444	5.55555556
ENSG00000085511	MAP3K4	0.83553469	4.30129398	149.687459	2.03E-34	6.12E-34	0.87982536	0	100	MAP3K4	0.74510557	4.18183564	97.3318065	5.86E-23	1.75E-22	0.68470845	0	100
ENSG00000170348	TMED10	-0.7515132	6.44698126	149.420148	2.32E-34	7.00E-34	-0.7477305	100	0	TMED10	-0.5301356	6.49142696	61.7035713	3.99E-15	9.52E-15	-0.5697895	100	0
ENSG00000156471	PTDSS1	-0.7538728	6.04969864	148.963297	2.92E-34	8.79E-34	-0.6719498	100	0	PTDSS1	-0.5659484	6.06068517	70.4529055	4.71E-17	1.19E-16	-0.6393982	100	0
ENSG00000162869	PPP1R21	0.94136386	3.44128819	148.539288	3.62E-34	1.09E-33	1.01971468	0	100	PPP1R21	0.62031116	3.19380889	50.7614569	1.04E-12	2.29E-12	0.64546043	5.55555556	94.4444444
ENSG00000138600	SPPL2A	-0.7854131	4.93284104	147.766003	5.34E-34	1.60E-33	-0.6806405	100	0	SPPL2A	-0.549031	4.99325866	61.1822554	5.20E-15	1.23E-14	-0.593174	97.2222222	2.77777778
ENSG00000198862	LTN1	0.76332739	5.45862138	147.748693	5.38E-34	1.61E-33	0.77609069	0	100	LTN1	0.74581227	5.36805572	116.350195	3.98E-27	1.32E-26	0.7093801	5.55555556	94.4444444
ENSG00000177963	RIC8A	0.75323602	6.03836257	147.542385	5.97E-34	1.79E-33	0.81155921	0	100	RIC8A	1.18960296	6.30062553	304.639879	3.21E-68	2.15E-67	1.20358612	0	100
ENSG00000134255	CEPT1	0.90506666	3.70867417	147.528662	6.01E-34	1.80E-33	0.86092406	2.85714286	97.1428571	CEPT1	0.82282673	3.64434389	100.508856	1.18E-23	3.58E-23	0.85829915	2.77777778	97.2222222
ENSG00000142867	BCL10	-0.7923487	4.75553036	147.429818	6.32E-34	1.89E-33	-0.7563349	100	0	BCL10	-0.5328525	4.80139634	56.6852387	5.11E-14	1.18E-13	-0.5533813	100	0
ENSG00000143811	PYCR2	0.82328912	4.3671928	147.326614	6.66E-34	1.99E-33	0.95459205	0	100	PYCR2	0.6553139	4.23191096	76.3485617	2.38E-18	6.21E-18	0.58120415	2.77777778	97.2222222
ENSG00000149809	TM7SF2	1.13265859	2.1987957	147.13483	7.33E-34	2.19E-33	1.18643044	0	100	TM7SF2	1.28271644	2.23452638	153.060988	3.71E-35	1.47E-34	1.28582512	0	100
ENSG00000272782	RP4-607J23.2	-1.2811055	1.35794313	146.859594	8.42E-34	2.51E-33	-1.2277366	100	0	RP4-607J23.2	-1.1366489	1.38305792	91.5069721	1.11E-21	3.21E-21	-1.1655293	100	0
ENSG00000054983	GALC	-0.8802405	3.84518405	146.698451	9.13E-34	2.72E-33	-0.8156253	100	0	GALC	-0.8619459	3.8365306	117.956182	1.77E-27	5.92E-27	-0.8619012	100	0
ENSG00000126561	STAT5A	0.74024186	6.98692277	146.466113	1.03E-33	3.06E-33	0.7972415	0	100	STAT5A	1.19285132	7.25167221	302.588698	8.99E-68	5.97E-67	1.06845173	0	100
ENSG00000101940	WDR13	-0.8482367	4.11395049	146.294157	1.12E-33	3.33E-33	-0.8087458	100	0	WDR13	-0.655672	4.11822105	73.1208611	1.22E-17	3.11E-17	-0.7736128	97.2222222	2.77777778
ENSG00000131148	EMC8	0.77904189	4.94723777	145.847926	1.40E-33	4.17E-33	0.81020748	0	100	EMC8	0.91962101	4.94259942	169.858113	7.95E-39	3.37E-38	0.89971075	0	100
ENSG00000110717	NDUFS8	0.80486003	4.5421463	145.785975	1.45E-33	4.30E-33	0.85357838	0	100	NDUFS8	0.73135501	4.47717388	99.53361	1.93E-23	5.83E-23	0.63876056	0	100
ENSG00000118246	FASTKD2	0.79204686	4.70139925	145.730683	1.49E-33	4.42E-33	0.87619946	0	100	FASTKD2	0.80663793	4.64332443	123.66647	9.97E-29	3.42E-28	0.7918232	2.77777778	97.2222222
ENSG00000105618	PRPF31	0.78409545	4.85803993	145.637861	1.56E-33	4.63E-33	0.78643864	0	100	PRPF31	0.83230635	4.85538392	137.084742	1.16E-31	4.25E-31	0.77659283	2.77777778	97.2222222
ENSG00000256223	ZNF10	0.87683442	3.87296916	145.622672	1.57E-33	4.66E-33	0.88398935	0	100	ZNF10	0.81609242	3.72341591	101.350337	7.71E-24	2.36E-23	0.7284172	2.77777778	97.2222222
ENSG00000100263	RHBDD3	1.07506753	2.47056139	145.112173	2.03E-33	6.02E-33	1.08096392	0	100	RHBDD3	0.94449476	2.33685	88.0570218	6.36E-21	1.80E-20	0.77869291	0	100
ENSG00000179094	PER1	0.73501915	9.32483892	144.879631	2.28E-33	6.76E-33	0.70202391	0	100	PER1	1.16225831	9.50695116	250.430463	2.09E-56	1.18E-55	1.08701754	0	100
ENSG00000188186	LAMTOR4	-0.7767087	4.92712835	144.701128	2.50E-33	7.39E-33	-0.6882303	100	0	LAMTOR4	-0.9616798	4.83700984	180.310901	4.15E-41	1.85E-40	-1.0743647	97.2222222	2.77777778
ENSG00000035141	FAM136A	0.76576646	5.07051654	143.707741	4.12E-33	1.21E-32	0.81803818	0	100	FAM136A	0.68830108	4.95773487	95.9952053	1.15E-22	3.41E-22	0.62128138	0	100

ENSG00000092140	G2E3	0.78273819	4.77239273	143.274637	5.12E-33	1.51E-32	0.80497605	0	100	G2E3	0.57111409	4.61241616	62.0689333	3.32E-15	7.91E-15	0.57418942	11.1111111	88.8888889
ENSG00000137312	FLOT1	-0.767207	5.09220524	143.160299	5.42E-33	1.60E-32	-0.6654463	94.2857143	5.71428571	FLOT1	-1.5347292	4.82370033	443.804909	1.61E-98	1.48E-97	-1.4989757	100	0
ENSG00000120875	DUSP4	-0.7381134	6.67389989	143.15291	5.44E-33	1.60E-32	-0.565295	91.4285714	8.57142857	DUSP4	-0.6773777	6.70915732	96.7305357	7.94E-23	2.36E-22	-0.8136279	88.8888889	11.1111111
ENSG00000146556	WASH2P	0.91304801	3.49584935	142.743435	6.69E-33	1.97E-32	0.92406521	0	100	WASH2P	0.87611194	3.42913162	107.967744	2.73E-25	8.67E-25	0.74136305	0	100
ENSG00000126001	CEP250	0.77591157	4.79022314	142.397584	7.96E-33	2.34E-32	0.84126475	0	100	CEP250	0.94601348	4.83474072	177.504346	1.70E-40	7.51E-40	0.87940161	0	100
ENSG00000134086	VHL	-0.7366933	6.33441902	142.392787	7.98E-33	2.34E-32	-0.6303682	100	0	VHL	-0.6978107	6.2574519	107.268883	3.89E-25	1.23E-24	-0.728792	100	0
ENSG00000131467	PSME3	-0.7344265	6.22789745	142.092533	9.28E-33	2.72E-32	-0.6522798	100	0	PSME3	-0.4229516	6.28048907	39.549992	3.20E-10	6.40E-10	-0.5037634	97.2222222	2.7777778
ENSG00000125734	GPR108	-0.8693755	3.82143853	141.89295	1.03E-32	3.01E-32	-0.7581355	100	0	GPR108	-0.6956599	3.81160412	76.4183485	2.30E-18	6.00E-18	-0.7903553	100	0
ENSG00000148730	EIF4EBP2	-0.7327263	6.23713208	141.017367	1.59E-32	4.67E-32	-0.6436586	100	0	EIF4EBP2	-0.5283407	6.27906964	61.6091615	4.19E-15	9.96E-15	-0.549086	100	0
ENSG00000165704	HPRT1	-0.9064856	3.4922976	140.966448	1.64E-32	4.78E-32	-0.832319	100	0	HPRT1	-0.7625834	3.47456412	83.5984491	6.06E-20	1.66E-19	-0.7635849	100	0
ENSG00000152240	HAUS1	-1.1755237	1.79205436	140.293699	2.30E-32	6.70E-32	-1.1128401	100	0	HAUS1	-0.6633209	1.94277205	38.2321559	6.28E-10	1.24E-09	-0.7426958	94.4444444	5.55555556
ENSG00000123066	MED13L	-0.7191899	8.34339577	140.08235	2.55E-32	7.44E-32	-0.6104874	100	0	MED13L	-0.6797458	8.30341722	94.9354585	1.97E-22	5.79E-22	-0.6710221	97.2222222	2.7777778
ENSG00000100599	RIN3	-0.7253162	7.18745986	140.052683	2.59E-32	7.55E-32	-0.6682861	94.2857143	5.71428571	RIN3	-0.9420511	7.0586424	191.50504	1.49E-43	6.90E-43	-1.0059398	100	0
ENSG00000107404	DVL1	0.7978133	4.44042971	139.878949	2.83E-32	8.23E-32	0.78919573	0	100	DVL1	0.70975524	4.32270389	90.4453014	1.90E-21	5.46E-21	0.61802019	0	100
ENSG00000168256	NKIRAS2	-0.7615454	4.94996764	139.743831	3.03E-32	8.79E-32	-0.699063	100	0	NKIRAS2	-0.8072914	4.91100759	130.386786	3.37E-30	1.20E-29	-0.9078901	100	0
ENSG00000198961	PJA2	-0.7179202	7.23236906	139.452619	3.51E-32	1.02E-31	-0.677483	100	0	PJA2	-0.6092396	7.22255406	80.8518273	2.43E-19	6.58E-19	-0.6126133	97.2222222	2.7777778
ENSG00000196498	NCOR2	-0.7199628	7.29483187	139.270212	3.84E-32	1.11E-31	-0.5943004	100	0	NCOR2	-0.9346712	7.18749301	185.829889	2.59E-42	1.17E-41	-0.9377373	97.2222222	2.7777778
ENSG00000105438	KDELR1	-0.8429774	3.99611717	139.254444	3.87E-32	1.12E-31	-0.7319541	100	0	KDELR1	-0.7733747	4.00358258	99.0656328	2.44E-23	7.36E-23	-0.8648579	100	0
ENSG00000173273	TNKS	0.74358983	5.31507635	139.032504	4.33E-32	1.25E-31	0.76271247	0	100	TNKS	0.72242135	5.26077678	109.426442	1.31E-25	4.19E-25	0.6873271	2.77777778	97.2222222
ENSG00000108061	SHOC2	-0.724623	6.40133137	138.785725	4.91E-32	1.42E-31	-0.6418086	100	0	SHOC2	-0.4798285	6.42783892	50.3723316	1.27E-12	2.79E-12	-0.5022458	91.6666667	8.33333333
ENSG00000213246	SUPT4H1	-0.7360987	5.58762375	138.52849	5.58E-32	1.61E-31	-0.6531396	100	0	SUPT4H1	-0.8053249	5.52937827	137.87879	7.75E-32	2.86E-31	-0.8851218	100	0
ENSG00000089048	ESF1	0.86621161	3.74376159	138.46651	5.76E-32	1.66E-31	0.97585475	0	100	ESF1	0.64684734	3.56344709	62.0820999	3.29E-15	7.86E-15	0.623476	2.77777778	97.2222222
ENSG00000131844	MCCC2	0.82660223	4.08277344	138.389361	5.99E-32	1.72E-31	0.91748616	0	100	MCCC2	0.59295114	3.916454	57.6286852	3.17E-14	7.34E-14	0.51294098	5.55555556	94.4444444
ENSG0000021355	SERPINB1	-0.7303453	5.94117965	137.878365	7.75E-32	2.23E-31	-0.7076581	97.1428571	2.85714286	SERPINB1	-0.8997111	5.86708741	174.567714	7.44E-40	3.24E-39	-0.9404664	100	0
ENSG00000137996	RTCA	0.79884898	4.35260643	137.782098	8.13E-32	2.33E-31	0.87025182	0	100	RTCA	0.95253479	4.40014343	165.220902	8.19E-38	3.41E-37	0.91272955	0	100
ENSG00000198874	TYW1	0.81444074	4.15039833	137.207615	1.09E-31	3.11E-31	0.88208964	0	100	TYW1	0.83789437	4.11027156	120.811566	4.20E-28	1.42E-27	0.75567501	0	100
ENSG00000147324	MFHAS1	-0.773873	4.71856663	137.026655	1.19E-31	3.40E-31	-0.6775763	91.4285714	8.57142857	MFHAS1	-2.355979	4.31620382	890.595039	1.09E-195	1.71E-194	-2.4331916	100	0
ENSG00000063587	ZNF275	0.77211334	4.65879764	136.273577	1.74E-31	4.97E-31	0.75266555	0	100	ZNF275	0.65453924	4.51704617	80.3666625	3.11E-19	8.38E-19	0.52828736	5.55555556	94.4444444
ENSG00000105612	DNASE2	-0.9240495	3.31574959	136.161752	1.84E-31	5.25E-31	-0.8994051	94.2857143	5.71428571	DNASE2	-1.0313597	3.27286462	139.226633	3.93E-32	1.46E-31	-1.1144524	100	0
ENSG00000215717	TMEM167B	-0.713332	6.68709053	136.02973	1.97E-31	5.61E-31	-0.6434381	100	0	TMEM167B	-0.661024	6.66905202	96.146544	1.07E-22	3.16E-22	-0.6962564	100	0
ENSG00000185947	ZNF267	-0.7299676	5.49190683	135.707917	2.31E-31	6.59E-31	-0.6320972	100	0	ZNF267	-0.7350209	5.44679909	114.406653	1.06E-26	3.47E-26	-0.7482646	100	0
ENSG00000141873	SLC39A3	-0.8426205	3.89005601	135.480967	2.59E-31	7.37E-31	-0.7858231	100	0	SLC39A3	-0.5564385	3.91925223	50.5311456	1.17E-12	2.57E-12	-0.5048642	100	0
ENSG0000059145	UNKL	0.84898557	3.83224842	135.399671	2.70E-31	7.67E-31	0.91651704	0	100	UNKL	0.85029143	3.79127384	112.787253	2.40E-26	7.80E-26	0.77338757	2.77777778	97.2222222
ENSG0000099917	MED15	0.70903832	7.08993816	135.014318	3.28E-31	9.29E-31	0.7859679	0	100	MED15	1.0978038	7.30708906	257.605922	5.71E-58	3.28E-57	1.0881729	0	100
ENSG00000108829	LRRC59	-0.7165531	6.04427005	134.55331	4.13E-31	1.17E-30	-0.6818201	100	0	LRRC59	-0.4900016	6.06513318	52.8683667	3.57E-13	7.96E-13	-0.5291203	100	0
ENSG00000167315	ACAA2	-0.8855649	3.52516979	134.360333	4.56E-31	1.29E-30	-0.8518627	100	0	ACAA2	-0.4623601	3.64978261	32.3014522	1.32E-08	2.46E-08	-0.5123755	86.1111111	13.8888889
ENSG00000182247	UBE2E2	-0.9770977	2.87178595	133.980459	5.52E-31	1.56E-30	-0.8308801	100	0	UBE2E2	-0.8503313	2.84012578	83.2857281	7.10E-20	1.95E-19	-0.8778762	100	0
ENSG00000172869	DMXL1	-0.728716	5.34337782	133.648036	6.52E-31	1.84E-30	-0.6159143	100	0	DMXL1	-0.5793075	5.32629452	70.8498891	3.85E-17	9.73E-17	-0.5826794	100	0
ENSG00000270184	RP11-568J23.5	1.33924444	0.80982233	133.377267	7.48E-31	2.11E-30	1.42643732	0	100	RP11-568J23.	1.61239771	0.90840774	150.253047	1.53E-34	5.98E-34	1.61658753	2.77777778	97.2222222
ENSG00000147130	ZMYM3	0.8406621	3.81476644	132.980607	9.13E-31	2.57E-30	0.88465561	0	100	ZMYM3	0.9623918	3.86313759	147.992069	4.76E-34	1.84E-33	0.89390418	2.77777778	97.2222222
ENSG00000172493	AFF1	-0.716637	6.12090642	132.05369	1.46E-30	4.09E-30	-0.5820025	88.5714286	11.4285714	AFF1	-0.8321871	5.98601901	148.791616	3.18E-34	1.24E-33	-0.8388788	100	0
ENSG00000148688	RPP30	0.78609069	4.29936856	131.975541	1.51E-30	4.25E-30	0.81241032	0	100	RPP30	0.66779962	4.1615801	77.8476996	1.11E-18	2.95E-18	0.58974094	2.77777778	97.2222222
ENSG00000197858	GPAA1	-0.7775481	4.37496845	131.153262	2.29E-30	6.41E-30	-0.7298905	100	0	GPAA1	-0.5331248	4.39958617	52.0358536	5.45E-13	1.21E-12	-0.6336026	91.6666667	8.33333333
ENSG0000078043	PIAS2	0.81358315	3.98255407	131.001696	2.47E-30	6.92E-30	0.88684069	0	100	PIAS2	0.86315288	3.9668771	123.287659	1.21E-28	4.13E-28	0.79673157	2.77777778	97.2222222
ENSG00000174885	NLRP6	0.97796956	2.78435448	130.708084	2.87E-30	8.02E-30	1.03479953	0	100	NLRP6	1.18163128	2.90247262	162.497349	3.22E-37	1.32E-36	1.16629786	0	100
ENSG0000021776	AQR	0.70840442	5.88275013	130.641617	2.97E-30	8.29E-30	0.75669004	0	100	AQR	0.82913857	5.90885324	147.968534	4.82E-34	1.86E-33	0.75151478	5.55555556	94.4444444
ENSG00000138071	ACTR2	-0.6948013	7.95745124	130.507802	3.17E-30	8.86E-30	-0.6368756	100	0	ACTR2	-0.6318162	7.95120352	84.3915111	4.06E-20	1.12E-19	-0.6190043	97.2222222	2.77777778
ENSG00000136146	MED4	0.72374459	5.28265943	130.421953	3.31E-30	9.25E-30	0.78044703	0	100	MED4	0.67545819	5.18814347	94.6027238	2.33E-22	6.83E-22	0.66776242	5.55555556	94.4444444
ENSG00000130749	ZC3H4	0.73698083	4.87808219	129.637543	4.92E-30	1.37E-29	0.75172773	2.85714286	97.1428571	ZC3H4	0.60033509	4.77525147	71.118088	3.36E-17	8.51E-17	0.58069226	8.33333333	91.6666667
ENSG00000108654	DDX5	0.69745911	10.389261	129.098397	6.45E-30	1.80E-29	0.72270037	0	100	DDX5	0.49682299	10.1760366	44.0137886	3.26E-11	6.76E-11	0.50625644	13.8888889	86.1111111
ENSG00000163798	SLC4A1AP	0.75874692	4.49570427	128.781231	7.57E-30	2.10E-29	0.84434425	0	100	SLC4A1AP	0.84382803	4.48872369	133.185912	8.23E-31	2.96E-30	0.79664993	0	100
ENSG00000196456	ZNF775	-0.7317235	4.99831051	128.530942	8.59E-30	2.39E-29	-0.5832742	94.2857143	5.71428571	ZNF775	-1.1153363	4.78534184	239.400358	5.31E-54	2.90E-53	-1.096399	100	0
ENSG00000175104	TRAF6	-0.7235118	5.08332472	128.500688	8.72E-30	2.42E-29	-0.6550636	100	0	TRAF6	-0.5844392	5.06903017	70.3100465	5.07E-17	1.28E-16	-0.531544	100	0

ENSG00000166913	YWHAB	-0.6903634	7.02392539	128.047556	1.10E-29	3.04E-29	-0.6569578	100	0	YWHAB	-0.647448	6.9741095	92.0600394	8.41E-22	2.43E-21	-0.6628202	100	0
ENSG00000146083	RNF44	0.68932013	7.00932735	127.825199	1.23E-29	3.39E-29	0.77807567	0	100	RNF44	0.61928251	6.89891705	83.9662525	5.03E-20	1.39E-19	0.59118621	5.55555556	94.4444444
ENSG00000254635	WAC-AS1	-0.8757338	3.40809837	127.655517	1.34E-29	3.69E-29	-0.7296575	97.1428571	2.85714286	WAC-AS1	-0.8697174	3.37033869	104.331285	1.71E-24	5.30E-24	-0.9960524	100	0
ENSG00000150961	SEC24D	-0.833101	3.73316775	127.29026	1.60E-29	4.43E-29	-0.8123508	100	0	SEC24D	-0.5822409	3.80594358	53.3737373	2.76E-13	6.18E-13	-0.5954523	94.4444444	5.55555556
ENSG00000102531	FNDC3A	0.72771566	4.89696459	127.136171	1.73E-29	4.79E-29	0.76328271	0	100	FNDC3A	0.88080952	4.95802788	155.683154	9.93E-36	3.96E-35	0.87619593	2.77777778	97.2222222
ENSG00000003056	M6PR	-0.800641	4.02113359	126.744514	2.11E-29	5.82E-29	-0.6997759	97.1428571	2.85714286	M6PR	-0.7363273	4.03400421	90.5694485	1.79E-21	5.13E-21	-0.8035868	94.4444444	5.55555556
ENSG00000198382	UVRAG	-0.7244231	4.95648568	126.595304	2.28E-29	6.27E-29	-0.6148359	100	0	UVRAG	-0.6956651	4.87459662	96.6660868	8.21E-23	2.44E-22	-0.7135681	100	0
ENSG00000015285	WAS	-0.7114087	5.30738177	126.186939	2.80E-29	7.70E-29	-0.6140249	97.1428571	2.85714286	WAS	-0.7159075	5.28719533	105.941753	7.59E-25	2.38E-24	-0.8299261	97.2222222	2.77777778
ENSG00000116906	GNPAT	0.85809895	3.51511395	126.020918	3.04E-29	8.36E-29	0.94289905	2.85714286	97.1428571	GNPAT	0.54680764	3.29850842	40.4584214	2.01E-10	4.05E-10	0.65801797	16.6666667	83.3333333
ENSG00000100911	PSME2	-0.7052182	5.42664578	125.527834	3.90E-29	1.07E-28	-0.534308	100	0	PSME2	-0.6265546	5.43711497	82.7284182	9.41E-20	2.57E-19	-0.6498804	94.4444444	5.55555556
ENSG00000095261	PSMD5	0.73266971	4.73291204	125.179962	4.65E-29	1.27E-28	0.78210205	0	100	PSMD5	0.63089914	4.63038024	76.6666232	2.02E-18	5.30E-18	0.60107061	5.55555556	94.4444444
ENSG00000170445	HARS	0.72120505	4.90950472	125.179408	4.65E-29	1.27E-28	0.80596081	0	100	HARS	1.01863774	5.02952212	210.294023	1.19E-47	5.89E-47	0.96586401	0	100
ENSG00000163348	PYGO2	0.74372972	4.53975022	125.06981	4.91E-29	1.34E-28	0.77954511	0	100	PYGO2	0.76079387	4.53213978	109.562737	1.22E-25	3.91E-25	0.6911484	0	100
ENSG00000180917	CMTR2	-0.797791	3.95533454	124.866626	5.44E-29	1.49E-28	-0.8103517	100	0	CMTR2	-0.7832904	3.87995063	99.3622712	2.10E-23	6.34E-23	-0.8411404	97.2222222	2.77777778
ENSG00000079739	PGM1	-0.9221763	2.97016679	124.802695	5.62E-29	1.53E-28	-0.8357123	100	0	PGM1	-0.5845041	3.08307303	43.881003	3.49E-11	7.22E-11	-0.5990773	100	0
ENSG00000122965	RBM19	0.72802003	4.77834844	124.532765	6.44E-29	1.76E-28	0.79155567	0	100	RBM19	0.80151033	4.75899277	125.513549	3.93E-29	1.36E-28	0.74508019	0	100
ENSG00000124151	NCOA3	-0.6781541	7.40403996	124.259345	7.39E-29	2.01E-28	-0.5270338	100	0	NCOA3	-0.6619324	7.35029337	94.874092	2.03E-22	5.97E-22	-0.6586736	97.2222222	2.77777778
ENSG00000001497	LAS1L	0.71418933	4.99789956	124.245243	7.44E-29	2.03E-28	0.80389425	0	100	LAS1L	0.62451818	4.87142687	78.5550353	7.78E-19	2.07E-18	0.53177202	0	100
ENSG00000164983	TMEM65	-0.9199509	2.9774233	124.138106	7.86E-29	2.14E-28	-0.7217627	100	0	TMEM65	-1.2764608	2.85080777	187.168876	1.32E-42	6.01E-42	-1.2266474	100	0
ENSG00000067248	DHX29	0.70399041	5.22267831	124.114005	7.95E-29	2.17E-28	0.78169554	0	100	DHX29	0.63919442	5.10831922	84.6494849	3.56E-20	9.85E-20	0.63176913	0	100
ENSG00000144357	UBR3	0.71748262	4.9222066	124.101325	8.00E-29	2.18E-28	0.77266544	0	100	UBR3	0.50302997	4.74751952	49.9228941	1.60E-12	3.48E-12	0.50584607	11.1111111	88.8888889
ENSG00000172831	CES2	0.74770937	4.4786056	124.099603	8.01E-29	2.18E-28	0.83408141	2.85714286	97.1428571	CES2	0.76111573	4.45718223	107.836198	2.92E-25	9.26E-25	0.71594598	2.77777778	97.2222222
ENSG00000103174	NAGPA	0.75642974	4.34407535	124.025336	8.32E-29	2.26E-28	0.8590549	0	100	NAGPA	0.66271291	4.21787351	77.7853796	1.15E-18	3.04E-18	0.60721196	0	100
ENSG00000135040	NAA35	0.855344	3.44747237	123.56083	1.05E-28	2.86E-28	0.87778916	0	100	NAA35	0.77345218	3.36805325	83.1664235	7.54E-20	2.07E-19	0.67670396	5.55555556	94.4444444
ENSG00000105708	ZNF14	0.74476974	4.57997338	123.398285	1.14E-28	3.10E-28	0.78385999	8.57142857	91.4285714	ZNF14	0.89755809	4.59756429	145.942002	1.34E-33	5.12E-33	0.91948357	13.8888889	86.1111111
ENSG00000131871	VIMP	-0.7678172	4.1886738	122.828369	1.52E-28	4.12E-28	-0.7305773	97.1428571	2.85714286	VIMP	-0.5086786	4.22400092	45.974925	1.20E-11	2.53E-11	-0.5697468	97.2222222	2.77777778
ENSG00000204282	TNRC6C-AS1	0.81436605	3.79261421	122.687729	1.63E-28	4.42E-28	0.88911442	2.85714286	97.1428571	TNRC6C-AS1	0.72646455	3.64106836	78.3839149	8.48E-19	2.26E-18	0.5928691	2.77777778	97.2222222
ENSG00000160888	IER2	-0.680922	7.84852024	122.670287	1.65E-28	4.46E-28	-0.6115687	85.7142857	14.2857143	IER2	-0.5002469	7.8756922	51.8755838	5.91E-13	1.31E-12	-0.5647715	86.1111111	13.8888889
ENSG00000196642	RABL6	0.69158547	5.65846563	122.3321	1.95E-28	5.28E-28	0.74493541	0	100	RABL6	0.77726246	5.6852963	127.73929	1.28E-29	4.49E-29	0.69560337	5.55555556	94.4444444
ENSG00000092439	TRPM7	0.67737219	6.64504044	122.286678	2.00E-28	5.40E-28	0.71502303	0	100	TRPM7	0.64347686	6.56580462	90.4316667	1.91E-21	5.49E-21	0.56883024	5.55555556	94.4444444
ENSG00000113300	CNOT6	0.72423799	4.70508523	122.273496	2.01E-28	5.43E-28	0.83429046	0	100	CNOT6	0.82064477	4.74573842	131.920907	1.56E-30	5.58E-30	0.76640744	0	100
ENSG00000110851	PRDM4	-0.6778111	6.48857447	121.410849	3.11E-28	8.38E-28	-0.5672979	97.1428571	2.85714286	PRDM4	-0.710793	6.41293568	110.31328	8.37E-26	2.69E-25	-0.6985357	100	0
ENSG00000122224	LY9	-0.6932685	5.86352314	120.956321	3.91E-28	1.05E-27	-0.6133798	85.7142857	14.2857143	LY9	-0.9817042	5.66975194	199.398783	2.83E-45	1.34E-44	-0.9966397	97.2222222	2.77777778
ENSG00000075785	RAB7A	-0.6719847	6.92610958	120.792077	4.24E-28	1.14E-27	-0.6454385	100	0	RAB7A	-0.7581622	6.84467784	125.651589	3.66E-29	1.27E-28	-0.812288	100	0
ENSG00000130703	OSBPL2	0.69368456	5.23199208	120.598951	4.68E-28	1.26E-27	0.75357718	0	100	OSBPL2	0.68017465	5.16945026	96.3281558	9.73E-23	2.89E-22	0.63013917	2.77777778	97.2222222
ENSG00000112893	MAN2A1	0.67395767	6.35282132	120.220501	5.66E-28	1.52E-27	0.74405753	0	100	MAN2A1	0.67845422	6.2929971	100.559459	1.15E-23	3.49E-23	0.59486524	5.55555556	94.4444444
ENSG00000121892	PDS5A	0.67445979	6.33935772	120.125241	5.94E-28	1.59E-27	0.75899699	0	100	PDS5A	0.60792496	6.21858523	81.1381866	2.10E-19	5.70E-19	0.62160275	8.33333333	91.6666667
ENSG00000187514	PTMA	-0.6738378	10.5897394	120.074312	6.09E-28	1.63E-27	-0.5901153	100	0	PTMA	-0.5222025	10.560058	47.3104824	6.06E-12	1.30E-11	-0.5552592	100	0
ENSG00000224078	SNHG14	0.74310785	4.38766554	119.998493	6.33E-28	1.70E-27	0.85950025	2.85714286	97.1428571	SNHG14	0.40822757	4.29023864	27.2742427	1.77E-07	3.48E-07	0.72284319	2.77777778	97.2222222
ENSG00000132549	VPS13B	0.68113314	5.86312479	119.694894	7.38E-28	1.98E-27	0.61829612	0	100	VPS13B	0.59286552	5.73536618	75.3979641	3.85E-18	9.98E-18	0.55475478	5.55555556	94.4444444
ENSG00000205413	SAMD9	-0.7172004	4.73994501	119.682738	7.42E-28	1.99E-27	-0.563122	100	0	SAMD9	-0.5186084	4.79699707	52.4625394	4.39E-13	9.76E-13	-0.5220553	86.1111111	13.8888889
ENSG00000103363	TCEB2	-0.6830024	5.65714169	118.863735	1.12E-27	3.00E-27	-0.6604128	91.4285714	8.57142857	TCEB2	-0.5161563	5.67356325	57.290466	3.76E-14	8.70E-14	-0.6171937	94.4444444	5.55555556
ENSG00000105953	OGDH	-0.8342464	3.50234509	118.758874	1.18E-27	3.15E-27	-0.7203855	100	0	OGDH	-0.4591821	3.53925774	30.7922107	2.87E-08	5.26E-08	-0.506447	88.8888889	11.1111111
ENSG00000127463	EMC1	0.7007889	4.93162205	118.57655	1.30E-27	3.46E-27	0.77687832	0	100	EMC1	0.84797414	4.97574492	145.634932	1.56E-33	5.97E-33	0.72632538	0	100
ENSG00000155115	GTF3C6	-0.7849393	3.87840338	118.261193	1.52E-27	4.05E-27	-0.7311024	100	0	GTF3C6	-0.4940542	3.93463957	40.2875702	2.19E-10	4.41E-10	-0.5476234	97.2222222	2.77777778
ENSG00000213024	NUP62	-0.6852373	5.33257579	118.254569	1.53E-27	4.06E-27	-0.5890684	100	0	NUP62	-0.5995753	5.29151172	75.8713412	3.03E-18	7.88E-18	-0.6313023	97.2222222	2.77777778
ENSG00000164105	SAP30	-1.1427463	1.37985345	118.001141	1.73E-27	4.61E-27	-1.131193	97.1428571	2.85714286	SAP30	-0.625499	1.527337	29.0833334	6.93E-08	1.25E-07	-0.5144808	94.4444444	5.55555556
ENSG00000163349	HIPK1	0.66126101	8.49417125	117.865942	1.86E-27	4.93E-27	0.70796512	0	100	HIPK1	1.02894216	8.63971688	210.078603	1.32E-47	6.56E-47	1.02872219	2.77777778	97.2222222
ENSG00000108854	SMURF2	0.68599083	5.22361417	117.690969	2.03E-27	5.38E-27	0.68363867	0	100	SMURF2	0.75012414	5.22406878	117.683976	2.03E-27	6.78E-27	0.62078356	0	100
ENSG00000089737	DDX24	0.65721742	8.45336667	117.521817	2.21E-27	5.86E-27	0.65653861	0	100	DDX24	0.85129343	8.48763953	147.862588	5.08E-34	1.96E-33	0.80044486	0	100
ENSG00000159110	IFNAR2	-0.7604386	4.08613703	117.391995	2.36E-27	6.25E-27	-0.7051442	100	0	IFNAR2	-1.3551996	3.88943174	288.699404	9.55E-65	6.02E-64	-1.3631652	100	0
ENSG00000182117	NOP10	-0.7294102	4.46397106	116.940433	2.96E-27	7.84E-27	-0.6831712	88.5714286	11.4285714	NOP10	-0.7308837	4.42678143	97.0825273	6.65E-23	1.98E-22	-0.8482205	97.2222222	2.77777778
ENSG00000204946	ZNF783	0.72552896	4.45690719	116.672312	3.39E-27	8.97E-27	0.80265616	2.85714286	97.1428571	ZNF783	0.68278485	4.35699268	84.7513209	3.38E-20	9.36E-20	0.58498016	2.77777778	97.2222222

ENSG00000105607	GCDH	0.94728304	2.60743583	116.477481	3.74E-27	9.89E-27	1.04563707	0	100	GCDH	0.82196958	2.44925923	68.4710772	1.29E-16	3.20E-16	0.65728244	2.77777778	97.2222222
ENSG00000239672	NME1	-1.0174349	2.11677957	116.396568	3.89E-27	1.03E-26	-0.9550745	100	0	NME1	-0.8551755	2.06380454	65.9860802	4.54E-16	1.11E-15	-0.9472766	100	0
ENSG00000174231	PRPF8	0.65494234	8.72877907	116.274194	4.14E-27	1.09E-26	0.65792592	0	100	PRPF8	0.8771047	8.77720182	152.391436	5.20E-35	2.06E-34	0.77255674	2.77777778	97.2222222
ENSG00000141627	DYM	-0.7228324	4.4653643	116.099662	4.52E-27	1.19E-26	-0.6230177	100	0	DYM	-0.7372005	4.38333968	99.4593964	2.00E-23	6.04E-23	-0.7118239	100	0
ENSG00000117523	PRRC2C	0.65561911	9.3594184	115.758633	5.37E-27	1.42E-26	0.63349342	0	100	PRRC2C	0.81882177	9.36850537	126.511843	2.38E-29	8.28E-29	0.81380144	2.77777778	97.2222222
ENSG00000113649	TCERG1	0.65778794	6.82211318	115.57292	5.90E-27	1.55E-26	0.68462332	0	100	TCERG1	0.63308833	6.72984476	87.980707	6.61E-21	1.87E-20	0.52789472	2.77777778	97.2222222
ENSG00000236104	ZBTB22	-0.803699	3.67038838	115.53015	6.02E-27	1.59E-26	-0.6820631	94.2857143	5.71428571	ZBTB22	-0.9203904	3.59789384	125.019657	5.04E-29	1.74E-28	-1.0764988	100	0
ENSG00000026508	CD44	-0.6541368	9.35932877	115.422271	6.36E-27	1.68E-26	-0.5898623	100	0	CD44	-0.5425413	9.34331229	56.661677	5.18E-14	1.19E-13	-0.5542006	100	0
ENSG00000246451	RP11-894P9.1	1.0784023	1.79828996	115.314405	6.72E-27	1.77E-26	1.17162588	5.71428571	94.2857143	RP11-894P9.1	1.21796719	1.82232682	117.219364	2.57E-27	8.54E-27	1.15658562	2.77777778	97.2222222
ENSG00000168228	ZCCHC4	0.89473169	2.90236281	115.124021	7.39E-27	1.95E-26	1.01970286	0	100	ZCCHC4	0.81551294	2.8138964	77.5851596	1.27E-18	3.36E-18	0.74103798	2.77777778	97.2222222
ENSG00000068323	TFE3	-0.6615995	6.05448579	114.820281	8.62E-27	2.26E-26	-0.5526744	100	0	TFE3	-0.6942871	5.99768261	105.221297	1.09E-24	3.40E-24	-0.7564063	100	0
ENSG00000151806	GUF1	0.72787508	4.33881925	114.705574	9.13E-27	2.40E-26	0.84729515	0	100	GUF1	0.6178043	4.21975517	67.374558	2.25E-16	5.55E-16	0.59895553	5.55555556	94.4444444
ENSG00000126005	MMP24-AS1	-0.7173338	4.47939383	114.668516	9.30E-27	2.44E-26	-0.6680912	100	0	MMP24-AS1	-0.5522329	4.52048591	57.1969175	3.94E-14	9.12E-14	-0.6755692	91.6666667	8.33333333
ENSG00000099940	SNAP29	-0.6769867	5.22367369	114.652033	9.38E-27	2.46E-26	-0.5680165	100	0	SNAP29	-0.4740079	5.26216465	47.4399962	5.67E-12	1.21E-11	-0.5217291	100	0
ENSG00000158769	F11R	-0.7551953	4.0232713	114.430809	1.05E-26	2.75E-26	-0.6874034	100	0	F11R	-0.6241502	4.02958347	65.9844915	4.54E-16	1.11E-15	-0.6522442	100	0
ENSG00000074695	LMAN1	0.68185448	5.07184077	114.240115	1.15E-26	3.02E-26	0.68879208	0	100	LMAN1	0.79278576	5.10509762	128.728503	7.78E-30	2.74E-29	0.75747328	2.77777778	97.2222222
ENSG00000175602	CCDC85B	-0.7198475	4.49972384	114.174634	1.19E-26	3.12E-26	-0.6522824	85.7142857	14.2857143	CCDC85B	-0.5121924	4.49771345	48.5847607	3.16E-12	6.82E-12	-0.5595095	88.8888889	11.1111111
ENSG00000100888	CHD8	0.64872496	7.63271175	114.106274	1.24E-26	3.23E-26	0.71496389	0	100	CHD8	0.74699002	7.6316707	119.184928	9.54E-28	3.21E-27	0.63322284	2.77777778	97.2222222
ENSG00000099910	KLHL22	0.82949398	3.36750277	114.091115	1.24E-26	3.26E-26	0.91413268	0	100	KLHL22	0.7926697	3.3270722	86.5141195	1.39E-20	3.89E-20	0.78480344	2.77777778	97.2222222
ENSG00000128534	LSM8	0.67486526	5.21060494	113.898136	1.37E-26	3.58E-26	0.70945732	0	100	LSM8	0.74617161	5.20370381	116.056834	4.62E-27	1.53E-26	0.69317714	0	100
ENSG00000176108	CHMP6	-0.9934439	2.2139851	113.866557	1.39E-26	3.64E-26	-0.8934878	100	0	CHMP6	-0.9085634	2.21944265	76.4565765	2.25E-18	5.89E-18	-0.9023378	100	0
ENSG00000225892	RP11-384K6.2	0.85162289	3.23975487	113.846277	1.41E-26	3.67E-26	0.94892688	2.85714286	97.1428571	RP11-384K6.2	1.18452916	3.46643553	195.596151	1.91E-44	8.89E-44	1.10855077	0	100
ENSG00000132467	UTP3	-0.7179163	4.43408226	113.796119	1.44E-26	3.77E-26	-0.5942978	100	0	UTP3	-0.5134228	4.44637216	49.2107977	2.30E-12	4.97E-12	-0.5243114	97.2222222	2.77777778
ENSG00000101558	VAPA	-0.6485123	7.17241319	113.682828	1.53E-26	3.99E-26	-0.5404285	100	0	VAPA	-0.6587851	7.08764071	94.7401182	2.17E-22	6.38E-22	-0.6891347	100	0
ENSG00000148843	PDCD11	0.68872757	4.82836874	113.143243	2.01E-26	5.23E-26	0.71645531	0	100	PDCD11	0.76950575	4.83327286	117.975579	1.76E-27	5.87E-27	0.68591276	2.77777778	97.2222222
ENSG00000110852	CLEC2B	-0.6554599	5.95780223	111.786063	3.98E-26	1.03E-25	-0.5943453	91.4285714	8.57142857	CLEC2B	-0.7218695	5.87280203	112.46515	2.83E-26	9.16E-26	-0.7426598	100	0
ENSG00000106617	PRKAG2	-0.6837785	4.89294176	111.769239	4.01E-26	1.04E-25	-0.6197478	94.2857143	5.71428571	PRKAG2	-0.9373603	4.73408833	170.099062	7.04E-39	3.00E-38	-0.953555	100	0
ENSG00000114127	XRN1	0.64642283	6.8351077	111.579927	4.42E-26	1.14E-25	0.67499553	0	100	XRN1	0.67346264	6.81849228	98.5311429	3.20E-23	9.60E-23	0.58767099	5.55555556	94.4444444
ENSG00000156170	NDUFAF6	0.80594676	3.48398362	111.280405	5.14E-26	1.33E-25	0.85867141	0	100	NDUFAF6	0.6458723	3.29149728	57.1707303	4.00E-14	9.23E-14	0.63206628	0	100
ENSG00000105254	TBCB	-0.7066696	4.48549902	111.261976	5.18E-26	1.34E-25	-0.6168132	100	0	TBCB	-0.4562138	4.50330569	38.9471358	4.35E-10	8.65E-10	-0.5357498	91.6666667	8.33333333
ENSG00000104671	DCTN6	0.7050292	4.54502612	111.251686	5.21E-26	1.35E-25	0.68241342	0	100	DCTN6	0.80219858	4.54868628	120.384172	5.21E-28	1.76E-27	0.77584483	5.55555556	94.4444444
ENSG00000188647	PTAR1	0.64900424	6.36579368	110.896034	6.24E-26	1.61E-25	0.66051981	0	100	PTAR1	0.54299913	6.24716844	64.1194607	1.17E-15	2.83E-15	0.55950539	16.6666667	83.3333333
ENSG00000101189	MRGBP	-0.8188654	3.36656465	110.888442	6.26E-26	1.62E-25	-0.7227901	100	0	MRGBP	-0.7751558	3.32502125	82.4617726	1.08E-19	2.94E-19	-0.838822	100	0
ENSG00000100865	CINP	-0.886013	2.8427236	110.78856	6.58E-26	1.70E-25	-0.8238653	100	0	CINP	-0.5269296	2.94270761	34.0713473	5.31E-09	1.01E-08	-0.5309153	100	0
ENSG00000126945	HNRNPH2	-0.6496032	6.24715209	110.71946	6.82E-26	1.76E-25	-0.5714828	97.1428571	2.85714286	HNRNPH2	-0.8010623	6.13520843	139.869003	2.84E-32	1.06E-31	-0.8270417	100	0
ENSG00000175931	UBE2O	0.66589159	5.22402701	110.593154	7.27E-26	1.87E-25	0.66955082	0	100	UBE2O	0.63976601	5.14643227	84.4606007	3.92E-20	1.08E-19	0.53208207	2.77777778	97.2222222
ENSG00000157045	NTAN1	-0.7227987	4.26014163	110.28934	8.47E-26	2.18E-25	-0.6749458	94.2857143	5.71428571	NTAN1	-0.7747134	4.13855067	103.254922	2.95E-24	9.06E-24	-0.902413	97.2222222	2.77777778
ENSG00000184990	SIVA1	0.64709239	6.07877313	110.242116	8.67E-26	2.24E-25	0.72198279	0	100	SIVA1	0.75368447	6.08852025	124.706166	5.90E-29	2.03E-28	0.66071721	0	100
ENSG00000251474	RPL32P3	0.86481715	3.0052921	110.115739	9.24E-26	2.38E-25	0.96445315	2.85714286	97.1428571	RPL32P3	0.80420552	2.89827425	76.9754719	1.73E-18	4.55E-18	0.69267878	0	100
ENSG00000108312	UBTF	0.63456739	7.56896449	109.634624	1.18E-25	3.03E-25	0.69217894	0	100	UBTF	0.73671282	7.57541467	116.952878	2.94E-27	9.75E-27	0.67541504	0	100
ENSG00000187954	CYHR1	0.67890139	4.82581236	109.533567	1.24E-25	3.19E-25	0.72396466	0	100	CYHR1	0.73786928	4.81881001	107.945601	2.76E-25	8.76E-25	0.64574508	0	100
ENSG00000106290	TAF6	0.797854	3.50972749	109.336315	1.37E-25	3.52E-25	0.92206408	2.85714286	97.1428571	TAF6	0.82439055	3.47623311	97.0821169	6.65E-23	1.98E-22	0.79081861	2.77777778	97.2222222
ENSG00000272153	RP1-286D6.5	1.3059425	0.25225899	109.103715	1.54E-25	3.95E-25	1.50634729	0	100	RP1-286D6.5	1.54236675	0.29781057	115.333889	6.65E-27	2.19E-26	1.4567082	0	100
ENSG00000164815	ORC5	0.85825627	3.00157193	108.846634	1.75E-25	4.49E-25	0.89547338	0	100	ORC5	0.75381857	2.88916983	67.2349646	2.41E-16	5.96E-16	0.64621778	5.55555556	94.4444444
ENSG00000168172	HOOK3	-0.6512502	5.49590078	108.567448	2.02E-25	5.16E-25	-0.6465868	100	0	HOOK3	-0.6683567	5.42527227	95.2081384	1.71E-22	5.05E-22	-0.6846382	97.2222222	2.77777778
ENSG00000173511	VEGFB	-0.7698274	3.69985768	108.556453	2.03E-25	5.19E-25	-0.6840635	100	0	VEGFB	-0.7487912	3.6346148	83.8069319	5.46E-20	1.50E-19	-0.8069552	97.2222222	2.77777778
ENSG00000131653	TRAF7	-0.6839172	4.67037215	108.552478	2.03E-25	5.19E-25	-0.6325913	100	0	TRAF7	-0.4839095	4.70676465	45.656608	1.41E-11	2.97E-11	-0.53922	88.8888889	11.1111111
ENSG00000068366	ACSL4	-0.6572967	5.32571471	108.458282	2.13E-25	5.44E-25	-0.6202548	97.1428571	2.85714286	ACSL4	-0.6939412	5.30883922	101.110858	8.70E-24	2.66E-23	-0.7129626	100	0
ENSG00000174373	RALGAPA1	0.65200394	5.46542077	108.354771	2.25E-25	5.73E-25	0.72103294	0	100	RALGAPA1	0.67980477	5.40786992	97.9097016	4.38E-23	1.31E-22	0.71891079	5.55555556	94.4444444
ENSG00000017260	ATP2C1	0.65894229	5.17561879	108.31365	2.29E-25	5.85E-25	0.64131721	0	100	ATP2C1	0.64747211	5.10187328	86.5372318	1.37E-20	3.85E-20	0.68081958	5.55555556	94.4444444
ENSG00000181026	AEN	-0.6708557	4.95409935	107.86362	2.88E-25	7.33E-25	-0.5602927	94.2857143	5.71428571	AEN	-0.6789665	4.8590187	92.0279942	8.55E-22	2.47E-21	-0.7613857	100	0
ENSG00000115524	SF3B1	0.63243297	9.33304591	107.577276	3.33E-25	8.45E-25	0.66452245	0	100	SF3B1	0.62829516	9.24589582	75.7996399	3.14E-18	8.16E-18	0.62438299	8.33333333	91.6666667
ENSG00000101639	CEP192	0.66913183	4.89354859	107.536407	3.40E-25	8.63E-25	0.71479599	0	100	CEP192	0.66547794	4.85468232	88.2926737	5.65E-21	1.60E-20	0.61644089	8.33333333	91.6666667

ENSG00000072121	ZFYVE26	0.68723052	4.57388957	107.523547	3.42E-25	8.68E-25	0.71048819	0	100	ZFYVE26	0.76244155	4.62056415	111.523455	4.54E-26	1.47E-25	0.65785475	0	100
ENSG00000147180	ZNF711	0.69638344	4.46862342	107.438185	3.57E-25	9.06E-25	0.68907536	0	100	ZNF711	0.7436541	4.34479991	98.9660557	2.57E-23	7.73E-23	0.69009726	5.55555556	94.4444444
ENSG00000135597	REPS1	0.64828195	5.4342847	107.404304	3.63E-25	9.21E-25	0.70917647	0	100	REPS1	0.73230385	5.42372018	114.476296	1.02E-26	3.36E-26	0.69463017	0	100
ENSG00000047346	FAM214A	0.63317501	6.67994395	107.077626	4.28E-25	1.09E-24	0.66296202	0	100	FAM214A	0.55129818	6.60416309	66.4607204	3.57E-16	8.76E-16	0.53222191	5.55555556	94.4444444
ENSG00000239900	ADSL	0.65801454	5.11951039	107.052139	4.34E-25	1.10E-24	0.67462821	0	100	ADSL	0.75096367	5.14296173	116.253509	4.18E-27	1.38E-26	0.66232346	0	100
ENSG00000070010	UFD1L	0.63647731	6.2044322	106.891257	4.70E-25	1.19E-24	0.67631627	0	100	UFD1L	0.69316468	6.18688877	104.996201	1.22E-24	3.80E-24	0.69942356	2.77777778	97.2222222
ENSG00000121741	ZMYM2	0.63102741	6.67874746	106.655412	5.30E-25	1.34E-24	0.65887197	0	100	ZMYM2	0.70164685	6.67354602	108.340803	2.26E-25	7.20E-25	0.66111066	2.77777778	97.2222222
ENSG00000119669	IRF2BPL	-0.6399407	6.24171349	106.237488	6.54E-25	1.65E-24	-0.5164037	91.4285714	8.57142857	IRF2BPL	-0.7950618	6.09230376	135.475694	2.60E-31	9.46E-31	-0.7913471	100	0
ENSG00000170035	UBE2E3	-0.7020465	4.34236937	106.232172	6.56E-25	1.66E-24	-0.6046484	97.1428571	2.85714286	UBE2E3	-0.5304538	4.34899868	51.4586784	7.31E-13	1.62E-12	-0.5987611	100	0
ENSG00000087152	ATXN7L3	-0.6287315	6.98862573	105.898204	7.76E-25	1.96E-24	-0.58609	97.1428571	2.85714286	ATXN7L3	-0.5025851	6.97527575	55.5994373	8.88E-14	2.03E-13	-0.6125719	100	0
ENSG00000197006	METTL9	-0.6309672	6.64024662	105.886984	7.81E-25	1.97E-24	-0.5975342	100	0	METTL9	-0.5914033	6.61025205	76.8257584	1.87E-18	4.90E-18	-0.6187254	100	0
ENSG00000146859	TMEM140	-0.7861598	3.48580531	105.461476	9.68E-25	2.43E-24	-0.6882834	100	0	TMEM140	-0.8458799	3.41735467	100.330749	1.29E-23	3.91E-23	-0.8793619	100	0
ENSG00000011638	TMEM159	-0.8774521	2.73898734	104.787366	1.36E-24	3.41E-24	-0.74167	100	0	TMEM159	-1.2033892	2.5758355	152.344166	5.33E-35	2.10E-34	-1.2484493	100	0
ENSG00000116560	SFPQ	0.6246449	9.41605437	104.748515	1.39E-24	3.48E-24	0.69312608	0	100	SFPQ	0.74138446	9.39538067	104.379343	1.67E-24	5.18E-24	0.72403321	2.77777778	97.2222222
ENSG00000121644	DESI2	-0.6543177	4.99360588	104.552183	1.53E-24	3.83E-24	-0.5709806	100	0	DESI2	-0.5517068	4.98090162	62.2010935	3.10E-15	7.41E-15	-0.6181714	97.2222222	2.77777778
ENSG00000144231	POLR2D	-0.6639076	4.7822488	104.379102	1.67E-24	4.18E-24	-0.5861134	97.1428571	2.85714286	POLR2D	-0.5430836	4.75381995	58.3791153	2.16E-14	5.03E-14	-0.5652493	97.2222222	2.77777778
ENSG00000112651	MRPL2	0.7668009	3.57613064	103.918232	2.11E-24	5.26E-24	0.84142871	0	100	MRPL2	0.76304479	3.52383282	85.1986992	2.70E-20	7.49E-20	0.64098416	0	100
ENSG00000139921	TMX1	-0.6910454	4.338598	103.535801	2.56E-24	6.37E-24	-0.634386	100	0	TMX1	-0.6077065	4.31054329	66.9371137	2.80E-16	6.91E-16	-0.6233794	97.2222222	2.77777778
ENSG00000181817	LSM10	-0.7771141	3.47791561	103.20408	3.02E-24	7.52E-24	-0.7254	100	0	LSM10	-0.5315964	3.54445417	41.3807082	1.25E-10	2.54E-10	-0.6393878	91.6666667	8.33333333
ENSG00000117450	PRDX1	-0.6882823	4.3839787	103.13456	3.13E-24	7.78E-24	-0.5907508	100	0	PRDX1	-0.577149	4.35964849	60.616275	6.94E-15	1.64E-14	-0.5398315	97.2222222	2.77777778
ENSG00000156171	DRAM2	-0.6491551	5.09172941	103.132083	3.14E-24	7.79E-24	-0.6389841	91.4285714	8.57142857	DRAM2	-0.9578564	4.92859856	181.550223	2.22E-41	9.95E-41	-0.9906894	100	0
ENSG00000179262	RAD23A	0.62361132	6.00337153	102.186427	5.05E-24	1.25E-23	0.67054907	0	100	RAD23A	0.58382164	5.93081017	74.4935205	6.08E-18	1.57E-17	0.50349274	5.55555556	94.4444444
ENSG00000149636	DSN1	0.81526738	3.12133231	102.152704	5.14E-24	1.27E-23	0.90420193	0	100	DSN1	0.85952748	3.07531887	93.4325389	4.20E-22	1.22E-21	0.79992143	0	100
ENSG00000107938	EDRF1	0.63323548	5.42173434	102.112608	5.25E-24	1.30E-23	0.64975225	0	100	EDRF1	0.62475572	5.33377706	82.3576802	1.14E-19	3.09E-19	0.54657303	5.55555556	94.4444444
ENSG00000012061	ERCC1	-0.7732926	3.49615603	102.080227	5.33E-24	1.32E-23	-0.7450262	100	0	ERCC1	-0.6750069	3.46321951	64.6132405	9.11E-16	2.21E-15	-0.8056402	94.4444444	5.55555556
ENSG00000159873	CCDC117	-0.6427917	5.08489936	102.040704	5.44E-24	1.35E-23	-0.5567118	97.1428571	2.85714286	CCDC117	-0.4710673	5.08213544	45.8112364	1.30E-11	2.74E-11	-0.5287656	97.2222222	2.77777778
ENSG00000131779	PEX11B	0.82195941	3.06689732	101.710798	6.42E-24	1.59E-23	0.90819964	0	100	PEX11B	0.54745892	2.84430259	35.2390557	2.92E-09	5.59E-09	0.51535755	19.4444444	80.5555556
ENSG00000111481	COPZ1	-0.6451431	5.01751799	101.578816	6.87E-24	1.70E-23	-0.5197116	100	0	COPZ1	-0.6249553	4.9810749	79.5533565	4.69E-19	1.26E-18	-0.6921319	100	0
ENSG00000250251	PKD1P6	0.69489524	4.20973369	101.362054	7.66E-24	1.89E-23	0.71605838	0	100	PKD1P6	0.63113833	4.1029214	67.616424	1.99E-16	4.92E-16	0.68449532	8.33333333	91.6666667
ENSG00000111860	CEP85L	0.62182081	5.97033761	101.0106	9.15E-24	2.25E-23	0.64282038	0	100	CEP85L	0.57779317	5.85949368	72.2427715	1.90E-17	4.84E-17	0.5017139	5.55555556	94.4444444
ENSG00000004399	PLXND1	-0.645265	5.17955412	100.92606	9.55E-24	2.35E-23	-0.5177073	91.4285714	8.57142857	PLXND1	-0.7760118	5.18882946	115.68249	5.58E-27	1.84E-26	-0.8624324	77.7777778	22.2222222
ENSG00000106268	NUDT1	-0.9098009	2.36235906	100.789554	1.02E-23	2.52E-23	-0.7593509	100	0	NUDT1	-0.6472465	2.41189897	42.4438264	7.27E-11	1.49E-10	-0.7555663	94.4444444	5.55555556
ENSG00000100324	TAB1	0.73744888	3.73398662	100.35623	1.27E-23	3.13E-23	0.82156825	0	100	TAB1	0.7529812	3.69511396	86.84539	1.17E-20	3.30E-20	0.66246963	2.77777778	97.2222222
ENSG00000225973	PIGBOS1	-1.0173646	1.57716651	100.270674	1.33E-23	3.27E-23	-0.884798	100	0	PIGBOS1	-0.794026	1.61397171	48.9403488	2.64E-12	5.70E-12	-0.8311908	97.2222222	2.77777778
ENSG00000008405	CRY1	0.62280688	5.73232749	100.239228	1.35E-23	3.32E-23	0.65896208	0	100	CRY1	0.92656338	5.83008218	184.281818	5.63E-42	2.54E-41	0.84670774	0	100
ENSG00000136108	CKAP2	0.63281808	5.2457255	100.122699	1.43E-23	3.52E-23	0.73752085	2.85714286	97.1428571	CKAP2	0.717319	5.21911121	106.414533	5.98E-25	1.88E-24	0.69414739	5.55555556	94.4444444
ENSG00000111727	HCFC2	0.68805477	4.210046	99.4464467	2.02E-23	4.94E-23	0.78150489	2.85714286	97.1428571	HCFC2	0.70543104	4.119757	85.7066489	2.09E-20	5.82E-20	0.64305458	2.77777778	97.2222222
ENSG00000198898	CAPZA2	-0.6136631	6.33822849	99.410229	2.05E-23	5.03E-23	-0.6047125	94.2857143	5.71428571	CAPZA2	-0.5883952	6.28085815	75.2664949	4.11E-18	1.07E-17	-0.6096928	97.2222222	2.77777778
ENSG00000142252	GEMIN7	-0.9317946	2.13475765	99.1394184	2.35E-23	5.76E-23	-0.9595128	94.2857143	5.71428571	GEMIN7	-0.6992225	2.15171133	45.625005	1.43E-11	3.01E-11	-0.7650789	94.4444444	5.55555556
ENSG00000106153	CHCHD2	-0.6069498	7.18227975	99.1244835	2.37E-23	5.80E-23	-0.5443005	97.1428571	2.85714286	CHCHD2	-0.4750606	7.17279324	49.3367058	2.16E-12	4.67E-12	-0.5392661	94.4444444	5.55555556
ENSG00000116106	EPHA4	0.63095323	5.22114211	99.0138417	2.51E-23	6.13E-23	0.66469014	0	100	EPHA4	0.89358608	5.4196009	163.993281	1.52E-37	6.28E-37	0.81358439	11.1111111	88.8888889
ENSG00000116459	ATP5F1	-0.6150989	5.99252233	98.9401027	2.60E-23	6.36E-23	-0.5142816	100	0	ATP5F1	-0.4994639	5.99851284	54.5456454	1.52E-13	3.44E-13	-0.5951274	97.2222222	2.77777778
ENSG00000214367	HAUS3	0.60706204	6.66983336	98.4585369	3.32E-23	8.08E-23	0.67602968	0	100	HAUS3	0.63304537	6.60193798	88.2014697	5.91E-21	1.68E-20	0.54466979	5.55555556	94.4444444
ENSG00000186866	POFUT2	0.65010681	4.69389982	98.3331841	3.54E-23	8.60E-23	0.66708266	0	100	POFUT2	0.92575226	4.8120412	169.041764	1.20E-38	5.07E-38	0.88270875	0	100
ENSG00000135002	RFK	-0.7107228	3.93351905	98.3156967	3.57E-23	8.67E-23	-0.6363526	97.1428571	2.85714286	RFK	-0.5367279	3.94294135	47.4199321	5.73E-12	1.23E-11	-0.5206056	94.4444444	5.55555556
ENSG00000078808	SDF4	-0.6205844	5.55516376	98.2137241	3.76E-23	9.13E-23	-0.6325995	94.2857143	5.71428571	SDF4	-0.4976861	5.57619398	52.705068	3.88E-13	8.65E-13	-0.6195318	86.1111111	13.8888889
ENSG00000128829	EIF2AK4	-0.6400451	4.88134534	97.998223	4.19E-23	1.02E-22	-0.6394716	94.2857143	5.71428571	EIF2AK4	-0.8803586	4.76452786	151.306283	8.98E-35	3.53E-34	-0.9433341	97.2222222	2.77777778
ENSG00000117528	ABCD3	0.69264383	4.08972365	97.9559698	4.28E-23	1.04E-22	0.70102404	0	100	ABCD3	0.7232346	4.07365949	89.0027401	3.94E-21	1.12E-20	0.6594913	2.77777778	97.2222222
ENSG00000111530	CAND1	0.6045986	6.841015	97.9546247	4.28E-23	1.04E-22	0.65183027	0	100	CAND1	0.621773	6.7557852	84.6273921	3.60E-20	9.95E-20	0.5753434	5.55555556	94.4444444
ENSG00000184924	PTRHD1	-0.7797387	3.28992758	97.9447832	4.30E-23	1.04E-22	-0.7211778	97.1428571	2.85714286	PTRHD1	-0.4178291	3.38529754	24.3087851	8.21E-07	1.40E-06	-0.5044262	86.1111111	13.8888889
ENSG00000182810	DDX28	-0.7168298	3.86425331	97.8753319	4.46E-23	1.08E-22	-0.6343187	94.2857143	5.71428571	DDX28	-0.6704894	3.81757543	71.0508479	3.48E-17	8.80E-17	-0.7301963	94.4444444	5.55555556
ENSG00000155957	TMBIM4	-0.8133292	3.00680627	97.7920393	4.65E-23	1.13E-22	-0.6997744	100	0	TMBIM4	-1.110596	2.87106642	143.894018	3.75E-33	1.42E-32	-1.1946858	100	0
ENSG00000160410	SHKBP1	-0.6180519	5.61551949	97.2510565	6.11E-23	1.48E-22	-0.6341787	85.7142857	14.2857143	SHKBP1	-0.6056707	5.61121297	76.6421036	2.05E-18	5.37E-18	-0.8556567	80.5555556	19.4444444

ENSG00000132475	H3F3B	-0.6067704	10.3737186	97.1717934	6.36E-23	1.54E-22	-0.5442664	91.4285714	8.57142857	H3F3B	-0.5119495	10.3407806	45.8123657	1.30E-11	2.74E-11	-0.5857724	91.6666667	8.33333333
ENSG00000055483	USP36	0.60102716	7.74978028	96.9604797	7.07E-23	1.71E-22	0.56825678	2.85714286	97.1428571	USP36	0.88216278	7.81812635	163.734848	1.73E-37	7.15E-37	0.75581062	0	100
ENSG00000234518	PTGES3P1	1.05148422	1.27163906	96.7478185	7.87E-23	1.90E-22	1.23866379	2.85714286	97.1428571	PTGES3P1	0.57878959	0.97287945	21.0026914	4.59E-06	7.47E-06	0.65475642	19.4444444	80.5555556
ENSG00000198406	BZW1P2	-1.0231587	1.45759031	96.6972651	8.08E-23	1.95E-22	-1.0790133	97.1428571	2.85714286	BZW1P2	-0.5799397	1.54573066	25.2761537	4.97E-07	8.57E-07	-0.6328252	88.8888889	11.1111111
ENSG00000171148	TADA3	-0.6908439	4.08642839	96.4842195	9.00E-23	2.17E-22	-0.5482035	94.2857143	5.71428571	TADA3	-0.5919765	4.07746268	59.3017084	1.35E-14	3.17E-14	-0.6017032	94.4444444	5.55555556
ENSG00000136997	MYC	-0.6097442	6.35687848	96.4613995	9.10E-23	2.19E-22	-0.5346372	88.5714286	11.4285714	MYC	-0.5992807	6.26933138	75.7723202	3.18E-18	8.27E-18	-0.7925754	80.5555556	19.4444444
ENSG00000129355	CDKN2D	-0.6091456	6.04708219	96.426938	9.26E-23	2.23E-22	-0.5418183	91.4285714	8.57142857	CDKN2D	-0.7920375	5.93247849	134.769764	3.71E-31	1.34E-30	-0.7871722	100	0
ENSG00000114125	RNF7	-0.6101817	5.65005022	96.2532502	1.01E-22	2.43E-22	-0.5203751	100	0	RNF7	-0.5116976	5.63588131	56.6408283	5.23E-14	1.20E-13	-0.5432859	97.2222222	2.77777778
ENSG00000124177	CHD6	0.59667763	7.18748741	96.2328935	1.02E-22	2.46E-22	0.63549571	0	100	CHD6	0.65189694	7.18556918	92.2501535	7.64E-22	2.21E-21	0.5738491	2.77777778	97.2222222
ENSG00000004961	HCCS	-0.7945176	3.07317339	95.9846907	1.16E-22	2.79E-22	-0.6700957	100	0	HCCS	-0.9438609	2.96466802	108.845095	1.75E-25	5.60E-25	-0.9456617	100	0
ENSG00000127084	FGD3	0.5996013	6.46334908	95.7782868	1.28E-22	3.09E-22	0.66699336	0	100	FGD3	0.60219225	6.39734238	79.9802113	3.78E-19	1.02E-18	0.5865038	2.77777778	97.2222222
ENSG00000006530	AGK	0.72125071	3.72861134	95.6439318	1.38E-22	3.30E-22	0.83280723	0	100	AGK	0.62681661	3.63399224	59.3985939	1.29E-14	3.03E-14	0.5451659	8.33333333	91.6666667
ENSG00000168374	ARF4	-0.6080512	5.74732619	95.6110561	1.40E-22	3.36E-22	-0.5610036	97.1428571	2.85714286	ARF4	-0.6392976	5.70540621	88.0444674	6.40E-21	1.81E-20	-0.6697315	100	0
ENSG00000151327	FAM177A1	0.60920209	5.73720192	95.6023472	1.40E-22	3.37E-22	0.64413799	0	100	FAM177A1	1.11174635	5.98586079	265.913295	8.82E-60	5.18E-59	1.02303791	0	100
ENSG00000115421	PAPOLG	0.6225538	5.07778959	95.5602587	1.43E-22	3.44E-22	0.66306433	0	100	PAPOLG	0.64336505	5.04038151	84.3078183	4.23E-20	1.17E-19	0.59615137	8.33333333	91.6666667
ENSG00000085788	DDHD2	0.60936303	5.50315124	95.3805496	1.57E-22	3.77E-22	0.67237208	0	100	DDHD2	0.61019162	5.42059695	79.5427034	4.72E-19	1.27E-18	0.5859241	8.33333333	91.6666667
ENSG00000134644	PUM1	0.59441231	6.95944442	95.1735725	1.74E-22	4.18E-22	0.61916559	0	100	PUM1	0.62322312	6.90326983	85.1910209	2.71E-20	7.52E-20	0.55670921	2.77777778	97.2222222
ENSG00000137364	TPMT	-0.7662255	3.29656522	94.5888713	2.34E-22	5.61E-22	-0.6847788	100	0	TPMT	-0.4850867	3.37038733	32.9717006	9.35E-09	1.75E-08	-0.5281579	97.2222222	2.77777778
ENSG00000165669	FAM204A	-0.6200102	5.02392343	94.4639175	2.50E-22	5.97E-22	-0.5776155	100	0	FAM204A	-0.5379434	5.0039492	59.4582924	1.25E-14	2.94E-14	-0.5135717	100	0
ENSG00000126214	KLC1	0.65436944	4.42392529	94.1790642	2.88E-22	6.88E-22	0.71291506	2.85714286	97.1428571	KLC1	0.67110983	4.37262018	82.1537434	1.26E-19	3.42E-19	0.67431191	2.77777778	97.2222222
ENSG00000124574	ABCC10	0.69882295	3.866491	93.6437422	3.78E-22	9.00E-22	0.74328583	0	100	ABCC10	0.93971598	3.96090217	144.318673	3.03E-33	1.15E-32	0.93441913	2.77777778	97.2222222
ENSG00000138495	COX17	-0.7430091	3.42659889	93.2391534	4.63E-22	1.10E-21	-0.7266419	100	0	COX17	-0.4822041	3.48582264	33.8277964	6.02E-09	1.14E-08	-0.5193182	97.2222222	2.77777778
ENSG00000181789	COPG1	0.59693542	5.76839253	92.8079509	5.76E-22	1.37E-21	0.65394219	0	100	COPG1	0.67769848	5.77206953	99.9482152	1.56E-23	4.74E-23	0.62596931	0	100
ENSG00000088179	PTPN4	0.6114272	5.14173128	92.745244	5.95E-22	1.41E-21	0.63941702	0	100	PTPN4	0.77994124	5.18025828	126.014694	3.05E-29	1.06E-28	0.78297322	2.77777778	97.2222222
ENSG00000158716	DUSP23	-1.0890084	0.90029934	92.5853768	6.45E-22	1.53E-21	-1.0991792	97.1428571	2.85714286	DUSP23	-1.0721571	0.89647227	68.5645077	1.23E-16	3.06E-16	-1.0837712	100	0
ENSG00000163428	LRRC58	0.59922939	5.75191701	92.5373061	6.61E-22	1.57E-21	0.65764986	2.85714286	97.1428571	LRRC58	0.58785168	5.63742428	72.9115375	1.36E-17	3.46E-17	0.62011153	13.8888889	86.1111111
ENSG00000204138	PHACTR4	0.63115867	4.6721795	92.3603793	7.22E-22	1.71E-21	0.68721975	2.85714286	97.1428571	PHACTR4	0.85614135	4.78946756	144.096027	3.39E-33	1.29E-32	0.83193365	0	100
ENSG00000049245	VAMP3	-0.5966942	5.77949151	92.2493941	7.64E-22	1.81E-21	-0.5846164	97.1428571	2.85714286	VAMP3	-0.6187354	5.71966358	82.8082225	9.04E-20	2.47E-19	-0.6455712	97.2222222	2.77777778
ENSG00000100523	DDHD1	0.62275859	4.83986354	92.187245	7.89E-22	1.87E-21	0.67523595	0	100	DDHD1	0.66168309	4.80049038	86.359152	1.50E-20	4.20E-20	0.56269795	2.77777778	97.2222222
ENSG00000149480	MTA2	0.5860383	6.66107699	91.8961312	9.13E-22	2.16E-21	0.6147646	0	100	MTA2	0.58391976	6.61868837	75.3039927	4.04E-18	1.05E-17	0.53123215	0	100
ENSG00000130349	C6orf203	0.81644485	2.71610844	91.2636258	1.26E-21	2.97E-21	0.86647923	0	100	C6orf203	0.63771748	2.54320448	43.554345	4.12E-11	8.51E-11	0.60013219	0	100
ENSG00000099385	BCL7C	-0.658167	4.2267444	91.1591544	1.33E-21	3.13E-21	-0.5648274	97.1428571	2.85714286	BCL7C	-0.6618348	4.17146244	76.2131225	2.55E-18	6.64E-18	-0.7259067	97.2222222	2.77777778
ENSG00000133997	MED6	0.61156546	4.9807577	91.144124	1.34E-21	3.15E-21	0.70802127	0	100	MED6	0.72564505	4.97884174	106.798992	4.93E-25	1.55E-24	0.65996541	2.77777778	97.2222222
ENSG00000126267	COX6B1	-0.5957004	5.61853397	91.113016	1.36E-21	3.20E-21	-0.553757	97.1428571	2.85714286	COX6B1	-0.4228584	5.65123562	38.3982262	5.77E-10	1.14E-09	-0.5029226	86.1111111	13.8888889
ENSG00000070831	CDC42	-0.5772473	8.53644822	90.9205886	1.50E-21	3.52E-21	-0.5497684	97.1428571	2.85714286	CDC42	-0.5347743	8.4850743	58.8431463	1.71E-14	3.99E-14	-0.5706906	100	0
ENSG00000163840	DTX3L	-0.6213936	4.75557224	90.8800037	1.53E-21	3.60E-21	-0.5640404	97.1428571	2.85714286	DTX3L	-0.8794555	4.64274426	148.213015	4.26E-34	1.65E-33	-0.8449201	100	0
ENSG00000172578	KLHL6	0.60481754	5.13898828	90.8737182	1.53E-21	3.61E-21	0.63558055	0	100	KLHL6	0.69036287	5.16098494	98.5313625	3.20E-23	9.60E-23	0.60572265	5.55555556	94.4444444
ENSG00000101882	NKAP	0.67880312	3.96313163	90.7873572	1.60E-21	3.76E-21	0.74755222	0	100	NKAP	0.72163538	3.93238885	85.7307088	2.06E-20	5.76E-20	0.60070599	2.77777778	97.2222222
ENSG00000181218	HIST3H2A	-1.0715154	0.96445442	90.7557771	1.63E-21	3.82E-21	-0.9599714	97.1428571	2.85714286	HIST3H2A	-0.4003382	1.16863017	10.5604772	0.00115531	0.00162067	-0.5023457	69.4444444	30.5555556
ENSG00000023191	RNH1	-0.5862194	6.32326503	90.558124	1.80E-21	4.22E-21	-0.5055481	91.4285714	8.57142857	RNH1	-0.4370146	6.33810592	41.7589699	1.03E-10	2.10E-10	-0.5603032	88.8888889	11.1111111
ENSG00000104866	PPP1R37	0.6425005	4.37837249	89.9267539	2.47E-21	5.79E-21	0.73943945	2.85714286	97.1428571	PPP1R37	0.79020351	4.4121835	114.742637	8.96E-27	2.94E-26	0.75360703	0	100
ENSG00000155324	GRAMD3	0.73125378	3.4124716	89.8323423	2.59E-21	6.07E-21	0.75556028	0	100	GRAMD3	0.53596246	3.2112698	38.3727658	5.84E-10	1.15E-09	0.50299919	8.33333333	91.6666667
ENSG00000075142	SRI	-0.6609073	4.11394745	89.7217336	2.74E-21	6.41E-21	-0.5521656	100	0	SRI	-0.4700622	4.14991476	38.6929162	4.96E-10	9.83E-10	-0.516303	97.2222222	2.77777778
ENSG00000182150	ERCC6L2	0.64542134	4.2921861	89.4474005	3.15E-21	7.36E-21	0.68174419	0	100	ERCC6L2	0.7864306	4.35938282	112.508905	2.76E-26	8.96E-26	0.81497052	2.77777778	97.2222222
ENSG00000101888	NXT2	-0.7447453	3.259473	89.2622119	3.46E-21	8.08E-21	-0.7535335	100	0	NXT2	-0.5283732	3.31766321	38.0851472	6.77E-10	1.33E-09	-0.5811148	94.4444444	5.55555556
ENSG00000214413	BBIP1	0.63977293	4.3974146	88.883834	4.19E-21	9.76E-21	0.68359392	5.71428571	94.2857143	BBIP1	0.79033885	4.42944547	113.931973	1.35E-26	4.40E-26	0.79938721	8.33333333	91.6666667
ENSG00000028116	VRK2	-0.814158	2.66103034	88.2961774	5.64E-21	1.31E-20	-0.6787429	97.1428571	2.85714286	VRK2	-1.0042416	2.57674552	106.618581	5.40E-25	1.70E-24	-0.9690217	100	0
ENSG00000145354	CISD2	-0.6360137	4.3693791	88.2209793	5.85E-21	1.36E-20	-0.580487	97.1428571	2.85714286	CISD2	-0.4941599	4.34424635	44.6056648	2.41E-11	5.02E-11	-0.507813	100	0
ENSG00000047621	C12orf4	0.71352574	3.49499665	88.1151094	6.18E-21	1.43E-20	0.82665344	0	100	C12orf4	0.62214474	3.39558118	54.5194595	1.54E-13	3.48E-13	0.60455681	2.77777778	97.2222222
ENSG00000164219	PGGT1B	-0.6168072	4.64680143	87.9423225	6.74E-21	1.56E-20	-0.5418951	94.2857143	5.71428571	PGGT1B	-0.466833	4.64655107	42.2106022	8.20E-11	1.67E-10	-0.5098908	88.8888889	11.1111111
ENSG00000064995	TAF11	0.61085836	4.75084825	87.9023922	6.88E-21	1.59E-20	0.66610424	0	100	TAF11	0.57740235	4.67037867	64.8752628	7.98E-16	1.94E-15	0.52440465	8.33333333	91.6666667
ENSG00000168476	REEP4	-0.7254192	3.41671224	87.8346612	7.12E-21	1.65E-20	-0.7330903	94.2857143	5.71428571	REEP4	-0.6697753	3.43925267	62.919323	2.15E-15	5.17E-15	-0.6927907	97.2222222	2.77777778
ENSG00000100239	PPP6R2	0.59919484	5.0310025	87.5116815	8.38E-21	1.94E-20	0.7098149	5.71428571	94.2857143	PPP6R2	0.73704313	5.02584732	108.809324	1.79E-25	5.70E-25	0.60559389	5.55555556	94.4444444

ENSG00000180098	TRNAU1AP	0.74381033	3.17417253	87.1494622	1.01E-20	2.32E-20	0.76447772	0	100	TRNAU1AP	0.58426496	3.0502542	43.3830403	4.50E-11	9.27E-11	0.5553817	0	100
ENSG00000062598	ELMO2	0.5801383	5.8651594	87.0284222	1.07E-20	2.47E-20	0.61443486	2.85714286	97.1428571	ELMO2	0.81716764	5.92321182	145.218375	1.92E-33	7.34E-33	0.70282944	0	100
ENSG00000165219	GAPVD1	0.57205324	6.20959663	86.4124411	1.46E-20	3.36E-20	0.53438272	0	100	GAPVD1	0.70049638	6.23833897	107.62951	3.24E-25	1.02E-24	0.60560535	2.77777778	97.2222222
ENSG00000004975	DVL2	0.64307043	4.18910665	86.2987318	1.55E-20	3.55E-20	0.70784584	0	100	DVL2	0.71852019	4.20155731	90.3770497	1.97E-21	5.64E-21	0.71218912	2.77777778	97.2222222
ENSG00000173653	RCE1	0.60493021	4.7418895	86.2310412	1.60E-20	3.67E-20	0.60596146	0	100	RCE1	0.79724833	4.77631547	125.571146	3.82E-29	1.32E-28	0.6639853	0	100
ENSG00000100325	ASCC2	0.58040755	5.44590769	86.1750156	1.65E-20	3.78E-20	0.64069437	0	100	ASCC2	0.69844957	5.45787628	104.15198	1.87E-24	5.79E-24	0.665613	2.77777778	97.2222222
ENSG00000048140	TSPAN17	-0.7119333	3.47282471	86.1120065	1.70E-20	3.90E-20	-0.5689984	97.1428571	2.85714286	TSPAN17	-0.772409	3.40555543	82.7777943	9.18E-20	2.51E-19	-0.7857068	100	0
ENSG00000198689	SLC9A6	0.59523637	5.01138507	86.0797576	1.73E-20	3.96E-20	0.61385653	2.85714286	97.1428571	SLC9A6	0.58818294	4.95015257	69.8075265	6.54E-17	1.64E-16	0.5031276	8.33333333	91.6666667
ENSG00000163444	TMEM183A	0.56278284	7.09414462	85.9828196	1.82E-20	4.16E-20	0.6452032	0	100	TMEM183A	0.6480936	7.05734164	92.3989818	7.09E-22	2.05E-21	0.61664753	2.77777778	97.2222222
ENSG00000108406	DHX40	0.57007533	6.20495598	85.9711612	1.83E-20	4.18E-20	0.63142326	0	100	DHX40	0.673306	6.16902729	99.386711	2.08E-23	6.26E-23	0.66450918	2.77777778	97.2222222
ENSG00000196843	ARID5A	0.56038634	8.45463758	85.8812277	1.91E-20	4.37E-20	0.5992616	0	100	ARID5A	0.53879974	8.39473301	60.1395547	8.84E-15	2.09E-14	0.51266742	2.77777778	97.2222222
ENSG00000138138	ATAD1	0.60820807	4.64875364	85.5012318	2.32E-20	5.29E-20	0.64280446	0	100	ATAD1	0.49983003	4.5425962	47.251989	6.24E-12	1.33E-11	0.51281012	11.1111111	88.8888889
ENSG00000255423	EBLN2	0.87975837	2.06803349	84.9569036	3.05E-20	6.95E-20	0.8256183	0	100	EBLN2	0.88440625	2.00929967	66.7730106	3.05E-16	7.50E-16	0.90582691	13.8888889	86.1111111
ENSG00000177463	NR2C2	0.65752668	3.9577945	84.8353617	3.24E-20	7.38E-20	0.79451181	0	100	NR2C2	0.61587345	3.89474661	61.6635572	4.07E-15	9.71E-15	0.54361534	5.55555556	94.4444444
ENSG00000149761	NUDT22	0.79632448	2.67621782	84.769518	3.35E-20	7.63E-20	0.89010646	0	100	NUDT22	0.61030989	2.51889298	38.9905626	4.26E-10	8.46E-10	0.52021892	11.1111111	88.8888889
ENSG00000154473	BUB3	0.56869019	6.20068607	84.5983068	3.66E-20	8.31E-20	0.60706893	5.71428571	94.2857143	BUB3	0.75098022	6.24959159	122.281742	2.00E-28	6.83E-28	0.77517059	8.33333333	91.6666667
ENSG00000103043	VAC14	0.60321845	4.67090514	84.5754435	3.70E-20	8.41E-20	0.66359465	0	100	VAC14	0.69407127	4.7107041	94.1874626	2.87E-22	8.40E-22	0.61779736	2.77777778	97.2222222
ENSG00000198355	PIM3	-0.5599357	8.28716649	84.4308502	3.98E-20	9.04E-20	-0.5513871	85.7142857	14.2857143	PIM3	-0.6554278	8.15001073	89.1723243	3.62E-21	1.03E-20	-0.6134087	97.2222222	2.77777778
ENSG00000160741	CRTC2	0.55955866	7.12065837	84.3879852	4.07E-20	9.23E-20	0.6692472	2.85714286	97.1428571	CRTC2	0.69083653	7.17324685	103.881068	2.15E-24	6.63E-24	0.61758651	0	100
ENSG00000093183	SEC22C	0.57130711	5.67251448	83.9862893	4.98E-20	1.13E-19	0.59663503	0	100	SEC22C	0.79464755	5.73459342	135.774815	2.23E-31	8.15E-31	0.67269882	5.55555556	94.4444444
ENSG00000013563	DNASE1L1	-0.7654566	2.98458286	83.9159691	5.16E-20	1.17E-19	-0.7764323	80	20	DNASE1L1	-0.9952285	2.89240938	113.898251	1.37E-26	4.47E-26	-1.1672095	91.6666667	8.33333333
ENSG00000124535	WRNIP1	0.60116268	4.65294315	83.7334128	5.66E-20	1.28E-19	0.63470216	0	100	WRNIP1	0.76418707	4.68230629	113.834387	1.42E-26	4.62E-26	0.69530621	0	100
ENSG00000257093	KIAA1147	0.55680224	6.94840868	83.4422664	6.56E-20	1.48E-19	0.56743057	0	100	KIAA1147	0.54970848	6.90144269	66.4111555	3.66E-16	8.98E-16	0.53041464	5.55555556	94.4444444
ENSG00000204514	ZNF814	0.69332365	3.55090705	83.4279842	6.61E-20	1.49E-19	0.70408676	0	100	ZNF814	0.78377878	3.51664669	88.6484011	4.72E-21	1.34E-20	0.61606763	2.77777778	97.2222222
ENSG00000163636	PSMD6	0.56023755	6.41706624	83.3777278	6.78E-20	1.53E-19	0.58238504	0	100	PSMD6	0.57629604	6.35119634	73.2684345	1.13E-17	2.89E-17	0.53005508	5.55555556	94.4444444
ENSG00000152291	TGOLN2	-0.5512683	8.15861718	83.1716093	7.52E-20	1.69E-19	-0.517455	100	0	TGOLN2	-0.5833786	8.08143778	71.7652794	2.42E-17	6.14E-17	-0.6077159	100	0
ENSG00000176438	SYNE3	-0.6365959	4.11676562	83.0751724	7.90E-20	1.78E-19	-0.5684601	97.1428571	2.85714286	SYNE3	-1.4300149	3.82656132	314.014033	2.92E-70	2.00E-69	-1.4359406	100	0
ENSG00000127884	ECHS1	-0.7678977	2.84450162	82.6567045	9.76E-20	2.19E-19	-0.7561492	97.1428571	2.85714286	ECHS1	-0.6580213	2.87719501	50.9315074	9.56E-13	2.11E-12	-0.7195019	94.4444444	5.55555556
ENSG00000168488	ATXN2L	0.54821165	7.54871603	81.8304187	1.48E-19	3.32E-19	0.63614026	0	100	ATXN2L	0.66235326	7.55388242	94.3775017	2.61E-22	7.64E-22	0.56631909	2.77777778	97.2222222
ENSG00000204186	ZDBF2	0.5547028	6.74040955	81.7760154	1.52E-19	3.41E-19	0.59341622	2.85714286	97.1428571	ZDBF2	0.67748653	6.70154656	98.6873749	2.96E-23	8.89E-23	0.76086613	8.33333333	91.6666667
ENSG00000115947	ORC4	0.61651353	4.27935271	81.6545593	1.62E-19	3.62E-19	0.68136189	0	100	ORC4	0.6512107	4.23810807	75.4429149	3.76E-18	9.76E-18	0.64283311	2.77777778	97.2222222
ENSG00000126767	ELK1	-0.5664354	5.46001774	81.5433135	1.71E-19	3.82E-19	-0.5476136	88.5714286	11.4285714	ELK1	-0.7919266	5.32615531	131.257323	2.18E-30	7.75E-30	-0.849714	100	0
ENSG00000102984	ZNF821	-0.6652164	3.74569251	81.4987757	1.75E-19	3.91E-19	-0.5214687	94.2857143	5.71428571	ZNF821	-0.5850198	3.67363554	52.3340466	4.68E-13	1.04E-12	-0.6549782	97.2222222	2.77777778
ENSG00000111790	FGFR1OP2	-0.5587669	5.67723831	81.0258675	2.23E-19	4.95E-19	-0.5234024	100	0	FGFR1OP2	-0.4713993	5.65355119	48.2952279	3.67E-12	7.89E-12	-0.5027321	100	0
ENSG00000079263	SP140	-0.6684831	3.72690898	80.9911887	2.27E-19	5.04E-19	-0.5546313	91.4285714	8.57142857	SP140	-0.8035414	3.5951764	94.7521846	2.16E-22	6.34E-22	-0.8804239	97.2222222	2.77777778
ENSG00000116120	FARSB	0.69989228	3.33879473	80.7906274	2.51E-19	5.57E-19	0.81021732	0	100	FARSB	0.59146352	3.23136836	47.0728669	6.84E-12	1.46E-11	0.54223442	2.77777778	97.2222222
ENSG00000151445	VIPAS39	0.72996978	3.05304357	80.6543493	2.69E-19	5.96E-19	0.82656721	0	100	VIPAS39	0.71244071	3.0009848	63.1153416	1.95E-15	4.69E-15	0.73969839	2.77777778	97.2222222
ENSG00000145414	NAF1	0.58775542	4.67200602	80.287593	3.24E-19	7.15E-19	0.676612	0	100	NAF1	0.66909866	4.62921859	86.5060149	1.39E-20	3.91E-20	0.64290514	2.77777778	97.2222222
ENSG00000041988	THAP3	0.7250669	3.07482399	80.2487408	3.30E-19	7.29E-19	0.77136061	0	100	THAP3	0.70832514	3.00290994	62.5156865	2.64E-15	6.33E-15	0.58041311	0	100
ENSG00000119787	ATL2	0.56134922	5.36472784	79.8547158	4.03E-19	8.88E-19	0.62309137	0	100	ATL2	0.59523244	5.29660056	74.282411	6.77E-18	1.74E-17	0.5921317	2.77777778	97.2222222
ENSG00000129484	PARP2	0.7322067	2.97583448	79.2943792	5.35E-19	1.18E-18	0.81084311	0	100	PARP2	0.7319861	2.88475116	64.0848039	1.19E-15	2.88E-15	0.66513377	2.77777778	97.2222222
ENSG00000011243	AKAP8L	0.54596386	6.26687312	79.0392839	6.09E-19	1.34E-18	0.61027522	0	100	AKAP8L	0.63359953	6.280281	88.673094	4.66E-21	1.33E-20	0.55083996	0	100
ENSG00000165526	RPUSD4	0.65375941	3.74467605	78.9249504	6.45E-19	1.42E-18	0.6617944	0	100	RPUSD4	0.68627823	3.69343241	72.5145419	1.66E-17	4.22E-17	0.56914187	0	100
ENSG00000054611	TBC1D22A	-0.6175382	4.14903086	78.2649625	9.01E-19	1.97E-18	-0.5532798	97.1428571	2.85714286	TBC1D22A	-0.6635545	4.03393703	73.4489003	1.03E-17	2.65E-17	-0.7189137	97.2222222	2.77777778
ENSG00000090661	CERS4	-0.7172989	3.07836965	78.2578081	9.04E-19	1.98E-18	-0.6193818	97.1428571	2.85714286	CERS4	-0.7321427	2.99629781	66.1989692	4.08E-16	9.99E-16	-0.8159555	100	0
ENSG00000213799	ZNF845	-0.6100049	4.2094076	78.1875991	9.37E-19	2.05E-18	-0.5305836	100	0	ZNF845	-0.7105209	4.10657078	86.4620251	1.42E-20	3.99E-20	-0.8070107	100	0
ENSG00000181274	FRAT2	-0.6385684	3.87744062	77.6444198	1.23E-18	2.69E-18	-0.6304814	88.5714286	11.4285714	FRAT2	-0.580903	3.84194949	53.6241246	2.43E-13	5.45E-13	-0.6526023	94.4444444	5.55555556
ENSG00000267352	SH3GL1P3	0.90118192	1.51793708	77.3569323	1.43E-18	3.11E-18	0.90476308	0	100	SH3GL1P3	1.01357107	1.56908216	77.0866251	1.64E-18	4.31E-18	0.78808177	0	100
ENSG00000146007	ZMAT2	-0.553934	5.24522509	77.2180319	1.53E-18	3.33E-18	-0.5075817	97.1428571	2.85714286	ZMAT2	-0.4876589	5.22895368	50.0438701	1.50E-12	3.28E-12	-0.5269785	97.2222222	2.77777778
ENSG00000138614	VWA9	0.59700431	4.30790636	76.8866325	1.81E-18	3.93E-18	0.65287771	0	100	VWA9	0.82343629	4.40894353	124.753216	5.76E-29	1.98E-28	0.76603685	0	100
ENSG00000128191	DGCR8	0.6126345	4.10593654	76.8860686	1.81E-18	3.93E-18	0.68937866	0	100	DGCR8	0.89792767	4.21646639	140.505151	2.06E-32	7.73E-32	0.81874054	2.77777778	97.2222222
ENSG00000196459	TRAPPC2	0.62147476	3.95959737	76.1197179	2.67E-18	5.77E-18	0.68647384	2.85714286	97.1428571	TRAPPC2	0.70754074	3.95432622	82.4619073	1.08E-19	2.94E-19	0.63033039	5.55555556	94.4444444
ENSG00000106400	ZNHIT1	0.55774598	4.99738986	76.0440267	2.77E-18	6.00E-18	0.63477077	2.85714286	97.1428571	ZNHIT1	0.85285014	5.1575714	150.043877	1.70E-34	6.63E-34	0.79690002	0	100

ENSG00000214026	MRPL23	-0.6247098	3.93346209	75.9739498	2.87E-18	6.21E-18	-0.6171124	91.4285714	8.57142857	MRPL23	-0.6442908	3.89884958	66.9669664	2.76E-16	6.81E-16	-0.7613122	94.4444444	5.55555556
ENSG00000133884	DPF2	0.54323513	5.4990645	75.8452396	3.07E-18	6.63E-18	0.57752524	0	100	DPF2	0.78353147	5.58879496	132.007803	1.49E-30	5.34E-30	0.67008318	0	100
ENSG00000158019	BRE	-0.6652395	3.48547503	75.8139429	3.12E-18	6.73E-18	-0.5658455	97.1428571	2.85714286	BRE	-0.5291696	3.48655047	40.45063	2.02E-10	4.06E-10	-0.5290766	100	0
ENSG00000232774	RP11-47I22.3	0.7570251	2.53094331	74.4336242	6.27E-18	1.35E-17	0.80933544	0	100	RP11-47I22.3	0.71334845	2.44870575	52.63011	4.03E-13	8.98E-13	0.70200926	2.77777778	97.2222222
ENSG00000127540	UQCR11	-0.5977651	4.18276252	74.4240489	6.30E-18	1.36E-17	-0.5196691	91.4285714	8.57142857	UQCR11	-0.5813178	4.15700166	58.567335	1.96E-14	4.58E-14	-0.7053501	94.4444444	5.55555556
ENSG00000083720	OXCT1	0.60523288	4.0689948	74.0986459	7.43E-18	1.60E-17	0.67859174	5.71428571	94.2857143	OXCT1	0.63407221	4.00445642	67.4233319	2.19E-16	5.42E-16	0.58763169	5.55555556	94.4444444
ENSG00000152443	ZNF776	-0.5443649	5.16372645	74.0286397	7.70E-18	1.65E-17	-0.5016946	100	0	ZNF776	-0.720508	5.04280803	106.023424	7.29E-25	2.28E-24	-0.7010485	100	0
ENSG00000168014	C2CD3	0.569792	4.57642702	73.8863186	8.27E-18	1.77E-17	0.66154412	2.85714286	97.1428571	C2CD3	0.69151911	4.58202243	91.178325	1.31E-21	3.78E-21	0.68854397	8.33333333	91.6666667
ENSG00000164080	RAD54L2	0.5322697	5.70238786	73.3960076	1.06E-17	2.27E-17	0.56448216	0	100	RAD54L2	0.65696792	5.74298591	92.8862199	5.54E-22	1.61E-21	0.61818336	5.55555556	94.4444444
ENSG00000101413	RPRD1B	0.54563381	5.17662076	73.3817714	1.07E-17	2.28E-17	0.5233996	5.71428571	94.2857143	RPRD1B	0.76741031	5.24891438	121.985233	2.33E-28	7.92E-28	0.72264709	2.77777778	97.2222222
ENSG00000105053	VRK3	0.595053	4.09934817	72.6462432	1.55E-17	3.30E-17	0.58292893	0	100	VRK3	0.88768977	4.21226884	138.681158	5.17E-32	1.92E-31	0.86408279	0	100
ENSG00000102606	ARHGEF7	0.52399808	6.54615716	72.5878822	1.60E-17	3.40E-17	0.54482931	2.85714286	97.1428571	ARHGEF7	1.29931304	7.02321365	357.29328	1.09E-79	8.19E-79	1.25863281	0	100
ENSG00000180329	CCDC43	0.56493548	4.53516526	72.3709434	1.78E-17	3.79E-17	0.58255127	0	100	CCDC43	0.76047348	4.57174939	110.078072	9.42E-26	3.02E-25	0.74431742	0	100
ENSG00000111331	OAS3	-0.6140471	4.05192139	72.3376215	1.81E-17	3.85E-17	-0.5619035	80	20	OAS3	-1.1361241	3.98811037	197.350402	7.91E-45	3.71E-44	-1.2583937	91.6666667	8.33333333
ENSG00000100395	L3MBTL2	0.60730285	3.91543073	72.0797319	2.07E-17	4.39E-17	0.7338539	0	100	L3MBTL2	0.88977697	4.03944736	133.143476	8.41E-31	3.03E-30	0.81682079	2.77777778	97.2222222
ENSG00000160785	SLC25A44	0.54467583	4.94581325	71.9429638	2.22E-17	4.69E-17	0.630101	2.85714286	97.1428571	SLC25A44	0.79944978	5.05794981	131.186925	2.25E-30	8.02E-30	0.75607775	0	100
ENSG00000175550	DRAP1	-0.531754	5.42360862	71.6136905	2.62E-17	5.54E-17	-0.549271	91.4285714	8.57142857	DRAP1	-0.445059	5.44254368	41.7294544	1.05E-10	2.13E-10	-0.5362972	91.6666667	8.33333333
ENSG00000127993	RBM48	0.54663117	4.83003542	71.5612883	2.69E-17	5.68E-17	0.57910905	0	100	RBM48	0.58282495	4.78595102	67.3869944	2.23E-16	5.52E-16	0.57139418	5.55555556	94.4444444
ENSG00000167969	ECI1	-0.7866177	2.15551749	71.3444344	3.00E-17	6.34E-17	-0.7440806	97.1428571	2.85714286	ECI1	-1.0994095	1.99938148	105.109588	1.16E-24	3.60E-24	-1.1081633	100	0
ENSG00000175166	PSMD2	0.51951312	6.33015077	71.1815878	3.26E-17	6.88E-17	0.595013	5.71428571	94.2857143	PSMD2	0.61699989	6.36060107	83.3799058	6.77E-20	1.86E-19	0.52115767	5.55555556	94.4444444
ENSG00000089022	MAPKAPK5	0.52590909	5.48128488	71.0741672	3.44E-17	7.27E-17	0.58541525	0	100	MAPKAPK5	0.60194774	5.47627883	77.7858753	1.15E-18	3.04E-18	0.51101384	0	100
ENSG00000110344	UBE4A	0.51578203	5.89221814	69.673028	7.00E-17	1.47E-16	0.54727163	0	100	UBE4A	0.68131555	5.93650257	100.848577	9.93E-24	3.03E-23	0.60713102	2.77777778	97.2222222
ENSG00000162194	C11orf48	0.59051882	3.97220676	69.4842549	7.70E-17	1.61E-16	0.69427045	0	100	C11orf48	0.79332267	4.03722138	106.478075	5.79E-25	1.82E-24	0.72583549	0	100
ENSG00000152359	POC5	0.67429399	3.04120985	68.8080835	1.09E-16	2.26E-16	0.71355542	0	100	POC5	0.72779104	3.02623996	66.312341	3.85E-16	9.44E-16	0.60929817	2.77777778	97.2222222
ENSG00000156709	AIFM1	0.68273412	2.98711581	68.6350533	1.18E-16	2.47E-16	0.7723282	2.85714286	97.1428571	AIFM1	0.84954389	3.06860146	91.012281	1.43E-21	4.10E-21	0.77384526	0	100
ENSG00000134987	WDR36	0.52620197	5.10054449	67.8572146	1.76E-16	3.65E-16	0.50305636	5.71428571	94.2857143	WDR36	0.61699833	5.04283222	77.2136693	1.53E-18	4.04E-18	0.61251383	2.77777778	97.2222222
ENSG00000159579	RSPRY1	0.5575079	4.33903605	67.6675622	1.94E-16	4.01E-16	0.61167447	0	100	RSPRY1	0.73288562	4.44061197	99.5179296	1.94E-23	5.87E-23	0.69904621	2.77777778	97.2222222
ENSG00000112983	BRD8	0.60352853	3.73621889	67.6185905	1.98E-16	4.11E-16	0.66525666	2.85714286	97.1428571	BRD8	0.80632613	3.79394113	102.722508	3.86E-24	1.18E-23	0.72348035	0	100
ENSG00000083814	ZNF671	0.6110474	3.62054713	66.971129	2.76E-16	5.68E-16	0.68841525	0	100	ZNF671	0.54195147	3.54928447	43.326246	4.63E-11	9.53E-11	0.53103768	5.55555556	94.4444444
ENSG00000130723	PRRC2B	0.49447052	8.255064	66.7803653	3.04E-16	6.25E-16	0.58289962	0	100	PRRC2B	0.6299516	8.28146789	82.1189221	1.28E-19	3.48E-19	0.53103694	5.55555556	94.4444444
ENSG00000147050	KDM6A	0.49875425	6.61430022	66.6295266	3.28E-16	6.74E-16	0.51982292	0	100	KDM6A	0.62616364	6.63234509	86.021621	1.78E-20	4.98E-20	0.5558631	5.55555556	94.4444444
ENSG00000112118	MCM3	0.61839247	3.60087085	66.5554759	3.40E-16	7.00E-16	0.83289306	20	80	MCM3	0.71440974	3.62889981	76.2808927	2.46E-18	6.42E-18	0.62360039	5.55555556	94.4444444
ENSG00000069493	CLEC2D	0.54995402	4.42354559	66.3254599	3.82E-16	7.86E-16	0.6185501	8.57142857	91.4285714	CLEC2D	0.5868389	4.34137907	62.3206849	2.92E-15	6.98E-15	0.59051948	11.1111111	88.8888889
ENSG00000145817	YIPF5	0.50329672	5.73434229	65.2804869	6.50E-16	1.33E-15	0.53698337	8.57142857	91.4285714	YIPF5	0.54664459	5.68762676	64.0074265	1.24E-15	3.00E-15	0.53524324	11.1111111	88.8888889
ENSG00000177732	SOX12	0.56925846	4.01389536	64.9484857	7.69E-16	1.57E-15	0.69759533	2.85714286	97.1428571	SOX12	0.71595069	4.02717343	85.809793	1.98E-20	5.54E-20	0.61185805	0	100
ENSG00000110536	PTPMT1	-0.635822	3.23023125	64.7266495	8.60E-16	1.75E-15	-0.6564483	100	0	PTPMT1	-0.4970287	3.21939998	33.2265903	8.20E-09	1.54E-08	-0.5836471	97.2222222	2.77777778
ENSG00000167552	TUBA1A	0.49244966	8.30171902	64.6958285	8.74E-16	1.78E-15	0.58927627	14.2857143	85.7142857	TUBA1A	0.95264749	8.57162529	175.273799	5.22E-40	2.28E-39	0.82627623	8.33333333	91.6666667
ENSG00000116717	GADD45A	0.50332047	5.54034425	64.4186691	1.01E-15	2.04E-15	0.59987244	8.57142857	91.4285714	GADD45A	0.90067126	5.68407919	172.407863	2.20E-39	9.51E-39	0.81728787	0	100
ENSG00000232119	MCTS1	-0.7246696	2.3499434	64.2111498	1.12E-15	2.27E-15	-0.5991851	100	0	MCTS1	-0.5925248	2.35375836	34.7874325	3.68E-09	7.02E-09	-0.6132119	97.2222222	2.77777778
ENSG00000147140	NONO	0.48476245	7.85354557	64.0880893	1.19E-15	2.41E-15	0.53587777	0	100	NONO	0.69703736	7.91496466	102.561156	4.18E-24	1.28E-23	0.66353094	0	100
ENSG00000111667	USP5	0.56909077	3.97679191	63.9922499	1.25E-15	2.53E-15	0.63300177	0	100	USP5	0.64637632	3.95946487	68.5560537	1.23E-16	3.07E-16	0.56527029	5.55555556	94.4444444
ENSG00000235677	NPM1P26	0.8449057	1.29734785	63.7005812	1.45E-15	2.93E-15	0.86117827	2.85714286	97.1428571	NPM1P26	1.01954153	1.23005188	69.8976239	6.25E-17	1.57E-16	1.05195566	5.55555556	94.4444444
ENSG00000091732	ZC3HC1	0.64536647	3.06407519	63.5809113	1.54E-15	3.11E-15	0.74095575	0	100	ZC3HC1	0.7125891	3.08191817	64.6823596	8.80E-16	2.14E-15	0.66991399	0	100
ENSG00000137547	MRPL15	-0.6769394	2.76052186	63.4421517	1.65E-15	3.33E-15	-0.666821	97.1428571	2.85714286	MRPL15	-0.5963333	2.72325883	40.2441055	2.24E-10	4.50E-10	-0.6141858	91.6666667	8.33333333
ENSG00000117222	RBBP5	0.502359	5.23027965	63.3358267	1.74E-15	3.51E-15	0.54823422	2.85714286	97.1428571	RBBP5	0.75353614	5.29196082	118.524749	1.33E-27	4.47E-27	0.71105309	5.55555556	94.4444444
ENSG00000139131	YARS2	0.6177454	3.33128907	63.2107006	1.86E-15	3.74E-15	0.67724035	0	100	YARS2	0.56766719	3.23026047	43.3330502	4.62E-11	9.50E-11	0.54034738	5.55555556	94.4444444
ENSG00000154305	MIA3	0.48637201	6.37380125	63.1361601	1.93E-15	3.88E-15	0.53750618	0	100	MIA3	0.65867679	6.40990886	95.7407159	1.31E-22	3.87E-22	0.63411945	2.77777778	97.2222222
ENSG00000106144	CASP2	0.50437205	5.08039694	62.7013351	2.41E-15	4.82E-15	0.53698134	5.71428571	94.2857143	CASP2	0.61455311	5.08557471	77.5360615	1.30E-18	3.44E-18	0.53907074	8.33333333	91.6666667
ENSG00000066027	PPP2R5A	0.48253615	6.58216096	62.3587247	2.86E-15	5.72E-15	0.54463394	0	100	PPP2R5A	0.62843696	6.59256464	86.4437862	1.44E-20	4.03E-20	0.58967031	2.77777778	97.2222222
ENSG00000145912	NHP2	-0.5484665	4.09999665	61.6147586	4.18E-15	8.31E-15	-0.5119683	91.4285714	8.57142857	NHP2	-0.386622	4.11478764	25.8072035	3.77E-07	6.55E-07	-0.5115293	88.8888889	11.1111111
ENSG00000177042	TMEM80	0.63167362	3.09095158	60.7773421	6.39E-15	1.27E-14	0.67809917	0	100	TMEM80	0.63557614	3.0046964	49.7559523	1.74E-12	3.79E-12	0.57248725	5.55555556	94.4444444
ENSG00000101343	CRNKL1	0.4837066	5.65198226	60.7459038	6.49E-15	1.29E-14	0.5428889	0	100	CRNKL1	0.65888328	5.68799512	93.9998168	3.16E-22	9.22E-22	0.57446355	2.77777778	97.2222222
ENSG00000167645	YIF1B	-0.6411851	3.00960164	59.8920306	1.00E-14	1.97E-14	-0.7390197	77.1428571	22.8571429	YIF1B	-0.9645444	2.86017836	104.709116	1.41E-24	4.39E-24	-1.2246252	88.8888889	11.1111111

ENSG00000162642	C1orf52	0.51005263	4.57047083	59.5796259	1.17E-14	2.31E-14	0.56329451	0	100	C1orf52	0.62809152	4.56134227	75.3794817	3.88E-18	1.01E-17	0.5392855	0	100
ENSG00000092929	UNC13D	0.48484557	5.44208617	59.3177756	1.34E-14	2.64E-14	0.52199311	11.4285714	88.5714286	UNC13D	0.73221906	5.52432736	111.820376	3.91E-26	1.26E-25	0.5883302	8.33333333	91.6666667
ENSG00000151612	ZNF827	0.48573891	5.13468455	58.6331	1.90E-14	3.72E-14	0.53574616	0	100	ZNF827	1.09855895	5.47503877	252.968835	5.85E-57	3.32E-56	1.01453982	0	100
ENSG00000126524	SBDS	0.46320147	7.67980024	58.4462097	2.09E-14	4.09E-14	0.53145851	2.85714286	97.1428571	SBDS	0.5247037	7.62927929	58.8164849	1.73E-14	4.04E-14	0.50222309	5.55555556	94.4444444
ENSG00000261416	RP11-455F5.5	0.80546234	1.30115943	58.3592685	2.18E-14	4.26E-14	0.91822919	2.85714286	97.1428571	RP11-455F5.5	0.88203488	1.2845093	53.7972054	2.22E-13	5.00E-13	0.78701131	2.77777778	97.2222222
ENSG00000068971	PPP2R5B	0.6203017	3.07958203	58.1511518	2.43E-14	4.74E-14	0.66276014	0	100	PPP2R5B	0.5723026	2.92329402	39.7332261	2.91E-10	5.83E-10	0.55731648	8.33333333	91.6666667
ENSG00000087191	PSMC5	0.47602142	5.47545431	58.0217525	2.59E-14	5.05E-14	0.51385398	0	100	PSMC5	0.70615585	5.5627387	106.791068	4.95E-25	1.56E-24	0.63322097	0	100
ENSG00000060688	SNRNP40	0.48765253	4.90550368	57.3796511	3.59E-14	6.98E-14	0.56991432	2.85714286	97.1428571	SNRNP40	0.76025384	5.00267666	117.469768	2.27E-27	7.54E-27	0.68124834	0	100
ENSG00000090273	NUDC	0.47439563	5.39736319	57.3608548	3.63E-14	7.04E-14	0.56513374	2.85714286	97.1428571	NUDC	0.63010013	5.44026129	84.6386421	3.58E-20	9.89E-20	0.54036803	2.77777778	97.2222222
ENSG00000176476	CCDC101	0.53360082	4.00407406	57.0024172	4.35E-14	8.42E-14	0.5690254	2.85714286	97.1428571	CCDC101	0.68473185	4.03950401	79.2168386	5.57E-19	1.49E-18	0.58381413	0	100
ENSG00000163481	RNF25	0.54569001	3.83022181	56.9595809	4.45E-14	8.60E-14	0.60256842	0	100	RNF25	0.67692023	3.86123744	73.905459	8.19E-18	2.10E-17	0.56966831	2.77777778	97.2222222
ENSG00000273271	AP000254.8	0.77576853	1.45383817	56.6683001	5.16E-14	9.97E-14	0.80985708	0	100	AP000254.8	0.66341947	1.35151796	31.3700697	2.13E-08	3.92E-08	0.61656252	5.55555556	94.4444444
ENSG00000185049	NELFA	0.47524324	5.1871779	56.6084803	5.32E-14	1.03E-13	0.51533723	0	100	NELFA	0.60576058	5.20083061	76.7056516	1.98E-18	5.20E-18	0.50000346	0	100
ENSG00000183495	EP400	0.46373785	6.07561465	56.5976968	5.35E-14	1.03E-13	0.55276326	0	100	EP400	0.70269936	6.17208863	107.597272	3.29E-25	1.04E-24	0.67830559	5.55555556	94.4444444
ENSG00000092931	MFSD11	0.53466708	3.95314298	56.4174276	5.86E-14	1.13E-13	0.61585351	0	100	MFSD11	0.61294374	3.98791953	63.0587332	2.01E-15	4.82E-15	0.55286943	0	100
ENSG00000136143	SUCLA2	0.62580462	2.86187623	56.3425669	6.09E-14	1.17E-13	0.71355049	0	100	SUCLA2	0.60773193	2.79956182	43.2075134	4.92E-11	1.01E-10	0.60174774	2.77777778	97.2222222
ENSG00000133142	TCEAL4	-0.6800768	2.29451867	56.0100092	7.21E-14	1.39E-13	-0.5787208	97.1428571	2.85714286	TCEAL4	-0.5366133	2.32698912	28.5795893	8.99E-08	1.61E-07	-0.6194737	94.4444444	5.55555556
ENSG00000110925	CSRNP2	0.56640909	3.49040006	55.499489	9.35E-14	1.79E-13	0.65503512	0	100	CSRNP2	0.72973417	3.50233166	77.3527789	1.43E-18	3.77E-18	0.64871496	2.77777778	97.2222222
ENSG00000008710	PKD1	0.45416512	5.82540672	53.5830521	2.48E-13	4.70E-13	0.5820032	5.71428571	94.2857143	PKD1	0.59900171	5.84634055	77.2410086	1.51E-18	3.99E-18	0.55445144	8.33333333	91.6666667
ENSG00000169738	DCXR	0.53279449	3.75282526	52.422286	4.48E-13	8.43E-13	0.5540053	2.85714286	97.1428571	DCXR	0.93891929	3.94823019	142.227285	8.67E-33	3.27E-32	0.85347471	2.77777778	97.2222222
ENSG00000166971	AKTIP	0.57062969	3.21800433	51.5251873	7.07E-13	1.32E-12	0.55539699	2.85714286	97.1428571	AKTIP	0.91685241	3.34798742	115.997064	4.76E-27	1.57E-26	0.85655622	2.77777778	97.2222222
ENSG00000163541	SUCLG1	0.49009306	4.26662238	51.46444	7.29E-13	1.36E-12	0.57773731	2.85714286	97.1428571	SUCLG1	0.49518824	4.21253776	43.5334548	4.17E-11	8.60E-11	0.51370455	5.55555556	94.4444444
ENSG00000117620	SLC35A3	0.46751391	4.67731146	50.8291583	1.01E-12	1.88E-12	0.51116004	0	100	SLC35A3	0.55225093	4.66978568	59.1392792	1.47E-14	3.44E-14	0.5752488	8.33333333	91.6666667
ENSG00000131351	HAUS8	0.54644681	3.36979695	49.8331937	1.67E-12	3.10E-12	0.6177698	2.85714286	97.1428571	HAUS8	0.54417244	3.30343422	40.5689037	1.90E-10	3.83E-10	0.53529138	2.77777778	97.2222222
ENSG00000204564	C6orf136	0.52719481	3.53620537	49.0054028	2.55E-12	4.71E-12	0.55640212	0	100	C6orf136	0.99861658	3.77134985	155.703544	9.83E-36	3.92E-35	0.88314163	0	100
ENSG00000139546	TARBP2	0.55274734	3.21556095	48.7755609	2.87E-12	5.29E-12	0.5907589	0	100	TARBP2	0.67495632	3.20283994	60.373328	7.85E-15	1.86E-14	0.61884433	2.77777778	97.2222222
ENSG00000172613	RAD9A	0.61552332	2.4918599	48.4572086	3.38E-12	6.22E-12	0.70144018	5.71428571	94.2857143	RAD9A	0.82703072	2.5592357	71.52569	2.74E-17	6.93E-17	0.64507454	5.55555556	94.4444444
ENSG00000250539	KRT8P33	0.66374964	1.91936569	47.933031	4.41E-12	8.09E-12	0.69535907	2.85714286	97.1428571	KRT8P33	0.65177256	1.89041811	36.4342277	1.58E-09	3.06E-09	0.62571536	5.55555556	94.4444444
ENSG00000154451	GBP5	0.43366047	5.29850157	46.5034961	9.15E-12	1.66E-11	0.50500171	20	80	GBP5	0.92124037	5.63540713	177.808256	1.46E-40	6.45E-40	0.85435501	2.77777778	97.2222222
ENSG00000103145	HCFC1R1	-0.6113959	2.3833633	46.4648857	9.33E-12	1.69E-11	-0.5428209	94.2857143	5.71428571	HCFC1R1	-0.6200155	2.3303536	37.7796006	7.92E-10	1.55E-09	-0.7773924	91.6666667	8.33333333
ENSG00000272779	LL22NC03-80A	-0.6617746	1.81996408	46.268179	1.03E-11	1.87E-11	-0.5988343	100	0	LL22NC03-80A	-0.5692155	1.80568968	26.8185329	2.23E-07	3.92E-07	-0.5923395	91.6666667	8.33333333
ENSG00000256885	NA	0.74166972	1.05581607	46.1797985	1.08E-11	1.95E-11	0.77863773	0	100	NA	0.90798867	1.12180995	52.9968206	3.34E-13	7.47E-13	0.92995735	8.33333333	91.6666667
ENSG00000132478	UNK	0.43237983	4.99081657	46.0482862	1.15E-11	2.09E-11	0.52247131	0	100	UNK	0.53528381	4.99303209	58.9256438	1.64E-14	3.83E-14	0.5038688	0	100
ENSG00000126746	ZNF384	0.41760657	5.96891185	45.9237265	1.23E-11	2.22E-11	0.50182555	0	100	ZNF384	0.61357552	6.02527609	82.589844	1.01E-19	2.76E-19	0.52483039	0	100
ENSG00000107281	NPDC1	0.60435271	2.66862594	45.8872254	1.25E-11	2.26E-11	0.5965989	20	80	NPDC1	1.37149121	3.03222842	218.336056	2.09E-49	1.07E-48	1.28572314	2.77777778	97.2222222
ENSG00000099800	TIMM13	-0.5513355	3.02755048	45.7834233	1.32E-11	2.38E-11	-0.5256281	94.2857143	5.71428571	TIMM13	-0.5764539	2.9597596	40.5182657	1.95E-10	3.93E-10	-0.662874	91.6666667	8.33333333
ENSG00000150779	TIMM8B	-0.6218345	2.16287346	44.98404	1.99E-11	3.55E-11	-0.5680318	88.5714286	11.4285714	TIMM8B	-0.5341627	2.16868442	26.755116	2.31E-07	4.05E-07	-0.5863509	91.6666667	8.33333333
ENSG00000268156	NA	0.84862762	0.07683486	44.9130569	2.06E-11	3.68E-11	1.06721269	14.2857143	85.7142857	NA	0.79447611	-0.0309657	28.7418964	8.27E-08	1.48E-07	0.61100569	16.6666667	83.3333333
ENSG00000164053	ATRIP	0.52289729	3.23750551	44.0096624	3.27E-11	5.81E-11	0.58575727	2.85714286	97.1428571	ATRIP	0.50470156	3.15748534	33.5079317	7.10E-09	1.34E-08	0.5054196	11.1111111	88.8888889
ENSG00000198912	C1orf174	0.44290295	4.44911278	43.9584579	3.35E-11	5.96E-11	0.56395775	0	100	C1orf174	0.56121068	4.44788909	59.0560836	1.53E-14	3.59E-14	0.50132984	0	100
ENSG00000164674	SYTL3	0.43320857	4.46473539	41.3826098	1.25E-10	2.17E-10	0.5960556	20	80	SYTL3	0.8400112	4.69124879	135.829314	2.17E-31	7.94E-31	0.79717124	5.55555556	94.4444444
ENSG00000120860	CCDC53	0.56440578	2.50209294	40.9059572	1.60E-10	2.76E-10	0.58697817	2.85714286	97.1428571	CCDC53	0.53082	2.44815762	29.0643142	7.00E-08	1.26E-07	0.54370963	13.8888889	86.1111111
ENSG00000167775	CD320	0.50129583	3.28211076	40.8486663	1.64E-10	2.85E-10	0.54845465	2.85714286	97.1428571	CD320	0.65278636	3.29785408	57.965504	2.67E-14	6.20E-14	0.52276381	5.55555556	94.4444444
ENSG00000197536	C5orf56	0.526781	2.82849932	39.2386575	3.75E-10	6.42E-10	0.61009029	5.71428571	94.2857143	C5orf56	0.55301922	2.81300933	35.6210136	2.40E-09	4.61E-09	0.56686323	11.1111111	88.8888889
ENSG00000100601	ALKBH1	0.48588804	3.12587728	36.797139	1.31E-09	2.20E-09	0.58188452	0	100	ALKBH1	0.6138381	3.16104337	49.3652656	2.12E-12	4.61E-12	0.56043491	2.77777778	97.2222222
ENSG00000138303	ASCC1	0.51067875	2.77738547	36.5164774	1.51E-09	2.53E-09	0.51211152	2.85714286	97.1428571	ASCC1	0.65776672	2.82342932	50.7635944	1.04E-12	2.29E-12	0.6318713	2.77777778	97.2222222
ENSG00000182973	CNOT10	0.43725251	3.81136539	36.4482121	1.57E-09	2.62E-09	0.54108822	2.85714286	97.1428571	CNOT10	0.5392095	3.78426714	46.2528748	1.04E-11	2.20E-11	0.50251619	5.55555556	94.4444444
ENSG00000166477	LEO1	0.51403263	2.67413221	36.0419462	1.93E-09	3.22E-09	0.53840821	0	100	LEO1	0.73062114	2.73440873	60.9097587	5.98E-15	1.42E-14	0.66606193	0	100
ENSG00000213443	CLEC2D	0.52605597	2.5129769	35.6884811	2.32E-09	3.85E-09	0.53211882	5.71428571	94.2857143	CLEC2D	0.60254281	2.46296564	37.554718	8.89E-10	1.74E-09	0.55359662	8.33333333	91.6666667
ENSG00000067365	METTL22	0.46281746	3.27602678	35.0135991	3.27E-09	5.41E-09	0.51947808	0	100	METTL22	0.54298175	3.31342632	40.793652	1.69E-10	3.42E-10	0.51166286	2.77777778	97.2222222
ENSG00000187688	TRPV2	0.42191251	3.69723667	32.4867612	1.20E-08	1.95E-08	0.53639057	11.4285714	88.5714286	TRPV2	0.53415997	3.69509157	43.6281945	3.97E-11	8.20E-11	0.52304137	11.1111111	88.8888889
ENSG00000267906	NA	0.69335319	0.18695682	31.5586778	1.94E-08	3.12E-08	0.73152848	5.71428571	94.2857143	NA	0.78926636	0.22091824	30.8245098	2.82E-08	5.17E-08	0.66767912	11.1111111	88.8888889
ENSG00000254910	RP11-326C3.7	0.66066407	0.49576015	31.321373	2.19E-08	3.51E-08	0.73311151	8.57142857	91.4285714	RP11-326C3.7	0.64251237	0.46942803	22.3834639	2.23E-06	3.71E-06	0.5970237	5.55555556	94.4444444

ENSG00000065559	MAP2K4	0.42584506	3.41950364	30.794005	2.87E-08	4.58E-08	0.50937981	5.71428571	94.2857143	MAP2K4	0.66362975	3.53826665	64.7074198	8.69E-16	2.11E-15	0.62897691	2.77777778	97.2222222
ENSG00000264577	SNORD4A	0.51523632	1.86964161	28.2603371	1.06E-07	1.66E-07	0.57297405	8.57142857	91.4285714	SNORD4A	0.63260796	1.85717202	33.8069159	6.09E-09	1.15E-08	0.68137661	11.1111111	88.8888889
ENSG00000156500	FAM122C	0.41932237	2.74250784	24.4371929	7.68E-07	1.16E-06	0.54122141	8.57142857	91.4285714	FAM122C	0.53926693	2.75471679	33.3772143	7.59E-09	1.43E-08	0.51097748	8.33333333	91.6666667
ENSG00000251578	TRBV21-1	0.53558335	0.24888698	19.3205484	1.11E-05	1.59E-05	0.52155952	5.71428571	94.2857143	TRBV21-1	0.51198948	0.19370654	12.8746686	0.00033306	0.00048617	0.55421944	16.6666667	83.3333333
ENSG00000224137	AC079767.4	-6.7926346	0.42707887	1796.30392	0	0	-7.1098029	100	0	AC079767.4	-5.1278003	0.38651391	1271.60461	1.67E-278	1.39E-276	-4.9561328	100	0
ENSG00000224397	LINC01272	-4.31315	1.60834762	1588.10756	0	0	-4.1032442	100	0	LINC01272	-6.1578137	1.54756902	1883.17262	0	0	-6.5586175	100	0
ENSG00000253701	AL928768.3	-7.6493973	-0.1549888	1540.83544	0	0	-10000	100	0	AL928768.3	-6.7653976	-0.1260765	1264.1544	6.97E-277	5.04E-275	-10000	100	0
ENSG00000269728	RP11-145M9.4	-3.9258885	1.92315933	1595.42623	0	0	-3.5513645	100	0	RP11-145M9.	-4.2120502	1.87419804	1341.09959	1.32E-293	1.92E-291	-3.901069	100	0
ENSG00000234184	RP5-887A10.1	-6.8968541	-0.2443392	1379.36137	6.42E-302	2.96E-300	-10000	100	0	RP5-887A10.1	-5.2611058	-0.2655509	966.122068	4.15E-212	1.60E-210	-5.2494327	100	0
ENSG00000211459	MT-RNR1	-2.1076277	10.3428567	1231.26838	9.77E-270	3.44E-268	-1.8321774	100	0	MT-RNR1	-1.444179	10.4699443	151.19292	9.51E-35	6.97E-34	-1.1449902	100	0
ENSG00000267174	CTC-510F12.4	-4.3667017	-0.1435735	1007.37577	4.48E-221	1.28E-219	-4.4170339	97.1428571	0	CTC-510F12.4	-5.7086003	-0.1509149	1145.85915	3.56E-251	2.06E-249	-6.1929431	100	0
ENSG00000272523	LINC01023	-3.3236581	-0.0552731	763.125318	5.62E-168	1.20E-166	-3.3245239	100	0	LINC01023	-2.2824235	0.02224949	357.944618	7.89E-80	1.34E-78	-2.0701364	100	0
ENSG00000253364	RP11-731F5.2	-6.1493045	-1.383569	665.448564	9.76E-147	1.95E-145	-10000	100	0	RP11-731F5.2	-5.7197127	-1.3836192	581.090062	2.17E-128	6.62E-127	-10000	97.2222222	2.77777778
ENSG00000260359	NA	-2.546703	1.16163457	656.008091	1.10E-144	2.13E-143	-2.2024773	100	0	NA	-1.5678451	1.32657088	225.150197	6.81E-51	7.73E-50	-1.177893	94.4444444	5.55555556
ENSG00000180422	LINC00304	2.59928129	1.04129814	620.339836	6.31E-137	1.18E-135	2.97747543	0	100	LINC00304	1.8506121	0.4694092	266.518781	6.51E-60	9.42E-59	2.08639522	0	100
ENSG00000272077	RP11-348P10.2	-2.7887813	-0.2061804	564.262355	9.94E-125	1.80E-123	-2.3589464	100	0	RP11-348P10.	-1.6627003	-0.0066049	200.429189	1.68E-45	1.60E-44	-1.4332976	94.4444444	5.55555556
ENSG00000172965	MIR4435-1HG	-2.0915622	1.80458339	547.403374	4.62E-121	7.91E-120	-1.7886509	100	0	MIR4435-1HG	-2.1949603	1.86064093	415.251077	2.64E-92	5.27E-91	-1.7061829	100	0
ENSG00000233901	RP11-65J3.1	-3.5575437	-1.0548535	520.447266	3.38E-115	5.48E-114	-3.394676	100	0	RP11-65J3.1	-4.3160341	-1.0716429	563.559736	1.41E-124	4.09E-123	-4.2950207	100	0
ENSG00000175898	CTD-2369P2.2	-1.9804665	2.19404545	492.270036	4.57E-109	7.02E-108	-1.6215094	100	0	CTD-2369P2.2	-2.3828413	2.04226277	535.360606	1.93E-118	5.31E-117	-2.0339457	100	0
ENSG00000268913	AC026806.2	-2.8141361	-0.6658963	484.961394	1.78E-107	2.66E-106	-2.5875749	100	0	AC026806.2	-2.92414	-0.6145388	426.759211	8.25E-95	1.77E-93	-2.6641038	100	0
ENSG00000259004	RP11-8L8.2	-3.8074388	-1.4470085	453.037486	1.57E-100	2.05E-99	-3.7183709	100	0	RP11-8L8.2	-4.0313573	-1.4831157	435.048609	1.29E-96	3.00E-95	-3.987525	100	0
ENSG00000272053	RP11-367G6.3	-1.8772462	1.23959025	393.350157	1.54E-87	1.85E-86	-1.6808566	100	0	RP11-367G6.3	-1.3003513	1.37339221	163.648367	1.81E-37	1.39E-36	-1.1280003	97.2222222	2.77777778
ENSG00000188070	C11orf95	-1.982524	3.02141062	390.085469	7.93E-87	9.31E-86	-1.6765277	100	0	C11orf95	-1.0618466	3.21393278	152.266714	5.54E-35	4.11E-34	-0.8407216	91.6666667	8.33333333
ENSG00000270055	CTD-3092A11.2	1.42938016	5.78316899	388.383811	1.86E-86	2.14E-85	1.70314396	0	100	CTD-3092A11.	1.11982335	5.56337549	178.923861	8.33E-41	7.42E-40	1.29918104	0	100
ENSG00000261455	LINC01003	-1.7132568	1.68651382	376.242402	8.19E-84	9.25E-83	-1.4213782	100	0	LINC01003	-1.6530353	1.65789071	265.550497	1.06E-59	1.49E-58	-1.3671332	100	0
ENSG00000225331	AP001055.6	-2.02356	0.11917588	348.785532	7.79E-78	7.91E-77	-1.5449377	100	0	AP001055.6	-2.613522	0.00906469	449.980431	7.28E-100	1.76E-98	-2.2604225	100	0
ENSG00000251301	RP11-81H14.2	-3.2356497	-1.3579215	348.468159	9.14E-78	9.12E-77	-3.0976942	97.1428571	2.85714286	RP11-81H14.2	-1.567292	-1.0214541	102.409005	4.52E-24	2.14E-23	-1.3375568	83.3333333	16.6666667
ENSG00000222041	LINC00152	-1.577758	2.17978088	329.403085	1.30E-73	1.25E-72	-1.3078671	97.1428571	2.85714286	LINC00152	-1.6755315	2.28894992	274.374166	1.26E-61	1.93E-60	-1.2805489	94.4444444	5.55555556
ENSG00000269290	RP11-869B15.1	1.93885444	0.0544986	306.32777	1.38E-68	1.25E-67	2.12322316	2.85714286	97.1428571	RP11-869B15.	1.0346688	-0.6382633	61.8248972	3.75E-15	1.14E-14	1.32186282	11.1111111	88.8888889
ENSG00000260006	RP11-469M7.1	-1.855559	4.23900225	298.857752	5.84E-67	5.19E-66	-1.4665234	100	0	RP11-469M7.	-1.1082016	4.39113748	194.853801	2.77E-44	2.59E-43	-0.7401092	100	0
ENSG00000270127	PRKXP1	1.84641768	0.53869689	298.843034	5.89E-67	5.19E-66	1.98587306	0	100	PRKXP1	1.13191183	-0.0701806	90.8825138	1.52E-21	6.49E-21	1.24989614	0	100
ENSG00000260910	LINC00565	1.49034348	2.1117465	297.549968	1.13E-66	9.78E-66	1.65872027	0	100	LINC00565	1.11193648	1.8487804	125.89559	3.24E-29	1.86E-28	1.30469186	0	100
ENSG00000272316	XXbac-BPGBPG	1.46303484	2.06281601	288.963228	8.36E-65	7.06E-64	1.61714674	0	100	XXbac-BPGBP	0.83196722	1.63044646	69.6051466	7.24E-17	2.45E-16	1.03487282	5.55555556	94.4444444
ENSG00000226137	BAIAP2-AS1	-1.6947454	0.79242735	283.245289	1.47E-63	1.23E-62	-1.3778186	97.1428571	2.85714286	BAIAP2-AS1	-2.656546	0.64983385	533.994614	3.82E-118	1.00E-116	-2.4509473	100	0
ENSG00000237438	CECR7	-1.727156	0.28353166	265.368332	1.16E-59	9.14E-59	-1.3658024	100	0	CECR7	-1.4201768	0.41856942	166.208399	4.98E-38	4.01E-37	-1.08309	97.2222222	2.77777778
ENSG00000266896	RP1-266L20.9	2.01457209	-0.6665399	262.409915	5.12E-59	3.93E-58	2.35721757	2.85714286	97.1428571	RP1-266L20.9	1.8189148	-0.7791017	165.229103	8.15E-38	6.47E-37	2.09254907	2.77777778	97.2222222
ENSG00000235499	AC073046.25	-1.4215799	1.53015978	253.606321	4.25E-57	3.18E-56	-1.0932193	100	0	AC073046.25	-1.0789521	1.60910882	116.246708	4.20E-27	2.23E-26	-0.7053929	97.2222222	2.77777778
ENSG00000261560	RP11-166B2.3	1.45190073	1.51405008	249.523343	3.30E-56	2.44E-55	1.63239529	0	100	RP11-166B2.3	1.7698792	1.69826514	289.53597	6.28E-65	1.01E-63	1.81993621	0	100
ENSG00000272086	CTD-2186M15.	-1.6295453	0.15543834	242.858131	9.37E-55	6.76E-54	-1.3726398	100	0	CTD-2186M15	-1.3188897	0.22851158	141.83678	1.06E-32	6.87E-32	-0.9620747	100	0
ENSG00000260306	RP11-645C24.5	1.69477236	0.07873055	242.439378	1.16E-54	8.24E-54	2.16589842	0	100	RP11-645C24.	0.96942327	-0.4976889	58.7875385	1.76E-14	5.11E-14	1.4028926	8.33333333	91.6666667
ENSG00000228223	HCG11	-1.3517389	1.7462207	240.203058	3.55E-54	2.50E-53	-0.996203	100	0	HCG11	-2.0201823	1.49797182	381.447179	6.02E-85	1.09E-83	-1.7151964	100	0
ENSG00000228106	RP11-452F19.3	-1.3437444	1.72521736	238.515824	8.29E-54	5.77E-53	-1.0616488	97.1428571	2.85714286	RP11-452F19.	-1.0363361	1.84277972	110.1237	9.21E-26	4.72E-25	-0.8437107	91.6666667	8.33333333
ENSG00000272849	RP11-347I19.8	1.55851293	0.60526796	225.883012	4.71E-51	3.21E-50	1.80634141	2.85714286	97.1428571	RP11-347I19.	1.34903944	0.37653884	147.661069	5.63E-34	3.92E-33	1.8042685	2.77777778	97.2222222
ENSG00000240350	AC017002.1	-1.5887787	0.40406113	220.440216	7.25E-50	4.67E-49	-1.316065	88.5714286	11.4285714	AC017002.1	-1.8068161	0.40111298	234.89193	5.11E-53	6.04E-52	-1.2301005	86.1111111	13.8888889
ENSG00000238142	RP11-108M9.4	-1.7385638	-0.7104535	211.211023	7.48E-48	4.62E-47	-1.3658024	100	0	RP11-108M9.	-1.4315255	-0.6691416	121.183741	3.48E-28	1.94E-27	-1.1510664	94.4444444	5.55555556
ENSG00000261355	NA	1.19901834	2.2225395	194.636665	3.09E-44	1.82E-43	1.49180322	2.85714286	97.1428571	NA	0.37695372	1.69613079	14.680652	0.00012735	0.00019821	0.55968221	5.55555556	94.4444444
ENSG00000272341	RP1-151F17.2	1.49557612	-0.0051418	191.191752	1.75E-43	1.02E-42	1.88353759	0	100	RP1-151F17.2	1.23827361	-0.1231438	108.704539	1.88E-25	9.48E-25	1.5321372	5.55555556	94.4444444
ENSG00000240905	RN7SL798P	-4.6450788	-2.9100695	182.680652	1.26E-41	7.18E-41	-10000	97.1428571	0	RN7SL798P	-3.0574696	-2.794208	130.776241	2.77E-30	1.67E-29	-3.9068797	94.4444444	5.55555556
ENSG00000260077	RP11-254F7.2	-1.3712845	0.26407657	178.396578	1.09E-40	6.08E-40	-1.0701652	94.2857143	5.71428571	RP11-254F7.2	-1.5073003	0.20560795	182.105656	1.68E-41	1.52E-40	-1.3903808	100	0
ENSG00000228434	AC004951.6	1.06394704	1.68168864	148.446366	3.79E-34	1.97E-33	1.46278815	2.85714286	97.1428571	AC004951.6	0.76239093	1.48467424	57.0475538	4.25E-14	1.22E-13	1.1695934	5.55555556	94.4444444
ENSG00000251867	RP11-48B3.5	-1.0881525	1.29769664	142.545996	7.39E-33	3.81E-32	-0.929875	94.2857143	5.71428571	RP11-48B3.5	-1.1935543	1.20661775	137.687244	8.53E-32	5.31E-31	-0.8357588	100	0
ENSG00000236194	AC003104.1	1.37733619	-0.561717	141.269414	1.40E-32	7.13E-32	1.678878	0	100	AC003104.1	1.1956613	-0.6776805	81.3760313	1.87E-19	7.16E-19	1.6305173	11.1111111	88.8888889
ENSG00000254615	RP11-395G23.	1.222503	0.43795812	141.045489	1.57E-32	7.92E-32	1.51887991	0	100	RP11-395G23.	1.16911734	0.24996101	111.200358	5.35E-26	2.76E-25	1.42506639	0	100

ENSG00000233261	LINC00264	1.25240135	0.06219516	140.11679	2.51E-32	1.25E-31	1.67914567	2.85714286	97.1428571	LINC00264	1.01658055	-0.1063059	75.4173231	3.81E-18	1.35E-17	1.32745927	0	100
ENSG00000231607	DLEU2	-1.1127256	0.97112681	136.310673	1.71E-31	8.38E-31	-0.7678532	100	0	DLEU2	-1.5646598	0.82666073	220.056261	8.79E-50	9.61E-49	-1.2414152	100	0
ENSG00000269996	NA	-1.0135602	1.50434968	131.667655	1.77E-30	8.34E-30	-0.7450478	91.4285714	8.57142857	NA	-1.6988366	1.34766848	271.856576	4.47E-61	6.64E-60	-1.2474216	100	0
ENSG00000267701	RP11-28F1.2	-2.0425613	-1.8306119	128.504214	8.71E-30	3.95E-29	-1.7786211	100	0	RP11-28F1.2	-1.857651	-1.8523306	103.052651	3.26E-24	1.57E-23	-1.7305275	91.6666667	8.33333333
ENSG00000261824	LINC00662	-1.1327787	0.3149384	125.171191	4.67E-29	2.09E-28	-0.7635914	100	0	LINC00662	-1.2706088	0.23116184	132.016881	1.48E-30	9.04E-30	-0.9952785	100	0
ENSG00000273352	RP11-61L19.3	-1.4432534	-1.0431036	122.593616	1.71E-28	7.54E-28	-0.9325673	91.4285714	8.57142857	RP11-61L19.3	-1.1279496	-0.9234789	67.084793	2.60E-16	8.41E-16	-0.7767928	83.3333333	16.6666667
ENSG00000215908	CROCCP2	1.12613435	4.50095522	121.979443	2.33E-28	1.02E-27	1.35838431	0	100	CROCCP2	1.45663323	4.52746087	384.228983	1.49E-85	1.21E-84	1.39444905	0	100
ENSG00000215908	CROCCP2	1.12613435	4.50095522	121.979443	2.33E-28	1.02E-27	1.35838431	0	100	CROCCP2	1.13487923	4.45627587	203.913016	2.92E-46	2.87E-45	1.39444905	0	100
ENSG00000232470	RP11-313D6.3	1.80906061	-1.6315111	112.70922	2.50E-26	1.03E-25	2.2543504	0	100	RP11-313D6.3	1.55423368	-1.8615322	72.4303295	1.73E-17	6.04E-17	1.97710821	0	100
ENSG00000259715	CTD-3110H11.1	1.90692877	-1.6301767	111.382446	4.88E-26	1.97E-25	2.4845966	2.85714286	97.1428571	CTD-3110H11.	1.44910506	-1.9979339	53.9019648	2.11E-13	5.84E-13	2.05983486	11.1111111	88.8888889
ENSG00000271938	RP11-589C21.6	1.18256728	-0.3157223	110.849033	6.39E-26	2.57E-25	1.39923979	2.85714286	97.1428571	RP11-589C21.	1.49951715	-0.2865528	145.18241	1.96E-33	1.33E-32	1.7636302	0	100
ENSG00000255989	NA	-1.0951041	-0.1638419	107.744734	3.06E-25	1.21E-24	-0.7504703	91.4285714	8.57142857	NA	-0.9709911	-0.1436338	68.9834784	9.93E-17	3.34E-16	-0.7569836	88.8888889	11.1111111
ENSG00000270972	RP11-326C3.15	1.65429656	-1.4432141	103.305841	2.87E-24	1.12E-23	1.87378968	8.57142857	91.4285714	RP11-326C3.1	1.09706076	-1.9450396	35.3617423	2.74E-09	5.98E-09	1.37388901	11.1111111	88.8888889
ENSG00000271843	RP11-245J9.5	1.16914826	-0.5820735	100.188648	1.39E-23	5.35E-23	1.52275721	5.71428571	94.2857143	RP11-245J9.5	0.99213383	-0.7291337	55.029807	1.19E-13	3.34E-13	1.40601028	8.33333333	91.6666667
ENSG00000227486	RP13-188A5.1	-1.3252278	-1.1106149	97.2536123	6.10E-23	2.30E-22	-0.9679819	82.8571429	17.1428571	RP13-188A5.1	-1.5151908	-1.241838	99.2121972	2.27E-23	1.05E-22	-1.3017979	91.6666667	8.33333333
ENSG00000271975	RP11-383J24.6	-0.8609207	1.35552564	92.9837863	5.27E-22	1.91E-21	-0.5433531	91.4285714	8.57142857	RP11-383J24.	-1.4679653	1.17805338	204.979475	1.71E-46	1.74E-45	-1.1431123	100	0
ENSG00000264112	RP11-159D12.2	0.9602367	4.66520381	91.945445	8.91E-22	3.22E-21	1.17206435	2.85714286	97.1428571	RP11-159D12.	0.97471027	4.71586226	147.194426	7.12E-34	4.90E-33	1.33301787	2.77777778	97.2222222
ENSG00000260539	GLG1	0.93106508	0.93214257	91.4476971	1.15E-21	4.11E-21	1.26600723	0	100	GLG1	0.48415655	0.64479745	20.7706831	5.18E-06	9.08E-06	0.65932128	16.6666667	83.3333333
ENSG00000222375	RN7SKP127	2.4826465	-2.5941428	90.632516	1.73E-21	6.13E-21	2.88156798	0	100	RN7SKP127	2.13805478	-2.8490724	66.2405859	3.99E-16	1.28E-15	2.6756889	2.77777778	91.6666667
ENSG00000152487	ARL5B-AS1	1.53879935	-1.5854301	88.9066991	4.14E-21	1.45E-20	1.9432007	2.85714286	97.1428571	ARL5B-AS1	1.40494802	-1.6755628	67.1283768	2.54E-16	8.27E-16	1.62035411	2.77777778	97.2222222
ENSG00000269086	CTC-523E23.5	0.88185295	1.08862501	87.1633852	9.99E-21	3.44E-20	1.23867548	0	100	CTC-523E23.5	0.90470375	1.12338928	77.3217909	1.45E-18	5.26E-18	1.20220481	0	100
ENSG00000270066	SCARNA2	1.41441644	-1.2787625	86.639548	1.30E-20	4.46E-20	1.53674332	2.85714286	97.1428571	SCARNA2	0.92045981	-1.8573902	26.3437275	2.86E-07	5.57E-07	1.1469396	13.8888889	86.1111111
ENSG00000273033	RP11-67L2.2	-0.9667587	3.82525915	82.6866155	9.62E-20	3.24E-19	-0.5733246	97.1428571	2.85714286	RP11-67L2.2	-1.3039892	3.68528862	254.798466	2.34E-57	3.00E-56	-0.9882202	100	0
ENSG00000204261	PSMB8-AS1	-0.8733973	3.09354211	79.863335	4.01E-19	1.33E-18	-0.5678526	94.2857143	5.71428571	PSMB8-AS1	-0.8651905	3.05898101	100.457209	1.21E-23	5.65E-23	-0.5163391	100	0
ENSG00000261526	CTB-31O20.2	0.89996087	4.30779858	73.6809907	9.18E-18	2.90E-17	1.22381845	0	100	CTB-31O20.2	0.77174499	4.18284686	94.6771077	2.24E-22	1.01E-21	1.01830299	2.77777778	97.2222222
ENSG00000230002	ALMS1-IT1	0.80726684	1.03970337	72.8989496	1.36E-17	4.26E-17	1.09138517	0	100	ALMS1-IT1	0.8469665	1.01609807	68.2968368	1.41E-16	4.65E-16	1.11543578	2.77777778	97.2222222
ENSG00000237491	RP11-206L10.9	0.79318311	0.77696465	66.0788618	4.33E-16	1.31E-15	1.06766314	5.71428571	94.2857143	RP11-206L10.	0.89821586	0.82921647	75.3057704	4.03E-18	1.42E-17	1.15459039	2.77777778	97.2222222
ENSG00000270704	SNORD64	1.23474847	-1.5442355	59.7866871	1.06E-14	3.02E-14	1.66114517	8.57142857	91.4285714	SNORD64	1.25646176	-1.5119706	59.2379094	1.40E-14	4.09E-14	1.76423841	5.55555556	94.4444444
ENSG00000269942	NA	1.40963465	-1.8507047	59.2171893	1.41E-14	3.99E-14	1.98856061	5.71428571	94.2857143	NA	1.24034205	-1.8965891	44.5598398	2.47E-11	6.05E-11	1.70988021	11.1111111	88.8888889
ENSG00000271869	RP11-51J9.5	0.72566339	3.05414844	56.3376327	6.10E-14	1.70E-13	1.00245913	0	100	RP11-51J9.5	0.76496184	3.04630366	78.1083893	9.75E-19	3.57E-18	1.00429901	0	100
ENSG00000271725	RP11-761I4.4	-0.8477544	-0.6740512	54.5623432	1.51E-13	4.14E-13	-0.5893161	88.5714286	11.4285714	RP11-761I4.4	-0.9547284	-0.7468425	52.9501028	3.42E-13	9.43E-13	-0.6711213	80.5555556	19.4444444
ENSG00000267481	CTC-559E9.5	0.72018171	0.64223774	52.8675796	3.57E-13	9.63E-13	0.96563225	0	100	CTC-559E9.5	0.36330251	0.43550431	11.714422	0.00062018	0.00090449	0.58418711	8.33333333	91.6666667
ENSG00000239884	RN7SL608P	1.0243318	-1.2478128	52.6310084	4.02E-13	1.08E-12	1.19902147	11.4285714	88.5714286	RN7SL608P	1.23880102	-1.1336359	69.6236886	7.18E-17	2.44E-16	1.61982787	5.55555556	94.4444444
ENSG00000260336	RP11-395B7.7	0.6487196	2.72544557	50.9554228	9.45E-13	2.49E-12	0.84820603	2.85714286	97.1428571	RP11-395B7.7	0.33630852	2.53199247	13.2823773	0.00026791	0.00040608	0.52292459	19.4444444	80.5555556
ENSG00000270419	CAHM	-0.9366824	-1.1951761	48.5107845	3.28E-12	8.55E-12	-0.601689	88.5714286	11.4285714	CAHM	-1.635266	-1.4125743	106.067643	7.13E-25	3.53E-24	-1.2444907	94.4444444	5.55555556
ENSG00000268205	CTC-444N24.11	0.61476736	2.58058261	48.0001372	4.26E-12	1.11E-11	0.86390751	5.71428571	94.2857143	CTC-444N24.1	0.29749538	2.35117259	10.0345967	0.00153627	0.00218551	0.56299821	19.4444444	80.5555556
ENSG00000222414	RNU2-59P	-1.5544359	-2.3062229	47.1120581	6.70E-12	1.72E-11	-2.023371	80	20	RNU2-59P	-0.9679482	-2.3501176	22.805567	1.79E-06	3.27E-06	-0.6551594	72.2222222	27.7777778
ENSG00000232412	RP1-315G1.3	-1.2560636	-1.9720018	46.3273209	1.00E-11	2.55E-11	-0.9265094	77.1428571	22.8571429	RP1-315G1.3	-0.9842486	-2.0018776	29.087641	6.92E-08	1.39E-07	-0.7398108	77.7777778	22.2222222
ENSG00000271347	RP11-701H24.7	1.38476273	-2.1739881	44.2898912	2.83E-11	7.13E-11	1.67842837	11.4285714	88.5714286	RP11-701H24.	1.06798429	-2.3625332	26.5281037	2.60E-07	5.08E-07	1.52687283	8.33333333	91.6666667
ENSG00000269900	RMRP	0.81296067	0.46842308	44.2289827	2.92E-11	7.32E-11	0.59874017	22.8571429	77.1428571	RMRP	0.68527739	-0.8518974	24.2629906	8.40E-07	1.57E-06	0.84715152	22.2222222	77.7777778
ENSG00000228485	GRK5-IT1	-0.9612369	-1.3931038	42.9811612	5.53E-11	1.33E-10	-0.6154948	80	20	GRK5-IT1	-1.075295	-1.5381088	43.8970279	3.46E-11	8.42E-11	-0.7127025	77.7777778	22.2222222
ENSG00000243339	RN7SL738P	-1.0225245	-1.5782762	42.7862915	6.11E-11	1.46E-10	-0.5686021	88.5714286	11.4285714	RN7SL738P	-1.0354754	-1.5907265	40.2079177	2.28E-10	5.29E-10	-0.8028758	80.5555556	19.4444444
ENSG00000196559	LINC00610	0.62939357	0.83485601	42.3687265	7.56E-11	1.80E-10	0.89169779	2.85714286	97.1428571	LINC00610	0.48203527	0.71806606	21.50396	3.53E-06	6.29E-06	0.78186148	5.55555556	94.4444444
ENSG00000263990	CTC-542B22.2	1.24200556	-2.042102	41.0050087	1.52E-10	3.54E-10	1.47276984	5.71428571	94.2857143	CTC-542B22.2	1.23356905	-2.1091639	40.9722849	1.54E-10	3.65E-10	1.48861851	8.33333333	91.6666667
ENSG00000272994	RP11-332H14.2	0.53546419	2.44216582	38.6122438	5.17E-10	1.17E-09	0.83743382	2.85714286	97.1428571	RP11-332H14.	0.52464535	2.41415963	31.9748665	1.56E-08	3.25E-08	0.83180728	0	100
ENSG00000260534	RP11-1006G14	0.59643321	0.74919459	37.6170398	8.61E-10	1.92E-09	0.91263352	2.85714286	97.1428571	RP11-1006G1	0.6208056	0.73698859	35.9913778	1.98E-09	4.38E-09	0.93282444	0	100
ENSG00000272432	RP3-465N24.6	-0.9533292	-1.7007015	34.4933957	4.28E-09	9.18E-09	-0.6841318	77.1428571	22.8571429	RP3-465N24.6	-0.8444762	-1.7006637	25.7551601	3.88E-07	7.46E-07	-0.6683622	69.4444444	30.5555556
ENSG00000269044	CTC-429P9.3	0.49093723	1.86124614	34.2271816	4.90E-09	1.04E-08	0.69236069	0	100	CTC-429P9.3	0.71852084	1.97502367	54.9515677	1.24E-13	3.44E-13	0.85200382	0	100
ENSG00000260404	RP11-384K6.6	0.59819703	4.42558631	33.8885981	5.84E-09	1.22E-08	0.81244772	2.85714286	97.1428571	RP11-384K6.6	0.74852366	4.53999911	88.2713696	5.71E-21	2.36E-20	0.92706353	2.77777778	97.2222222
ENSG00000269958	RP11-73M18.8	0.48864053	1.83090548	33.6848716	6.48E-09	1.35E-08	0.76065349	2.85714286	97.1428571	RP11-73M18.	0.47306515	1.78145605	23.6279858	1.17E-06	2.16E-06	0.65971792	2.77777778	97.2222222
ENSG00000228107	AP000692.9	0.86062583	-1.4879536	32.3004854	1.32E-08	2.73E-08	0.90145348	0	100	AP000692.9	0.68310364	-1.5680979	17.9299859	2.29E-05	3.84E-05	0.87275468	11.1111111	88.8888889
ENSG00000273142	RP11-458F8.4	0.4649805	2.01865512	31.0021838	2.58E-08	5.15E-08	0.851752	8.57142857	91.4285714	RP11-458F8.4	0.64614523	2.10261104	45.5208253	1.51E-11	3.74E-11	0.71802768	2.77777778	97.2222222
ENSG00000236337	FMR1-IT1	1.21688041	-2.4917902	28.540659	9.18E-08	1.77E-07	1.70379266	8.57142857	91.4285714	FMR1-IT1	1.06579254	-2.537506	23.9103436	1.01E-06	1.87E-06	1.13536582	13.8888889	86.1111111

ENSG00000231560	AC091814.3	0.52163777	0.70604539	28.3544168	1.01E-07	1.93E-07	0.85675442	5.71428571	94.2857143	AC091814.3	0.88892145	1.03388281	73.1574467	1.20E-17	4.20E-17	1.1436547	5.55555556	94.4444444
ENSG00000225975	AC074138.3	0.59218485	-0.7525362	25.9941895	3.42E-07	6.39E-07	0.83609784	5.71428571	94.2857143	AC074138.3	0.81529481	-0.6881691	40.0919824	2.42E-10	5.57E-10	1.03400343	2.77777778	97.2222222
ENSG00000270108	RP11-73M18.6	0.54260167	-0.3090027	25.4906956	4.45E-07	8.17E-07	0.87950444	14.2857143	85.7142857	RP11-73M18.	0.48458829	-0.3620723	16.0128096	6.29E-05	0.00010147	0.70075436	19.4444444	80.5555556
ENSG00000242853	RN7SL749P	-0.8410255	-1.7352397	25.457735	4.52E-07	8.23E-07	-0.5704067	74.2857143	25.7142857	RN7SL749P	-0.8834276	-1.8336675	25.3109249	4.88E-07	9.25E-07	-0.6640104	77.7777778	22.2222222
ENSG00000252464	RN7SKP70	1.04318787	-2.2491663	24.964869	5.84E-07	1.06E-06	1.38579965	14.2857143	85.7142857	RN7SKP70	0.88766392	-2.2329989	19.169088	1.20E-05	2.04E-05	1.31126497	19.4444444	80.5555556
ENSG00000207445	SNORD15B	1.39408708	-2.6566155	24.846839	6.21E-07	1.12E-06	2.18396107	11.4285714	88.5714286	SNORD15B	0.93628582	-3.1853523	11.3129788	0.00076967	0.0011141	1.04973488	22.2222222	75
ENSG00000268087	CTC-429P9.2	0.61418051	-0.9844489	24.3389216	8.08E-07	1.45E-06	0.97114614	2.85714286	97.1428571	CTC-429P9.2	0.65007236	-0.9422609	22.8199105	1.78E-06	3.26E-06	0.99526609	8.33333333	91.6666667
ENSG00000224078	SNHG14	0.49931382	4.35172604	23.6282673	1.17E-06	2.06E-06	0.85950025	2.85714286	97.1428571	SNHG14	0.40822757	4.29023864	27.2742427	1.77E-07	3.48E-07	0.72284319	2.77777778	97.2222222
ENSG00000252010	SCARNA5	1.04443443	-1.8904968	23.354162	1.35E-06	2.35E-06	0.98110366	25.7142857	74.2857143	SCARNA5	0.93049636	-2.7411429	15.4727168	8.37E-05	0.00013388	1.13994692	19.4444444	80.5555556
ENSG00000265802	RN7SL49P	1.09043186	-2.4949185	23.1040503	1.53E-06	2.66E-06	1.73656217	8.57142857	91.4285714	RN7SL49P	0.54878701	-2.7176231	5.92110263	0.01496059	0.01899602	1.02356421	22.2222222	77.7777778
ENSG00000260257	RP5-1085F17.3	0.41612858	1.58823951	23.0134388	1.61E-06	2.78E-06	0.66533987	8.57142857	91.4285714	RP5-1085F17.	0.45701763	1.57885091	21.2051085	4.13E-06	7.31E-06	0.6465356	11.1111111	88.8888889
ENSG00000264608	RP11-192H23.8	0.64526077	-1.2617306	22.1123513	2.57E-06	4.39E-06	1.10451625	8.57142857	91.4285714	RP11-192H23.	0.37506101	-1.4348948	6.01106569	0.01421644	0.01813066	0.66460018	25	75
ENSG00000271862	RP11-343L5.2	0.47784906	0.15250568	22.0375505	2.67E-06	4.54E-06	0.8287758	2.85714286	97.1428571	RP11-343L5.2	0.32604502	0.0617318	8.56010182	0.0034361	0.00472566	0.74917608	19.4444444	80.5555556
ENSG00000259321	RP11-468E2.5	0.68201907	-1.5033034	20.34269	6.47E-06	1.07E-05	1.02633138	8.57142857	91.4285714	RP11-468E2.5	0.59281829	-1.5934106	13.5030098	0.00023818	0.00036196	0.8882744	19.4444444	80.5555556
ENSG00000232300	FAM215B	0.37342377	2.06893564	19.6278426	9.41E-06	1.54E-05	0.68876129	14.2857143	85.7142857	FAM215B	0.33239926	2.03861463	11.6323664	0.00064814	0.0009429	0.66045942	16.6666667	83.3333333
ENSG00000263621	NA	0.44141438	0.12704282	18.5161448	1.68E-05	2.73E-05	0.7758935	14.2857143	85.7142857	NA	0.50264228	0.13651189	20.1378144	7.21E-06	1.26E-05	0.80117049	11.1111111	88.8888889
ENSG00000259380	RP11-346D14.1	0.33613606	2.07488942	15.9928574	6.36E-05	9.89E-05	0.53577888	14.2857143	85.7142857	RP11-346D14.	0.42768851	2.18096322	19.3117185	1.11E-05	1.90E-05	0.61703887	8.33333333	91.6666667
ENSG00000202538	RNU4-2	0.7623301	-1.4485325	15.4042162	8.68E-05	0.00013365	1.40359811	31.4285714	68.5714286	RNU4-2	0.68887211	-2.1061803	9.76845299	0.00177532	0.0025071	1.13089771	30.5555556	69.4444444
ENSG00000267904	CTC-429P9.5	0.40991547	-0.5664241	13.5399147	0.00023354	0.00034973	0.54029393	5.71428571	94.2857143	CTC-429P9.5	0.46071651	-0.5624797	13.5096613	0.00023734	0.00036163	0.70323852	19.4444444	80.5555556
ENSG00000232164	AC092669.3	0.29931369	2.18103058	12.659424	0.00037368	0.00055267	0.58043915	8.57142857	91.4285714	AC092669.3	0.35792209	2.28083867	13.8590502	0.00019705	0.00030262	0.54441425	22.2222222	77.7777778
ENSG00000225528	RP3-370M22.8	0.35764184	-0.2569858	11.3854856	0.0007402	0.00107617	0.80627553	20	80	RP3-370M22.	1.07916933	0.16263766	92.4028977	7.07E-22	3.15E-21	1.30394372	0	100
ENSG00000269952	RP11-324I22.3	0.43328927	-1.0923612	10.594637	0.00113416	0.00161753	1.06313283	22.8571429	77.1428571	RP11-324I22.	0.89455004	-0.9412935	40.6034373	1.86E-10	4.37E-10	1.47110755	13.8888889	86.1111111
ENSG00000232686	NA	0.43269249	-1.1591816	10.4717041	0.00121217	0.00172059	0.69942621	20	80	NA	0.60467798	-1.1230866	17.9105051	2.32E-05	3.86E-05	0.89136975	13.8888889	86.1111111
ENSG00000267074	RP11-1094M14	0.44252575	-1.1899688	10.3418629	0.00130047	0.00184156	0.72786095	25.7142857	74.2857143	RP11-1094M1	0.82386388	-0.9785091	33.485993	7.18E-09	1.53E-08	0.94718893	11.1111111	88.8888889
ENSG00000166770	ZNF667-AS1	0.29520388	0.66321166	9.12094183	0.002527	0.0035449	0.63913536	0	100	ZNF667-AS1	1.15717269	1.20558015	127.38626	1.53E-29	8.94E-29	1.39817971	2.77777778	97.2222222
ENSG00000263607	NA	0.60066496	-2.3226957	8.23702219	0.00410444	0.0056389	0.77682262	14.2857143	85.7142857	NA	0.89774601	-2.1913692	20.9243111	4.78E-06	8.43E-06	1.30740433	13.8888889	86.1111111
ENSG00000260808	CTD-2007L18.5	0.39955916	-1.464078	7.32325382	0.00680681	0.00918306	0.62087568	11.4285714	88.5714286	CTD-2007L18.	0.67640773	-1.3607226	19.6506774	9.30E-06	1.60E-05	1.0525078	13.8888889	86.1111111
ENSG00000269867	CTD-2583A14.8	0.4049728	-1.5427047	7.03891254	0.00797574	0.01071182	0.73622683	11.4285714	88.5714286	CTD-2583A14.	0.41950142	-1.5881276	6.82467563	0.00899069	0.01183093	0.74043534	19.4444444	80.5555556
ENSG00000269940	RP11-73M18.7	0.28382722	-0.6105158	6.38870776	0.01148486	0.01515293	0.63198088	22.8571429	77.1428571	RP11-73M18.	0.37945226	-0.5795718	9.21650072	0.00239844	0.00334625	0.73874413	16.6666667	83.3333333
ENSG00000256582	RP11-75L1.1	0.2547249	0.09211461	6.1803188	0.0129179	0.01693178	0.58598212	5.71428571	94.2857143	RP11-75L1.1	0.26498844	0.1126828	5.68862667	0.01707521	0.0214925	0.50190004	8.33333333	91.6666667
ENSG00000214293	APTR	0.24411223	0.0843766	5.75358942	0.016455	0.02152084	0.58565292	8.57142857	91.4285714	APTR	0.27225162	0.09309656	6.11666532	0.01339132	0.01715392	0.51241133	2.77777778	97.2222222
ENSG00000212443	SNORA53	0.51609212	-2.4922035	5.07061348	0.02433477	0.03108002	0.9820688	28.5714286	71.4285714	SNORA53	0.79712251	-2.4006553	14.4079809	0.00014718	0.00022846	1.09443259	33.3333333	66.6666667
ENSG00000178440	LINC00843	0.26290097	-0.8387798	4.93349849	0.02634094	0.03342844	0.53561429	17.1428571	82.8571429	LINC00843	0.37224284	-0.8308246	7.95574067	0.00479351	0.00653045	0.73115464	22.2222222	77.7777778
ENSG00000272054	RP11-423P10.2	0.21131912	0.83244405	4.75613852	0.02919397	0.0367378	0.51355966	20	80	RP11-423P10.	0.64070314	1.03674223	38.5204182	5.42E-10	1.23E-09	0.85223286	13.8888889	86.1111111
ENSG00000257499	NA	0.21367619	0.17127374	4.44061825	0.03509354	0.04370276	0.62528379	14.2857143	85.7142857	NA	0.57891494	0.29069235	28.4206573	9.76E-08	1.95E-07	0.84164508	5.55555556	94.4444444

Supplementary Table 4A: Number of DE genes in Case-Control comparisons accross different fractions.

Total Number of Genes = 63677
Coding Genes = 45618
Non-coding Genes = 18247
Genes belonging to both groups = 188

Number of Genes:	**CD4+**		**CD8+**		**CD4-CD8-**		**PBMC**	
Analysis Type:	**Over All Timepoints**	**12 months before SC**	**Over All Timepoints**	**12 months before SC**	**Over All Timepoints**	**12 months before SC**	**Over All Timepoints**	**12 months before SC**
FILTERING STEP 1								
RPKM > 0	38380	31939	41014	31392	40970	39018	36593	32941
Coding genes with RPKM > 0	32046	27343	33937	26937	33880	32630	30743	28120
Non-coding genes with RPKM > 0	6498	4738	7246	4588	7263	6557	6006	4966
FILTERING STEP 2								
Coding genes with RPKM > 3	7129	6992	7009	6903	7424	7348	7341	7255
Non-coding genes with RPKM > 0.5	580	550	573	565	570	565	503	497
FILTERING STEP 3	**erential expression analysis takes place before filtering ste**		**erential expression analysis takes place before filtering ste**		**erential expression analysis takes place before filtering ste**		**erential expression analysis takes place before filtering ste**	
Coding Genes								
*(|medianLogFC| > 0.5) + Percent Up/Down-regulation > 65%	40	16	58	77	114	22	68	27
(|medianLogFC| > 0.5) + Percent Up/Down-regulation > 75%	12	11	25	45	46	6	13	6
Non-coding Genes								
*(|medianLogFC| > 0.5) + Percent Up/Down-regulation > 65%	11	1	12	3	29	1	17	0
(|medianLogFC| > 0.5) + Percent Up/Down-regulation > 75%	2	1	4	2	16	0	2	0

***NOTE**: Genes with |medianLogFC| > 0.5 and Percent Up/Down-regulation > 65% were considered differentially expressed

Supplementary Table 4B. Protein coding DE genes between Cases and Controls

Ensembl Gene IDs	Gene Names	IPA ANNOTATION				Previously published	Median LogFC								FDR								Percent Up								Percent Down							
							Over All Timepoints				12 mo before SC				Over All Timepoints				12 mo before SC				Over All Timepoints				12 mo before SC				Over All Timepoints				12 mo before SC			
		Symbol	Entrez Gene Name	Location	Type(s)		CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC
ENSG00000215513	NA						-2.16	-2.00	-2.28		-2.35	-2.00	-1.95		0.00	0.00	0.00		0.00	0.00	0.00		22	24	24		20	27	33		78	76	76		80	73	67	
ENSG00000205246	RPSAP58						1.34	1.71	1.47	1.32	0.59	1.83	1.83	1.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	67	70	71	71	60	82	67	58	33	30	29	29	40	18	33	42
ENSG00000181404	XXbac-YRM2039.2	WASHC1	WASH complex subunit 1	Cytoplasm	other		-2.07	-1.65	-1.33		-1.73	-0.98	-0.92		0.00	0.00	0.00		0.00	0.00	0.01		14	11	24		10	18	25		86	89	76		90	82	75	
ENSG00000129925	TMEM8A	TMEM8A	transmembrane protein 8A	Plasma Membrane	other		0.90	0.52	0.30	0.63	0.65	0.77	0.40	0.70	0.00	0.00	0.00	0.00	0.00	0.00	0.51	0.00	75	81	79	84	70	82	75	92	25	19	21	16	30	18	25	8
ENSG00000008517	IL32	IL32	interleukin 32	Extracellular Space	cytokine		1.09	1.12	1.28	1.02	0.96	1.14	1.26	1.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	78	70	92	84	80	73	83	83	22	30	8	16	20	27	17	17
ENSG00000237506	RPSAP15	RPSAP15	ribosomal protein SA pseu	Other	other		1.44	1.60	1.62	1.53	0.63	2.93	2.04	1.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	75	76	74	76	60	82	67	75	25	24	26	24	40	18	33	25
ENSG00000186470	BTN3A2	BTN3A2	butyrophilin subfamily 3 m	Plasma Membrane	other		0.75	0.69	0.80	0.89	0.55	0.68	0.76	1.01	0.00	0.01	0.00	0.00	0.45	0.00	0.01	0.00	78	73	82	76	80	82	83	83	22	27	18	24	20	18	17	17
ENSG00000188820	FAM26F	FAM26F	family with sequence simil	Other	other	Kallionpää et al. 2014	1.30		0.27	0.20	0.25		0.05	-0.19	0.00		0.09	0.15	1.00		1.00	1.00	75		71	58	50		58	42	25		29	42	50		42	58
ENSG00000137801	THBS1	THBS1	thrombospondin 1	Extracellular Space	other		0.62	0.70	0.47	0.40	0.71	0.37	0.28	0.63	0.00	0.06	0.00	0.00	0.00	0.07	0.13	0.00	69	54	61	71	90	55	58	83	31	46	39	29	10	45	42	17
ENSG00000088899	LZTS3	LZTS3	leucine zipper tumor suppr	Cytoplasm	other		-0.62	-0.43	-0.27	-0.38	-0.16	-0.10	-0.05	-0.18	0.00	0.06	0.01	0.00	1.00	0.95	1.00	1.00	25	32	39	34	30	45	50	33	75	68	61	66	70	55	50	67
ENSG00000133706	LARS	LARS	leucyl-tRNA synthetase	Cytoplasm	enzyme		0.50	0.82		0.81					0.00	0.00		0.00					75	73		71					25	27		29				
ENSG00000160593	AMICA1	JAML	junction adhesion molecul	Plasma Membrane	other		0.81	0.74	0.56	0.62	0.67	0.74	0.45	0.49	0.00	0.00	0.00	0.01	0.08	0.00	1.00	1.00	75	89	66	66	70	91	75	75	25	11	34	34	30	9	25	25
ENSG00000090857	PDPR	PDPR	pyruvate dehydrogenase pl	Cytoplasm	enzyme	Kallionpää et al. 2014	0.55	0.45	0.52	0.48	0.60	0.36	0.72	0.41	0.00	0.06	0.00	0.00	0.00	0.00	0.03	0.22	83	70	68	68	90	64	75	67	17	30	32	32	10	36	25	33
ENSG00000130222	GADD45G	GADD45G	growth arrest and DNA dar	Nucleus	other		-0.58	-0.74	-0.24	-0.43	-0.23	-0.14	0.09	0.12	0.00	0.00	0.10	0.01	1.00	0.68	1.00	1.00	22	19	32	29	40	36	58	58	78	81	68	71	60	64	42	42
ENSG00000165029	ABCA1	ABCA1	ATP binding cassette subfa	Plasma Membrane	transporter	Kallionpää et al. 2014	-0.61	-0.17	-0.26	-0.44	-0.19	-0.16	-0.23	-0.36	0.00	0.16	0.00	0.00	1.00	0.40	1.00	1.00	31	35	34	29	40	27	33	25	69	65	66	71	60	73	67	75
ENSG00000226210	WASH7P	LOC100288778	WAS protein family homolo	Other	other		0.64	0.68	0.87	0.78	0.45	0.64	0.88	0.71	0.00	0.01	0.00	0.00	1.00	0.17	0.57	0.31	83	78	84	84	80	82	83	83	17	22	16	16	20	18	17	17
ENSG00000145214	DGKQ	DGKQ	diacylglycerol kinase theta	Cytoplasm	kinase		0.51	0.20	0.54	0.69	0.47	0.31	0.84	0.86	0.00	0.47	0.00	0.00	0.24	0.07	0.01	0.00	81	68	84	87	90	73	92	92	19	32	16	13	10	27	8	8
ENSG00000169220	RGS14	RGS14	regulator of G-protein sign	Cytoplasm	other		0.73	0.85	0.39	0.65	0.68	1.06	0.27	0.63	0.00	0.01	0.00	0.00	1.00	0.00	1.00	0.32	67	65	66	63	60	82	75	67	33	35	34	37	40	18	25	33
ENSG00000169442	CD52	CD52	CD52 molecule	Plasma Membrane	other	Reynier et al. 2010	0.50	0.49	-0.11	0.25	0.60	0.49	-0.17	0.16	0.00	0.47	0.55	0.27	0.68	0.11	1.00	1.00	75	68	45	58	70	73	42	50	25	32	55	42	30	27	58	50
ENSG00000160179	ABCG1	ABCG1	ATP binding cassette subfa	Plasma Membrane	transporter		-0.55	-0.25	-0.35	-0.54	0.13	-0.14	-0.22	-0.23	0.00	0.20	0.00	0.00	1.00	0.97	1.00	1.00	22	30	24	32	60	36	42	42	78	70	76	68	40	64	58	58
ENSG00000110090	CPT1A	CPT1A	carnitine palmitoyltransfer	Cytoplasm	enzyme		0.75	0.21	0.29	0.43			-0.29	0.07	0.00	0.31	0.03	0.00			1.00	1.00	69	59	63	68			42	58	31	41	37	32			58	42
ENSG00000109762	SNX25	SNX25	sorting nexin 25	Cytoplasm	other		-0.65	-0.33	-0.14	-0.07		-0.40	0.13	-0.06	0.00	0.45	0.28	0.51		0.75	1.00	1.00	14	30	45	42		27	58	42	86	70	55	58		73	42	58
ENSG00000178927	C17orf62	C17orf62	chromosome 17 open read	Other	other		0.50	0.47	0.33	0.49		0.89	0.30	0.53	0.00	0.00	0.00	0.00		0.00	0.68	0.30	69	76	68	68		91	58	75	31	24	32	32		9	42	25
ENSG00000189060	H1F0	H1F0	H1 histone family member	Nucleus	other		0.51		-0.11	-0.01	0.20		0.01	-0.18	0.00		0.85	0.91	1.00		1.00	1.00	69		47	50	70		50	42	31		53	50	30		50	58
ENSG00000254912	RP11-632K20.2						-0.88	-0.52			-0.72	-0.65			0.00	0.07			1.00	0.01			25	30			20	18			75	70			80	82		
ENSG00000147813	NAPRT1	NAPRT	nicotinate phosphoribosyltr	Cytoplasm	enzyme		-0.52		-0.47	-0.21	-0.85		-0.54		0.00		0.02	0.48	0.14		1.00		25		34	42	30		25		75		66	58	70		75	
ENSG00000100092	SH3BP1	SH3BP1	SH3 domain binding protei	Other	other		0.51	0.32	-0.01	0.32	0.25	0.29	-0.32	0.11	0.00	0.66	0.97	0.21	1.00	0.15	1.00	1.00	69	57	50	63	60	64	33	58	31	43	50	37	40	36	67	42
ENSG00000211710	TRBV4-1	TRBV4-1	T cell receptor beta variabl	Other	other		0.95	1.11		1.05		1.23		1.18	0.00	0.01		0.00		0.08		0.30	72	59		82		64		83	28	41		18		36		17
ENSG00000164056	SPRY1	SPRY1	sprouty RTK signaling anta	Cytoplasm	other		-0.50	-0.24	-0.12	-0.41	-0.42	-0.12	-0.13	-0.15	0.00	0.44	0.45	0.03	1.00	0.92	1.00	1.00	17	35	34	32	20	45	33	42	83	65	66	68	80	55	67	58
ENSG00000215302	CTD-3092A11.1						-0.56	-0.02	-0.05		-0.75	-0.07	-0.06	0.06	0.00	0.80	0.98		0.68	0.87	1.00	1.00	31	49	47		30	36	42	50	69	51	53		70	64	58	50
ENSG00000022267	FHL1	FHL1	four and a half LIM domair	Cytoplasm	other		-0.54			-0.15	-0.77			-0.24	0.00			0.55	0.37			1.00	31			37	20			25	69			63	80			75
ENSG00000188290	HES4	HES4	hes family bHLH transcripti	Other	other		-0.65		-0.04		-0.65		0.69		0.00		0.76		1.00		1.00		28		50		40		67		72		50		60		33	
ENSG00000158555	GDPD5	GDPD5	glycerophosphodiester pho	Plasma Membrane	enzyme	Kallionpää et al. 2014	-0.64	-0.71	-0.08		-0.45				0.00	0.00	0.08		1.00				33	22	42		30				67	78	58		70			
ENSG00000128383	APOBEC3A	APOBEC3A	apolipoprotein B mRNA edi	Cytoplasm	enzyme	Kallionpää et al. 2014 Ferreira et al. Diabetes 2014	1.08		0.59	0.28	1.24		0.08	0.00	0.00		0.11	0.23	1.00		1.00	1.00	69		58	55	70		50	50	31		42	45	30		50	50
ENSG00000111843	TMEM14C	TMEM14C	transmembrane protein 14	Plasma Membrane	other		0.51	0.44	0.55	0.58	0.56	0.45	0.41	0.58	0.00	0.37	0.02	0.00	1.00	0.26	1.00	1.00	69	73	76	74	80	91	75	75	31	27	24	26	20	9	25	25
ENSG00000188690	UROS	UROS	uroporphyrinogen III synth	Cytoplasm	enzyme		0.54	0.46	0.51	0.49	0.60	0.53	0.48	0.45	0.00	0.29	0.00	0.01	1.00	0.15	1.00	1.00	78	73	74	71	80	73	67	75	22	27	26	29	20	27	33	25
ENSG00000095370	SH2D3C	SH2D3C	SH2 domain containing 3C	Cytoplasm	other		-0.50	-0.32	-0.14	-0.31	-0.86	-0.59	-0.41	-0.50	0.00	0.31	0.38	0.15	0.03	0.01	0.50	0.38	28	32	42	32	10	18	17	8	72	68	58	68	90	82	83	92
ENSG00000260708	CTA-29F11.1						-0.58	-0.31	-0.42	-0.55	-0.73	-0.26	-0.43	-0.43	0.00	0.18	0.02	0.00	0.37	0.57	1.00	0.59	25	30	37	26	20	27	42	33	75	70	63	74	80	73	58	67
ENSG00000145649	GZMA	GZMA	granzyme A	Cytoplasm	peptidase	Kallionpää et al. 2014	0.66	0.19	0.40	0.45	0.48	0.21	0.60	0.28	0.00	0.86	0.00	0.00	1.00	0.67	0.35	0.39	67	57	71	68	60	64	67	75	33	43	29	32	40	36	33	25
ENSG00000025708	TYMP	TYMP	thymidine phosphorylase	Extracellular Space	growth factor		0.89		0.29	0.44			0.15	-0.02	0.01		0.23	0.18			1.00	1.00	69		58	61			50	50	31		42	39			50	50
ENSG00000115523	GNLY	GNLY	granulysin	Cytoplasm	other	Kallionpää et al. 2014	0.27	-1.27	0.05	-0.28	0.12	-1.06	0.17	-0.08	0.69	0.00	0.58	0.34	1.00	0.00	1.00	1.00	58	16	53	42	50	18	67	50	42	84	47	58	50	82	33	50
ENSG00000100302	RASD2	RASD2	RASD family member 2	Cytoplasm	enzyme			-1.08	-0.28	-0.23		-0.57		0.21		0.00	0.07	0.00		0.00		1.00		30	47	47		27		75		70	53	53		73		25
ENSG00000115414	FN1	FN1	fibronectin 1	Extracellular Space	enzyme			0.80				0.55	-0.92			0.00				0.07	1.00			68				55	42			32				45	58	
ENSG00000073861	TBX21	TBX21	T-box 21	Nucleus	transcription regulator	Kallionpää et al. 2014, Heninger et al. 2017		-0.74	0.13	-0.07		-0.78	0.27	0.19		0.00	0.33	0.95		0.00	1.00	1.00		16	58	50		9	58	58		84	42	50		91	42	42
ENSG00000176845	METRNL	METRNL	meteorin like, glial cell diff	Cytoplasm	other		-0.19	-0.78	-0.19	-0.30	0.32	-0.31	-0.08	-0.10	0.83	0.00	0.16	0.09	1.00	0.00	1.00	1.00	42	19	45	37	60	9	50	50	58	81	55	63	40	91	50	50
ENSG00000152492	CCDC50	CCDC50	coiled-coil domain containi	Cytoplasm	other		-0.45	-1.10	-0.26	-0.48	-0.65	-1.19	-0.36	-0.54	0.00	0.00	0.00	0.00	0.11	0.00	0.91	0.20	25	22	16	16	30	18	17	8	75	78	84	84	70	82	83	92
ENSG00000135114	OASL	OASL	2'-5'-oligoadenylate synthe	Cytoplasm	enzyme	Kallionpää et al. 2014, Reynier et al. 2010, Ferreira et al. 2014	-0.03	-0.66	-0.26	-0.08	0.53	-0.54	-0.35	-0.14	0.81	0.00	0.01	0.02	1.00	0.00	1.00	1.00	50	27	37	47	60	27	25	42	50	73	63	53	40	73	75	58
ENSG00000107317	PTGDS	PTGDS	prostaglandin D2 synthase	Cytoplasm	enzyme			-0.91	0.09	-0.14			0.09	-0.13		0.00	0.83	0.18			1.00	1.00		27	55	42			58	42		73	45	58			42	58
ENSG00000211689	TRGC1	TARP	TCR gamma alternate reac	Cytoplasm	other			-0.85								0.00								16								84						
ENSG00000075234	TTC38	TTC38	tetratricopeptide repeat dc	Cytoplasm	other			-0.73	0.11	0.32			0.33	0.46		0.00	0.16	0.05			1.00	0.51		22	55	66			58	75		78	45	34			42	25
ENSG00000135047	CTSL	CTSL	cathepsin L	Cytoplasm	peptidase		0.29	1.11	-0.25	-0.05	0.86		0.38	0.46	0.00	0.00	0.89	0.17	0.80		1.00	0.52	56	70	45	50	60		50	50	44	30	55	50	40		50	50
ENSG00000158747	NBL1	MINOS1-NBL1/NBL1	neuroblastoma 1, DAN fam	Nucleus	other			-0.65		-0.36		-0.37				0.00		0.01		0.27				24		37		36				76		63		64		
ENSG00000065989	PDE4A	PDE4A	phosphodiesterase 4A	Cytoplasm	enzyme			-0.72	-0.13	-0.33		0.06	0.07	-0.33		0.00	0.07	0.05		0.56	1.00	1.00		32	37	37		55	50	42		68	63	63		45	50	58
ENSG00000188404	SELL	SELL	selectin L	Plasma Membrane	transmembrane receptor	Elo et al. 2010	0.38	0.59	0.80	0.81	0.19	0.53	0.48	0.24	0.00	0.00	0.00	0.00	1.00	0.00	1.00	1.00	64	68	61	61	80	73	58	58	36	32	39	39	20	27	42	42
ENSG00000111537	IFNG	IFNG	interferon gamma	Extracellular Space	cytokine	Ferreira et al. Diabetes 2014, Reinert-Hartwall et al. 2015		-0.73	-0.29	-0.11		-1.02	-0.42	-0.43		0.00	0.74	0.99		0.00	1.00	1.00		32	45	47		18	33	33		68	55	53		82	67	67
ENSG00000158869	FCER1G	FCER1G	Fc fragment of IgE recepto	Plasma Membrane	transmembrane receptor		0.64	0.97	0.11	0.45	1.11	0.96	-0.29	0.21	0.00	0.00	0.10	0.10	1.00	0.07	1.00	1.00	64	73	55	61	70	73	42	58	36	27	45	39	30	27	58	42
ENSG00000073605	GSDMB	GSDMB	gasdermin B	Cytoplasm	other		0.30	0.65							0.01	0.00							61	73							39	27						
ENSG00000176083	ZNF683	ZNF683	zinc finger protein 683	Other	other			-0.69		-0.54		-0.48		-0.11		0.00		0.13		0.00		1.00		32		45		45		50		68		55		55		50
ENSG00000105374	NKG7	NKG7	natural killer cell granule p	Plasma Membrane	other		0.42	-0.86	0.19	0.08	0.13	-1.15	0.39	0.14	0.36	0.00	0.00	0.41	1.00	0.00	0.79	1.00	61	30	61	53	60	18	58	58	39	70	39	47	40	82	42	42
ENSG00000158122	AAED1	AAED1	AhpC/TSA antioxidant enzy	Other	other			-0.60	-0.08	-0.27		-0.28	0.02	0.09		0.00	0.82	0.20		0.11	1.00	1.00		19	45	39		27	50	50		81	55	61		73	50	50
ENSG00000127311	HELB	HELB	DNA helicase B	Nucleus	enzyme	Ferreira et al. Diabetes 2014	0.22	0.57		0.48	0.13	0.37		0.43	0.01	0.00		0.00	1.00	0.28		0.72	64	89		79	60	82		67	36	11		21	40	18		33
ENSG00000143878	RHOB	RHOB	ras homolog family memb	Cytoplasm	enzyme		-0.29	-0.59	0.21	0.00	0.12	-0.09	0.03	0.14	0.11	0.00	0.37	0.13	1.00	0.62	1.00	1.00	44	30	55	50	60	45	50	58	56	70	45	50	40	55	50	42
ENSG00000131149	GSE1	GSE1	Gse1 coiled-coil protein	Extracellular Space	other			-0.77	-0.32	-0.35		-1.03	-0.32	-0.38		0.00	0.00	0.00		0.00	1.00	0.90		16	18	26		18	17	17		84	82	74		82	83	83
ENSG00000196126	HLA-DRB1	HLA-DRB1	major histocompatibility c	Plasma Membrane	transmembrane receptor	Elo et al. 2010	-0.42	-0.73	-0.40	-0.69	-0.21	-0.86	-0.23	-0.33	0.11	0.00	0.00	0.00	1.00	0.02	0.60	0.30	39	32	26	29	40	27	33	42	61	68	74	71	60	73	67	58
ENSG00000188483	IER5L	IER5L	immediate early response	Other	other			-0.65	-0.11	-0.25		0.27	0.24	0.09		0.00	0.80	0.17		0.99	1.00	1.00		27	45	34		55	58	50		73	55	66		45	42	50
ENSG00000147443	DOK2	DOK2	docking protein 2	Plasma Membrane	other		-0.03	-0.58	0.02	-0.04	-0.01	-0.58	-0.11	-0.03	0.39	0.00	0.60	0.78	1.00	0.08	1.00	1.00	39	24	53	47	40	27	50	50	61	76	47	53	60	73	50	50
ENSG00000117318	ID3	ID3	inhibitor of DNA binding 3,	Nucleus	transcription regulator		-0.22	-1.15	-0.19	-0.37	0.30	-0.20	0.23	0.28	0.42	0.00	0.42	0.08	1.00	0.74	1.00	1.00	47	27	42	39	70	36	58	67	53	73	58	61	30	64	42	33
ENSG00000223745	RP4-717I23.3	CCDC18-AS1	CCDC18 antisense RNA 1	Other	other		0.09	0.59	0.45		-0.52	0.17	0.81		0.08	0.00	0.05		1.00	0.00	0.42		50	68	71		40	64	83		50	32	29		60	36	17	
ENSG00000134539	KLRD1	KLRD1	killer cell lectin like recept	Plasma Membrane	transmembrane receptor	Kallionpää et al. 2014		-0.59	0.41	0.38			0.30	0.47		0.00	0.00	0.01			0.42	0.76		24	74	61			67	58		76	26	39			33	42
ENSG00000211694	TRGV10	TRGV10	T cell receptor gamma var	Other	other			-0.61		-0.05		-0.49		0.20		0.01		0.77		0.30		1.00		24		50		18		58		76		50		82		42
ENSG00000169554	ZEB2	ZEB2	zinc finger E-box binding h	Nucleus	transcription regulator			-0.53	-0.16	-0.15		-0.92	-0.07	-0.05		0.01	0.19	0.17		0.00	1.00	1.00		27	34	39		9	33	50		73	66	61		91	67	50
ENSG00000134107	BHLHE40	BHLHE40	basic helix-loop-helix famil	Nucleus	transcription regulator		-0.21	-0.63	-0.14	-0.23	0.13	-0.55	-0.07	0.10	0.74	0.01	0.69	0.19	1.00	0.01	1.00	1.00	39	24	37	39	50	9	42	58	61	76	63	61	50	91	58	42
ENSG00000143185	XCL2	XCL2	X-C motif chemokine ligan	Extracellular Space	cytokine			-0.66	0.27	0.14			0.46	0.63		0.01	0.97	0.90			1.00	1.00		30	55	58			67	75		70	45	42			33	25
ENSG00000145882	PCYOX1L	PCYOX1L	prenylcysteine oxidase 1 li	Other	other		0.27	0.69			0.13	0.47			0.00	0.01			1.00	0.00			61	76			60	82			39	24			40	18		
ENSG00000160789	LMNA	LMNA	lamin A/C	Nucleus	other	Elo et al. 2010, Kallionpää et al. 2014	-0.40	-0.75	-0.30	-0.25	0.61	-0.08	0.04	0.09	0.07	0.01	0.10	0.00	0.37	0.41	1.00	1.00	36	32	42	37	60	45	58	50	64	68	58	63	40	55	42	50

ENSG00000148484	RSU1	RSU1	Ras suppressor protein 1	Cytoplasm	other		0.08	0.63	0.54	0.50	0.05	0.85	0.51	0.60	0.00	0.02	0.00	0.00	1.00	0.00	0.93	0.45	58	68	76	68	50	73	75	67	42	32	24	32	50	27	25	33
ENSG00000114812	VIPR1	VIPR1	vasoactive intestinal peptid	Plasma Membrane	G-protein coupled receptor		0.42	0.53		0.58	0.35	0.98			0.00	0.02		0.00	1.00	0.00			75	73		84	70	91			25	27		16	30	9		
ENSG00000186810	CXCR3	CXCR3	C-X-C motif chemokine rec	Plasma Membrane	G-protein coupled receptor			-0.73	-0.09	-0.06		-0.44	0.35	0.43		0.02	0.56	0.87		0.60	1.00	0.82		30	42	50		36	58	67		70	58	50		64	42	33
ENSG00000183735	TBK1	TBK1	TANK binding kinase 1	Cytoplasm	kinase			-0.52	-0.26	-0.33			-0.23	-0.35		0.03	0.02	0.05			1.00	1.00		27	26	34			33	42		73	74	66			67	58
ENSG00000077585	GPR137B	GPR137B	G protein-coupled receptor	Plasma Membrane	other			-0.54	-0.12	-0.14			0.08	-0.07		0.03	0.25	0.20			1.00	1.00		22	42	42			58	42		78	58	58			42	58
ENSG00000110665	C11orf21	C11orf21	chromosome 11 open read	Cytoplasm	other		0.09	0.51	0.48	0.22	-0.25	0.51	0.32	0.31	0.19	0.03	0.00	0.12	1.00	0.00	1.00	1.00	53	73	66	58	40	73	58	67	47	27	34	42	60	27	42	33
ENSG00000179588	ZFPM1	ZFPM1	zinc finger protein, FOG fa	Nucleus	transcription regulator			-0.55		0.25		-0.16				0.03		0.79		0.81				30		61		36				70		39		64		
ENSG00000185112	FAM43A	FAM43A	family with sequence simil	Other	other			-0.70	0.28	-0.13		-0.69	0.43	0.33		0.04	0.04	0.97		0.25	0.73	1.00		30	55	47		27	67	67		70	45	53		73	33	33
ENSG00000160223	ICOSLG	ICOSLG/LOC102723996	inducible T-cell costimulat	Plasma Membrane	other		-0.56	-0.66	-0.20	-0.35	0.01	-0.11	0.15	-0.09	0.11	0.04	0.04	0.00	1.00	0.88	1.00	1.00	28	30	32	29	50	36	58	42	72	70	68	71	50	64	42	58
ENSG00000136213	CHST12							-0.64	0.24	0.09			0.02	0.03		0.04	0.21	0.39			1.00	1.00		24	58	53			50	50		76	42	47			50	50
ENSG00000184939	ZFP90	ZFP90	ZFP90 zinc finger protein	Nucleus	transcription regulator		0.32	0.56		0.44	0.37	0.10		0.29	0.16	0.05		0.00	1.00	0.39		0.97	58	73		76	70	55		83	42	27		24	30	45		17
ENSG00000179344	HLA-DQB1	HLA-DQB1	major histocompatibility c	Plasma Membrane	other	Elo et al. 2010			-0.57	-0.42			-0.32	0.11			0.00	0.00			0.00	0.32			32	37			33	50			68	63			67	50
ENSG00000101057	MYBL2	MYBL2	MYB proto-oncogene like 2	Nucleus	transcription regulator				-0.86	-0.98			-0.50	-0.51			0.00	0.00			0.04	0.02			21	21			33	25			79	79			67	75
ENSG00000211940	NA								0.76	1.04			1.27	1.08			0.00	0.00			0.00	0.00			79	68			75	67			21	32			25	33
ENSG00000091409	ITGA6	ITGA6	integrin subunit alpha 6	Plasma Membrane	transmembrane receptor		0.17	0.38	0.75	0.34	0.06	0.26	0.61	0.12	0.00	0.04	0.00	0.00	1.00	0.01	0.05	0.67	61	62	76	63	60	55	67	58	39	38	24	37	40	45	33	42
ENSG00000196735	HLA-DQA1	HLA-DQA1	major histocompatibility c	Plasma Membrane	transmembrane receptor	Kallionpää et al. 2014			-0.54	-0.33			-0.43	-0.06			0.00	0.00			0.00	1.00			34	39			25	50			66	61			75	50
ENSG00000168685	IL7R	IL7R	interleukin 7 receptor	Plasma Membrane	transmembrane receptor		0.01	0.17	0.70	0.48	-0.04	0.14	0.45	0.12	0.29	0.71	0.00	0.00	1.00	0.91	1.00	1.00	53	59	74	66	50	64	58	58	47	41	26	34	50	36	42	42
ENSG00000113263	ITK	ITK	IL2 inducible T-cell kinase	Cytoplasm	kinase		0.14	0.25	0.71	0.31	0.06	0.06	0.46	0.11	0.07	0.61	0.00	0.00	1.00	0.72	0.17	0.99	61	70	79	74	50	64	75	75	39	30	21	26	50	36	25	25
ENSG00000138795	LEF1	LEF1	lymphoid enhancer binding	Nucleus	transcription regulator	Kallionpää et al. 2014	0.03	0.12	0.61	0.32	-0.12	0.10	0.47	0.18	0.51	0.84	0.00	0.02	1.00	0.91	0.83	1.00	53	62	79	76	30	64	67	67	47	38	21	24	70	36	33	33
ENSG00000182866	LCK	LCK	LCK proto-oncogene, Src fa	Cytoplasm	kinase		-0.07	0.01	0.68	0.31	-0.19	-0.01	0.57	0.37	0.43	0.68	0.00	0.00	1.00	0.79	0.56	0.68	44	51	79	74	30	36	67	75	56	49	21	26	70	64	33	25
ENSG00000229164	NA						0.05	0.06	0.80	0.23	-0.11	-0.09	0.47	0.13	0.53	0.91	0.00	0.02	1.00	0.99	1.00	1.00	53	54	82	74	40	45	67	58	47	46	18	26	60	55	33	42
ENSG00000082074	FYB	FYB	FYN binding protein	Nucleus	other		-0.04	0.33	0.62	0.39	-0.07	0.33	0.18	0.38	0.29	0.32	0.00	0.00	1.00	0.19	1.00	1.00	47	76	76	74	40	82	67	75	53	24	24	26	60	18	33	25
ENSG00000117602	RCAN3	RCAN3	RCAN family member 3	Other	other		0.12	0.12	0.68	0.29	-0.02	0.00	0.20	-0.02	0.39	0.70	0.00	0.01	1.00	0.97	0.91	1.00	56	62	84	66	30	55	67	42	44	38	16	34	70	45	33	58
ENSG00000211953	NA								0.82	0.48			0.64	0.19			0.00	0.00			0.14	0.30			68	68			75	67			32	32			25	33
ENSG00000111913	FAM65B	FAM65B	family with sequence simil	Cytoplasm	other		0.26	0.19	0.53	0.39	0.22	0.19	0.50	0.39	0.00	0.07	0.00	0.00	1.00	0.08	1.00	0.55	69	73	74	74	70	73	58	75	31	27	26	26	30	27	42	25
ENSG00000184613	NELL2	NELL2	neural EGFL like 2	Extracellular Space	other		-0.04	0.20	0.68	0.44	-0.11	0.20	0.57	0.39	0.84	0.87	0.00	0.00	1.00	0.91	0.61	0.97	44	62	71	68	20	55	67	67	56	38	29	32	80	45	33	33
ENSG00000167286	CD3D	CD3D	CD3d molecule	Plasma Membrane	transmembrane receptor	Reynier et al. 2010	0.07	0.06	0.64	0.26	0.12	0.03	0.63	0.22	0.19	0.76	0.00	0.00	1.00	0.63	0.92	1.00	56	57	79	79	60	64	67	83	44	43	21	21	40	36	33	17
ENSG00000205268	PDE7A	PDE7A	phosphodiesterase 7A	Cytoplasm	enzyme		0.22	0.24	0.63	0.50	0.11	0.27	0.64	0.30	0.00	0.09	0.00	0.00	1.00	0.00	0.18	0.35	69	68	87	68	60	64	83	58	31	32	13	32	40	36	17	42
ENSG00000162894	FAIM3	FCMR	Fc fragment of IgM recept	Plasma Membrane	other		0.04	0.28	0.62	0.30	0.03	0.16	0.33	0.38	0.06	0.29	0.00	0.00	1.00	0.08	0.86	0.80	56	65	71	68	50	73	58	67	44	35	29	32	50	27	42	33
ENSG00000172005	MAL	MAL	mal, T-cell differentiation	Plasma Membrane	transporter	Elo et al. 2010	0.12	0.07	0.85	0.31	0.05	0.05	0.66	0.16	0.22	0.98	0.00	0.03	1.00	0.94	0.96	1.00	64	57	79	74	60	64	67	58	36	43	21	26	40	36	33	42
ENSG00000034053	APBA2	APBA2	amyloid beta precursor pr	Cytoplasm	transporter	Kallionpää et al. 2014	-0.08	0.22	0.66	0.32	-0.25	0.22	0.49	0.21	0.80	0.67	0.00	0.00	1.00	0.30	0.31	0.87	47	59	76	74	30	64	75	67	53	41	24	26	70	36	25	33
ENSG00000186854	TRABD2A						0.13	0.21	0.71	0.45	0.04	0.31	0.54	0.34	0.03	0.45	0.00	0.00	1.00	0.09	0.73	1.00	61	68	71	74	50	73	67	67	39	32	29	26	50	27	33	33
ENSG00000189339	SLC35E2B	SLC35E2B	solute carrier family 35 m	Other	other		0.20	0.24	0.52	0.37	0.14	0.18	0.39	0.41	0.00	0.02	0.00	0.00	1.00	0.01	0.44	0.18	58	68	68	68	60	73	67	83	42	32	32	32	40	27	33	17
ENSG00000196329	GIMAP5	GIMAP5	GTPase, IMAP family mem	Cytoplasm	other		0.16	0.35	0.75	0.52	-0.03	0.35	0.56	0.31	0.02	0.33	0.00	0.00	1.00	0.01	0.45	1.00	61	68	74	68	40	73	58	58	39	32	26	32	60	27	42	42
ENSG00000157303	SUSD3	SUSD3	sushi domain containing 3	Plasma Membrane	other		0.39	0.34	0.68	0.46	0.17	0.52	0.57	0.62	0.00	0.03	0.00	0.00	1.00	0.00	0.77	0.19	69	84	82	71	80	100	75	83	31	16	18	29	20	0	25	17
ENSG00000111817	DSE	DSE	dermatan sulfate epimeras	Cytoplasm	enzyme				-0.74	-0.62			-0.64	-0.52			0.00	0.00			0.42	0.75			29	29			33	33			71	71			67	67
ENSG00000175352	NRIP3	NRIP3	nuclear receptor interactin	Other	other				-0.53	-0.41			-0.51	0.00			0.00	0.00			1.00	1.00			24	37			42	50			76	63			58	50
ENSG00000143515	ATP8B2	ATP8B2	ATPase phospholipid trans	Plasma Membrane	transporter		0.36	0.41	0.53	0.37	0.32	0.48	0.37	0.86	0.00	0.06	0.00	0.00	1.00	0.00	0.46	0.02	58	70	74	61	60	91	75	67	42	30	26	39	40	9	25	33
ENSG00000147408	CSGALNACT1	CSGALNACT1	chondroitin sulfate N-acety	Cytoplasm	enzyme	Kallionpää et al. 2014	0.32	0.72	0.62	0.32	0.17	0.89	0.69	0.24	0.00	0.14	0.00	0.04	1.00	0.00	0.04	0.82	69	65	82	74	70	73	75	75	31	35	18	26	30	27	25	25
ENSG00000178562	CD28	CD28	CD28 molecule	Plasma Membrane	transmembrane receptor		0.09	0.10	0.58	0.37	-0.09	0.04	0.34	0.25	0.76	0.72	0.00	0.07	1.00	0.31	1.00	1.00	58	65	79	71	50	73	67	58	42	35	21	29	50	27	33	42
ENSG00000165929	TC2N	TC2N	tandem C2 domains, nucle	Nucleus	transporter		-0.08	0.33	0.53	0.33	-0.19	-0.13	0.44	0.02	0.82	0.30	0.00	0.00	1.00	0.84	0.91	1.00	39	62	82	68	20	45	75	50	61	38	18	32	80	55	25	50
ENSG00000111801	BTN3A3	BTN3A3	butyrophilin subfamily 3 m	Plasma Membrane	other		0.42	0.49	0.67	0.79	0.40	0.50		0.83	0.00	0.02	0.00	0.00	1.00	0.00		0.08	78	73	76	74	90	91		83	22	27	24	26	10	9		17
ENSG00000244682	FCGR2C	FCGR2C	Fc fragment of IgG recept	Plasma Membrane	transmembrane receptor				-0.83				-1.16				0.00				0.00				32				33				68				67	
ENSG00000105483	CARD8	CARD8	caspase recruitment doma	Nucleus	other		0.19	0.32	0.64	0.64	0.10	0.39		0.58	0.00	0.01	0.00	0.00	1.00	0.00		0.21	61	73	74	71	50	82		75	39	27	26	29	50	18		25
ENSG00000197283	SYNGAP1						0.15	0.34	0.65	0.28	0.27	0.48	0.48	0.46	0.11	0.50	0.00	0.01	1.00	0.01	0.45	0.67	56	65	76	74	70	82	75	67	44	35	24	26	30	18	25	33
ENSG00000135426	TESPA1	TESPA1	thymocyte expressed, posit	Cytoplasm	other	Kallionpää et al. 2014	0.01	0.17	0.64	0.26	-0.18	0.12	0.23	0.05	0.73	0.48	0.00	0.03	1.00	0.62	1.00	1.00	53	68	76	71	30	64	67	58	47	32	24	29	70	36	33	42
ENSG00000176014	TUBB6	TUBB6	tubulin beta 6 class V	Cytoplasm	other				-0.63	-0.68			-0.42	0.01			0.00	0.00			0.98	1.00			21	29			33	50			79	71			67	50
ENSG00000152056	AP1S3	AP1S3	adaptor related protein co	Cytoplasm	transporter				-0.69				-0.02				0.00				0.83				26				42				74				58	
ENSG00000065675	PRKCQ	PRKCQ	protein kinase C theta	Cytoplasm	kinase		-0.07	0.00	0.64	0.36	-0.11	-0.20	0.52	0.27	0.11	0.75	0.00	0.01	1.00	0.97	1.00	1.00	47	51	74	63	40	36	67	58	53	49	26	37	60	64	33	42
ENSG00000127152	BCL11B	BCL11B	B-cell CLL/lymphoma 11B	Nucleus	transcription regulator		0.04	0.01	0.60	0.25	-0.09	0.00	0.31	0.02	0.99	0.98	0.00	0.30	1.00	0.99	0.72	1.00	50	54	71	68	30	45	58	50	50	46	29	32	70	55	42	50
ENSG00000116824	CD2	CD2	CD2 molecule	Plasma Membrane	transmembrane receptor		0.01	0.06	0.59	0.28	0.06	0.23	0.63	0.35	0.89	0.78	0.00	0.01	1.00	0.41	0.78	1.00	53	59	76	74	70	73	67	67	47	41	24	26	30	27	33	33
ENSG00000176749	CDK5R1	CDK5R1	cyclin dependent kinase 5 r	Nucleus	kinase	Kallionpää et al. 2014	0.47	0.42	0.63	0.42	0.57	0.45	0.59	0.66	0.00	0.06	0.00	0.00	0.12	0.05	0.28	0.31	83	84	82	71	80	82	83	83	17	16	18	29	20	18	17	17
ENSG00000160654	CD3G	CD3G	CD3g molecule	Plasma Membrane	transmembrane receptor		-0.01	-0.12	0.80	0.30	-0.09	-0.27	0.40	-0.01	0.30	0.90	0.00	0.01	1.00	0.86	1.00	1.00	50	46	76	61	30	36	67	42	50	54	24	39	70	64	33	58
ENSG00000179144	GIMAP7	GIMAP7	GTPase, IMAP family mem	Cytoplasm	enzyme		0.27	0.37	0.58	0.25	0.37	0.58	0.49	0.17	0.09	0.76	0.00	0.06	1.00	0.15	1.00	1.00	67	65	71	66	60	73	58	67	33	35	29	34	40	27	42	33
ENSG00000157978	LDLRAP1	LDLRAP1	low density lipoprotein rec	Cytoplasm	transporter		0.21	0.48	0.53	0.41	-0.02	0.15		0.28	0.02	0.14	0.00	0.00	1.00	0.30		1.00	56	62	76	71	40	55		67	44	38	24	29	60	45		33
ENSG00000196187	TMEM63A	TMEM63A	transmembrane protein 63	Cytoplasm	other		0.24	0.35	0.71	0.42	-0.14	0.35	0.58	0.33	0.09	0.04	0.00	0.00	1.00	0.02	0.75	0.96	58	78	74	68	40	91	75	67	42	22	26	32	60	9	25	33
ENSG00000225217	HSPA7	HSPA7	heat shock protein family A	Cytoplasm	other				-0.91				-1.50				0.00				0.02				34				42				66				58	
ENSG00000122877	EGR2	EGR2	early growth response 2	Nucleus	transcription regulator	Heninger et al. 2017			-0.57	-0.31			-0.28	-0.33			0.00	0.00			0.94	0.53			24	29			33	25			76	71			67	75
ENSG00000184384	MAML2	MAML2	mastermind like transcripti	Nucleus	transcription regulator		0.23	0.55	0.64	0.47	0.16	0.79	0.34	0.37	0.17	0.06	0.00	0.03	1.00	0.00	0.81	1.00	64	70	76	66	70	82	75	58	36	30	24	34	30	18	25	42
ENSG00000074966	TXK	TXK	TXK tyrosine kinase	Cytoplasm	kinase	Kallionpää et al. 2014	-0.10	0.30	0.62	0.50	-0.31	0.41	0.42	0.36	0.57	0.18	0.00	0.00	1.00	0.01	0.48	0.41	42	62	74	68	30	73	75	67	58	38	26	32	70	27	25	33
ENSG00000110203	FOLR3	FOLR3	folate receptor 3	Extracellular Space	other	Kallionpää et al. 2014			1.49	0.89			1.19	0.83			0.00	0.00			0.90	1.00			68	68			67	67			32	32			33	33
ENSG00000177575	CD163	CD163	CD163 molecule	Plasma Membrane	transmembrane receptor	Ferreira et al. Diabetes 2014			0.85	0.67			0.64	0.41			0.00	0.00			0.76	0.78			66	71			67	67			34	29			33	33
ENSG00000137507	LRRC32	LRRC32	leucine rich repeat contain	Plasma Membrane	other				-0.61	-0.35			-0.36	-0.30			0.00	0.00			0.42	0.80			29	24			25	25			71	76			75	75
ENSG00000178295	GEN1	GEN1	GEN1, Holliday junction 5' f	Cytoplasm	enzyme				-0.51				-0.43				0.00				1.00				26				42				74				58	
ENSG00000167664	TMIGD2	TMIGD2	transmembrane and immu	Other	other		0.24	0.31	0.77	0.44	0.05	0.62	0.60	0.50	0.19	0.45	0.00	0.00	1.00	0.03	0.79	0.21	56	65	71	68	50	91	67	75	44	35	29	32	50	9	33	25
ENSG00000159674	SPON2	SPON2	spondin 2	Extracellular Space	other	Kallionpää et al. 2014		-0.18	0.51	0.43		-0.18	0.69	0.31		0.38	0.00	0.00		1.00	0.01	0.03		41	68	66		45	67	58		59	32	34		55	33	42
ENSG00000081059	TCF7	TCF7	transcription factor 7 (T-ce	Nucleus	transcription regulator		0.01	0.06	0.54	0.24	-0.07	0.06	0.42	0.23	0.58	0.96	0.00	0.03	1.00	0.89	0.84	1.00	53	62	82	71	30	64	83	58	47	38	18	29	70	36	17	42
ENSG00000119487	MAPKAP1	MAPKAP1	mitogen-activated protein	Cytoplasm	other		0.26	0.45	0.68	0.45	0.39	0.83	0.72	0.48	0.02	0.36	0.00	0.01	1.00	0.00	0.28	0.44	58	59	66	61	60	73	75	67	42	41	34	39	40	27	25	33
ENSG00000160305	DIP2A	DIP2A	disco interacting protein 2	Nucleus	transcription regulator		0.00	0.40	0.51	0.27	0.00	0.44	0.61	0.35	0.35	0.65	0.00	0.00	1.00	0.27	0.28	0.15	50	65	66	74	50	64	75	83	50	35	34	26	50	36	25	17
ENSG00000013573	DDX11	DDX11	DEAD/H-box helicase 11	Cytoplasm	enzyme		-0.63	-0.41	-0.66		-1.15	-0.95	-0.35		0.00	0.01	0.00		0.00	0.00	0.68		39	38	34		20	36	42		61	62	66		80	64	58	
ENSG00000100385	IL2RB	IL2RB	interleukin 2 receptor subu	Plasma Membrane	transmembrane receptor		-0.10	-0.18	0.52	0.15	0.12	0.08	0.59	0.33	0.75	0.44	0.00	0.04	1.00	0.91	0.17	0.17	47	38	74	61	50	55	67	75	53	62	26	39	50	45	33	25
ENSG00000215788	TNFRSF25	TNFRSF25	TNF receptor superfamily r	Plasma Membrane	transmembrane receptor		0.00	0.10	0.50	0.13	-0.12	0.00	0.76	0.29	0.85	0.75	0.00	0.09	1.00	0.75	0.42	1.00	50	59	68	61	50	55	75	67	50	41	32	39	50	45	25	33
ENSG00000160185	UBASH3A	UBASH3A	ubiquitin associated and SH	Cytoplasm	enzyme		-0.05	0.09	0.61	0.10	-0.06	0.06		0.04	0.87	0.99	0.00	0.27	1.00	0.99		1.00	42	57	79	63	30	55		58	58	43	21	37	70	45		42
ENSG00000110448	CD5	CD5	CD5 molecule	Plasma Membrane	transmembrane receptor		-0.14	-0.11	0.56	0.01	-0.05	0.04	0.53	0.18	0.36	0.85	0.00	0.91	1.00	0.98	1.00	1.00	31	41	76	50	30	55	67	58	69	59	24	50	70	45	33	42
ENSG00000197540	GZMM	GZMM	granzyme M	Cytoplasm	peptidase		0.17	0.10	0.51	0.39	0.36	0.27	0.41	0.75	0.11	0.89	0.00	0.01	1.00	0.28	0.42	0.05	64	51	66	68	80	73	58	75	36	49	34	32	20	27	42	25
ENSG00000145287	PLAC8	PLAC8	placenta specific 8	Nucleus	other		0.11	0.29	0.55	0.29	0.01	0.19	0.10	0.14	0.11	0.65	0.00	0.01	1.00	0.62	1.00	1.00	58	65	76	68	50	55	58	58	42	35	24	32	50	45	42	42
ENSG00000163516	ANKZF1	ANKZF1	ankyrin repeat and zinc fin	Nucleus	transcription regulator		0.12	0.30	0.51	0.28	-0.30	0.25	0.40		0.05	0.28	0.00	0.02	1.00	0.43	0.83		56	68	76	76	30	64	75		44	32	24	24	70	36	25	
ENSG00000168936	TMEM129	TMEM129	transmembrane protein 12	Cytoplasm	enzyme		0.24	0.38	0.52	0.38	0.04	0.21	0.34	0.20	0.03	0.38	0.00	0.00	1.00	0.50	1.00	0.99	61	78	74	82	50	73	75	83	39	22	26	18	50	27	25	17

ENSG00000162729	IGSF8	IGSF8	immunoglobulin superfami	Plasma Membrane	other		0.20	0.31	0.57	0.37	-0.11	0.25		0.36	0.26	0.45	0.00	0.01	1.00	0.67		1.00	61	65	79	68	50	64		75	39	35	21	32	50	36		25
ENSG00000172340	SUCLG2	SUCLG2	succinate-CoA ligase GDP-f	Cytoplasm	enzyme		0.14	0.50	0.61	0.45	0.27	0.79	0.61	0.62	0.08	0.35	0.00	0.03	1.00	0.01	0.99	0.99	56	59	71	61	50	73	75	67	44	41	29	39	50	27	25	33
ENSG00000183019	MCEMP1	MCEMP1	mast cell expressed memb	Cytoplasm	other				-0.52	-0.23			-0.51	-0.27			0.00	0.09			0.42	1.00			32	42			25	33			68	58			75	67
ENSG00000162892	IL24	IL24	interleukin 24	Extracellular Space	cytokine		-0.02	0.41	0.63	0.29	0.02	0.33	0.37	0.18	0.23	0.04	0.00	0.00	1.00	0.45	1.00	1.00	47	73	76	71	50	73	67	67	53	27	24	29	50	27	33	33
ENSG00000172116	CD8B	CD8B	CD8b molecule	Plasma Membrane	other			0.08	0.53	0.68		0.13	0.20	0.73		0.76	0.00	0.00		0.45	1.00	0.05		54	71	66		73	58	67		46	29	34		27	42	33
ENSG00000163823	CCR1	CCR1	C-C motif chemokine recep	Plasma Membrane	G-protein coupled receptor				-0.56	-0.40			-0.78	-0.15			0.00	0.02			0.05	0.99			32	47			25	50			68	53			75	50
ENSG00000140398	NEIL1	NEIL1	nei like DNA glycosylase 1	Nucleus	enzyme		-0.19	-0.11	-0.55	-0.34		-0.38	0.28	-0.19	0.98	0.41	0.00	0.00		0.51	1.00	1.00	42	38	34	26		27	58	42	58	62	66	74		73	42	58
ENSG00000139193	CD27	CD27	CD27 molecule	Plasma Membrane	transmembrane receptor		0.13	0.12	0.70	0.30	0.21	0.04	0.52	0.39	0.22	0.87	0.00	0.00	1.00	0.88	1.00	1.00	58	57	71	66	70	55	67	67	42	43	29	34	30	45	33	33
ENSG00000137070	IL11RA	IL11RA	interleukin 11 receptor sub	Plasma Membrane	transmembrane receptor		0.20	0.20	0.55		-0.21	0.20	0.55		0.11	0.27	0.00		1.00	0.03	0.60		56	59	71		40	55	75		44	41	29		60	45	25	
ENSG00000211734	TRBV5-1	TRBV5-1	T cell receptor beta variabl	Other	other		0.19	0.40	0.86	0.09	0.19	0.02	0.38	0.04	0.15	0.76	0.00	0.08	1.00	0.93	1.00	1.00	53	57	74	63	50	55	75	67	47	43	26	37	50	45	25	33
ENSG00000035115	SH3YL1	SH3YL1	SH3 and SYLF domain conta	Plasma Membrane	other	Kallionpää et al. 2014	0.21	0.26	0.55	0.40	0.41	0.02	0.42	0.28	0.07	0.72	0.00	0.04	1.00	0.45	1.00	1.00	61	62	76	63	60	64	75	58	39	38	24	37	40	36	25	42
ENSG00000231475	IGHV4-31	IGHV4-31	immunoglobulin heavy vari	Other	other				0.62	0.36			0.20	0.46			0.00	0.01			1.00	0.82			68	63			58	75			32	37			42	25
ENSG00000226660	TRBV2	TRBV2	T cell receptor beta variabl	Other	other		0.22	0.22	0.85	0.25	-0.14	0.22		0.10	0.22	0.53	0.00	0.11	1.00	0.51		1.00	58	73	84	71	40	91		58	42	27	16	29	60	9		42
ENSG00000106560	GIMAP2	GIMAP2	GTPase, IMAP family mem	Cytoplasm	other		0.18	0.33	0.78	0.36	0.33	0.60	0.58	0.46	0.14	0.68	0.00	0.04	1.00	0.22	1.00	1.00	58	59	71	61	60	64	83	67	42	41	29	39	40	36	17	33
ENSG00000166825	ANPEP	ANPEP	alanyl aminopeptidase, me	Plasma Membrane	peptidase	Kallionpää et al. 2014	0.08		-0.55	-0.64	0.16		-0.40	-0.73	0.96		0.00	0.00	1.00		1.00	1.00	56		34	37	60		33	42	44		66	63	40		67	58
ENSG00000181035	SLC25A42	SLC25A42	solute carrier family 25 me	Cytoplasm	transporter		0.15	0.16	0.54		-0.32	0.16			0.22	0.66	0.00		1.00	0.47			56	57	71		40	64			44	43	29		60	36		
ENSG00000013725	CD6	CD6	CD6 molecule	Plasma Membrane	transmembrane receptor		-0.07	-0.10	0.51	0.14	-0.02	0.12	0.51	0.18	0.19	0.87	0.00	0.41	1.00	0.95	0.84	1.00	36	46	68	61	50	55	75	67	64	54	32	39	50	45	25	33
ENSG00000064886	CHI3L2	CHI3L2	chitinase 3 like 2	Extracellular Space	enzyme		0.05	-0.10	0.59	0.13	0.10	-0.16	0.07	-0.08	0.79	0.98	0.00	0.27	1.00	0.97	1.00	1.00	56	46	68	55	60	36	58	42	44	54	32	45	40	64	42	58
ENSG00000026950	BTN3A1	BTN3A1	butyrophilin subfamily 3 m	Extracellular Space	other		0.38	0.35	0.61	0.50	-0.29	0.09	0.65	0.70	0.02	0.42	0.00	0.00	1.00	0.49	0.69	0.02	61	59	68	76	40	55	75	75	39	41	32	24	60	45	25	25
ENSG00000226752	PSMD5-AS1	PSMD5-AS1	PSMD5 antisense RNA 1 (h	Other	other		0.33	0.36	0.52	0.59	0.16	0.11		0.30	0.10	0.66	0.00	0.00	1.00	0.97		1.00	58	59	68	74	60	55		75	42	41	32	26	40	45		25
ENSG00000211747	TRBV20-1	TRBV20-1	T cell receptor beta variabl	Other	other		0.02	-0.03	0.53	0.28	0.02	0.29	0.16	0.38	0.76	0.98	0.00	0.07	1.00	0.98	1.00	1.00	53	49	68	66	60	55	58	67	47	51	32	34	40	45	42	33
ENSG00000232869	TRBV29-1	TRBV29-1	T cell receptor beta variabl	Other	other		-0.17	-0.02	0.57	0.14	-0.30	-0.10	0.36	-0.07	0.73	0.84	0.01	0.67	1.00	0.96	1.00	1.00	47	46	71	61	40	45	58	50	53	54	29	39	60	55	42	50
ENSG00000130598	TNNI2	TNNI2	troponin I2, fast skeletal ty	Cytoplasm	enzyme				-0.53	-0.48			-0.48	-0.37			0.01	0.05			0.69	1.00			29	32			33	42			71	68			67	58
ENSG00000166681	NGFRAP1	BEX3	brain expressed X-linked 3	Cytoplasm	other		0.27	0.26	0.65	0.47	-0.06	0.18	0.59	0.10	0.00	0.72	0.01	0.00	1.00	0.70	1.00	1.00	64	68	79	76	50	55	75	75	36	32	21	24	50	45	25	25
ENSG00000213930	GALT	GALT	galactose-1-phosphate urid	Cytoplasm	enzyme		0.33	0.24	0.53		0.05	0.42	0.53		0.08	0.24	0.01		1.00	0.04	1.00		69	73	68		60	91	58		31	27	32		40	9	42	
ENSG00000176171	BNIP3	BNIP3	BCL2 interacting protein 3	Cytoplasm	other		0.07	0.13	0.60	0.32	-0.08	0.10	0.19	0.32	0.76	0.84	0.01	0.13	1.00	0.90	1.00	1.00	64	62	71	66	50	64	58	58	36	38	29	34	50	36	42	42
ENSG00000090554	FLT3LG	FLT3LG	fms related tyrosine kinase	Extracellular Space	cytokine		0.15	0.26	0.50	0.30	0.31	0.57	0.68	0.40	0.31	0.85	0.01	0.09	0.32	0.08	0.99	0.58	64	68	71	71	90	82	75	100	36	32	29	29	10	18	25	0
ENSG00000198937	CCDC167	CCDC167	coiled-coil domain contain	Other	other		0.12	0.22	0.75	0.60	0.18	0.02	0.64	0.79	0.35	0.86	0.01	0.04	1.00	0.94	1.00	1.00	56	59	68	66	60	55	67	75	44	41	32	34	40	45	33	25
ENSG00000136630	HLX	HLX	H2.0 like homeobox	Nucleus	transcription regulator				-0.54	-0.20			-0.51	-0.20			0.02	0.13			0.78	1.00			32	39			33	42			68	61			67	58
ENSG00000227191	TRGC2	TRGC2	T cell receptor gamma con	Other	other			-0.21	0.61	0.39		-0.06		0.35		0.41	0.02	0.39		0.84		1.00		41	74	66		45		67		59	26	34		55		33
ENSG00000170310	STX8	STX8	syntaxin 8	Plasma Membrane	other		0.35	0.38	0.53	0.28	0.35	0.56	0.52	0.10	0.27	0.75	0.02	0.09	1.00	0.62	1.00	1.00	64	62	68	61	60	64	67	67	36	38	32	39	40	36	33	33
ENSG00000123342	MMP19	MMP19	matrix metallopeptidase 1	Extracellular Space	peptidase				-0.54				0.11				0.02				1.00				34				50				66				50	
ENSG00000211677	IGLC2	IGLC2	immunoglobulin lambda c	Extracellular Space	other				-0.60	-0.48			-0.34	-0.51			0.02	0.13			1.00	1.00			34	37			33	33			66	63			67	67
ENSG00000104951	IL4I1	IL4I1	interleukin 4 induced 1	Cytoplasm	enzyme	Ferreira et al. Diabetes 2014			0.54				0.69				0.03				1.00				66				67				34				33	
ENSG00000115263	GCG	GCG	glucagon	Plasma Membrane	other					0.57				0.39				0.00				0.00				74				75				26				25
ENSG00000118785	SPP1	SPP1	secreted phosphoprotein 1	Extracellular Space	cytokine					1.62								0.00								76								24				
ENSG00000074706	IPCEF1	IPCEF1	interaction protein for cyto	Cytoplasm	enzyme		0.41	0.30		0.87	0.22	0.09		0.31	0.00	0.07		0.00	1.00	0.50		0.82	67	76		71	60	73		58	33	24		29	40	27		42
ENSG00000254647	INS	INS	insulin	Extracellular Space	other					0.74				0.51				0.00				0.06				74				67				26				33
ENSG00000150867	PIP4K2A	PIP4K2A	phosphatidylinositol-5-phos	Cytoplasm	kinase		0.35	0.31	0.33	0.53	0.45	0.78	0.28	0.72	0.00	0.04	0.00	0.00	1.00	0.00	0.26	0.03	64	70	74	68	70	73	67	75	36	30	26	32	30	27	33	25
ENSG00000180357	ZNF609	ZNF609	zinc finger protein 609	Nucleus	other		0.39	0.36		0.56	0.40			0.74	0.00	0.00		0.00	1.00			0.02	64	68		68	70			75	36	32		32	30			25
ENSG00000151702	FLI1	FLI1	Fli-1 proto-oncogene, ETS t	Nucleus	transcription regulator	Kallionpää et al. 2014	0.49	0.43	0.38	0.83	0.56	0.43	0.22	0.85	0.00	0.02	0.00	0.00	1.00	0.00	0.97	0.03	64	68	66	66	60	82	67	75	36	32	34	34	40	18	33	25
ENSG00000115386	REG1A	REG1A	regenerating family memb	Extracellular Space	growth factor					0.52				0.38				0.00				0.36				66				58				34				42
ENSG00000101017	CD40	CD40	CD40 molecule	Plasma Membrane	transmembrane receptor				-0.43	-0.68			-0.31	-0.47			0.00	0.00			0.35	0.07			13	18			8	17			87	82			92	83
ENSG00000198502	HLA-DRB5	HLA-DRB5	major histocompatibility c	Plasma Membrane	transmembrane receptor	Elo et al. 2010			-0.39	-0.87			-0.10	-0.93			0.00	0.00			1.00	0.90			29	32			50	42			71	68			50	58
ENSG00000197043	ANXA6	ANXA6	annexin A6	Plasma Membrane	ion channel		0.25	0.35	0.49	0.61	0.29	0.56	0.49	0.69	0.00	0.65	0.00	0.00	1.00	0.11	0.75	0.25	64	59	66	68	80	73	75	75	36	41	34	32	20	27	25	25
ENSG00000111331	OAS3	OAS3	2'-5'-oligoadenylate synthe	Cytoplasm	enzyme	Kallionpää et al. 2014, Reynier et al. 2010, Ferreira et al. 2014				0.53								0.00								66								34				
ENSG00000204642	HLA-F	HLA-F	major histocompatibility c	Plasma Membrane	transmembrane receptor	Elo et al. 2010	0.49	0.47	0.44	0.69	0.43	0.60	0.27	0.34	0.00	0.18	0.00	0.00	0.24	0.00	0.83	0.21	75	73	74	74	80	82	67	83	25	27	26	26	20	18	33	17
ENSG00000214078	CPNE1	CPNE1	copine 1	Nucleus	transporter		0.24	0.45	0.39	0.67	0.20	0.61	0.39	0.67	0.00	0.25	0.00	0.00	1.00	0.00	0.57	0.31	69	65	76	68	70	73	83	67	31	35	24	32	30	27	17	33
ENSG00000171130	ATP6V0E2	ATP6V0E2	ATPase H+ transporting V0	Cytoplasm	enzyme		0.37	0.38		0.63	0.36	0.77		0.72	0.00	0.27		0.00	1.00	0.01		0.31	72	65		68	80	82		75	28	35		32	20	18		25
ENSG00000077984	CST7	CST7	cystatin F	Extracellular Space	other	Kallionpää et al. 2014	0.52	-0.51	0.46	0.52		-0.36	0.69	0.70	0.14	0.03	0.00	0.00		0.15	0.06	0.01	61	41	79	66		36	58	75	39	59	21	34		64	42	25
ENSG00000178952	TUFM						0.14	0.26	0.37	0.58	0.09	0.26	0.34	0.62	0.13	0.74	0.01	0.00	1.00	0.55	1.00	0.29	75	65	82	82	70	64	83	75	25	35	18	18	30	36	17	25
ENSG00000105953	OGDH	OGDH	oxoglutarate dehydrogena	Cytoplasm	enzyme			0.40	0.27	0.63				0.75		0.61	0.01	0.00				0.44		59	66	68				75		41	34	32				25
ENSG00000147955	SIGMAR1	SIGMAR1	sigma non-opioid intracellu	Plasma Membrane	transmembrane receptor		0.30	0.28		0.53	-0.01			0.73	0.01	0.31		0.00	1.00			0.82	61	62		71	50			75	39	38		29	50			25
ENSG00000189057	FAM111B	FAM111B	family with sequence simil	Other	other				-0.50	-0.58			-0.72	-0.63			0.00	0.00			0.35	0.12			34	26			33	25			66	74			67	75
ENSG00000010292	NCAPD2	NCAPD2	non-SMC condensin I comp	Nucleus	other		0.12	0.23		0.51	0.00			0.59	0.18	0.48		0.00	1.00			0.74	58	68		68	50			67	42	32		32	50			33
ENSG00000154229	PRKCA	PRKCA	protein kinase C alpha	Cytoplasm	kinase		0.11	0.25		0.51	0.04	0.04		0.10	0.31	0.56		0.00	1.00	0.27		0.76	67	68		68	70	64		58	33	32		32	30	36		42
ENSG00000126266	FFAR1	FFAR1	free fatty acid receptor 1	Plasma Membrane	G-protein coupled receptor				-0.34	-0.53			-0.37	-0.02			0.00	0.00			1.00	1.00			34	34			42	50			66	66			58	50
ENSG00000153406	NMRAL1	NMRAL1	NmrA like redox sensor 1	Nucleus	other		0.17	0.31		0.65	-0.05	0.52		0.61	0.17	0.25		0.00	1.00	0.19		0.76	64	65		74	40	64		75	36	35		26	60	36		25
ENSG00000131634	TMEM204	TMEM204	transmembrane protein 20	Plasma Membrane	other		0.29	0.62		0.59	0.25	0.71		0.35	0.01	0.07		0.00	1.00	0.07		1.00	69	70		66	60	82		58	31	30		34	40	18		42
ENSG00000083454	P2RX5	P2RX5	purinergic receptor P2X 5	Plasma Membrane	ion channel				0.50	0.55			0.55	0.27			0.00	0.00			1.00	1.00			71	74			67	58			29	26			33	42
ENSG00000188191	PRKAR1B	PRKAR1B	protein kinase cAMP-depe	Cytoplasm	kinase		0.11	0.39		0.52	-0.07	0.41		0.24	0.27	0.59		0.00	1.00	0.06		0.98	69	68		82	50	82		83	31	32		18	50	18		17
ENSG00000211746	TRBV19	TRBV19	T cell receptor beta variabl	Other	other	Elo et al. 2010	0.41	0.15		0.59	0.43	0.07		0.47	0.10	0.61		0.00	1.00	0.94		1.00	67	65		74	70	55		75	33	35		26	30	45		25
ENSG00000181754	AMIGO1	AMIGO1	adhesion molecule with Ig	Plasma Membrane	other		-0.04	0.16		0.52	-0.31			-0.05	0.30	0.55		0.00	1.00			1.00	47	59		71	10			50	53	41		29	90			50
ENSG00000122694	GLIPR2	GLIPR2	GLI pathogenesis related 2	Cytoplasm	other				0.12	0.57			0.06	0.38			0.02	0.00			1.00	1.00			58	68			50	83			42	32			50	17
ENSG00000167815	PRDX2	PRDX2	peroxiredoxin 2	Cytoplasm	enzyme		0.43	0.44	0.61	0.55	0.47	0.71	0.62	1.00	0.03	0.81	0.03	0.00	1.00	0.19	1.00	0.63	61	59	61	68	70	73	67	75	39	41	39	32	30	27	33	25
ENSG00000149531	FRG1B	FRG1BP	FSHD region gene 1 family	Other	other		-0.66	-0.69	-0.30	-0.61	-0.70	-0.79	-0.52	-0.77	0.01	0.05	0.10	0.01	1.00	0.13	0.48	0.30	39	30	37	34	30	27	25	25	61	70	63	66	70	73	75	75
ENSG00000106397	PLOD3	PLOD3	procollagen-lysine,2-oxogl	Cytoplasm	enzyme				0.25	0.52			0.21	0.35			0.01	0.01			1.00	1.00			68	74			58	67			32	26			42	33
ENSG00000137959	IFI44L	IFI44L	interferon induced protein	Nucleus	other	Kallionpää et al. 2014, Ferreira et al. 2014	0.06	0.80	0.29	0.55	-0.24	-0.83	-0.69	-0.64	0.26	0.18	0.37	0.01	0.14	0.00	0.48	0.68	56	59	58	66	30	18	33	42	44	41	42	34	70	82	67	58
ENSG00000223350	IGLV9-49	IGLV9-49	immunoglobulin lambda va	Other	other				0.48	0.67			0.67	0.89			0.03	0.02			1.00	0.86			71	71			75	75			29	29			25	25
ENSG00000198951	NAGA	NAGA	alpha-N-acetylgalactosami	Cytoplasm	enzyme				0.42	0.57			0.19	0.42			0.00	0.02			1.00	1.00			63	68			67	75			37	32			33	25
ENSG00000134291	TMEM106C	TMEM106C	transmembrane protein 10	Other	other		0.18	0.27		0.50	-0.12			0.48	0.23	0.49		0.03	1.00			1.00	67	62		68	40			67	33	38		32	60			33
ENSG00000164111	ANXA5	ANXA5	annexin A5	Plasma Membrane	transporter		0.35	-0.19	0.22	0.56	0.24	-0.19	0.25	0.34	0.09	0.78	0.55	0.04	1.00	0.64	1.00	1.00	61	41	58	66	60	27	58	67	39	59	42	34	40	73	42	33
ENSG00000104974	LILRA1	LILRA1	leukocyte immunoglobulin	Plasma Membrane	transmembrane receptor				0.17	0.61							0.14	0.04							55	66							45	34				
ENSG00000225630	MTND2P28	MTND2P28	mitochondrially encoded N	Other	other		0.37	0.10	0.19	0.06	0.99	0.36	0.15	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	61	57	63	53	80	64	67	50	39	43	37	47	20	36	33	50
ENSG00000124882	EREG	EREG	epiregulin	Extracellular Space	growth factor	Ferreira et al. Diabetes 2014	0.46	0.75	0.36	0.19	1.19		0.33	0.86	0.00	0.01	0.01	0.01	0.00		0.88	0.00	67	62	68	58	70		58	75	33	38	32	42	30		42	25
ENSG00000134531	EMP1	EMP1	epithelial membrane prote	Plasma Membrane	other		-0.08	0.00	-0.25	-0.27	0.80	0.88	0.06	0.41	0.97	0.77	0.12	0.20	0.00	0.08	1.00	0.89	47	51	42	39	80	64	58	50	53	49	58	61	20	36	42	50
ENSG00000060138	YBX3	YBX3	Y-box binding protein 3	Nucleus	transcription regulator		0.20	0.35	0.01	0.00	0.77	0.44	0.17	0.26	0.02	0.55	0.72	0.67	0.00	0.00	1.00	1.00	56	68	50	50	80	82	58	67	44	32	50	50	20	18	42	33
ENSG00000135046	ANXA1	ANXA1	annexin A1	Plasma Membrane	enzyme		0.08	-0.02	-0.10	0.22	0.84	0.28	-0.28	0.56	0.11	0.96	0.98	0.14	0.00	0.68	1.00	1.00	56	49	42	61	70	64	42	67	44	51	58	39	30	36	58	33

ENSG00000186407	CD300E	CD300E	CD300e molecule	Plasma Membrane	other		0.49		0.10	-0.04	1.28		0.43	0.92	0.00		0.76	0.98	0.00		1.00	1.00	64		50	50	70		58	58	36		50	50	30		42	42
ENSG00000124942	AHNAK	AHNAK	AHNAK nucleoprotein	Nucleus	other		0.24	0.34	-0.20	0.11	0.67	0.61	0.07	0.35	0.34	0.97	0.64	0.41	0.02	0.77	1.00	1.00	58	51	45	53	70	64	50	67	42	49	55	47	30	36	50	33
ENSG00000078804	TP53INP2	TP53INP2	tumor protein p53 inducibl	Nucleus	other		0.13	0.01	-0.10	-0.28	0.55	0.25	-0.02	0.31	0.56	0.72	0.51	0.01	0.02	0.77	1.00	1.00	58	51	37	32	80	64	42	58	42	49	63	68	20	36	58	42
ENSG00000154451	GBP5	GBP5	guanylate binding protein	Plasma Membrane	enzyme	Kallionpää et al. 2014, Reynier et al. 2010, Ferreira et al. 2014	-0.29	-0.59	0.00	-0.13	-0.39	-0.85	-0.15	-0.21	0.02	0.08	0.97	0.67	0.76	0.00	1.00	1.00	42	30	50	42	30	9	42	33	58	70	50	58	70	91	58	67
ENSG00000132386	SERPINF1	SERPINF1	serpin family F member 1	Extracellular Space	other	Kallionpää et al. 2014	0.31	0.24	-0.26	0.29	0.64	1.21	-0.37	0.32	0.09	0.08	0.70	0.28	0.55	0.00	1.00	1.00	58	54	37	66	60	73	33	67	42	46	63	34	40	27	67	33
ENSG00000163013	FBXO41	FBXO41	F-box protein 41	Cytoplasm	enzyme		0.40	0.53	0.40	0.38	0.51	0.87		0.79	0.00	0.09	0.00	0.00	0.81	0.00		0.10	75	78	84	74	70	73		67	25	22	16	26	30	27		33
ENSG00000136997	MYC	MYC	v-myc avian myelocytomat	Nucleus	transcription regulator		0.22	0.28	-0.04	0.13	0.44	0.60	-0.11	0.14	0.13	0.83	0.89	0.18	0.22	0.00	1.00	1.00	56	57	45	53	70	82	42	50	44	43	55	47	30	18	58	50
ENSG00000071073	MGAT4A	MGAT4A	mannosyl (alpha-1,3-)-glyco	Cytoplasm	enzyme		0.39	0.35	0.43	0.48	0.43	0.68	0.43	0.51	0.00	0.19	0.00	0.00	0.37	0.00	0.28	0.30	72	70	84	84	90	91	83	100	28	30	16	16	10	9	17	0
ENSG00000026297	RNASET2	RNASET2	ribonuclease T2	Cytoplasm	enzyme		0.07	0.37	0.01	0.11	0.48	0.85	0.01	0.08	0.26	0.66	0.62	0.51	1.00	0.00	1.00	1.00	56	59	58	58	60	73	58	58	44	41	42	42	40	27	42	42
ENSG00000040933	INPP4A	INPP4A	inositol polyphosphate-4-pl	Cytoplasm	phosphatase		0.10	0.20		0.42	0.07	0.54		0.50	0.21	0.18		0.00	1.00	0.00		0.00	53	59		66	50	73		75	47	41		34	50	27		25
ENSG00000153551	CMTM7	CMTM7	CKLF like MARVEL transme	Extracellular Space	cytokine		0.50	0.53	0.48	0.41	0.52	0.54	0.23	0.52	0.00	0.05	0.00	0.00	0.24	0.00	1.00	0.29	83	70	68	82	80	100	58	92	17	30	32	18	20	0	42	8
ENSG00000178199	ZC3H12D	ZC3H12D	zinc finger CCCH-type cont	Cytoplasm	other		-0.04	0.04	0.17	0.20	0.10	0.86	0.37	0.34	0.49	0.98	0.43	0.56	1.00	0.00	1.00	1.00	44	51	63	61	60	73	67	75	56	49	37	39	40	27	33	25
ENSG00000127663	KDM4B	KDM4B	lysine demethylase 4B	Nucleus	enzyme		0.16	0.25	0.07	0.15	0.30	0.56	0.50	0.64	0.48	0.83	0.82	0.42	0.99	0.00	0.84	0.22	56	62	55	63	70	82	83	83	44	38	45	37	30	18	17	17
ENSG00000130775	THEMIS2	THEMIS2	thymocyte selection associ	Other	other		0.50	0.57	0.00	-0.14	0.53	0.57	-0.32	-0.09	0.00	0.01	0.93	0.74	0.86	0.00	1.00	1.00	78	62	50	42	70	73	33	50	22	38	50	58	30	27	67	50
ENSG00000117643	MAN1C1	MAN1C1	mannosidase alpha class 1	Cytoplasm	enzyme		0.11	0.48		0.48	0.22	0.52		0.54	0.21	0.20		0.00	1.00	0.00		0.08	58	68		74	70	82		83	42	32		26	30	18		17
ENSG00000121281	ADCY7	ADCY7	adenylate cyclase 7	Plasma Membrane	enzyme		0.23	0.38	0.44	0.47	-0.06	0.77	0.48	0.58	0.00	0.08	0.00	0.00	1.00	0.00	1.00	0.16	61	73	74	71	50	82	67	83	39	27	26	29	50	18	33	17
ENSG00000167261	DPEP2	DPEP2	dipeptidase 2	Plasma Membrane	peptidase		0.29	0.40	0.26	0.16	0.27	0.56	0.20	0.09	0.00	0.01	0.01	0.07	1.00	0.00	1.00	1.00	67	76	68	55	60	91	75	58	33	24	32	45	40	9	25	42
ENSG00000143466	NA						0.21	0.38		0.44	0.06	0.69		0.44	0.02	0.02		0.00	1.00	0.00		0.82	64	70		61	50	82		75	36	30		39	50	18		25
ENSG00000172543	CTSW	CTSW	cathepsin W	Cytoplasm	peptidase		0.46	-0.35	0.30	-0.01	0.12	-0.57	0.35	-0.17	0.49	0.20	0.12	0.99	1.00	0.00	1.00	1.00	64	41	66	47	60	27	67	42	36	59	34	53	40	73	33	58
ENSG00000120875	DUSP4	DUSP4	dual specificity phosphatas	Nucleus	phosphatase		-0.30	-0.41	-0.13	-0.24	-0.10	-0.80	-0.05	0.12	0.08	0.03	0.48	0.02	1.00	0.00	1.00	1.00	42	27	45	37	50	27	50	50	58	73	55	63	50	73	50	50
ENSG00000162777	DENND2D	DENND2D	DENN domain containing 2	Cytoplasm	other		0.28	0.39	0.48	0.49	0.59	0.64	0.45	0.85	0.00	0.00	0.00	0.00	1.00	0.01	0.53	0.18	64	65	79	74	70	82	75	83	36	35	21	26	30	18	25	17
ENSG00000113319	RASGRF2	RASGRF2	Ras protein specific guanin	Cytoplasm	other		0.44	0.48			0.45	0.66			0.00	0.44			0.41	0.01			69	62			60	73			31	38			40	27		
ENSG00000099326	MZF1	MZF1	myeloid zinc finger 1	Nucleus	transcription regulator		0.27	0.43			0.10	0.58			0.03	0.08			1.00	0.01			72	81			80	100			28	19			20	0		
ENSG00000137478	FCHSD2	FCHSD2	FCH and double SH3 domai	Other	other		0.22	0.42	0.44	0.08	0.34	0.58	0.35	0.37	0.01	0.14	0.00	0.31	1.00	0.01	1.00	1.00	58	62	61	55	70	73	58	58	42	38	39	45	30	27	42	42
ENSG00000169896	ITGAM	ITGAM	integrin subunit alpha M	Plasma Membrane	transmembrane receptor			-0.45	-0.08	-0.02		-0.67	-0.08	-0.02		0.01	0.82	0.67		0.01	1.00	1.00		30	47	50		27	42	50		70	53	50		73	58	50
ENSG00000055332	EIF2AK2	EIF2AK2	eukaryotic translation initi	Cytoplasm	kinase		-0.22	-0.14	-0.10	0.02	-0.28	-0.59	-0.41	-0.42	0.19	0.70	0.34	0.35	1.00	0.01	0.83	0.96	39	43	39	53	30	9	25	33	61	57	61	47	70	91	75	67
ENSG00000178035	IMPDH2	IMPDH2	inosine monophosphate de	Cytoplasm	enzyme		0.15	0.18	0.23	0.21	0.15	0.50	0.23	0.49	0.31	0.80	0.09	0.06	1.00	0.01	1.00	0.99	58	62	63	63	50	82	67	75	42	38	37	37	50	18	33	25
ENSG00000107819	SFXN3	SFXN3	sideroflexin 3	Cytoplasm	transporter		0.37	0.31	0.08	0.19	0.66	0.61	0.48	0.39	0.16	0.48	0.77	0.25	0.55	0.01	1.00	1.00	64	73	61	63	70	82	67	67	36	27	39	37	30	18	33	33
ENSG00000185504	C17orf70	FAAP100	Fanconi anemia core comp	Nucleus	other		0.36	0.35	0.36	0.45	0.43	0.52	0.46	0.59	0.00	0.63	0.00	0.01	1.00	0.01	0.97	0.31	69	65	76	66	70	91	83	75	31	35	24	34	30	9	17	25
ENSG00000010295	IFFO1	IFFO1	intermediate filament fami	Other	other		0.38	0.27	0.38		0.22	0.58	0.51		0.03	0.14	0.02		1.00	0.02	1.00		69	70	68		70	91	67		31	30	32		30	9	33	
ENSG00000181896	ZNF101	ZNF101	zinc finger protein 101	Nucleus	other		-0.04	-0.12	0.13	-0.01	-0.43	-0.59	-0.05	-0.26	0.21	0.74	0.90	0.47	0.28	0.02	1.00	0.69	50	35	63	50	10	0	50	25	50	65	37	50	90	100	50	75
ENSG00000130164	LDLR						0.23	0.17	-0.02	0.48	0.56	0.68	0.08	0.61	0.78	0.97	0.90	0.14	0.23	0.02	1.00	0.07	53	59	47	58	70	73	50	67	47	41	53	42	30	27	50	33
ENSG00000137312	FLOT1	FLOT1	flotillin 1	Plasma Membrane	other		0.17	0.37	0.06	0.20	0.09	0.51	-0.12	0.20	0.00	0.16	0.90	0.15	1.00	0.02	1.00	1.00	67	62	53	61	60	73	50	67	33	38	47	39	40	27	50	33
ENSG00000225138	CTD-2228K2.7											0.53								0.02								91								9		
ENSG00000158062	UBXN11	UBXN11	UBX domain protein 11	Cytoplasm	other		-0.06	0.22	0.00	0.01	0.09	0.52	0.10	-0.03	0.38	0.36	0.58	0.96	1.00	0.02	1.00	1.00	50	62	50	55	50	73	58	50	50	38	50	45	50	27	42	50
ENSG00000161381	PLXDC1	PLXDC1	plexin domain containing 1	Plasma Membrane	other		-0.22	0.44			0.26	0.70			0.79	0.41			1.00	0.03			42	59			60	73			58	41			40	27		
ENSG00000198771	RCSD1	RCSD1	RCSD domain containing 1	Other	other		0.34	0.48	0.40	0.41	0.33	0.64	0.47	0.53	0.00	0.06	0.00	0.00	1.00	0.03	1.00	0.86	64	68	76	66	70	73	75	75	36	32	24	34	30	27	25	25
ENSG00000106003	LFNG	LFNG	LFNG O-fucosylpeptide 3-b	Cytoplasm	enzyme		0.18	0.33	0.15	0.15	-0.03	0.61	0.10	0.21	0.06	0.65	0.33	0.15	1.00	0.04	1.00	1.00	58	59	58	61	50	73	50	58	42	41	42	39	50	27	50	42
ENSG00000068878	PSME4	PSME4	proteasome activator subu	Cytoplasm	other		-0.34	-0.54	-0.24	-0.29	-0.38	-0.63	-0.17	-0.29	0.00	0.18	0.00	0.04	1.00	0.04	1.00	1.00	19	30	21	26	20	18	25	25	81	70	79	74	80	82	75	75
ENSG00000128185	DGCR6L	DGCR6L	DiGeorge syndrome critica	Nucleus	other		0.32	0.28	0.34	0.26	0.30	0.66	0.22	0.54	0.13	0.78	0.03	0.04	1.00	0.04	1.00	0.99	64	59	71	66	60	73	58	75	36	41	29	34	40	27	42	25
ENSG00000160271	RALGDS	RALGDS	ral guanine nucleotide diss	Cytoplasm	other		-0.05	0.10	-0.16	-0.09	0.32	0.54	0.24	0.04	0.97	0.97	0.36	0.79	1.00	0.04	1.00	1.00	47	51	42	47	60	73	58	50	53	49	58	53	40	27	42	50
ENSG00000142089	IFITM3	IFITM3	interferon induced transm	Plasma Membrane	other	Kallionpää et al 2014	0.42	-0.04	-0.07	0.20	-0.37	-0.32	-0.51	-0.61	0.23	0.87	0.74	0.44	1.00	0.98	0.00	0.00	58	49	42	55	40	45	17	33	42	51	58	45	60	55	83	67
ENSG00000126709	IFI6	IFI6	interferon alpha inducible	Cytoplasm	other	Kallionpää et al 2014	0.31	0.38	0.12	0.38	-0.31	0.15	-1.16	-0.95	0.42	0.85	0.99	0.86	1.00	0.94	0.00	0.05	67	62	55	55	50	55	25	33	33	38	45	45	50	45	75	67
ENSG00000131401	NAPSB	NAPSB	napsin B aspartic peptidas	Other	other				-0.34	-0.37			-0.73	-0.43			0.00	0.00			0.01	0.00			37	32			25	25			63	68			75	75
ENSG00000085265	FCN1	FCN1	ficolin 1	Extracellular Space	peptidase		-0.14	-0.08	-0.51	-0.47	1.01	-0.08	-0.88	-0.55	0.69	0.95	0.00	0.00	1.00	0.97	0.01	0.01	44	49	39	39	60	45	25	25	56	51	61	61	40	55	75	75
ENSG00000244734	HBB	HBB	hemoglobin subunit beta	Cytoplasm	transporter			-0.14	-0.43	-0.97		0.10	-1.28	-1.46		0.27	0.00	0.00		0.99	0.01	0.00		43	45	42		55	33	42		54	55	58		45	67	58
ENSG00000110077	MS4A6A	MS4A6A	membrane spanning 4-dom	Other	other				-0.25	0.04			-0.72	-0.13			0.55	0.70			0.02	0.29			47	50			33	42			53	50			67	58
ENSG00000157933	SKI	SKI	SKI proto-oncogene	Nucleus	transcription regulator		0.18	0.29	0.31	0.34	0.25	0.43	0.75	0.40	0.17	0.99	0.10	0.04	0.03	0.00	0.03	0.11	64	57	63	68	80	91	83	83	36	43	37	32	20	9	17	17
ENSG00000121316	PLBD1	PLBD1	phospholipase B domain co	Extracellular Space	enzyme				-0.42	-0.16			-0.51	-0.61			0.01	0.00			0.03	0.01			34	39			25	33			66	61			75	67
ENSG00000173762	CD7	CD7	CD7 molecule	Plasma Membrane	other		0.00	-0.11	0.27	0.16	0.14	-0.03	0.55	0.54	0.90	0.75	0.00	0.07	1.00	0.72	0.04	0.30	50	35	82	71	60	45	100	92	50	65	18	29	40	55	0	8
ENSG00000188536	HBA2	HBA1/HBA2	hemoglobin subunit alpha	Extracellular Space	transporter			-1.27	-0.62	-1.52			-0.76	-1.64		0.08	0.00	0.00			0.26	0.00		38	42	42			42	33		59	58	58			58	67
ENSG00000206172	HBA1	HBA1/HBA2	hemoglobin subunit alpha	Extracellular Space	transporter				0.04	-0.78			-0.55	-1.59			0.21	0.00			0.70	0.00			53	42			50	33			47	58			50	67
ENSG00000196565	HBG2	HBG2	hemoglobin subunit gamm	Cytoplasm	other	Kallionpää et al. 2014			-0.30				-0.31	-2.12			0.19				0.98	0.00			45				33	33			55				67	67
ENSG00000206341	HLA-H	HLA-H	major histocompatibility c	Plasma Membrane	other		0.14	0.27	0.43	0.29	0.07	0.98	0.52	0.81	0.00	0.40	0.00	0.00	1.00	0.01	0.33	0.01	58	57	63	58	50	55	67	75	42	43	37	42	50	45	33	25
ENSG00000221957	KIR2DS4	KIR2DS4 (includes oth	killer cell immunoglobulin	Plasma Membrane	transmembrane receptor								1.55	1.06							0.03	0.02							58	75							42	25
ENSG00000167680	SEMA6B	SEMA6B	semaphorin 6B	Plasma Membrane	other				0.19	0.61			0.61	0.95			0.80	0.53			0.91	0.02			53	55			58	67			47	45			42	33
ENSG00000188486	H2AFX	H2AFX	H2A histone family membe	Nucleus	transcription regulator		-0.16	-0.25	0.15	0.03	0.25	0.03	0.45	0.57	0.34	0.49	0.27	0.85	1.00	0.88	0.83	0.05	39	38	66	50	50	64	83	83	61	62	34	50	50	36	17	17

Supplementary Table 4C. Non-coding DE genes between Cases and Controls

		IPA ANNOTATION				Previously	Human lncRNA ATLAS Hon et al. Nature 2017:543;199-20			Median LogFC								FDR								Percent Up								Percent Down							
										Over All Timepoints				12 mo before SC				Over All Timepoints				12 mo before SC				Over All Timepoints				12 mo before SC				Over All Timepoints				12 mo before SC			
Ensembl Gene IDs	Gene Names	Symbol	Entrez Gene Name	Location	Type(s)	published	FANTOM CAT tool	CAT gene class	CAT gene category	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC	CD4+	CD8+	CD4-CD8-	PBMC
ENSG00000228463	AP006222.2									0.83								0.00								78								22							
ENSG00000260711	RP11-747H7.3									0.71								0.00								69								31							
ENSG00000260065	CTA-445C9.15						No implications in coex	lncRNA intergen	e_lncRNA	0.63	0.05	0.12	0.26		-0.24	0.06	0.32	0.00	0.81	0.23	0.04		0.92	1.00	0.99	69	54	66	63		45	58	58	31	46	34	37		55	42	42
ENSG00000249667	LINC01259	LINC01259	long intergenic non-protein coding RNA 1259	Other	other		No implications in coex	lncRNA intergen	others	0.55	0.55		0.80	0.65			0.76	0.00	0.02		0.00	0.73			0.60	67	65		68	80			67	33	35		32	20			33
ENSG00000271938	RP11-589C21.6						1 eQTL linked co-expre	lncRNA intergen	p_lncRNA_intergen	-0.59	-0.72	-0.27	-0.36	0.12	-0.45	-0.12	-0.29	0.01	0.00	0.07	0.07	0.99	0.50	0.99	0.81	33	24	26	26	50	36	33	33	67	76	74	74	50	64	67	67
ENSG00000234449	RP11-706O15.3									0.64	0.82				0.85			0.01	0.01				0.33			69	73				73			31	27				27		
ENSG00000235576	AC092580.4						No implications in coex	lncRNA intergen	e_lncRNA	1.08	-0.18	0.77	0.10	1.08	-0.51	1.72	0.06	0.01	0.38	0.00	0.15	0.56	0.70	0.66	0.99	75	46	66	58	90	27	58	58	25	54	34	42	10	73	42	42
ENSG00000269996	NA						No implications in coex	lncRNA intergen	others	0.63	0.41	0.06	0.29	0.74	0.43	-0.21	0.03	0.01	0.32	0.99	0.54	0.65	0.75	0.99	1.00	81	70	55	61	80	73	42	50	19	30	45	39	20	27	58	50
ENSG00000232677	LINC00665	LINC00665	long intergenic non-protein coding RNA 665	Other	other		6 eQTL linked co-expre	lncRNA divergen	p_lncRNA_divergen	-0.67	-0.50	-0.17	-0.22	-0.94	-0.50	-0.18	-0.50	0.02	0.04	0.80	0.98	0.04	0.55	0.99	0.78	28	30	39	37	10	18	25	17	72	70	61	63	90	82	75	83
ENSG00000223692	DIP2A-IT1	DIP2A-IT1	DIP2A intronic transcript 1	Other	other					-0.66	-0.76	-0.20	-0.29	0.00	-0.98	-0.25	0.25	0.02	0.00	0.98	0.22	0.99	0.43	1.00	0.99	28	32	34	42	50	36	33	58	72	68	66	58	50	64	67	42
ENSG00000270127	PRKXP1									0.58	1.03		1.13	0.24	1.41			0.02	0.00		0.00	0.99	0.19			72	76		66	50	73			28	24		34	50	27		
ENSG00000261685	RP11-401P9.4									0.44	0.70		0.60	0.43	0.65		0.53	0.05	0.00		0.01	0.70	0.26		0.58	61	73		68	60	64		75	39	27		32	40	36		25
ENSG00000259715	CTD-3110H11.1									0.29	0.96	0.40		-0.23	-0.08	0.50		0.40	0.00	0.52		0.99	0.95	1.00		64	81	63		40	45	67		36	19	37		60	55	33	
ENSG00000273038	RP11-479G22.8									-0.15	-0.66	-0.45	-0.27	-0.30	-0.56	0.21	-0.47	0.43	0.01	0.01	0.05	0.99	0.10	0.99	0.61	47	27	29	39	40	18	50	42	53	73	71	61	60	82	50	58
ENSG00000254419	RP11-261P9.4									0.37	0.68	0.41		0.12	0.47	0.73		0.39	0.01	0.25		0.99	0.33	0.80		61	73	63		60	73	92		39	27	37		40	27	8	
ENSG00000235532	LINC00402	LINC00402	long intergenic non-protein coding RNA 402	Other	other		No implications in coex	lncRNA intergen	others	0.35	0.87		0.38					0.16	0.01		0.00					58	70		71					42	30		29				
ENSG00000227403	AC009299.3	LINC01806	long intergenic non-protein coding RNA 1806	Other	other		No implications in coex	lncRNA intergen	p_lncRNA_intergen	0.41	0.57	0.73	0.65	0.41	0.59	0.85	0.73	0.05	0.01	0.00	0.00	0.99	0.03	0.25	0.11	78	86	79	84	70	91	67	83	22	14	21	16	30	9	33	17
ENSG00000260461	RP11-541N10.3						No implications in coex	lncRNA intergen	e_lncRNA	0.16	0.68		0.19	0.05			-0.08	0.20	0.01		0.02	0.99			0.99	69	70		58	50			42	31	30		42	50			58
ENSG00000223745	RP4-717I23.3	CCDC18-AS1	CCDC18 antisense RNA 1	Other	other		4 eQTL linked co-expre	lncRNA divergen	p_lncRNA_divergen	0.09	0.59	0.45	0.17	-0.52	0.17	0.81	0.15	0.40	0.02	0.11	0.14	0.99	0.26	0.33	0.99	50	68	71	63	40	64	83	58	50	32	29	37	60	36	17	42
ENSG00000265185	SNORD3B-1	SNORD3B-1	small nucleolar RNA, C/D box 3B-1	Other	other		No implications in coex	lncRNA intergen	others			-1.45								0.00								8								92					
ENSG00000245164	LINC00861	LINC00861	long intergenic non-protein coding RNA 861	Other	other		No implications in coex	lncRNA intergen	others	0.63	0.33	1.10	0.80	0.73	1.53	1.19	1.28	0.06	0.08	0.00	0.00	0.99	0.01	0.09	0.24	58	59	76	58	60	73	75	67	42	41	24	42	40	27	25	33
ENSG00000237943	PRKCQ-AS1	PRKCQ-AS1	PRKCQ antisense RNA 1	Other	other		1 eQTL linked co-expres	lncRNA divergen	p_lncRNA_divergen	0.14	0.29	0.77	0.29	-0.24	0.32	0.70	0.20	0.77	0.57	0.00	0.10	0.99	0.77	0.66	0.99	56	59	82	66	40	73	75	67	44	41	18	34	60	27	25	33
ENSG00000202198	RN7SK	RN7SK	RNA, 7SK small nuclear	Nucleus	other		No implications in coex	lncRNA divergen	p_lncRNA_divergen	0.38	0.05	-0.61	-0.20	0.96	0.05	-0.56	-0.31	0.48	0.91	0.00	0.23	0.89	0.83	0.01	0.99	56	57	24	42	80	55	25	42	44	43	76	58	20	45	75	58
ENSG00000256576	RP13-977J11.2	LOC100996246	uncharacterized LOC100996246	Other	other		1 eQTL linked co-expres	lncRNA intergen	p_lncRNA_intergen	0.05	0.08	0.72	0.34	-0.03	0.03	0.62	0.30	0.99	0.98	0.00	0.04	0.99	1.00	0.66	0.99	53	57	84	74	40	55	75	75	47	43	16	26	60	45	25	25
ENSG00000272282	RP11-222K16.2						No implications in coex	lncRNA intergen	p_lncRNA_intergenic		-0.13	0.52	0.52						0.55	0.00	0.01						43	76	71						57	24	29				
ENSG00000261574	RP1-168P16.2										-0.66	-0.59	-0.65		-0.67	-0.27	-0.35		0.03	0.00	0.00		0.62	0.80	0.99		38	18	29		27	25	25		62	82	71		73	75	75
ENSG00000235437	LINC01278	LINC01278	long intergenic non-protein coding RNA 1278	Other	other		1 eQTL linked co-expres	lncRNA intergen	p_lncRNA_intergen	0.18	0.38	0.50	0.47	0.18	0.35	0.32	0.49	0.24	0.34	0.00	0.01	0.99	0.42	0.80	0.58	64	62	79	63	70	73	75	67	36	38	21	37	30	27	25	33
ENSG00000212232	SNORD17	SNORD17	small nucleolar RNA, C/D box 17	Other	other		Best associated with hir	small RNA	others	-0.49	-0.28	-1.07	0.02	1.33	-0.50	-1.47	0.20	0.25	0.27	0.00	0.98	0.99	0.77	0.25	0.99	47	38	32	50	70	18	33	58	53	62	68	50	30	82	67	42
ENSG00000245937	LINC01184	LINC01184	long intergenic non-protein coding RNA 1184	Other	other		No implications in coex	lncRNA divergen	p_lncRNA_divergen	0.35	0.09	0.54	0.61	0.22	0.47	0.46	0.60	0.27	0.54	0.00	0.02	0.99	0.77	0.99	0.91	58	57	68	66	70	64	67	75	42	43	32	34	30	36	33	25
ENSG00000272048	NA						No implications in coex	lncRNA intergen	others	0.19	0.27	0.79	0.54	0.13	0.30	0.44	-0.03	0.48	0.57	0.00	0.03	0.99	0.77	0.80	0.99	64	65	84	66	60	73	75	50	36	35	16	34	40	27	25	50
ENSG00000237772	AC092620.3											-0.61	-0.52			-0.62				0.00	0.04			0.34				24	39			17				76	61			83	
ENSG00000273272	CTA-384D8.34						No implications in coex	lncRNA intergen	e_lncRNA			-0.59				-0.63				0.00				0.32				29				17				71				83	
ENSG00000212694	LINC01089	LINC01089	long intergenic non-protein coding RNA 1089	Other	other		1 eQTL linked co-expres	lncRNA sense int	others	0.04	0.28	0.51	0.31	-0.07	0.21	0.53	0.39	0.50	0.59	0.00	0.47	0.99	0.85	0.83	0.99	58	68	79	74	30	73	75	75	42	32	21	26	70	27	25	25
ENSG00000272849	RP11-347I19.8						No implications in coex	lncRNA antisens	others	0.21	0.39	0.70	0.41	-0.07	0.04	0.52	0.06	0.39	0.20	0.00	0.45	1.00	0.77	0.80	0.99	58	76	74	63	40	64	67	50	42	24	26	37	60	36	33	50
ENSG00000235314	LINC00957	LINC00957	long intergenic non-protein coding RNA 957	Other	other					0.12	0.50	0.52	0.38	-0.25	0.14	0.19	-0.01	0.48	0.48	0.00	0.07	0.99	0.88	1.00	0.99	58	76	76	71	20	73	67	50	42	24	24	29	80	27	33	50
ENSG00000255135	RP11-111M22.3						1 eQTL linked co-expres	lncRNA divergen	p_lncRNA_divergen	0.18	0.37	0.82	0.05	-0.07	0.31	0.82	0.00	0.35	0.76	0.01	0.34	0.99	0.96	0.99	0.99	64	62	68	55	50	55	58	50	36	38	32	45	50	45	42	50
ENSG00000240905	RN7SL798P	RN7SL798P		Other	other							-0.91	-0.01			-0.95	-0.28			0.01	0.81			0.59	0.99			24	50			33	42			76	50			67	58
ENSG00000225978	HAR1A	HAR1A	highly accelerated region 1A (non-protein co	Other	other		No implications in coex	lncRNA intergen	p_lncRNA_intergen	0.00	-0.14	0.62	0.19	-0.38	0.18	0.55	0.38	0.88	0.33	0.01	0.82	0.99	0.99	0.66	0.99	50	49	68	63	30	55	67	75	50	51	32	37	70	45	33	25
ENSG00000266274	RN7SL138P	RN7SL138P		Other	other							-0.58	-0.65			-0.86	-1.48			0.01	0.07			0.66	0.68			32	37			33	33			68	63			67	67
ENSG00000269900	RMRP	RMRP	RNA component of mitochondrial RNA proce	Cytoplas	other		No implications in coex	lncRNA divergen	p_lncRNA_divergen	0.13	-0.41	-0.66	-0.34	1.00	-0.41	-1.14	-0.35	0.30	0.12	0.01	0.14	0.77	0.93	0.14	0.99	50	30	32	32	70	36	25	33	50	70	68	68	30	64	75	67
ENSG00000260910	LINC00565	LINC00565	long intergenic non-protein coding RNA 565	Other	other		2 eQTL linked co-expres	lncRNA intergen	e_lncRNA	0.18	0.12	0.62	0.56	0.34	0.35	0.78	0.57	0.81	0.90	0.01	0.14	0.99	0.77	0.30	0.99	53	54	74	66	60	64	83	67	47	46	26	34	40	36	17	33
ENSG00000271948	RP11-242F4.2									0.49	0.16	0.67	0.16	0.51	0.36	0.77	0.05	0.02	0.61	0.01	0.21	0.76	0.81	0.66	0.99	81	62	76	55	90	73	75	50	19	38	24	45	10	27	25	50
ENSG00000253948	RP11-410L14.2	LOC105375666		Other	other		No implications in coex	lncRNA divergen	p_lncRNA_divergen	0.36	0.61	0.74	0.59	0.34	0.69	0.72	0.49	0.07	0.33	0.03	0.04	0.99	0.55	1.00	0.99	58	57	66	71	60	64	67	75	42	43	34	29	40	36	33	25
ENSG00000272812	RP5-855D21.3						No implications in coex	lncRNA divergen	p_lncRNA_divergen	0.27	0.33	0.57		0.17	0.74	0.45	0.50	0.40	0.61	0.03		0.99	0.55	0.80	0.99	64	68	68		70	73	75	75	36	32	32		30	27	25	25
ENSG00000262074	SNORD3B-2	SNORD3B-2	small nucleolar RNA, C/D box 3B-2	Other	other		No implications in coex	lncRNA intergen	p_lncRNA_intergen	-0.49		-0.58	-0.69			-0.32	-0.71	0.14		0.03	0.01			0.80	0.35	36		34	26			33	17	64		66	74			67	83
ENSG00000257613	RP11-320P7.1	LINC01481	long intergenic non-protein coding RNA 1481	Other	other					0.24	0.32	0.58	0.16	0.03	-0.06	0.33	0.23	0.48	0.55	0.05	0.81	0.99	1.00	1.00	0.99	56	59	76	63	50	45	83	75	44	41	24	37	50	55	17	25
ENSG00000260539	GLG1						No implications in coex	lncRNA intergen	e_lncRNA	0.36	0.54	0.36	0.84	0.36	0.54	0.59	0.72	0.01	0.05	0.00	0.00	0.99	0.50	0.30	0.20	75	68	66	68	70	73	67	67	25	32	34	32	30	27	33	33
ENSG00000223891	OSER1-AS1	OSER1-AS1	OSER1 antisense RNA 1 (head to head)	Other	other		1 eQTL linked co-expres	lncRNA divergen	p_lncRNA_divergent		0.58		0.68				0.54		0.27		0.00				0.65		59		79				92		41		21				8
ENSG00000260804	PKI55	LINC01963	long intergenic non-protein coding RNA 1963	Other	other		No implications in coex	lncRNA intergen	e_lncRNA				0.63								0.00								68								32				
ENSG00000270091	RP11-78O7.2									0.03	0.44		0.57				0.08	0.57	0.33		0.00				0.81	53	59		66				58	47	41		34				42
ENSG00000203875	SNHG5	SNHG5	small nucleolar RNA host gene 5	Other	other		No implications in coex	lncRNA intergen	p_lncRNA_intergen	-0.36	-0.37	-0.32	-0.55	-0.41	-0.37	-0.47	-0.52	0.02	0.11	0.28	0.01	0.00	0.50	0.99	0.20	28	27	32	29	10	18	25	25	72	73	68	71	90	82	75	75
ENSG00000226423	AC093642.4						1 eQTL linked co-expres	lncRNA intergen	others	0.15	0.48		0.61	0.12	0.52		0.84	0.39	0.15		0.01	0.99	0.55		0.20	61	70		66	50	73		83	39	30		34	50	27		17
ENSG00000237310	GS1-124K5.4	GS1-124K5.4	uncharacterized LOC100289098	Other	other		2 eQTL linked co-expres	lncRNA antisens	others	0.25	0.33	0.45	0.52	0.03	0.13		0.65	0.27	0.71	0.06	0.03	0.99	1.00		0.61	64	62	76	68	50	64		67	36	38	24	32	50	36		33
ENSG00000237940	AC093642.3	LINC01238	long intergenic non-protein coding RNA 1238	Other	other		4 eQTL linked co-expres	lncRNA sense int	others	0.20	0.48	0.44	0.29	0.20	0.74	0.54	0.11	0.02	0.00	0.03	0.30	0.99	0.03	0.80	0.99	72	76	68	61	80	82	58	50	28	24	32	39	20	18	42	50

Supplementary Table 5A. IL32, IFNG and INS coregulated genes selected based on Euclidean distance calculated from log2 fold change of Case-Ctrl RPKM values

IL32 coregulated genes

CD4+		**CD8+**		**CD4-CD8-**		**PBMC**	
Gene	Median Euclidia	Gene	Median Eucli	Gene	Median Euclidi:	Gene	Median Euclidian distance
IL32	0.00	**IL32**	0.00	**IL32**	0.00	**IL32**	0.00
CD52	1.18						
TMEM14C	1.20					**TMEM14C**	2.13
BTN3A2	1.36	**BTN3A2**	1.91	**BTN3A2**	1.32	**BTN3A2**	1.60
TRBV4-1	1.56					**TRBV4.1**	1.86
LARS	1.74	**LARS**	2.06			**LARS**	1.85
CTA-445C915	1.83						
RGS14	1.85						
UROS	1.89			**UROS**	1.03		
SH3BP1	1.92						
RP11-747H7.3	2.13						
AMICA1	2.15			**AMICA1**	2.22	**AMICA1**	2.02
ENSG00000269996	2.18						
C17orf62	2.30						
WASH7P	2.33			**WASH7P**	1.99		
		RSU1	1.93	**RSU1**	2.10	**RSU1**	2.02
		FCER1G	2.35				
				AC092580.4	2.20		
				ATP8B2	1.63		
				BTN3A3	1.87	**BTN3A3**	1.95
				CARD8	1.95	**CARD8**	1.84
				CCDC167	2.16	**CCDC167**	2.08
				CD2	1.55		
				CD27	1.32		
				CD3D	1.49		
				ENSG00000211953	2.14		
				ENSG00000229164	2.05		
				FAIM3	1.98		
				FAM65B	2.17		
				FLT3LG	2.19		
				FYB	1.94		
				GIMAP2	2.03		
				GIMAP5	2.27		
				GZMM	2.41		
				HAR1A	2.45		
				IGHV4.31	2.37		
				IGSF8	1.91		
				IL24	2.27		
				LCK	1.94		
				LDLRAP1	2.20		
				LINC00861	2.26		
				LINC01184	1.79	**LINC01184**	1.58
				LINC01278	1.40		
				MAL	2.17		
				MAML2	1.83		
				MAPKAP1	2.27		
				PDE7A	1.80		
				PLAC8	2.11		
				PRKCQ	2.23		
				PRKCQ-AS1	2.02		
				PSMD5-AS1	2.31		
				RP11-111M22.3	2.04		
				RP11-222K16.2	2.16		
				SH3YL1	2.22		
				STX8	2.14		
				SUCLG2	2.18		
				SUSD3	2.41		
				SYNGAP1	2.05		
				TC2N	1.90		
				TESPA1	2.31		
				TMIGD2	1.95		
				TRABD2A	2.02		
				TRBV2	1.83		
				TRBV20.1	1.76		
				TXK	2.11		
				UBASH3A	2.42		
						ANXA5	2.37
						ANXA6	1.57
						ATP6V0E2	1.83
						CD8B	2.03
						CPNE1	1.59
						CST7	2.01
						DGKQ	2.08
						FLI1	2.33
						GLG1	2.41
						GLIPR2	2.34
						HLA.F	1.42
						IPCEF1	2.29
						LILRA1	2.10
						NAGA	2.18
						NCAPD2	1.67
						NMRAL1	1.46
						OGDH	2.02
						OSER1.AS1	2.49

						P2RX5	1.96
						PIP4K2A	1.41
						PKI55	2.42
						PLOD3	2.47
						PRDX2	0.91
						RP11.410L14.2	2.30
						SIGMAR1	1.48
						TMEM106C	1.61
						TMEM8A	2.40
						TRBV19	1.63
						TUFM	1.85
						ZNF609	2.21

IFNG coregulated genes

CD8+

Gene	Median Euclidian distance
IFNG	0.00
NKG7	1.56
ZEB2	1.61
TBX21	1.88
BHLHE40	2.02
OASL	2.29
KLRD1	2.30

INS coregulated genes

PBMC

Gene	Median Euclidian distance
INS	0.00
GCG	1.12
REG1A	1.74

Supplementary Table 5B: Transfac promoter analysis of IL32 and coclustered genes for overpresented transcription factor binding sites with FDR < 0.05

Fmatch tool (search for overpresented TF binding sites), background = randomly seected gene set, default parameters,
using best supported promoter (-10 000 to +1000 region of the gene's promoter), P-value threshold 1.
P values were corrected with Benjamini Hochberg method (FDR). FDR<0.05 were cosidered significant and are shown below.

CD4+ IL32 cocluster* **Profile (group of matrices): Taxon: Vertebrate_non_redundant_minFP**

Matrix	**Accession**	**Factor name**	**Yes**	**No**	**Yes/No**	**p value**	**FDR(BH corre**	**Genes with matrices count**
V$CPBP_Q6	M01822	KLF6	42.9	27.3	1.6	0.00	0.00	AMICA1, SH3BP1, UROS, IL32, CD52, RGS14, TMEM14C, LARS, BTN3A2, WASH7P (LOC100288778), RP11-747H7.3 (ENSG00000260711), C17orf62
V$IK_Q5_01	M07260	Ikaros	13.3	7.4	1.8	0.00	0.00	AMICA1, SH3BP1, UROS, IL32, CD52, RGS14, TMEM14C, LARS, BTN3A2, WASH7P (LOC100288778), RP11-747H7.3 (ENSG00000260711), C17orf62
V$ING4_01	M01743	ING4	15.3	9.5	1.6	0.00	0.00	AMICA1, SH3BP1, UROS, IL32, CD52, RGS14, TMEM14C, LARS, BTN3A2, WASH7P (LOC100288778), RP11-747H7.3 (ENSG00000260711), C17orf62
V$GKLF_Q4	M01835	KLF4 group	10.1	5.8	1.8	0.00	0.00	AMICA1, SH3BP1, UROS, IL32, CD52, RGS14, TMEM14C, LARS, BTN3A2, WASH7P (LOC100288778), RP11-747H7.3 (ENSG00000260711), C17orf62
V$RREB1_01	M00257	RREB-1	2.0	0.4	4.8	0.00	0.00	AMICA1, SH3BP1, UROS, IL32, CD52, RGS14, TMEM14C, LARS, WASH7P (LOC100288778)
V$ERALPHA_0	M01801	ER group	1.3	0.2	8.0	0.00	0.01	AMICA1, SH3BP1, UROS, IL32, CD52, RGS14, TMEM14C, LARS

*ENSG00000269996, TRBV4-1 and CTA-445C9.15 excluded due to unavailable promoter sequence

CD8+ IL32 cocluster **Profile (group of matrices): Taxon: Vertebrate_non_redundant_minFP**

Matrix	**Accession**	**Factor name**	**Yes**	**No**	**Yes/No**	**p value**	**FDR(BH corre**	**Genes with matrices count**
No findings with FDR < 0.05								

CD4-CD8-IL32 cocluster* **Profile (group of matrices): Taxon: Vertebrate_non_redundant_minFP**

Matrix	**Accession**	**Factor name**	**Yes**	**No**	**Yes/No**	**p value**	**FDR(BH corre**	**Genes with matrices count**
No findings with FDR < 0.05								

*ENSG00000211953, ENSG00000229164, PRKCQ-AS1, PSMD5-AS1, and HAR1A excluded due to unavailable promoter sequence

PBMC IL32 cocluster* **Profile (group of matrices): Taxon: Vertebrate_non_redundant_minFP**

Matrix	**Accession**	**Factor name**	**Yes**	**No**	**Yes/No**	**p value**	**FDR(BH corre**	**Genes with matrices count**
V$IK_Q5_01	M07260	Ikaros	12.9	9.0	1.4	0.00	0.00	AMICA1, ANXA5, ANXA6, ATP6V0E2, BTN3A2, BTN3A3, CARD8, CCDC167, CD8B, CPNE1, CST7, DGKQ, FLI1, GLIPR2, HLA-F, IL32, IPCEF1, LARS, LILRA1, LINC01184, RP11-410L14.2 (LOC105375666), NAGA, NCAPD2, NMRAL1, OGDH, OSER1-AS1, P2RX5, PIP4K2A, PKI55, PLOD3, PRDX2, RSU1, SIGMAR1, TMEM106C, TMEM14C, TMEM8A, TUFM, ZNF609
V$CPBP_Q6	M01822	KLF6	38.2	33.0	1.2	0.00	0.00	AMICA1, ANXA5, ANXA6, ATP6V0E2, BTN3A2, BTN3A3, CARD8, CCDC167, CD8B, CPNE1, CST7, DGKQ, FLI1, GLIPR2, HLA-F, IL32, IPCEF1, LARS, LILRA1, LINC01184, RP11-410L14.2 (LOC105375666), NAGA, NCAPD2, NMRAL1, OGDH, OSER1-AS1, P2RX5, PIP4K2A, PKI55, PLOD3, PRDX2, RSU1, SIGMAR1, TMEM106C, TMEM14C, TMEM8A, TUFM, ZNF609
V$ING4_01	M01743	ING4	14.5	11.4	1.3	0.00	0.00	AMICA1, ANXA5, ANXA6, ATP6V0E2, BTN3A2, BTN3A3, CARD8, CCDC167, CD8B, CPNE1, CST7, DGKQ, FLI1, GLIPR2, HLA-F, IL32, IPCEF1, LARS, LILRA1, LINC01184, RP11-410L14.2 (LOC105375666), NAGA, NCAPD2, NMRAL1, OGDH, OSER1-AS1, P2RX5, PIP4K2A, PKI55, PLOD3, PRDX2, RSU1, SIGMAR1, TMEM106C, TMEM14C, TMEM8A, TUFM, ZNF609

*GLG1, TRBV19 and TRBV4.1 excluded due to unavailable promoter sequence

Description of column names

Matrix	The TF matrix that was enriched
Accession	The TRANSFAC ID of the matrix
Factor name	Name of the factor corresponding to the matrix
Yes	The frequency wih which the matrix was found on the promoters of the test set
No	The frequency wih which the matrix was found on the promoters of the background set
Yes/No	The ratio of the two frequencies
p value	the p-value of the enrichment
FDR (BH corre	Benjamini Hoschberg corrected p-value
Genes with m	Genes whose promoter had the matrix in them

Supplementary Table 6A: Details on the single-cell RNA-Seq data after pre-processing using Cell Ranger

			After Cell Ranger's Pre-processing Pipeline			
PBMC sample	**Age**	**Selection Basis**	**# of cells**	**Mean reads / cell**	**Median genes / cell**	**Total genes detected**
Case 2	24 months	IL32 high	1,394	155,454	933	16,397
Control 2	24 months		2,803	105,769	749	16,737
Case 5	12 months	IL32 low, INS high	1,499	184,116	968	16,068
Control 5	12 months		3,412	75,855	776	16,940
Case 3	12 months	IL32 high	3,373	56,940	823	16,927
Control 3	18 months		1,468	199,172	846	15,235
Case 9	24 months	IL32 very high, INS high	3,342	60,377	950	17,366
Control 9	18 months		3,079	76,789	776	16,595

Supplementary Table 6B: Clusters and their proportions after merging the data from eight scRNA-seq samples (4 Cases + 4 controls)

	Number of individual cells	
Naive T cells	8438	45.87%
RGCC+ T cells	2033	11.05%
CD62L+ T cells	1559	8.47%
B cells	1465	7.96%
Act. Th cells	1432	7.78%
Act. GNLY+ CD8+	1078	5.86%
Act. NK cells	976	5.31%
Act. GZMA+ CD8+ T cells	824	4.48%
Monocytes/DCs	339	1.84%
Act. prolif. GZMA+ CD8+ T cells	162	0.88%
Developing T cells	66	0.36%
Platelets	24	0.13%
Total	**18396**	