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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-sequencingbased analysis of 306 samples including fractionated samples of CD4+ and CD8+ T cells as well as CD4-CD8- cells 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 IFNy (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 | median log₂FC| > 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 10⁶ 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 DNasel (Invitrogen), and cDNA was synthesized with Transcriptor First Strand cDNA Synthesis Kit (Roche). For isoform-specific ($IL32\alpha$, β , and γ) assay, qPCR analysis was performed in triplicate runs using SYBR Select master mix (Applied Biosystems). Δ Ct values were calculated relative to $EF1\alpha$. 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 DNasel and cDNA was synthesized with SuperScript II Reverse Transcriptase (18064014, Invitrogen). For the detection of global $IL32_{\perp}$ qPCR reactions were run using a custom TaqMan Gene Expression Assay reagent (#AJ5IQA9, Thermo Scientific) in duplicate and in two separate runs. Δ Ct 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-32 α antibody (R&D, IC30402A) and FITC-conjugated IFN γ 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- β H1 human beta-cell line was obtained from Univercell Biosolution S.A.S., France. The cells were cultured as described (26). EndoC- β H1 cells were stimulated with either IL-32 γ alone (100 ng/ml, R&D Systems) or in combination with a cocktail of IL-1 β (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 2.5 ng/ml if IL-12 (R&D). Cells were activated with plate bound CD3 (0.5 μ g/well of a

24 well-plate) and soluble CD28 (0.5 μ g/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 IFN γ neutralization, anti-IFN γ antibody (10 μ g/ml, R&D: MAB285) was used. For reactivation, cells were treated with 5ng/ml PMA (Calbiochem) and 0.5pg/ml lonomycin (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 ($IL32\alpha$, $IL-32\theta$ and $IL32\gamma$) 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, $IL-32\gamma$ was expressed at the highest level, followed by $IL-32\theta$ and $IL-32\alpha$.

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 IFNy, was expressed both in Th0 as well as Th1 cells (Fig. 4A). Interestingly in Th1 cells, most IFNy-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 IFNy-producing Th1 cells than in Th0 cells (Fig. 4B-C). Furthermore, neutralization of IFNy significantly reduced IL-32 secretion by Th1 cells (Fig. 4D) confirming that IFNy 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-32y transgenic mice exhibit impaired glucose tolerance, increased levels of IFNy 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 cellsurface 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 log₂FC (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 log₂ 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 IL32y 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

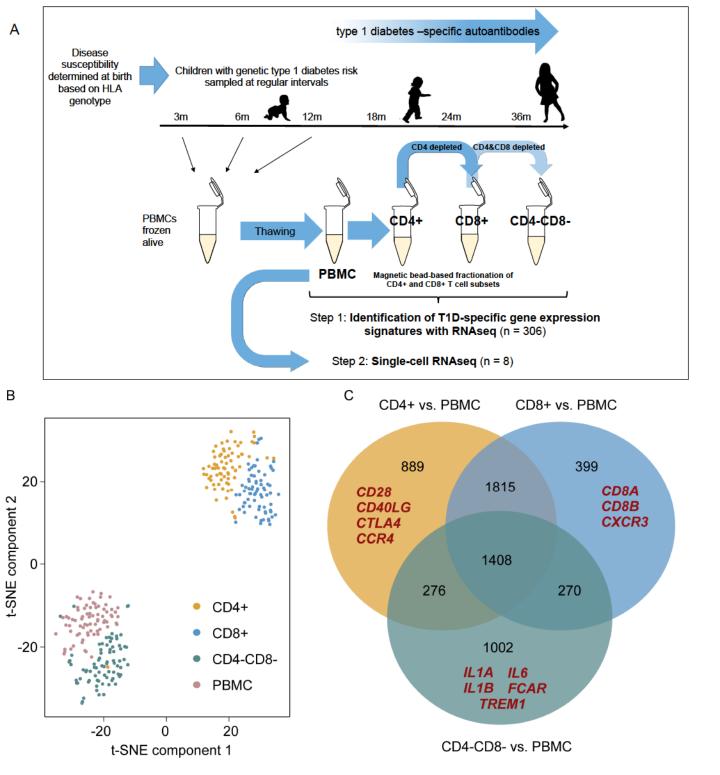
A) Representative FACS dot plots showing IFN-γ and IL-32 double staining in ThO and Th1 polarized CD4+ cells. Staining controls and two other replicates are shown in **Supplementary** Fig. 13A. Percent IL-32 positive cells as well as Median Fluorescence Intensity (MFI) data (mean+/- SD) from all the 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-32y as measured by the Tagman 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-32y, followed by washing and re-stimulation by PMA and ionomycin for 48 h. The expression plotted is relative to ThO (-). 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.

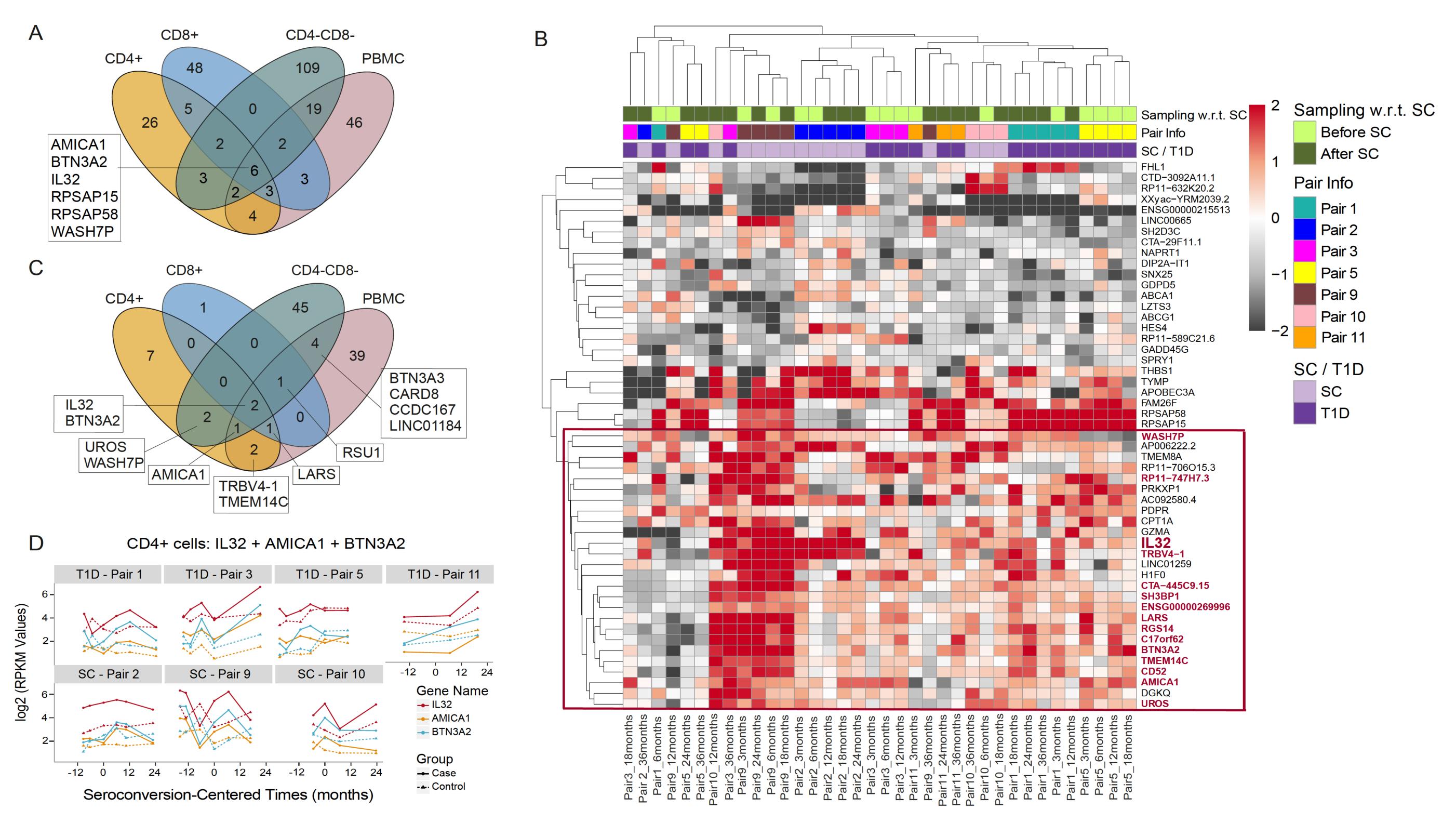
TABLES

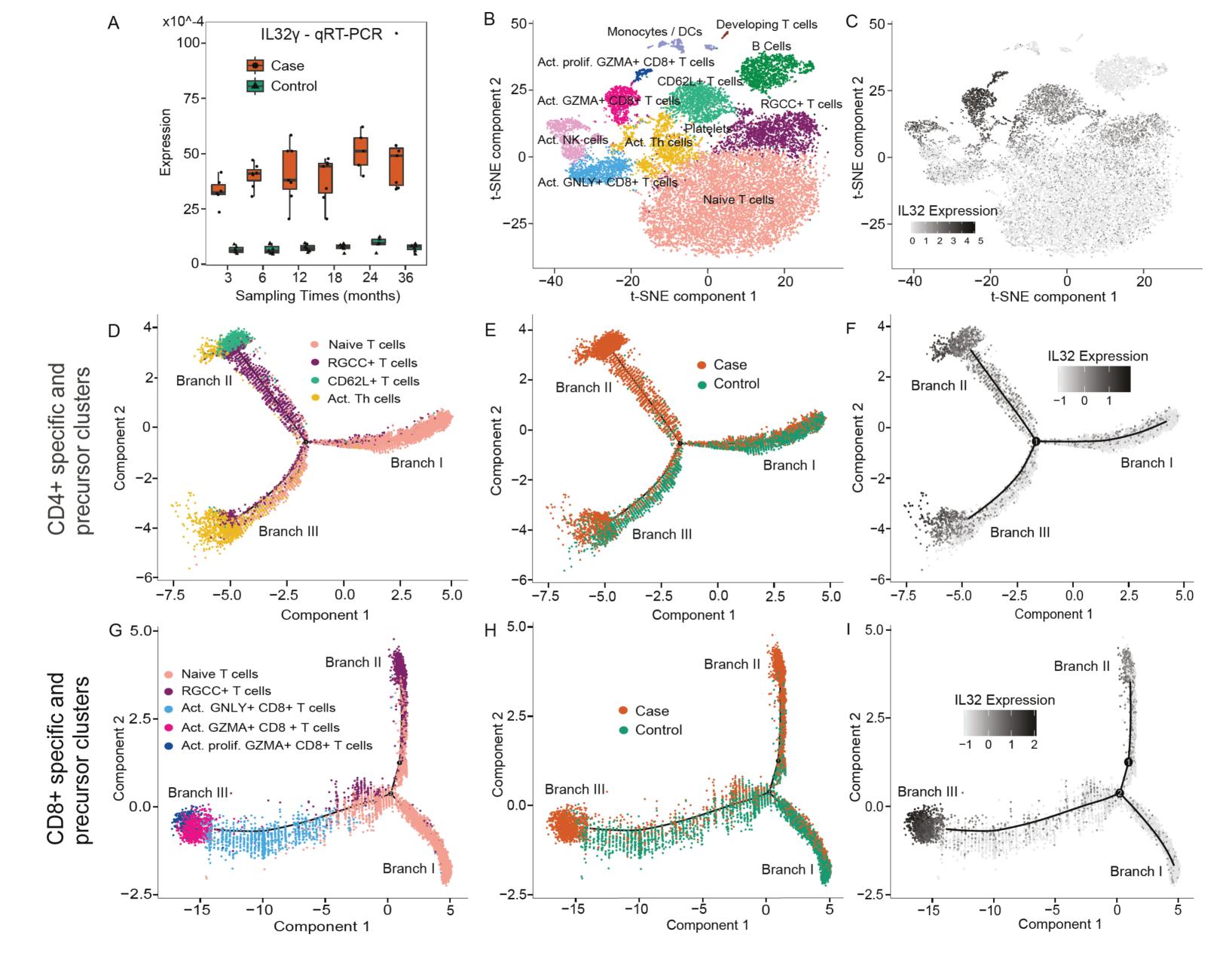
Table 1. Summary of the Case and Control children sampled at the age of 3–36 months.					
Case #	Gender	Seroconversion*	First	Age at T1D	Matched
		age	autoantibodies	diagnosis	control #
Case 1	Female	12 mo	IAA, GADA	3.2 y	Control 1
Case 2	Male	12 mo	IAA	-	Control 2
Case 3	Male	18 mo	IAA, ICA	3.7 y	Control 3
Case 5	Female	24 mo	IAA, IA-2A, ZnT8A,	2.6 y	Control 5
			ICA		
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

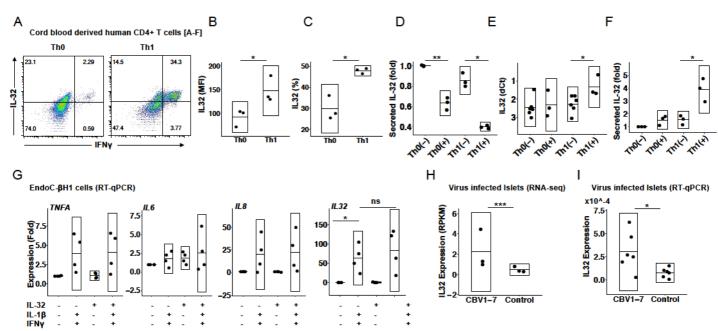
^{*}First detection of T1D-associated autoantibodies.

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



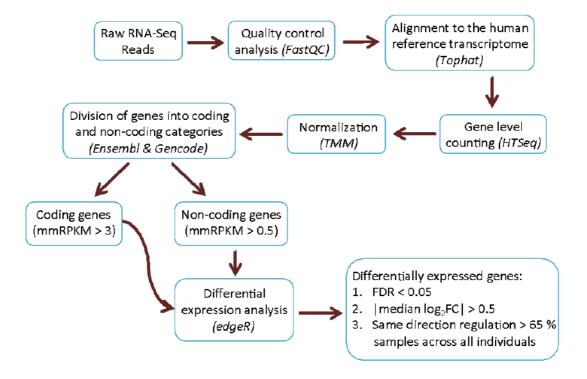






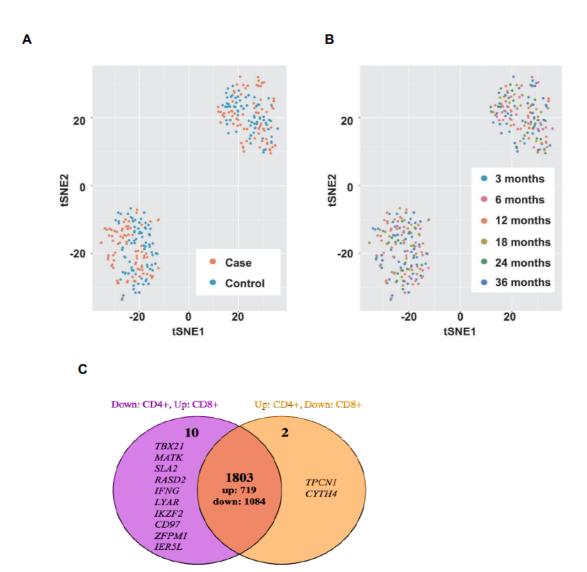
Supplementary Figures

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



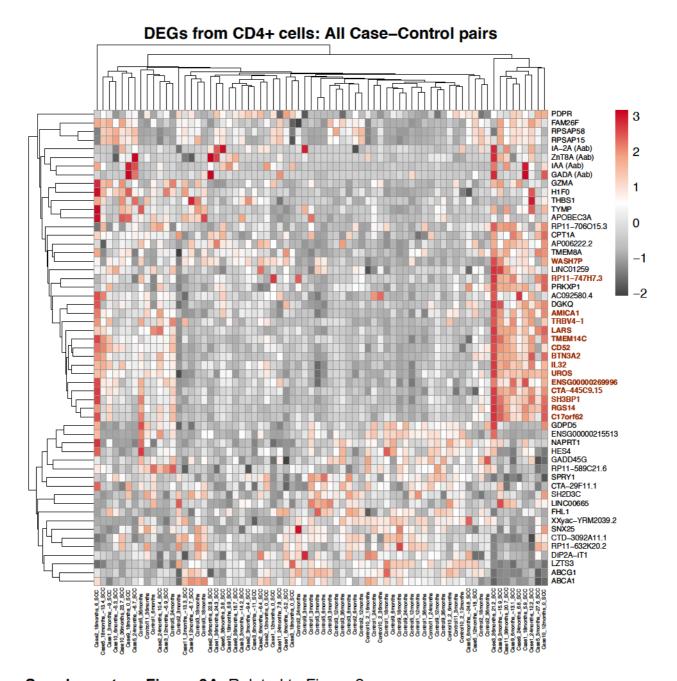
Supplementary Figure 1. Related to Figure 2.

Flow chart depicting the steps taken in the differential expression analyses of the RNAseq data in this study.



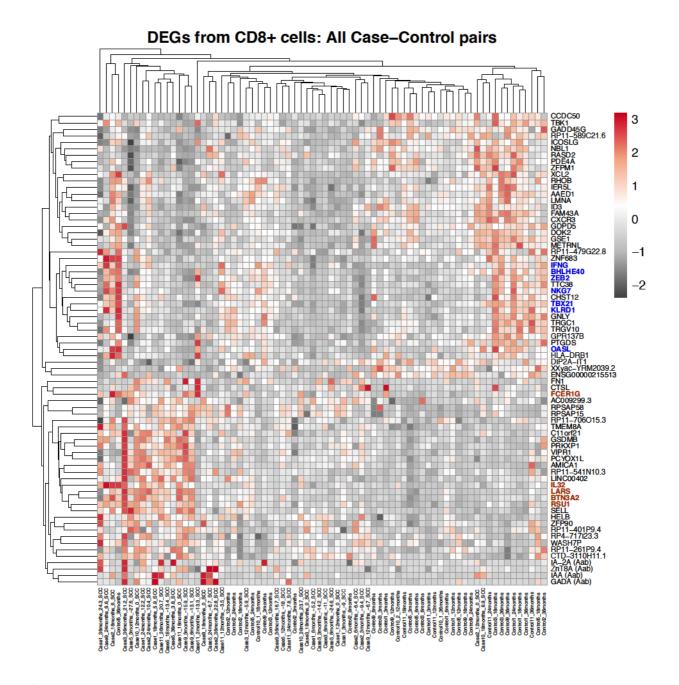
Supplementary Figure 2. Related to Figure 1.

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**.



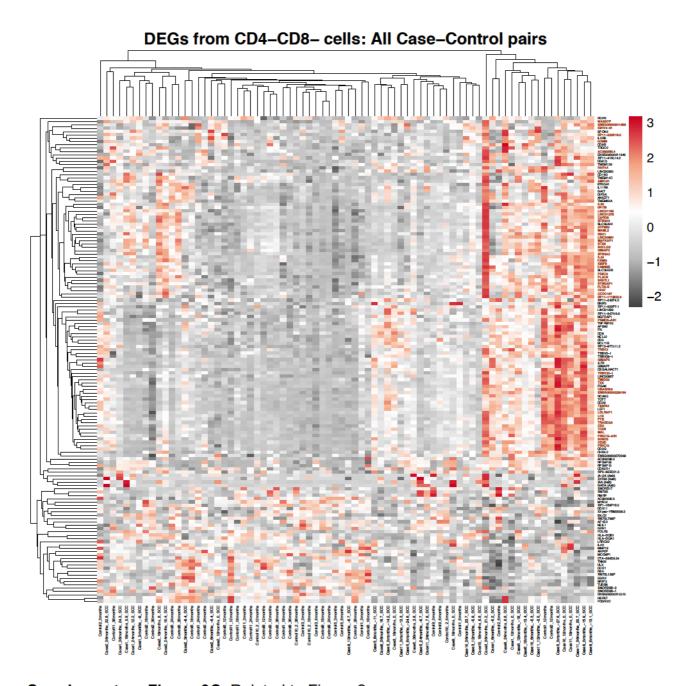
Supplementary Figure 3A. Related to Figure 2.

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.



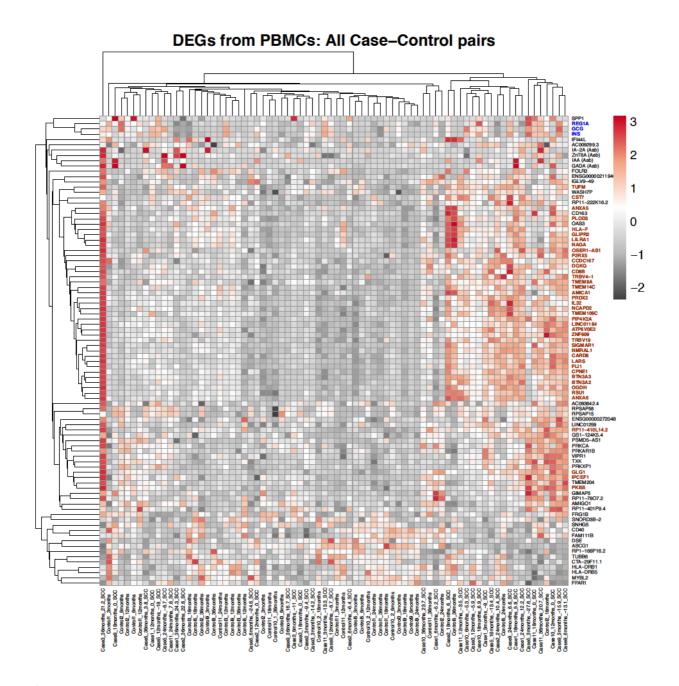
Supplementary Figure 3B. Related to Figure 2.

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.

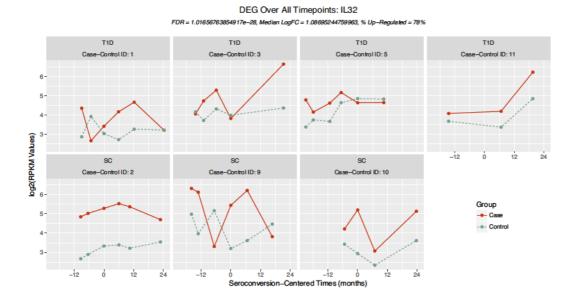


Supplementary Figure 3D. Related to Figure 2.

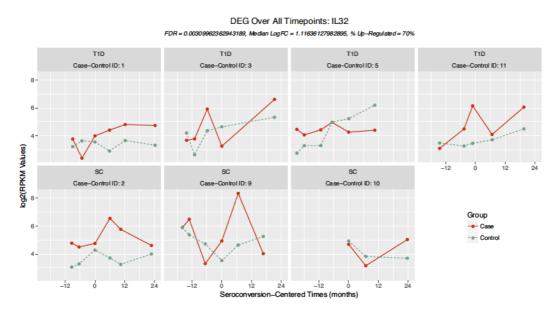
Hierarchical clustering of the levels of standardized autoantibodies (IAA, IA-2A, ZnT8A, and GADA) and the 85 DE genes between the Cases and Controls detected in the PBMC population. Each gene's expression was standardized across samples from each case-control pair individually. Genes with an Euclidean 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:



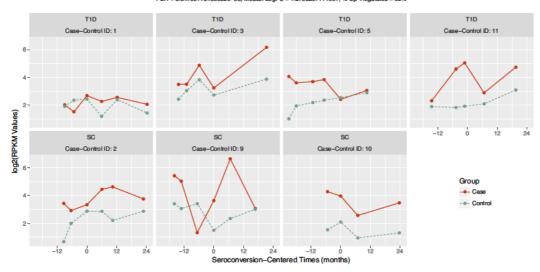
A) Expression levels of IL-32 gene in CD4+ cells.



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

DEG Over All Timepoints: IL32

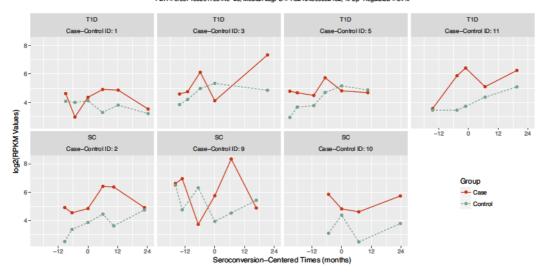
FDR = 3.34750773439632e-33, Median LogFC = 1.2753207171961, % Up-Regulated = 92%



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

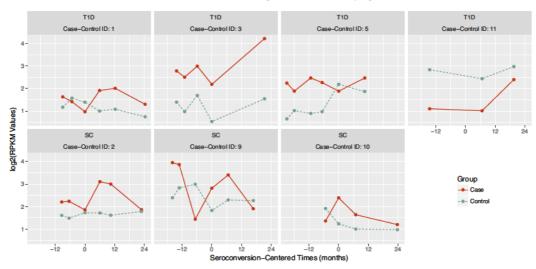
DEG Over All Timepoints: IL32

FDR = 5.00715039175544e-26, Median LogFC = 1.02104899092152, % Up-Regulated = 84 %



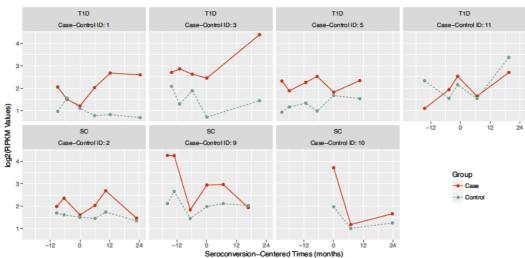
D) Expression levels of IL-32 gene in PBMCs.

DEG Over All Timepoints: AMICA1 FDR = 231370877035674e-09, Median LogFC = 0.806214764405675, % Up-Regulated = 75%



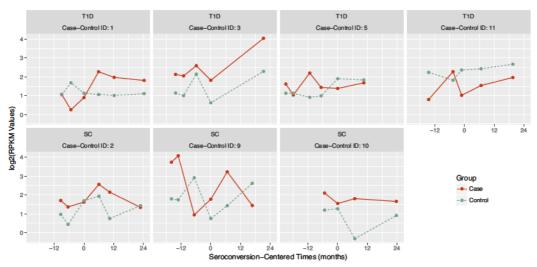
E) Expression levels of AMICA1 gene in CD4+ cells.





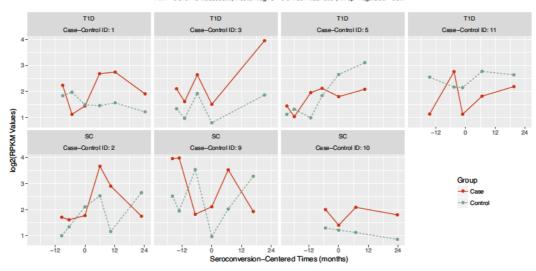
F) Expression levels of AMICA1 gene in CD8+ cells.

DEG Over All Timepoints: AMICA1 FDR = 0.000434825570123128, Median LogFC = 0.560439291296879, % Up-Regulated = 66%



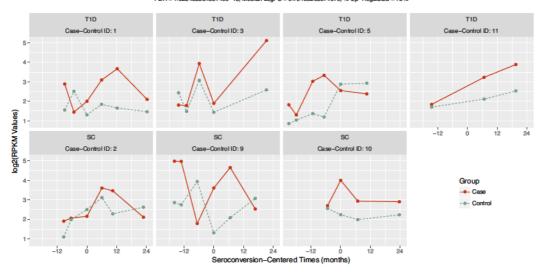
G) Expression levels of AMICA1 gene in CD4-CD8- cells.





H) Expression levels of AMICA1 gene in PBMCs.

DEG Over All Timepoints: BTN3A2 FDR = 1.0234838456149e-13, Median LogFC = 0.75165263074075, % Up-Regulated = 78%

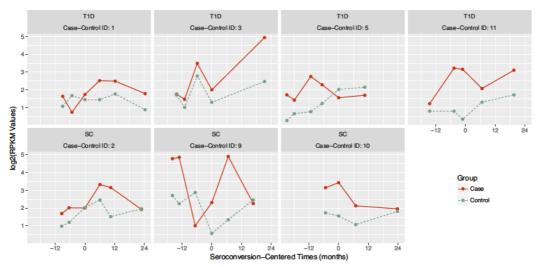


I) Expression levels of BTN3A2 gene in CD4+ cells.



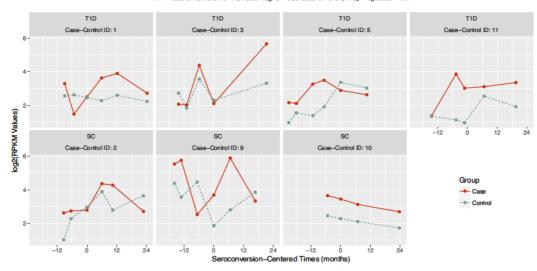
J) Expression levels of BTN3A2 gene in CD8+ cells.

DEG Over All Timepoints: BTN3A2 FDR = 2.01189886944382e-17, Median LogFC = 0.795428777816898, % Up-Regulated = 82%



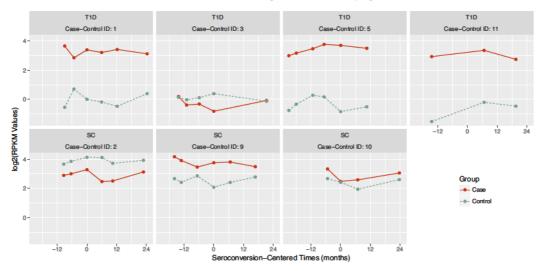
K) Expression levels of BTN3A2 gene in CD4-CD8- cells.



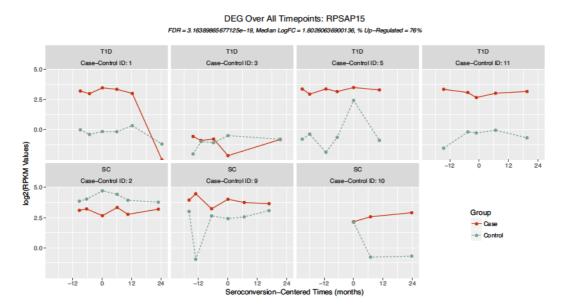


L) Expression levels of BTN3A2 gene in PBMCs.

DEG Over All Timepoints: RPSAP15 FDR = 5.82127700825433e-26, Median LogFC = 1.44472640284937, % Up-Regulated = 75%

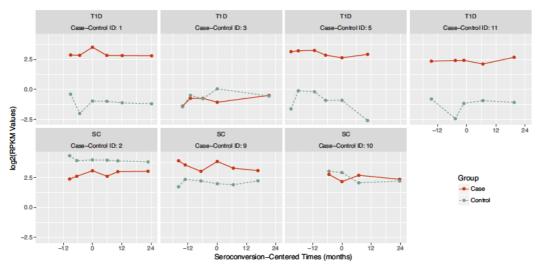


M) Expression levels of RPSAP15 gene in CD4+ cells.



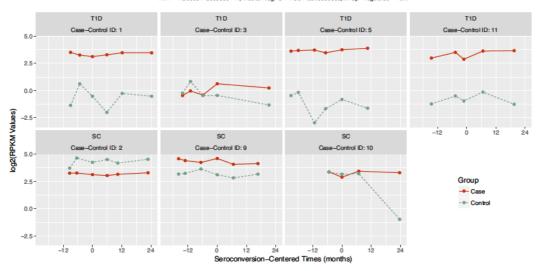
N) Expression levels of RPSAP15 gene in CD8+ cells.

DEG Over All Timepoints: RPSAP15 FDR = 5.32314905726484e-26, Median LogFC = 1.62142730156426, % Up-Regulated = 74%



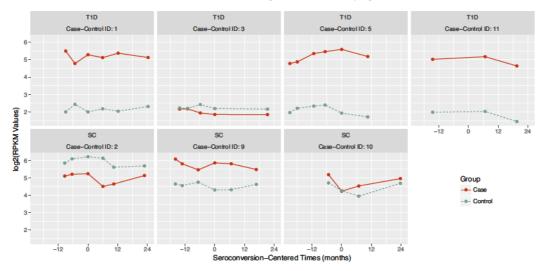
O) Expression levels of RPSAP15 gene in CD4-CD8- cells.





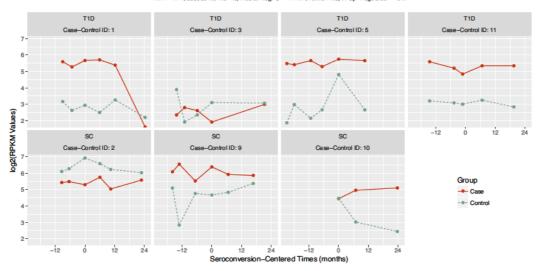
P) Expression levels of RPSAP15 gene in PBMCs.

DEG Over All Timepoints: RPSAP58 FDR = 1.0656775476997e-42, Median LogFC = 1.34071165073582, % Up-Regulated = 67%



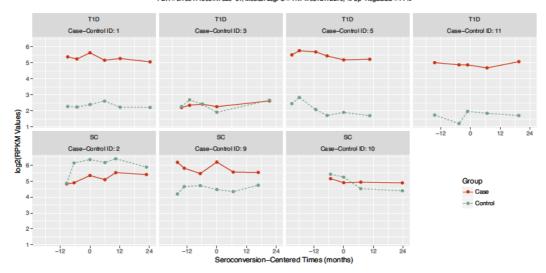
Q) Expression levels of RPSAP58 gene in CD4+ cells.





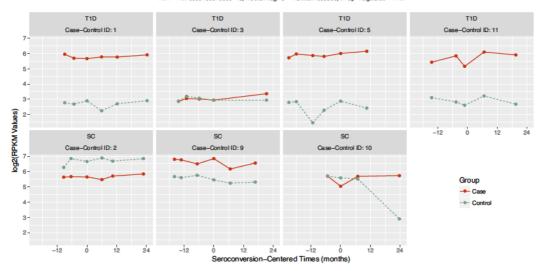
R) Expression levels of RPSAP58 gene in CD8+ cells.

DEG Over All Timepoints: RPSAP58 FDR = 6.70517105944752e-51, Median LogFC = 1.47479372172279, % Up-Regulated = 71 %



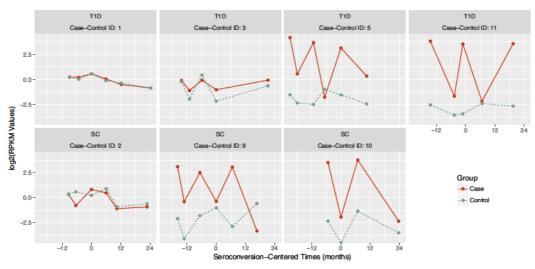
S) Expression levels of RPSAP58 gene in CD4-CD8- cells.



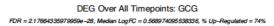


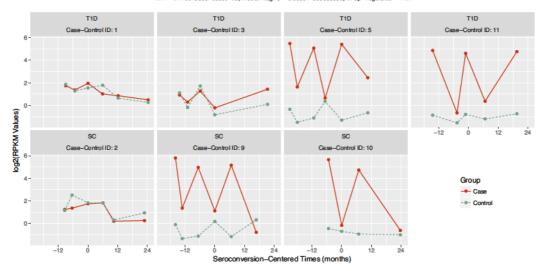
T) Expression levels of RPSAP58 gene in PBMCs.

DEG Over All Timepoints: INS FDR = 9.3351601477442e-11, Median LogFC = 0.739926117529327, % Up-Regulated = 74%



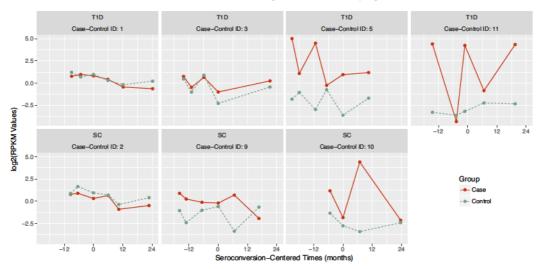
U) Expression levels of INS gene in PBMCs.



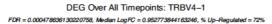


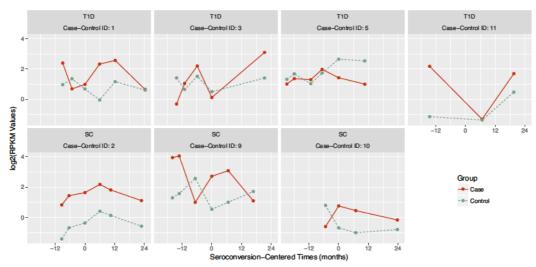
V) Expression levels of GCG gene in PBMCs.

DEG Over All Timepoints: REG1A FDR = 4.98145775801475e-08, Median LogFC = 0.517199222755978, % Up-Regulated = 66%



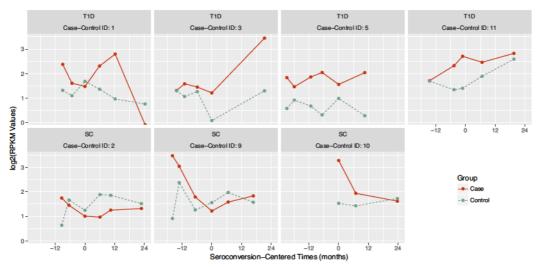
W) Expression levels of REG1A gene in PBMCs.



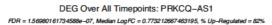


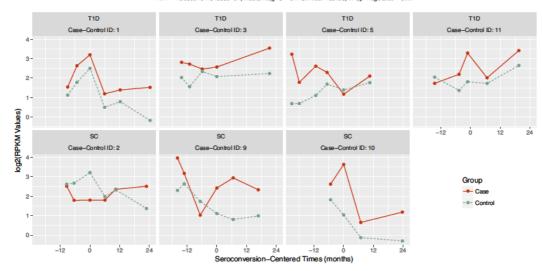
X) Expression levels of TRBV4-1 gene in CD4+ cells.

DEG Over All Timepoints: VIPR1 FDR = 0.0192216332832046, Median LogFC = 0.52712894908211, % Up-Regulated = 73%



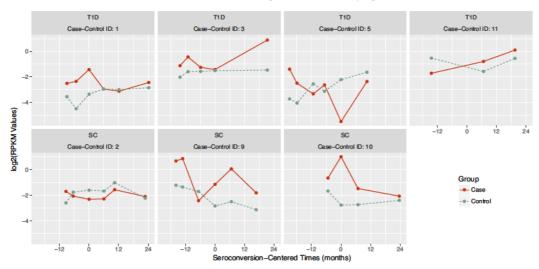
Y) Expression levels of VIPR1 gene in CD8+ cells.



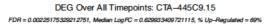


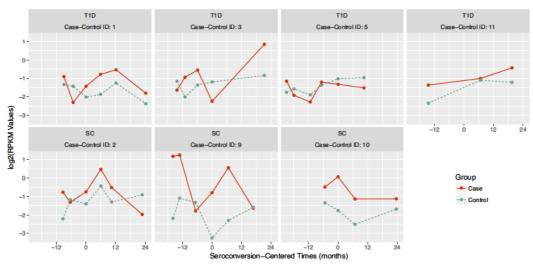
Z) Expression levels of PRKCQ-AS1 gene in CD4-CD8- cells.

DEG Over All Timepoints: RP11–747H7.3 FDR = 0.000778155971399923, Median LogFC = 0.711745514222584, % Up-Regulated = 69%

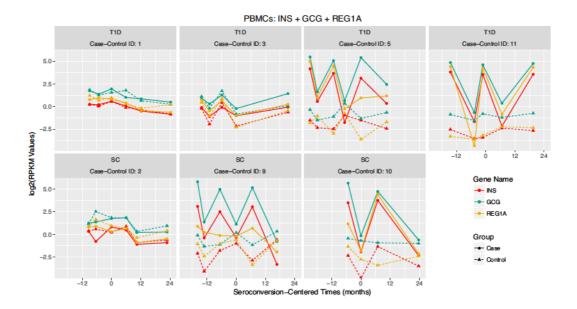


AA) Expression levels of RP11-747H7.3 gene in CD4+ cells.



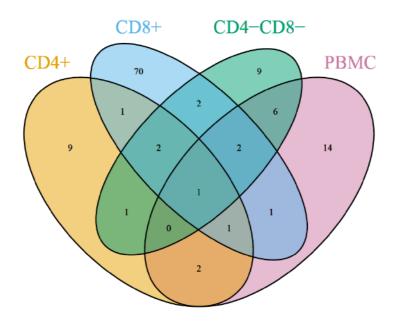


AB) Expression levels of CTA-445C9.15 gene in CD4+ cells.



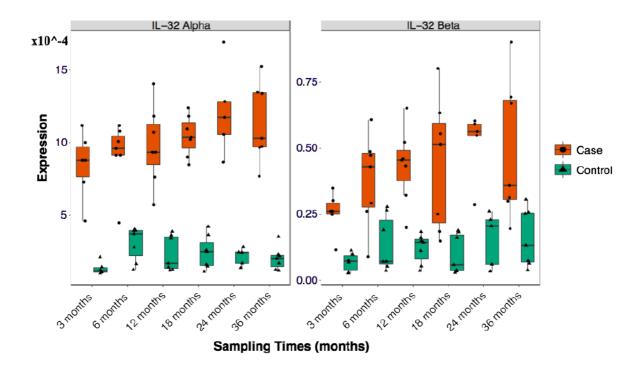
Supplementary Figure 5. Related to Figure 2.

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.



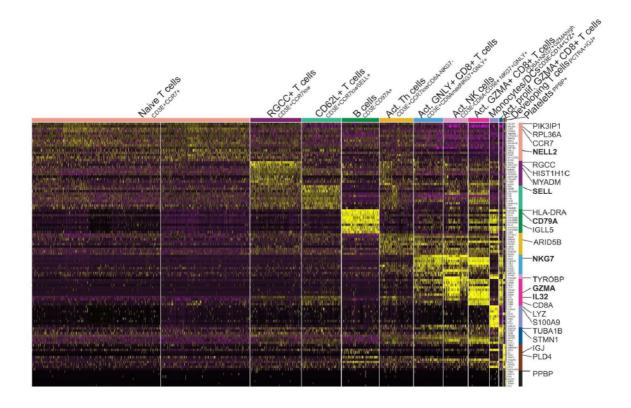
Supplementary Figure 6. Related to Figure 2.

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 \geq 65% of the Cases). For complete listing, see Supplementary Table 3 columns "12 mo before SC".



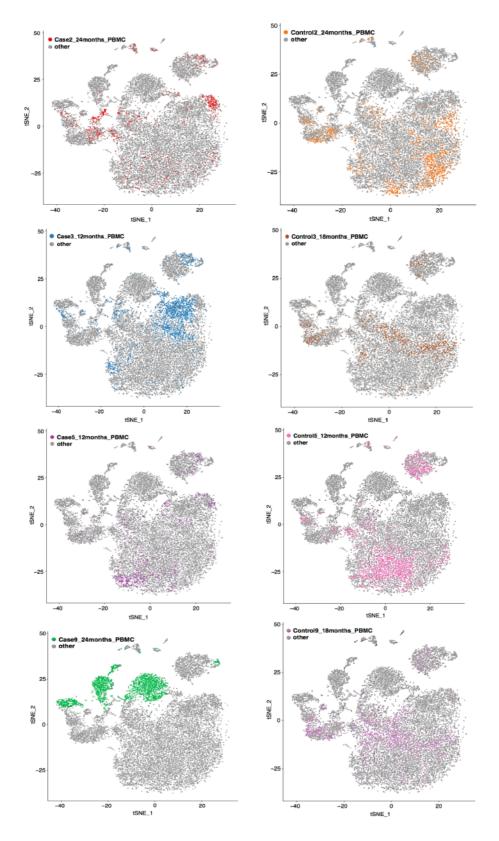
Supplementary Figure 7. Related to Figure 3A.

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 IL32 γ isoform, please refer to **Figure 3A**.



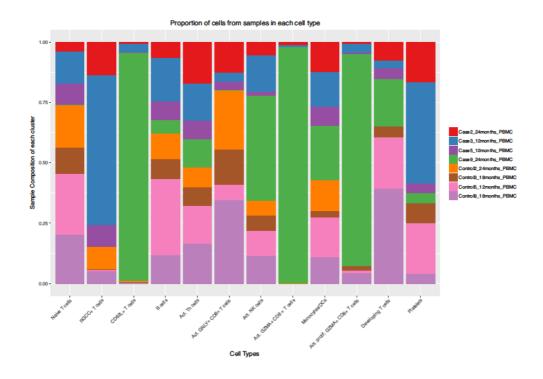
Supplementary Figure 8. Related to Figure 3.

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**).

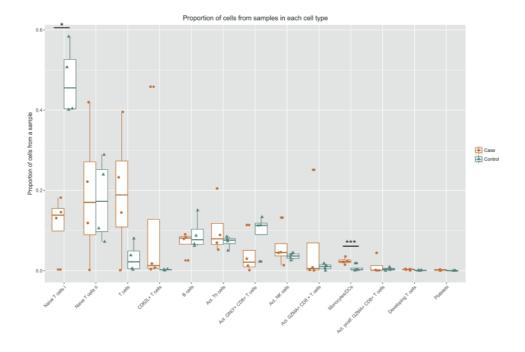


Supplementary Figure 9. Related to Figure 3.

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

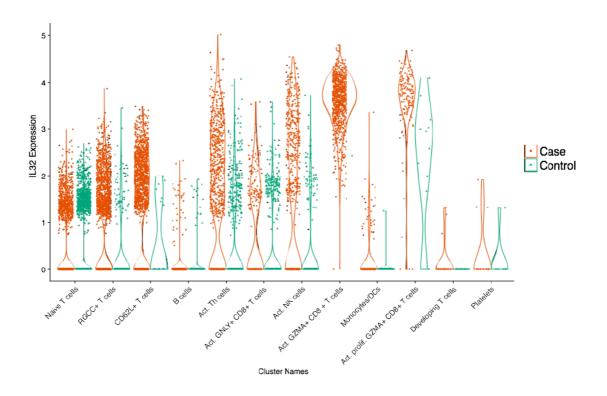


В



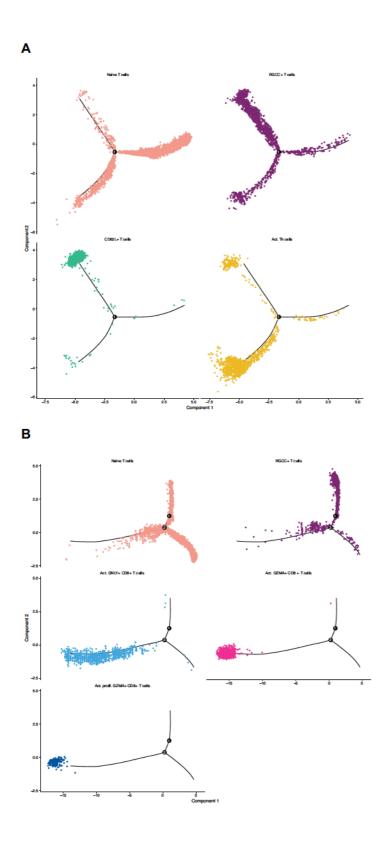
Supplementary Figure 10. Related to Figure 3.

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.



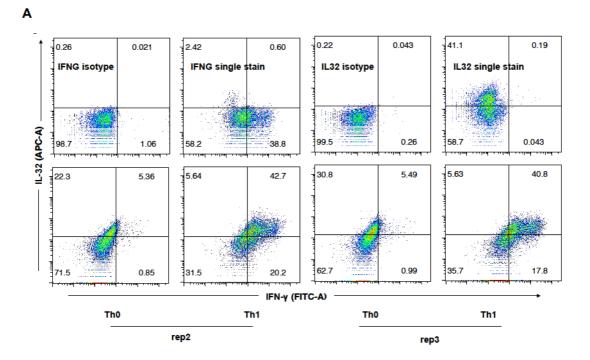
Supplementary Figure 11. Related to Figure 3.

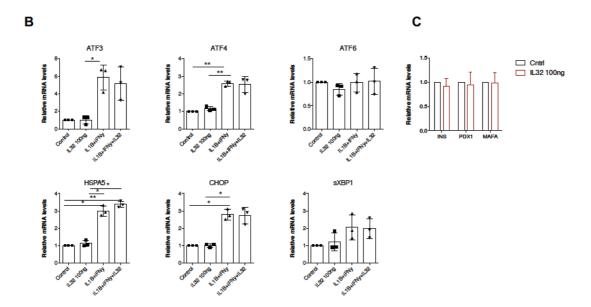
Violin plot showing the expression of *IL32* in the 12 cell clusters identified from the single-cell RNA-Seq data, displayed separately for Cases (orange) and Controls (green).



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-1 β and IFN γ , 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- β H1 cells with 100 ng of IL-32 γ 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 RNA-seq the data using FastQC (version 0.10.0. on raw 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 htseqcount function from the HTSeg 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 log₂FC filtering, where DE genes with a |median log₂FC| > 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 *Ime4* 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 setup. 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 log₂ 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 coregulated features.

To summarize over the *IL32*-clusters from the seven case-control pairs, a feature coclustering 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.

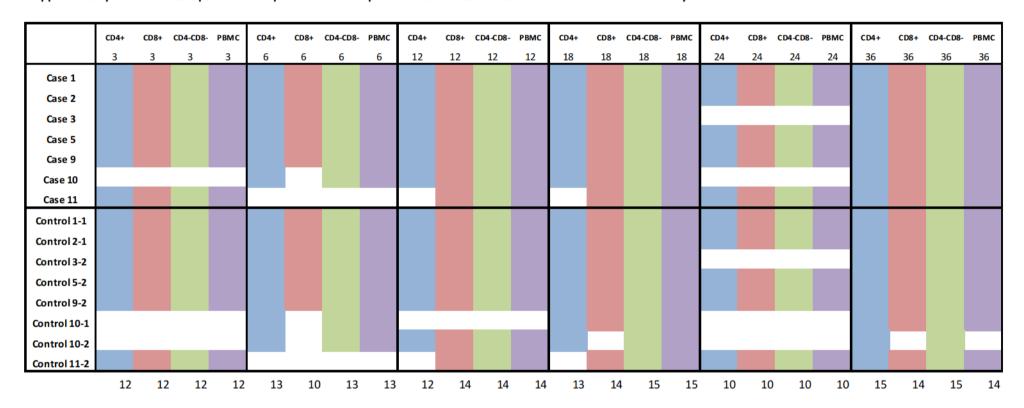
To determine the cell type represented in each cluster, markers defining the clusters were determined via differential expression algorithm implemented in Seurat, where cells of a single cluster were compared to the cells of all other clusters combined. A gene was considered a marker of a cluster if 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



Total Number of Samples = 306

Coloured = Sampled Empty = Not Sampled

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

Case 1 FINLAND Female Yes 3.2 Moderately increased Father age 9 E003251 0 0.32 0.18 0.06 3 0.01 0 0.08 6 0.45 0 0.16 12 14.08 21.75 0.08 18 53.07 1933.3 88.23 24 14.44 305.98 510.62 36 2.3 119.94 678.3 Case 2 FINLAND Male No Moderately increased Father age 27 E003989 0 0 0 0 0.13 3 0 0 0 0.14 6 0 0.15 12 13.46 0 0.15	0.07 0.06 0.08 0.3 6.37 12.89 22.46 0.05	3 0 0 0 374 747 512
6 0.45 0 0.16 12 14.08 21.75 0.08 18 53.07 1933.3 88.23 24 14.44 305.98 510.62 36 2.3 119.94 678.3 Case 2 FINLAND Male No Moderately increased Father age 27 E003989 0 0 0 0 0.13 3 0 0 0 0.14 6 0 0 0 0.15 12 13.46 0 0.15	0.08 0.3 6.37 12.89 22.46 0.05	0 0 374 747
12	0.3 6.37 12.89 22.46 0.05	0 374 747
Case 2 FINLAND Male No Moderately increased Father age 27 E003989 0 0 0 0.13 6 0 0 0.15 18 53.07 1933.3 88.23 24 14.44 305.98 510.62 36 2.3 119.94 678.3 3 0 0 0.13 6 0 0 0.15 12 13.46 0 0.15	6.37 12.89 22.46 0.05	374 747
Case 2 FINLAND Male No Moderately increased Father age 27 E003989 0 0 0 0 0.13 119.94 678.3 12 13.46 0 0.15 12 13.46 0 0.15 12 13.46 0 0.15 12 13.46 0 0.15 12 13.46 0 0.15 0.1	12.89 22.46 0.05	747
Case 2 FINLAND Male No Moderately increased Father age 27 E003989 0 0 0 0 0.13 3 0 0 0 0.14 6 0 0 0.15 12 13.46 0 0.15	22.46 0.05	
Case 2 FINLAND Male No Moderately increased Father age 27 E003989 0 0 0 0.13 3 0 0 0.14 6 0 0 0.15 12 13.46 0 0.15 0.15	0.05	512
3 0 0 0.14 6 0 0 0.15 12 13.46 0 0.15		312
6 0 0 0.15 12 13.46 0 0.15		0
12 13.46 0 0.15	0.06	0
	0.06	0
	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	ŀ
12 0.7 0.07 0.1	0.05	ļ
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
120.391.43 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 Io, transient abs Slightly increased T013815 0 0 0 0.13	0.15	0
60.04 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 0.983.95 0.09	0.11	0
18	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	ŀ

						6	0	0	0.08	0.06	
						12	0.28	0.07	0.09	0.07	
						18	0.28	0.07	0.07	0.07	
						24	0.28	1.56	0.09	0.13	
						36	0.92	0.71	0.11	0.13	
Control 2	FINLAND Male	No	Moderatelyincreased		E001463	0	0.31	0.71	0.02	0.18	
Control 2	FINLAND IVIALE	NO	wioder atery micreased		E001463	3	0.14	0	0.02	0.18	
						6	0.63	0	0.02	0.07	
						12	0.63	0	0.06	0.06	
						18	0.2	0	0.16	0.06	
						24	0				
						36	0.14	0.93 0	0.1 0.1	0.05 0.09	
6	FINILAND AALL	N.	Madantal dan arad		F0.066.46						
Control 3	FINLAND Male	No	Moderatelyincreased		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	Moderatelyincreased		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 Tcells

Target cDNA	Sequence of 5'-primer (F)	Sequence of 3'-primer (R)	Probe (if applicable)
IL32α	5'-GCTGGAGGACGACTTCAAAGA-3'	5'-GGGCTCCGTAGGACTTGTCA-3'	
IL32β	5'-TCTGTCTCTCGGGCCTTG-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
	ILO	CCAGAGCTGTGCAGATGAGT	GGGTCAGGGGTGGTTATTGC
*	TNFa	GATCCCTGACATCTGGAATCTG	GAAACATCTGGAGAGAGGAAGG
*	BAD	ATCATGGAGGCGCTG	CTTAAAGGAGTCCACAAACTC
*	BAX	AACTGGACAGTAACATGGAG	TTGCTGGCAAAGTAGAAAAG
	HSPA5 (BIP)	TGGCTGGAAAGCCACCAAGATGCT	GGGGAGGCCTGCACTTCCAT
	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

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HAND COLOR NO. 1	RCIII NPA	MCD2 phaphalpaseCpress 2	Olive sher Oliveism exigne Manua Mentrane phophatase	4.00	-530 -636	1.39	0.00	500	600			100	=	200	
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HAND COD COD COD COD COD COD COD COD COD CO	HEACHA HEACHA	PORMA/PORMA (Frequented by Early Prepare to the MAYOR	Planta Memirane di comemirane recepto della Marina bana di bone di bone quidare Planta Memirane di comemirane recepto	480	-6.01 -6.22 -1.01	-081 0.38 0.39	0.00	648 648	628 628		:	:	=	97 200 97	e e
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HANDERS SAN	EEC IEWA	ADDRESS adhesion of paste los expeller expeller ESS ESSES Immunophila Interpresentated ESSES Immunophila Interpresentated 4	Manual territorie siber Manual territorie protein copied ecopie totale fair Tipes siber Totale fair Tipes siber	42	-635 -635 -338	0.33 -083 -083	0.00 0.00		627 660 660	:		-	=	200	
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S MAND CERCOT 188-1 S MAND CERCOT 188-9 S MAND CERCOT 188-9 S MAND CERCOT 188-0	HEVY-M HEVY-M HEVY-M	EXY-E tomos qui ai tri mide seratio 2 di EXY-E tomos qui ai tri mide seratio 2 di EXY-E tomos qui ai tri mide seratio 2 di EXY-E tomos qui ai tri mide seratio 2 di		68 68 96 96	-6.8 -6.8 -5.80*	-011 -011	120	600 600	660 660	:	:	27	2	20	
PROCESS SALE	HEAD-IN	EEV2-23 Immunopical televalue sarticle 2-28 EEV2-21 Immunopical televalue sociale sarticle 2-28 EEV2-24 Immunopical televalue sarticle 2-28 EEV2-24 Immunopical televalue sarticle 2-24	Chier sther Extraorbier Space sther Extraorbier Space sther	4.00	100° 100 400 400	-040 -047 -048	1.0	620 620	620 620			34 34	20	20	
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B MANDO CET COT SHE B B MANDO CET COT SHE S B MANDO CET COT SHE S	EBN/318 EBN/921	1906-11. Introducing to let to know your risks of 11 (go only or other 1906-10). Introducing to let to know your risks of 20 (1906-10). Introducing to let to know your risks of 20 (1906-10). Introducing the let to know your risks of 21 (1906-10). Introducing the let to know your risks of 21 (1906-10). Introducing the let to know your risks of 22 (1906-10).	Other aller	4.80	-6.3E -6.0E	-684 -628	0.00	6.00 6.00	000				=	300 300	
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S MANDO CEC CON 1984 9 S MANDO CEC CON 1983 2 S MANDO CEC CON 1984 9 S MANDO CEC CON 1984 9 S MANDO CEC CON 1984 7 S MANDO CEC CON 1984 7 S MANDO CEC CON 1987 9 S MANDO CEC CON 1987 9	EDOVERS CHES	EDAS 40 Immungitial Inhang or risk a 5-40 EDAS 40 Immungitial Inhang or risk a 5-40 CLECS ship by no of the channel 3	Other after Other after Males brokered	4.75 4.36 4.39	-6.00 -6.00 -5.00	-038 -033 -003	0.00 0.00 0.00		600 600		:		=	20	
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	HLA-CP/G	MACPEL study of listenance fields; complex, size 8, 10% and 12, 10	Other siter i ju Other siter 2 Mematembrane a summirane recepto	48	-680 -680	-044 0.38 -014	0.00	600 600	600 601 608		:	:	=	20	E.
I MARIO CED CER 147% I MARIO CED CER 1464 I MARIO CED CER 147% I MARIO CED CER 147% I MARIO CED CER 1464	HADORS HADORS HADORS HADORS	NACO many barance fields consist a first Colors	Clie aler	4.07	-625 -626 -630	-631 -633 -614	0.00	6.00 6.00	600				2	200	
I MANGEMENT IN A STREET OF THE	MANUAL MA	HA-CE IN major listic comparticity complex, size 8 , CC) in the CE III of the CE III o	Optoplem majore Manual Ambrose a commitme recepto 7. Manual Ambrose a commitme recepto	411	-080 -630 -638	-014 0.00 0.00	120	640 640	587 587 580 580			107 70	-	500 500	
HARCECON 1	mw.c		Extraorbior Space poptibles Places to the contrast of the cont	4.72	-629 -738	-011 -021	0.00	600	600			27 42 82	120	300 300	
FREE CECCO CON T FREE CECCO CON CON C	100 VS -07 100 VS -08	USBC be despited conserving state in the case plan AS SERV-S to immunophis had to be pare somethin 5 of SERV-S to immunophis had to be pare somethin 5 of SERV-SS to immunophis had to be pare somethin 5 of SERV-SS to immunophis had to be pare somethin 5 of	Clie der Laborate Space der	9	-6.00 -6.00	-643 -643	1.0	5.00 5.00	600 600	:			=	200	-
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HANGED CO. CO. C.	HERVE OF HOSE LYN	MINTY-27 Internating in but to be year our table 1-07 100 International instances between 1500 1500 International	Optophem transporter I condection Optophem binase 630027, erbeid tells, de	4.00 4.00 4.00 4.00 4.00 4.00 4.00 4.00	-6.00 -6.00 -6.00 -6.00 2.84	-626 -620 630 -627	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	600 600	600 600 600				=	100 14 200 200	
HAND GER CET MEST	ETH HELLS PTD-EBIGLE BCSM EMM	TOP of the country to	Manual Ambanian Sampane clumb	1.86	284 -142 -647	1.56	0.00	600	0.00	200	30	-	-	97	
PRODUCTE CT. TOP 3 PRODUCTE CT. TOP 3	PRICE DOMES	ETRES protectioner option PRIES protectioner option CEPELS speak growth fator receptor the S	Optoplasm minyme Optoplasm bloase Cepadas atthator, ing Other aller	48	-180	0.88 0.88	0.00	5.00 5.00	620 620 678		:		=	20	1
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I MICCECOLORS	MANAGE SPG	DC DC contributing protein	Plantable militare projetime Optoplant after	2.00 2.00	-8.80 3.08 -6.67	0.80 0.87 1.83	0.00	540 540	520 520 520	200	100	100	-	200 0 200	
I MANICOLD CON 753 3 I MANICOLD CON RECK	INC EHMS	MC MC problemagere, more optically solve bloose EMMS in high texture landing protein 1 MCMS by droppe length and in coptical 2 COMEA COMEA not compared to the	Optopherm bloom tedenth, EC-C, je une Optopherm sither	1.00 2.07 4.00 4.22 4.31	-650 221 -628	0.86	1.0	5.00 5.00		200	100	100	100	100	
PROCEEDINGS	COMEGA	COMEA COMEs make alle TERRI I just sed manang me on/byptophen benerang:	Manual Ambrase a nonembrase recepto ma Optoplaco trans della completar	42	-00	1.00 0.07 -048	0.00	5.00 5.00	6A3 660				=	93 90	
HAND CERCECTO	TREES.	THE TAKE leading time of TAKE STATE	Qiquiam binase Estacelair Spice baspoter andester, melliquis	410	-2.98 -1.38 -6.00 -6.22	-026 0.89 -032	0.00 0.00	6.00 6.00 6.00	633 680 688			122	=	200 97 88 200	
FRANCISCO SHI N FRANCISCO SHI N FRANCISCO SHI N	O ME EXAMP ROS		Other after Nation time dylanogalour	4.11 4.25 4.21 4.05 4.37	-6.22 -5.00 -5.00	1.68 1.69 -01h	1.0	600 600	600 600 600 600	:		100	20	20	- 1
HAND CONTRACTOR OF THE CONTRACTOR OF T	FOR MED 1	MEST MEST MEST MEST 1	Other siber Plannahl milaser is numericase recepto Optoplasm siber	419	-0.00	1.61	1.0	600	600		:	27 120 26	=	200	71 0 22
HANGED COMMAN	1000178 10077	1997 Inch Regreshis for India protein 7	Other other Extraorities Space Semporter Other other	4.00 1.00 1.00 1.00*	-038 -638 5-88*	6.27 -624 -648	0.00 0.00 0.00	648 648	621 621				12 12	200	-
I MICCECCION 1 I MICCECCION 1	MERFE BARA BARA BRANG BEPRE GPT SEGRA GPT BRETE BETER CORRECT	NOTE HOOK landing protein I	Optoplasm after Marine transdythorogulator Optoplasm minuse	4.00	-226	-603	0.00	600 600	600 614			100	=	10	u M
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I MICCOLON 76 A	091 1204		Otopian kespate Otopian kespate	48	-1.0 -1.0 -1.0	0.00 -0.04 0.38	: a	Ξ	587 633 588				=	20	
HANGGEGE TO TO	MPT IN	COREC CORECINE COR	Optoplasm existre Plasma Mambrase in commissione recepto	48	-638	0.37	1.0	=	614 600			-	=	20	
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	THE MICH MICHAEL SHOULD	ASSA may into	Table Tabl	1.8 4.0 4.0 4.0 4.0 4.0	-186 -188 -130	-cos 0.38	0.00 0.00 0.00	680 680	000 000 609 000			a 2	=	20 20 20	
I MINICODECTA 340 7	MARIE	RPM phospholystylasphotoce1	Honald misus phaphetus	4.0		0.86	1.00		660	•		w w	100		

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FMICOECUSORY NEEDS	1000 NCCC, cylectrones addressorably prairie Graphon	aler	4.8 -3.6 -4.8 -4.0 -4.0 -4.0 -4.0 -4.0 -4.0 -4.0 -4.0	0.8 0.0 -0.18 -0.28 -0.10	1.0	500	638 600 603			=	20	
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E MANDERSCHONNE BETT. E MANDERSCHONNEY MEDICE E MANDERSCHONNEY MEDICE	RETS lone removalured oil adject Plantablembare NEE/RD NEE/RAN binding pulstakeD Optoplane	aler	4.71 -680 4.86 -580 2.87	-688	0.00	540	600	0 0		120	200	12
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I MICCECCO TO 1	BPDKI TRAX	MACCO	tratie mangiospherodelpingman 1 Labeline jake Si	Quantum major fe-Sqliteatri, mede Quantum aller i hindranifemanisis	4.9 4.9 4.9 1.0 1.0 1.0	141 -138 -638	-628 0.86	0.00	5.00 5.00	618 600	0 0	:	6	120	200 87	:
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I MICCOCK MA	HOLE	INFE INDI ARIMS	sould make a 1996 of the long complete pulpopular is recorded for the advance leaders and the 1(r he finding A bloom a riched og protein the sking the seconds bell protein 13 he for damed committeining of ACP r line cylet has factor CEP one a clima bing protein 1.	Males ster Name to entree engre	1.31	-137	-0.39 0.37 -0.37 -0.33 1.32 0.38 0.38	0.00	68	620 620 620	20	320	100	-	87	
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PRICE CE CU PA 1	URL MARK	um.	DM by or 1	Nation stops	1.0	538 589 -586	0.36	0.00	68 68	600	20	er e	-	-	200	
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I MICCOCO MAI	HEICHTS PARTHERS	NODE NADM dependent difference dut are 1 Optophore existere 1 MACRICEZ family of the squeece dent only 300 revenior 82 Other called	1.80	180	0.67	0.00	500	600	20	**	-	:	:	:
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I MINICOLOGIANO I MINICOLOGIANO	CLUMPS	MART seld excel de dominious epistets. Qiopiam transporter latidose triologic CLUPR slottered introduced to handing pre-adopted. Other other	1.36 1.37	141 100 581	0.87 0.37	0.00	5.00	600	200	100	-		:	14 10
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I MICCORD CO MILE I MICCORD CO WOLL	NAA ATB	RAMA RAMA, mancher Mittanag me ib nity Qippiana suppre ACTE at ib late Question state:	422	-040 -047	0.72 -0.18 -0.67	0.00	500	600	:			1	97 94	
FREEDERS AND A STREET CO.	PING PING	CEDCHR coded-cal dura to come trange to Citie other STANS. que attention, one replacação 3 Plante attentame attent CEPCHR communication to Cities Communication attention to Central Communication attention attention.	1.07	-036 335 306	-644 0.38	0.00	680 680	600	200	320		120 0	0	27
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I MICCECU VIII I	ATMEC HACCE	A79.9CC A79.co/det respecting VCodeoit c Qioplani Sesporte NA-DDB region bits competitely complex, cle. 8, DD bate Manina M endoare a respective	4.00	-086 -188	-640 0.67	0.00	5.00 5.00	600 600	:	:	n n	320 M	100 97	n N
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HANGED CLYCKS	THE MENT	ESST Intervals topped Consistent Plane of Employee a manufacture recepts TMS MICE Commenture protein 20 Quiplom Anniverse company TMS MICE Lanconnecture protein 25 Quiplom Anniverse	4.30	-0.00 -0.00	-633 1.86	0.00	EAST EAST	520 520	0		-	120	200	
FRANCISCO CONTROL O CONTRO	PAUR PAUR	ECRES SE degradat considerating a lyte examinable on the pret. Optoplaces encapses. PARE forth and degrations. PERC 1. Mail on the Constitution of the Constitution	1.01	218 272	-681 0.M 0.46	0.00	6.00 6.00	G4 (42)	20	-	- :		14	
PROCEEDINGS	1761	Total Color Colo	1.66	128 118	0.86	0.00	640 640	600 600	20	er se	E E		- 1	•
FRANCISCO CON NOTE OF THE PROPERTY OF THE PROP	OCA ATRIACOS	200 DC - Into Stage MEXTupe containing d - Madines - other - ICCS - go mainti - Opposium - other - AT MEXICOS - AT world-to-mapped big Vitrodocali di - Opposium - bampun ter - bampun ter	48	-2.58 -2.58	-630 0.40 0.38	0.00	540 540	600 600 600			38 28	10	20	2 2
HAROCOCKION?	PR R.R.S	PSE PE diese besetztet geschieften eine in der men i für Gesphan in der Scharften und der ges Gesphan in dem Applichen der Scharften und der gestellen Gesphan im dem Applichen Gesphan gescharften Gesphan mengen GROSS Chief die Metsward und gesphan mengen	1.30	-08 -05 111	0.40 0.34 0.36 0.48		=	600	200	-	100	100		:
I MARIO CELCAL DALA I MARIO CELCAL STOTA I MARIO CELCAL STOTA I MARIO CELCAL STAIA	# 160 10091	CHICA CHICA SE SEASE SE CONTROL CONTRO	1.00 1.00 1.07	-com 118	-618 6.80	0.00	5.00	528 520	0 107	e 17		122	200	я.
HANDERS RES	PLIENCE.		48	-0.00 -0.05 -0.07	0.61 -634 0.61 0.62	0.00	5.00 5.00	620 620	:	:	27	32	20	-
	MCM7 MARK	MCMT mits divanisame na blane nac complex component? Mai ma mayora MCMS contra modera plane this pilota pilota C. Mai ma state MCMS — sente modera pilota modera na 2. Mai ma monora	1.30	129	0.40	1.0	-	600	20	-	-	:	:	- 1
HANDER COLUMN	MIMITE HIMBAT OPTEA BLODNER	PRIMES providing the methylanderse 2 Mains mayor HMMAS laghmelding-properties 3 Mains been glober glober CPTS condition-publiship to selve 2 Mains mayor perhed the NCDAS solds coming Smith 2 member 23 Optopium beaugants	6 M 6 M	-1.07 -0.00	-601 0.35 0.62	0.00	5.00 5.00	EAS EAS	0			=	90 97 73	-
PROCEEDINGS PROCEEDINGS PROCEEDINGS PROCEEDINGS PROCEEDINGS PROCEEDINGS	GATE CARCE	SCEACS value corter family 20 member 25 Qrisplann baseporter GMCS optionible transmitter and mility component 3 Marines. State dystering sistem	4.38 4.36 1.34 1.34	-CIR CR2 CR7	0.70 0.70	0.00	646 646	683 660 660	200 200	U U	10. 107		75 1	:
I MAND CENTRO MAN I MAND CENTR	TD0 CT	LDCCS. brustninger downing derfor cases the Other sher AMIRS angel benefig 3 Malina sher	4.27	114 117	0.01 0.02 0.08	0.00	640 640	524 520 520	0 200 200	-		320 0	83.	*
HANGED COMMAN	AMERICA STANDA EMAL SONDA PELA LEPAR PERIO	Assess and benefit to the Assessment of the Asse	1.35 1.30 4.35 1.38 1.38	-0.00	-671 -622	0.00 0.00 0.00 0.00	500	601	200	100	1	320	200	
FREEDOM OUT	USP CO.	PCES Chip pier range new, of dylat nakust. Opiquian surject dae, is stradenjen. USS dayses quant is yearbe SE. Recent Membrane profitse. PSS SE version of the second se	1.30 1.34 4.85	118 682 -188	1.38 0.30 -628		640 640	600 600	200 200	ur er	100	:		- :
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HANCOTON SET	DAJARI	CREATION and an internated region 2. Opposition to the collect of	1.00 1.00 4.30 1.07 4.00	-6.8	-628	0.00	646 646	650	200	320	100	0 320	0 200	
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HANGED CLUBS	CHOIL	URSTM drings the companing or opine ST M Opine State Marine CHOS characteristics of CHASTAN parameters. National entrying	1.38 4.33 1.37	-CMI	-019	0.00	500	600	0 20			320 0	97	3
PRICE CE CE SE	192	NTSMC probled siffer homes a finish number 2 Quiplant problem TSC1 takens salesh 1 Quiplant siler TSC1 takens salesh 1 Quiplant siler MMCS1 salesh 1 Steps of methods problem 12 Quiplant MCS1 probled silfer homes a finish number 2 Quiplant problem	1.30 1.38 4.86	126 589 -677 -586	0.48 0.48 0.52 -607	0.00	600 600 600	520 520 580	200 200 0			300	87	- :
I MILECOLOU VEA I MILECOLOU VAA I MILECOLOU CON ACIO	MARIETTA TARRE	MTMIC All prices with specified Opinionis Prices	4.86 4.08 1.39 4.98	-030 -030 -030	1.39 -681	0.00	600 600 600	628 620 620	200	300	100	1	20	
FREE CECENTRY	EU/ED MASS	TUM Labelinian bis 1 La	420	-046 -046	0.39 1.39 -G19	0.00 0.00 0.00	6.00 6.00	614 600 600			300 300	320 M 320	20 20	
HAND GEOGRAPHS	TABLE HEADYZ	MALS installment til staget programs game 1 Gelephinn stiper. TURES 1 Michine politick 1 MICHAEL START STAR	1.81	108	0.78	0.00			20	100		:		
HAND GEOGRAPHS	AUPATS NADIVES	CIPIL suberdese Star of open tals 2 like Grapison other MCCRIS MACQUERE AL Quarter August Au	1.0 1.0 1.0 4.0 1.0	138 -146 670	-114 0.73		600 600 600	600 600 600	0 200		- :	120	200	U I
FREEDERS WIT FREEDERS WIT	MIDAD-AG MAAA	Matter M	1.00	142 -238 -187	1.26 0.86 -CAR	0.00	640 640	600 600	0	87 0		120	200	2
I MICCECU THE I MICCECU TO 4	MENCH MENCH	WIDSS WD repeal does in 24 Cliev other MESSS on the toc appeal or 2 Quipeloon Sungarior	1.00	CAL .		0.00	-		200	M				
I MEGICINAL	BIPT MY-NOR	COUNT COUN	2.00 6.00 6.00 1.00	-0.00 -0.00	-618 -685 -687	0.00 0.00 0.00	600 600	600 600		÷	-	12	97	20 EL
FREE CECTS CO. 4	MARKET HE MARKET HE MARKET	THE STATE IS ASSESSED TO THE STATE OF THE ST	1.38 1.38	128	-631 6.87	0.00	5.00	676	20 20 20	320 87			0 8	
FRANCISCO CO C	MENT MENT	Martin	1.37 1.36 1.88	581 119	0.75	0.00		600	20	120 17	100	:	:	:
HANGE COLUMN	NEEDEL NEEDEL	WILLIAM MOTORAL MANNES STATE I TOMBAN MANNES STATE	1.80	580 312	1.00	0.00	680 680		200	20	100	:		
FREE CECETARY	HATEN	EXEC entirelit evopro tele. National Molecules and or retail to compensation of the state of the	1.0	107 -CIB	0.62 1.67	0.00	600	600	30 30	20	100		83	:
I MANO CORDO COMO A I MANO CORDO COMO A	CHARGE AND	SET AMERICAN STATE OF THE STATE	4.0	-0.0 -0.0	0.E 0.E 0.B	1.00	640 640	620 644 620	:	:	1	=	97 300 83	
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FRANCISCO NO. A FRANCISCO COL 1870 FRANCISCO COL 1870	PFE.	16ALCI Mr. Family of Brogorous And only 20 rounder A. Clier other . 1972. Family on Pyllor Calculus . Marina. Marina mayor . 2.599. galadeless account bely promit. Marina. National Service Spherony details.	1.00 1.00 1.00	275 225 228	1.01		680 680	683 680 680	20 20	120	100	:	:	
HANDGE CO. ST. 2	HMG.	U.S. speaker in manus or practice. In the case of the	1.30 1.30 1.30	181	1.00	0.00	620 620	620 620	20 20 20		100	120	87	
FRANCISCO STATE FRANCISCO STAT	MERCE METER MERCE MERCE MERCE MERCE MERCE MERCE MERCE MERCE MERCE MERCE MERCE MERCE MERCE METER	MINES EMbhailig naif praint 2 Maí na dher MERC MEY (No Mandy) saint a bri ly nambe 2 Maí na mayor ME SE SE calculation control brill prainted F Manual Manhales Emprairie AREL SAIN and San control brill 1, I search than it no brill and Embarra Saint dybrang datar	1.00	128 -646 677	1.33 -0.09 0.75	0.00	600	600	300	1	100 6 100	320	62	
I MICCECCIONA I MICCECCIONA	BECT STORY	MCD MCC - And on the charge of the controller of the charge of the charg	1.0 4.0	-CAS -CAS -CAS	-0.09 0.76 0.88 0.88	0.00 0.00		600 600 600	100 0	11		10		
HEREGE CU AVI	HEISTON	CDES (qui sin predesti mer 18 Qippinon binne RLI2 RDJ, quiptan i qui de Qippinon braquiter et alumini, fin claim METSERS is directione 2 ISS limity remine o Ball ma. other	4.0	-136 -037	-628	0.00	600	618	0	:	2	220 U	300 84	3
FRANCISCO SAFE FRANCISCO SAFE FRANCISCO SAFE	MANA MANA MENSA	CDCID code-cal dorst incode big 10 Optigion after MAR (22 product after 1 Maria Minister Incode and American	1.0 4.0 1.0 4.0 4.0 4.0 1.0 1.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4	-138 671	0.E -613 1.33	0.00	646 646	601 601	200	107	20 E0			
I MICCECURET	TRAIL	TOTAL	1.00	130 119 -630 -687 -138	-618	0.00	0.00 0.00	666	100 0		:	100	200	E.
HAND COLOR WILL HAND COLOR WILL	APM/S #HIAPA	ATHER ATTENDED AND ADDRESS OF A STATE AND ADDRESS OF A STATE ADDRESS O	G ME G ME 1.82	-120 CA1 CA1	-618 -682 0.02	0.00 0.00 0.00	648 648 648	0.00 0.00 0.00			-	-	100 100 14 11	e e
I MICCECLION? I MICCECLION?	HARD ALL HARD HARD	T-120	1.00 4.00 1.07 1.00	- CAS - CAS - CAS	0.m 0.M	0.00 0.00 0.00	640 640	600	0 0 200			120	11 100	
FRANCISCO COLORS 1	OPEL CHES	1991 GOO, consider to telestrate graph for marginar 1 Florina Marriagone y protein coupled a copia 1991 GOO, consideration and the condition public in 1886 A label and the condition of the condition public in 1886 A POD II ship product companies on ARTON complex 2 Quiplom other companies and conditions in 1887 RECENT REPORT of the product condition of the condition of the condition of the conditions are conditions or conditions and conditions of the conditions are conditions and conditions are conditions are conditions and conditions are conditions and conditions are conditions are conditions and conditions are conditionally as a condition of conditions are conditions are conditionally as a condition of conditions are conditionally as a condition of conditions are conditions are conditions are conditionally as a condition of conditions are conditionally as a c	1.0	101	0.00	0.00		660	300 300	-	100		20	
HANGED CO-407	BETOR DHR	MT Market in Aur Market	1.8 4.0 1.0 1.0 1.0 4.0 1.0	100	0.00 0.00	0.00	600	GA1 GD0	200	96 86	-		:	
FREE CECECOCY	CMP98.1 HDAGSD	OAZ urstille des buyle a stryez Geplane aller CMP181 CMP181, od op de socied (I, ponke) Clier aller MCCCO is d'acrefessifice TO Naina Vanca Spissor agrido relinado (, prisantel MCCCO is d'acrefessifice TO	1.M 1.M	-0.00 33.0 32.0	0.00	0.00	680 680	670	300 300	300 07		:		:
I MICCECTI MAN I MICCECTI MAN I MICCECTI MAN	PO NESE DI RES.	POCCO I sear-develope D Nation See different place in one different place in one by the control payment of the Control of the	GM GM	-138 -68 130	0.00 -035 0.70	0.00	0.00 0.00	620 620	:	:	3	=	200	2 2
	HGG J HGGGGG GGGGGGGGGGGGGGGGGGGGGGGGGGG	March Marc	6 M 6 M 1.21 1.32 1.33 1.34 4.31	126	0.00 1.08 0.08 0.00	0.00	640 640	600 600	200 200 200 0	=	100	:	:	:
FRANCISCO SMA	MADE MACY	COMMar membranes aust selecting Chilgie flager S. Ophylaum maywe RASCE RASC bindly sember 2. Ophylaum maywe ARSCY admiciglamospetistus Ophylaum maywe with ophwech A,1	1.00 4.00	128 128 -08	0.00 -633 -689	0.00	646 646	620 620 620	0 0	-	-	10	14	

HANDGE CO. SHA HANDGE CO. FEET	CARD AMPG	MASO MADIFICIAl de la la majora de la majora promoto de comples de la majora de la	Optoplesm mayore Marine stiler	1.38 1.30 1.88	585 592 381	0.80	0.00 0.00 0.00	6.00 6.00	0.00	20	=	e			•
NAME OF CO. FOR Y NAME OF CO. ANY Y NAME OF CO.	BOOK STATE	MARCS analysis primating complex schedul. 1008-119. Sed denied received to the S _i endoped to A.S. per- MARCS reg of his mode; MARCS Sed Search and denied to LYBERS LITERATE containing S. LYBERS LITERATE containing S.	Mains aller	1.00 1.00	181 -180 682	-028		620 620 620	525	0	- 1		-	17	
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HAND GEORGE 7 HAND GEORGE 74.7 HAND GEORGE 74.802	NA NA	ICO1 gyangkapkabén plagkabénna 1 MICCI faniya k egene éni aty Minester G	Graphin Marie Salar Sala	1.07	111 -681	-011 -025 0.40	0.00	6.00 6.00	600 600	200	100			83 0	:
NAME OF COLUMN	MARINETS MATTER	MINTO protect the disease New highway in the sale	Optoplace scapes Malma scapes	1.66	100	1.0	0.00	600	0.00	200	10				я
HANGED CO. CO. C.	TAKEN TAKEN UNION	TACE In submitting and do no find and contacting protein 2 EMADERS. ETACERS because the EPSAZ makeyaki to minimum betatom is also date.	Qualitate silver Qualitate silver Oddalare basis businesistan	1.00 4.00 1.60	-C-0 137	-012 -028	0.00	640 640	500	200 0 200			120	92	
MICCECH 60 MICCECT 86	COUR	CMBC a title to a skewl grad hinds to family month CDB CDB release	Clie der Henationism ausmissermpts	4.07 1.08	-128 -627	-014 -141	0.00	-	500	200		*	330	100	E 20
HARMON CO. CO.	HEITEL ACTOR	CSD Makes	Manual destrone phosphatose Optophon mayne Obtophon mayne	6 M	128 -686 182	1.98 -089	0.00	680 680	600	900 900	- :		100	300	=
HANDSECTION 7	P NO.	PRE Interferon gamma TEST Let at hop-yet bis as yes t domain ST	Estandiar Space options Nation tiles	4.00 1.07	CAR CA1	0.46	0.00	-	500	200		2	ML 0		n n
PRINCED CHES	100 MISS	HALLS HALLS against be complex calcust to TABLESS to commitme protein SS SPACES against advertigation associated S the S	Qiquison after Nation binchared	1.0 4.38	-1.61 -6.00	0.00	0.00	646 646	556	0	0 27	100	33	200	
I MINICESCHETTE	HEED LEWIS	ECE moji Cut détai sare sur 2 LOSS LOS desarris sing 1	Optoplace majore Mail ma base dythologyaktor	1.00	330 684	0.00	0.00	500		200	100	-	:	:	
FRANCISCO CARRA	D by	DOT NE in called publish capital to the picture of COSEs, complete 2 COSES. confering in the income using ESS.	Optoplasm phosphatase Optoplasm escapes	1.07	000 000 -100	1.0	0.00	=	600	100 M	2		:		
I MICCECUMA	E112	ECS investigis de tos EXQUA compresQUA	Optoplace after Optoplace after	1.0	388 388	1.37	0.00	600	000	200	100			0	' i
1 Marcate (12 M/1 1 Marcate (14 7 M/1	30 100	TABLE 1 CONTROL OF THE SER	Graphon mayor Manadi entrare diler	1.07	338 685	1.00 0.00	0.00	-	500	200	120 17	1 m	:	. :	
HANGE CE SAG	DATE	1994 signal-toloand profession economic d.1 Desired class profes landy (topic) member (2 BATSA lytine are lytines for each	Optoplace after Optoplace acquire	6.07 1.32	-000 0.76	-017 0.38	0.00	6.0 6.0	681 681	200		-		87	
FRANCISCH MAC	1863 19697	SATEA Igains are igit read or one 2 A UMSE USA disease counts trang 2 CHMP7 charged multimated at leady protein 7 in a legal 1.1 200726 cite forger protein 27%	Clie aller Optopion kampater	1.01	676 680	0.30 0.80 -0.03	0.00	680	500	20		11		14	
I MICCE CLIES	20027 N WENT 6		Naina aler Naina aler	1.0	-125 338 687 376	0.36 0.38 1.48	0.00 0.00 0.00	680 680	6.00 6.00	200	100	30	:		
FRANCODCU NO 1	1971L3	1773 ope pitt grant le 2 1804 d'auturi rettemme d'alconsomme 6 19032 interfero épis indutté prie 1127t le 2	Optoplace steer Marina transporter	1.86	576 678	1.00	0.00	680	600	20	100	180	:		
HANGED CO. SEC.	IZE-MET	GRIDO G palet recept after the 200 ACEP and open dependent TRI opinion paters.	Nematterizae printrapidença	1.07	126	-630 138 -688	0.00 0.00 0.00	500	500	17	-	-	1 12	200	11
I MICCOCCIO DE I	MACH MACH	ADTEP and organization and the option option protects protecting to a support or any other medicine in the COMP. It is proported by the control of the complete option of the complete of the complete option o	Remarks after Other after Others more	1.00	184	0.97 1.08	0.00	500	6.00 6.00	20	-	100 100		97	
FRANCISCO VINT.	MARTE COVE	PRACTI Favor to facility member 2 CDVS CDVS benedag POR probje-bylanojag	Optoplasm solver	6 M	-1.86 -6.67	0.00 -048 -018	0.00 0.00 0.00	640 640	600 600 600			-	**	87 200	32 32
FREEDERS STR	MCMA MCMA	NO. public light spine when better NO. white carrier frontly 1 member 5	Optoplace surproter	4.38	-617 101	-018 0.86 0.80	0.00	638 630	6.00 6.00	0		34 36 100	120	84	34 0
HANDERSON 7	RAPORE SPEED	EPER Esp gartie recleable exhauge factor & SPEE upodic perspingle 25 (subscens) recentle, black good	Name Maniero aller Mane Maniero migra	1.0	-138	-681 -682 -117	0.00	500	666	200		1	100	10 07	-
HAROCECCA COLO	1953A 2	NCSE2 NCSE the hydronic operation component NCSE After the ody, AAAA contract contract NCSE	Optoplasm transporter Marina after	1.0	188 677 148	0.48	0.00	680	600 600	20	=				
PRINCED COTORS	AMPI	PPERS proteinhautete 1 regulatry substitit MONTL MCL appears de de mateiles > lie (emi)	Qrapton aller Qrapton phaptains	4.00 1.00	-187 130	1.88 -617 0.75 0.87	0.00	600	661 660	0 20		6	120	200	i (
HAND GER CLU THE	MAN .		Manual desirate after Malina Mapendest nation rec	1.31	-080	0.00	0.00	500	500	100 11 0			-	12	n
I MINISTERNATION I	2000	Could charactered operating from 8 200001. 20000 Developitie POTEPS. Sphaphosphar phopheters 1	Other other Opposition phosphatase	4.07 1.00	-687	-611 -611	0.00		600	200	*	:	10	11	
HAND GEORGE CO. 2	MAZIN MACI	FORE FOR dense name trong 8 1001 character property dense fore 1	Extraor Saler Space other Optoplasm phosphatase	687	-ca	-017 -017	0.00	648 648	6.00 6.03		n 0	1 27	10	20	
PROGRAMMA PROGRAMMA	HOPE LONG	NEP2 NEP2 maleste protein	Nation there Organism position	1.01 1.01	131 108	-014 1.89 0.88	0.00	649 649	600 600	20	=	100	0		
I MICCECCOMI I MICCECCOMI	PT30	1972 Intelligets transpot 20	Optoplace after Optoplace phosphatase	1.39	344 648	0.00	0.00	0.00 0.00	666	200	-		:	14	
HANDERSON NO.	ANY ANY	PSS pole-glos as a discrete depotes 1 PSS security prime extra chanding 6	Maina aler Grapium majne Other aler	1.0	E85 E85 -138	0.80 0.37 0.39	0.00	6.00 6.00	600 600 648	200		TI UT		200	
	March Marc	DES. delete digital by a 1	Called Annual Control of Control	4.00	687	0.30 0.38	0.00	0.00	5.00 5.07	200			320 0		
HANDSESSONS HANDSESSONS	QMCHG.	PCSC1 PC imprepart contring 1 CRESC glaburate to b1	Other after Mains after Mains areas	1.0	-08 011 040	0.00 0.00	0.00	68 68	620 620	20	=	100	120	87	
HAND GEORGE TALE	PENG. MARKE	USS2 ship-th praish by self component recognit 2 PCMS periodicide reservi 1 MARIE mirrolables following bits a d	Original aler Original lines	1.00	585 586 -573	0.00	0.00	6.00 6.00	0.00 0.81	200	**	-	120	87	. :
HANDODONALA HANDODODONA	MA DISCREA	DODGE DESCRIPTION OF THE PROPERTY.	Males aler	1.30	278 226	0.8E 0.8D	0.00	640 640	000	200	-	100		11 0	:
HANGED CONTROL	VII.	VME VME, CD RVT complex sales of VC. should be sales of TO REA. Local of and y E member A.	Annual misus majos Organism majos	1.31 4.32 6.88	-536 -639	0.00 0.00	0.00	646 646	621 621 620			100	120	20 20	1
PROGESTION	MINNS IMES	MSPA protects were nines protein, and open indused 1 MSD2 proof and AT+tch interaction denote use of 2	Manual entrare after Nation transsplanning dater	CM CM	-08 -00	0.00 0.00	0.00	600	600	:		100	16 320	20	:
HANDER COOKS	20 M2	2CRCB on Super CENTUpe containing 26 18972 and ICRC+th Sales 2 16082 methods collects 95	Naina dier Clie dier	687	0.78 -1.09 -1.07	-082 -086		520	620 620	0		N N	=	87	
PROCEEDINGS	1162	TABLE Tred at batter that I have at batter or since	Optopleum aller	1.0	087 -530	1.00		-		100				20	
FRANCIECTIVASO	IMES.	MEEN seurgiaks PRES Interferon eistedenei opnentel regulatur 1 APRES adaptur presen ja phagis objective in ding ur b PRES	Qisphon siler Nai na siler Nai na siler	1.07	388	0.93 1.89 0.38		-	600 600	20	-	100	:	:	:
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NAME OF CUI AND NAME OF THE OFFICE OF	ACTES MORE	ACTES MORE	immediate and y response 31 stems ding posterior. ANY to other risk ted protein 5 homolog. MC report done in 1	Optoplace National Extraordale Space	ater ater	1.01 0.00	-040 3318 -040	-040 0.78 0.78	0.00 0.00	5.00 5.00 5.00	600 600 611	200	100	100	-	97	
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HAND CODE COLUMNS	EII MIRPI	MIRE.	ten man yanan matar Si. ISB, rene piar riskandi pratana manakandi pratato 2 arigi teren quellin nasarpine mikusi 13 tahida tar of CONA, kanding 11, MEM pratana MEMI tahina oling pratana 3 (1523 kalunikin)	Maine tone-plan	· ····································	6.79 0.36	603 647	0.0	0.00	CAD CAD	520 520	* *	100	- :	100 0	80 0	*
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F MARIO COD COA COM S	983 088	1902 1900 1900	THESE attacks 1944.1 Immediate and y require 2 of for still y exposed in INCP 2 thanking SAS (22 protein all later 45; providence SAS, marsher 1941 congress for thylines	Optoplace alle		68	-08	-637 1.88		600	600 600	M 8	*	100		11	
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I MICCOECU AFE I MICCOECU MAN I MICCOECU MA	VISE VANCO		vacable protein setting 33 hand og 8 sted besigte met fildensin containing 9	March Marc	arter	6.00	EAS -EAS	0.61 -610		00 00	600	20	M.	a a		:	u m
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I HAND COM TO A NEW O	CTADAR	CHARGE	OTU dana bosodo bing 6.0	Other stler	0.38	638	0.86	0.00	cox	000	B 07	-	n		
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HALLOTT CO. TO.	110	-	establishmen PROTemby 2 salifamily 8 member 1 Rab bitmail og I yessemal palatin proteinly sed self mas 2	Qtopison stler Qtopison bloss C1-507	0.44		0.86	0.00		000	er er		١.		:
I MINICOLOGICAL NO.	MARK	MAGC	fent hand opt 07 landing protein 2 8 de	Naine transplacements	63	-680	0.00	0.30	600	550				96	
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I MANIC CED CON SMILT	cocw	COCH	adel of district and the 187	Oliv dier	62	-638	-678	0.00	500	660	e 4			**	
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PRINCES CONTRACTOR	HI.	PH.	function of the same of the 1	Optoplace majore	63	-68	-682	om om	0.00	000	M 11	- :		29	
PRINCIPAL COLOR	BMES	SMACS.	and nation 1904 the log complex polymptable to	Malma tona deliceregulator	0.0	-cm	-688	0.00 0.44	5.00	000	N .			92	-
I MINICOLOGO CON II	ALBERT .	ALIBNA	al lith analog E, lycke derestly lace	Optoplace maybe	0.30	-631	-672 -689	0.00 0.00 0.01	6.0 6.0 6.0	650 650 650 650	n a			11 11 42	=
9 MARIE (222 C23 MAR 2	ERS.MA	BANKS.	rise and past of the people and	Clier aller	0.00	618	-689	0.25	638	000		-		42	m.
PRINCEPON REA	CHIPS	CHIPS	of lith conducy at, justice do red by lace. If the conducy do the LEE by an adoption the quartee or highwayer at I conduction a product H conduction a product H conduction product H conduction produce or the China color pick spill about 1 contact aggrade that conduction 2 disposition design for one E 2 disposition design for one of one of one of the spill one for	Naine aler	en	-030	-682	0.00	500	000	2 2		н	72	-
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11000000007	Chets	COM/10	decrease 2 quered glare 12	ttler aler	40	-680	-684	0.00	0.00	0.00	м м			- 11	
HANGGEGERAT	PROF	PINET	2 magnateut de 1°5 hap fate 10 hydra och phaphat djet handa et se 10 methytra subrase	Option major	4.0	-046	-688	0.00	640	600	N 2	- :		73 94	
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HAROGE CLUBS	MACIZA	MAKEERA	Family of the space and only 200 remier A. The gaster recipitals exchange factor 21.	Naina aler	0.36	638	-682	0.00	-	000		- 1		42	
FREE CECTOR SHIP	APHIRP11 Chief ZB	ANNUAL CONTRACTOR	the gaste redestib exhaugefator 11 characterist presenting force 28	Other siler	63	-638	0.m -0.02	0.00	627	660		-	70	87	
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FRANCISCO ON 1	SCANA.	123,510	CMA palymer are delta 2, accessory subsetti small CQ all subjequestfol EMA 9 accled-call disma to contacting E2 function allo-bunding protein 1	Other after	0.86		0.00	0.00		000		2	Ι.,		
PRODUCTION OF	PICHE	PION	factor do harding protect 1	Optoplasm after	I		0.00		_	000		- I	I ~	-	2
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HAND GET COLUMN	BES	100	the large and SCAN dated constituting to immediate and prospers to	Clie ster	ca	524	0.00	0.00	64B	600 600 600 600 600	: :	**	er er	41	
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HANGER CO. TOTAL	RPS	POPE	FOR handing chanciles of Philippideses	Males mayor	6 B	-610	-080	0.07	C/R	000		=	2	**	
HARCOTTON TON	March .	DAME:	rise and part of the provide me Ti	Clie dier	62	-03	-687	0.20	CAS CAS	000	77 4 15 2	27	Ĩ.		20
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HARICGE CO. 7017	PD-MINA				0.46 0.44	556	-687	0.00	630	6.00 6.00	er e				
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	PTO-MENTA HERE HELL HELLWIS AMELINES AMELINES PTO-MEDIAL	HELENAGE		Qrisplania mayore	0.00	-60	-Ch7 0.45 0.46 0.46 -Ch2 -Ch2 -Ch4	1.0	678	600 600 600 600		-		72	×
HAROGE CIRCLE	APRES NO. 3	HE-0101	recording over according to complex asserting to	distance makes	0.38 0.34	618 628	-682 -682	0.00 0.00	6.00 6.00	000	7 7			72 28 83	M.
PRODUCTION OF	#10-M1081				6.34	-638	-684	0.38	6.07	000	n	2		81	N N
	a warm.					-			***						

Supplementary Table	e 38. Differentially	expressed non-coding genes in CD4+, CD8+ and CD4-CD8- fraction con	spared to the original PBMC fi	action (using			en only).				_				_
Ensembl Gene IDs		Symbol Entrez Gene Name	Location Type(s) Drug(s)	CD 4+ vs PBM	Median Lo	C CD4-CD8-vs. PBM C			CD4CD8- vs. PBMC			C CD4-CD8- vs. PBMC	CD4+ vs PBM	Percent Dow	CD4-CD8-vs. PBM
ENSG00000224137 ENSG00000224397	AC079767.4 LINC01272	UNC01857 long intergenic non-protein coding RNA 1857 SMIM25 small integral membrane protein 25	Other other Other other	-7.11 -4.10	-4.96 -6.56	0.37 0.29	0.00	0.00	0.07 0.42	0	0	70 65	100 100	100 100	30 35
ENSG000000251562 ENSG000000253701	MALAT1 AL928768.3	MALAT1 metastasis associated lung adenocarcinoma transcript 1		1.78 "-INF"	1.53 "-INF"	1.26 -0.28	0.00	0.00	000	97	100	89 27	100	100	11 73
ENSG00000255717 ENSG00000256039		SNHG1 small nucleolar RNA host gene 1	Other other	1.55 -6.67	157 191	0.78 -2.82	0.00	0.00	000	100	100 100	100	100	0	100
ENSG000000260682 ENSG000000269728	75 K RP11-145M9.4	RN7SKP176 RNA, 7SK small nuclear pseudogene 176	Other other	-4.77 -3.55	-1.42 -3.90	1.36 -0.04	0.00	0.00	000	0	0	100 43	100 100	100 100	0 57
ENSG00000272379 ENSG00000234184	RP1-257A7.5 RP5-887A10.1	LINCOL781 long intergenic non-protein coding RNA1781	Other other	-3.81 "-INF"	-4.00 -5.25	087 001	0.00	0.00	0.00	0	0	95 51	100 100	100 100	5 49
ENSG00000272016 ENSG00000273472	RP11-215G15.5 RP11-102N12.3			-3.76 -5.34	-3.22 -4.79	0.61 0.75	0.00	0.00	0.00	0	0	95 97	100 100	100 100	5
ENSG00000230709 ENSG00000211459	AC104024.1 MT-RNR1	LOC284191 uncharacterized LOC284191 MT-RNR1 s-rRNA	Other other Cytoplasm other	-6.88 -1.83	-5.36 -1.14	106 005	0.00	0.00	000	0	0	92 57	100 100	100 100	8 43
ENSG00000250834 ENSG00000260655	LINC00989 CTA-250010.23	UNC00989 long intergenic non-protein coding RNA 989	Other other	-5.95 -3.67	"-INF" -2.39	-0.98 0.83	0.00	0.00	0.00	0	0	16 97	100 100	100 100	84 3
ENSG00000247982 ENSG00000267174	LINC00926 CTC-510F12.4	LINC00926 long intergenic non-protein coding RNA 926 HSPC102 uncharacterized HSPC102	Other other	-3.46 -4.42	-2.56 -6.19	2.02 0.20	0.00	0.00	0.00	0	0	100 62	100 97	100 100	0
ENSG00000237604 ENSG00000260065	AP001056.1			-4.87 -2.49	-5.17 0.08	0.64	0.00	0.00	0.00	0	0 56	89 16	100	100	11 84
ENSG00000271614 ENSG00000268734	LINC00936 CTB-61M7.2	ATP281-AS1 ATP281 entirense RNA1	Other other	-2.56 -2.94	-2.83 -4.70	116 195	0.00	0.00	0.00	0	0	100 100	100	100 100	0
ENSG00000241163 ENSG00000186594	LINC00877 MIR22HG	LINCOD877 long intergenic non-protein coding RNA 877	Other other	-2.97 -1.86	-4.13 -1.65	151	0.00	0.00	0.00	0	0	100	100	100	0
ENSG00000272523 ENSG00000230438	LINCOLO23 SERPINB9P1	UNC01023 long intergenic non-protein coding RNA1023	Other other Other other	-3.32 -2.21	-2.07 -1.92	038 054	0.00	0.00	000	0	0	95 97	100	100	5
ENSG000000253364	RP11-731F5.2	SERPNB9P1 serpin family 8 member 9 pseudogene 1	Coner dener	"-INF"	"INF"	-0.34	0.00	0.00	0.00	0	3	35	100	97	65 24
ENSG00000260859 ENSG00000180422 ENSG00000272077	NA LINC00304 RP11-348P10.2	UNC00304 long intergenic non-protein coding RNA304	Other other	-2.20 2.98 -2.36	-1.18 2.09	031	0.00	0.00	0.00	100	100	76	0	94	19
ENSG000000272888	AC013394.2	UNC01578 long intergenic non-protein coding RNA1578	Other other	0.66	-1.43 0.41	0.38 -0.11	0.00	0.00	0.28	100	86	32	0	94	68
ENSG00000172965 ENSG00000232931	LINC00342	MR4435-2HG MIR4435-2 host gene UNC00342 long intergenic non-protein coding RNA342	Other other	-1.79 2.51	-1.71 1.92	0.28	0.00	0.00	0.40	100	97	73 81	0	100 3	27 19
ENSG000000233901 ENSG000000255760		UNC01503 long intergenic non-protein coding RNA 1503 LOC105369723	Other other	-3.39 "-INF"	-4.30	-0.08 0.32	0.00	0.00	0.03 0.61	0	0	49 59	100 100	100	51 41
ENSG00000175898 ENSG000000268913	CTD-2369P2.2 AC026806.2			-1.62 -2.59	-2.08 -2.66	0.26 -0.18	0.00	0.00	0.03 0.01	0	0	73 43	100 100	100 100	27 57
ENSG00000263126 ENSG00000233056	CTC-479C5.10 ERVH48-1	ERVH48-1 endagenaus retrovirus graup 48 member 1	racellular Sp other	2.02 2.27	190 -0.43	0.84 -0.96	0.00	0.00	000	100 100	100 22	95 5	0	0 78	5 95
ENSG000000261005 ENSG000000210082	NA MT-RNR2	MT-RNR2 L-RNA	Other other	-156 -188	-1.57 -1.40	0.82 -0.54	0.00	0.00	0.00	0	3 0	89 16	100 100	97 100	11 84
ENSG00000223511 ENSG00000259004		LOC101929422uncharacterized LOC101929422	Other other	2.50 -3.72	2.17 -3.99	1.59 0.35	0.00	0.00	0.00	100	100	89 86	100	100	11 14
ENSG00000234741 ENSG000000223745	GASS RP4-717123.3	GASS growth arrest specific 5 (non-protein coding) CCDC18-AS1 CCDC18 antisense RNA 1	Other other	0.53	0.43	-0.27 1.47	0.00	0.18	000	100	94 97	5 86	0	6	95 14
ENSG00000233746 ENSG00000230606 ENSG00000272053		CCDC18-AS1 CCDC18 antiseme RNA1 LOC100506123uncharacterized LOC100506123	Other other	2.45 -1.68	213 -1.13	0.98	0.00	0.00	000	100	100	86 89 41	0	97	14 11 59
ENSG00000188070	C11crf95	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 ENSG00000261455	CTD-3092A11.2 LINC01003	LINCO1003 long intergenic non-protein coding RNA 1003	Other other	-1.42	-1.37	0.25	0.00	0.00	0.45	0	0	73 76	100	100	27
ENSG000000260807 ENSG00000240219		LMF1 lipase maturation factor 1 LOC105371692uncharacterized LOC105371692	Cytoplasm other Other other	2.25 2.27	0.78 1.71	-0.78 1.32	0.00	0.00	000	100 97	89 97	27 95	3	11 3	73 5
ENSG00000232891 ENSG00000196295	RP11-136K14.1 AC005154.6			-2.44 2.24	-2.20 1.68	0.99 1.83	0.00	0.00	0.00	97	100	100 92	100	100	8
ENSG00000225331 ENSG000000251301		LINC01678 LOC10050719Suncharacterized LOC100507195	Other other Other other	-154 -3.10	-2.26 -1.34	0.16 0.41	0.00	0.00	0.81 0.58	0 3	0 17	73 62	100 97	100 83	27 38
ENSG00000267279 ENSG000000222041	RP11-879F14.2 LINC00152	CYTOR cytositeleton regulator RNA	Other other	"-INF" -1.31	-1.28	-0.61 0.02	0.00	0.00	0.00 0.04	3	6	27 51	97 97	94	73 49
ENSG000000251136 ENSG000000261490		LOC1 01 92 97 09 uncharact or ked LOC10 19 29 70 9	Other other	-1.47 2.08	-1.24 1.08	0.78 0.76	0.00	0.00	0.00	97	0 94	100 89	100	100 6	0 11
ENSG00000188971 ENSG00000269290	RP11-427H3.3 RP11-869815.1			1.35 2.12	0.75 1.32	-0.77 0.44	0.00	0.00	0.00	100 97	94 89	3 65	0	6 11	97 35
ENSG00000250006 ENSG00000270127	RP11-469M7.1 PRIXIP1			-1.47 1.99	-0.74 1.25	-0.18	0.00	0.00	0.00	0	100	30	100	100	70
ENSG00000260910 ENSG00000225783	LINC00565 MIAT	UNC00565 long intergenic non-protein coding RNA 565 MIAT myccardial infanction associated transcript (non-protein	Other other	1.66	130	-0.44 1.05	0.00	0.00	0.00	100	100	19 86	0	0	81 14
ENSG00000272316 ENSG00000272316 ENSG00002726137			Other other Other other	1.62 -1.38	103 -245	002	0.00	0.00	0.03	100	94	51	0	6	14
ENSG000000228784	LINC00954	BAIAP2-AS1 BAIAP2 art sense RNA 1 (head to head) LINC00954 long intergenic non-protein coding RNA 954	Other other	1.98	1.45	0.66	0.00	0.00	0.00	100	97	51 86	0	3	14
ENSG00000270060 ENSG00000235576	RP11-390K5.6 AC092580.4			1.78 -2.33	2.08 0.78	138 -1.53	0.00	0.00	0.00	100	100 81	86 5	100	19	14 95
ENSG00000237438 ENSG00000260787	CECR7 NA RP1-266/2019	ŒCR7 cat eye syndrome chromosome region, candidate 7 (non	Other other	-137 197	-108 150	037 152	0.00	0.00	0.00	100	92	89 86	0	97 8	11
ENSG00000266896 ENSG00000243650	RN7SL834P	RN7SL834P RNA, 7SL, cytopia smic 834, pseudogene	Other other	2.96	2.09	2.63	0.00	0.00	0.00	97 97	97 92	92	3	8	8
ENSG00000235499 ENSG00000261560				-109 163	-0.71 1.82	-0.04 0.45	0.00	0.00	0.02	100	100	43 59	0	97	57 41
ENSG00000254419 ENSG00000272086				2.56 -1.37	194 -0.96	156 011	0.00	0.00	0.00 0.15	0	97	81 57	100	100	19 43
ENSG00000260806 ENSG00000228223	H0511	RRN3P1 RRNS homolog, RNA polymerase I transcription factor pol HCG11 HLA complex group 11 (non-protein coding)	Other other	2.17 -1.00	1.40 -1.72	-0.43	0.00	0.00	0.00	100	92 0	8	100	100	92
	CTD-2521M249	LOC102724017uncharacterized LOC102724017	Other other	-106 -104	-0.84 -0.82	0.30 -0.66	0.00	0.00	0.00	3 0	8 6	68 8	97 100	92 94	32 92
ENSG00000272849 ENSG000000142396	RP11-347119.8 ERVK3-1	BRVK3-1	Other other	181 152	180 166	-0.02 1.00	0.00	0.00	0.14	97 100	97 100	49 89	3	3 0	51 11
ENSG00000197989 ENSG00000260101		SNHG 12 small nucleolar RNA host gene 12 LOC1 01 92 7402uncharacterized LOC10 1927 402	Other other Other other	1.86 -1.28	1.94 -1.59	1.42 0.61	0.00	0.00	000 000	100	100	100 81	97	100	0 19
ENSG00000266709 ENSG00000240850	MGC12916 AC017002.1	MGC12916 uncharacterized protein MGC12916	Other other	-1.14 -1.32	-0.90 -1.23	107 033	0.00	0.00	0.00	17 11	8 14	95 76	83 89	92 86	5 24
ENSG000000267302 ENSG000000258659		LOC1 01 92 77 55 unchar act or lized LOC10 19 27 75 5	Other other	1.58 1.96	168 197	0.70 1.23	0.00	0.00	0.00	100 100	94 97	76 92	0	6	24
ENSG00000263470 ENSG00000238142	RP11-16005.1	100105376805	Other other	-2.62 -1.37	-1.73 -1.15	0.61	0.00	0.00	0.03	0	0	76 38	100	100 94	24 62
ENSG00000260751 ENSG00000266274		RM75L1389	Other other	1.76 "-INF"	179	0.95 0.74	0.00	0.00	000	100	94	92 84	0	6	8 16
ENSG00000235373 ENSG00000259928				166	169 096	132	0.00	0.00	000	97	97 97	89 92	3	3	11 8
ENSG00000261355 ENSG00000272341	NA NA RP1.151F172			1.49	0.56	0.41	0.00	0.00	0.00	97	94	92 81	3	6	19
ENSG00000272168	CASC15	CASC15 cancer susceptibility 15 (non-protein coding)	Other other	1.88	153		0.00	0.00		100	94		0	6	_
ENSG00000240905 ENSG00000262370		RM SL7989	Other other	"-INF" 154	-3.91 -0.14	0.47 1.43	0.00	0.00	000	94	44	65 89	97 6	94 56	35 11
ENSG00000260077 ENSG00000265242				-1.07 -0.84	-1.39 -0.66	-0.60	0.00	0.00	000	0	6	89 5	94 100	100 94	11 95
ENSG000000260948 ENSG000000234883	M R155HG			1.66 -1.04	1.00 -1.06	1.05 1.05	0.00	0.00	000	97 17	92 6	81 100	3 83	94	19 0
ENSG000000260905 ENSG000000230415	RP11-105C19.1 RP5-902P8.10			1.89 1.97	131 136	0.83 0.61	0.00	0.00	0.00	100 100	89 89	81 76	0	11 11	19 24
ENSG00000236871 ENSG00000237513	LINC00106 RP11-325F22.2	LINC00106 long intergenic non-protein coding RNA 106 LOC1 01927902uncharacterized LOC101927902	Other other	3.29 -0.85	3.02 -0.80	3.15 0.72	0.00	0.00	000 000	100 6	94 11	97 100	0 94	6 89	0
ENSG00000228434 ENSG00000251867	AC004951.6 RP11-4883.5			1.46	117	0.49	0.00	0.00	000	97	94	84	3 94	6	16 86
ENSG00000264772 ENSG00000236194	SNORA67 AC009104.1			137	147	126 043	0.00	0.00	0.00	100	97 89	100	0	3	0
ENSG00000254615 ENSG00000233261		UNC00264 long intergenic non-protein coding RNA264	Other other	152	143	034 005	0.00	0.00	0.03	100	100	76 51	0	0	24
ENSG00000224478 ENSG00000231607	RP11-13/5.1 DLEU2	mir-15 microRNA 15a	Cytoplasm nicroRNA	-1.62 -0.77	-166 -124	098 001	0.00	0.00	000	9	6	97 51	91 100	94	3
ENSG00000249532 ENSG00000238795	RP11-14886.1 SCARNA12	mir-302 microRNA 302c SCARNA12 small Cajal body-specific RNA12	Cytoplasm ricroRNA Other other	2.15	2.14	178 0.99	0.00	0.00	000	97	100	97	3	0	3
ENSG000000260114	CTD-2574022.4	KCTD13 potassium channel tetramerization domain containing 15	Nucleus in channel	1.46	190 146	0.81	0.00	0.00	0.00	97	89 97	84 86	3	3	14
ENSG00000230724 ENSG00000269996	NA.	001 (includes dong intergenic non-protein coding RNA 1347	Other other	1.33 -0.75	-1.25	0.99	0.00	0.00	0.00	100	97	97 81	91	100	3 19
ENSG000000261220 ENSG000000261114				-1.13 -0.88	-0.83 -0.46	141 0.66	0.00	0.00	000	11 14	11 31	97 86	89 86	89 69	3 14
ENSG000000262766 ENSG000000261270	RP11-196G11.4 RP11-325K4.3			1.44 -1.17	154 -0.38	138 065	0.00	0.00	0.00	97 11	94 31	92 92	3 20	6 69	8
ENSG00000267701 ENSG00000260841	RP11-28F1.2 CTC-205M6.5			-1.78 -0.81	-1.73 -0.15	0.64	0.00	0.00	0.16 0.00	0 11	8 39	54 95	100 89	92 61	46 5
ENSG00000261824 ENSG00000212694	LINC00662 LINC01089	UNC00662 long intergenic non-protein coding RNA 662 UNC01089 long intergenic non-protein coding RNA 1089	Other other	-0.76 1.28	-1.00 0.79	-0.19 -0.58	0.00	0.00	0.00	0	97	27 8	100	100	73 92
ENSG00000273352 ENSG00000215908		CROCCP2 ciliaryroadet coile 6 coil, roadetin pseudogene 2	Other other	-0.93 1.36	-0.78 1.39	-0.08 0.36	0.00	0.00	0.00	9	17	43 89	91	83	57 11
ENSG00000215908 ENSG00000254985 ENSG00000253764	CROCC92 RSF1-IT2 RP11-439C15.4	CROCCP2 cilia ryrocdet colled-coil, roodetin pseudogene 2 RSF1-IT2 RSF1 intronic transcript 2	Other other	-0.99 3.05	-0.16	-0.33	0.00 0.00 0.00	0.00	0.00	100 9 97	100 39	30	91 3	61	70
ENSG00000206140	TMEM191C	M1918/TMEMtransmembrane protein 191C	Other other	1.28	455	***	0.00		444	100	or.		0		
ENSG00000240731 ENSG00000226423	AC098642.4			1.74 1.50	173 054	1.10 -1.12	0.00	0.02	000	100 97	97 75	86 14	3	3 25	14 86
ENSG00000259758 ENSG00000266918	CASC7 RP11-798G7.8			-0.50 1.45	-0.32 1.27	0.27	0.00	0.00	0.00	20 94	19 94	32 86	80 6	81 6	68 14
ENSG00000232470 ENSG00000261338	RP11-378A13.1			2.25 -0.78	1.98 -0.50	-0.66	0.00	0.00	0.00	100	100 25	24	91	75	76
ENSG00000261094 ENSG00000259715	CTD-3110H11.1			1.21 2.48	146 206	0.74	0.00	0.00	0.00	100 97	100 89	95	0 3	0 11	5
ENSG000000271938 ENSG000000270172				1.40 1.41	176 096	0.24 0.64	0.00	0.00	0.33	97 97	100 97	62 92	3	0 3	38 8
ENSG00000255989				-0.75	-0.76	021	0.00	0.00	0.78	9	11	68	91	89	32

ENS900000241860	RP11-34P13.13			1.28	123	146	0.00	0.00	0.00	97	94	95	3	6	5
ENSG00000270972 ENSG00000270157				187	137	0.53	0.00	0.00	0.00	91 97	89 97	86	9	11 3	14
ENSG00000271843 ENSG00000269444	RP11-24509.5 CTB-180A7.6			1.52	1.41	-0.22 1.34	0.00	0.00	000	94	92 97	35 95	6	8	65
ENSG00000251323 ENSG00000244459		LOC101928865uncharacterized LOC101928865	Other other	134	2.34	234	0.00		430	100	21	23	0 94		,
ENSG00000227486 ENSG00000273192	RP13-188A5.1 CITF22-1A6.3			-0.97 1.44	-1.30 1.38	0.29	0.00	0.00	0.27	17 97	100	68 84	83	92	32 16
ENSG00000267532 ENSG00000239002	M R497HG SCARNA10	SCARNA10 small Cajal body-specific RNA10	Other other	125	230	493	0.00	440	450	100	100	84	0	•	-
ENSG00000227518 ENSG00000237940	M R1302-2 AC098642.3	mir-1302 microRNA 1302-5	Cytoplasm nicroRNA	1.14	104	0.63 0.60	0.00	0.00	0.00	97	92 89	81 89	3	8	19 11
ENSG00000271975 ENSG00000264112	RP11-383/24.6	UNC01238 long intergenic non-protein coding RNA1238	Nucleus other	-0.54 1.17	-1.14 1.33	-0.05	0.00	0.00	0.00	9	0 97	43 54	91	100	57 46
ENSG000000260539	GLG1	SRSF1 serine and arginine rich splicing factor 1	Nucleus other	1.27	0.66		0.00	0.00		100	83		0	17	
ENSG00000229227 ENSG00000222375	RM7SIP127	RN75XP1.27	Other other	1.38 2.88	1.10 2.68	0.74	0.00	0.00	0.00	97 100	94 92	89	3 0	6 3	11
ENSG000000261574 ENSG000000152487	RP1-168P16.2 ARL58-AS1			-1.20 1.94	1.62	0.66	0.00	0.00	0.00	97	97	84	100 3	67 3	16
ENSG000000212464 ENSG000000268802	SNORA12 NA	SNORA12 small nucleolar RNA, H/ACA box 12	Other other	4.84 -0.57	-1.10	0.64	0.00	0.00	0.00	91 20	3	84	80	97	16
ENSG00000269086 ENSG00000270066	CTC-523E23.5 SCARNA2	SCARNA2 small Cajal body-specific RNA2	Other other	1.24 1.54	120 115		0.00	0.00		100 97	100 86		3	0 14	
ENSG00000261685 ENSG00000238039	RP11-401P9.A AF011889.2			1.14 2.54	-0.20	-1.20	0.00	0.00	0.00	94 94	47	3	6 6	53	97
ENSG00000273033 ENSG00000272894	RP11-67L2.2 RP5-1159O4.1	LINC02035 long intergenic non-protein coding RNA 2035	Other other	-0.57 1.32	-0.99	0.40 2.25	0.00	0.00	0.00	3 94	0	89 100	97 6	100	11 0
ENSG00000100181 ENSG00000204261	TPTEP1 PSM88-AS1	TPTEP1 transmembrane phosphatase with tensin homology pseu- PSM88-AS1 PSM88 antisense RNA1 (head to head)	Other other Other other	-0.61 -0.57	0.12 -0.52	-0.07 -0.33	0.00	0.12	000	11 6	64 0	35 22	89 94	36 100	65 78
ENSG00000260591 ENSG00000272462	RP11-817013.6 U91328.19			3.68 -0.56	-0.29	-0.05	0.00	0.00	0.01	91 3	11	41	6 97	89	59
ENSG00000273015 ENSG00000202198	LINC00938 RN7SK	RN7SX RNA, 7SX small nuclear	Nucleus other	-0.56 0.93	-0.47 0.70	-0.38 0.95	0.00	0.00	0.00	0 83	8 75	3 86	100 17	92 25	97 14
ENSG00000249456 ENSG00000227946	RP11-298/20.4 AC007383.3			-0.63 -0.59	-0.37 -0.04	-0.13 0.33	0.00	0.00	0.00 0.14	11 6	28 44	35 81	89 94	72 56	65 19
ENSG00000261526 ENSG00000270659	CTB-31 O 20 2 RP11-105N14.1			1.22 -0.58	1.02 -0.61	-0.87	0.00	0.00	0.01	100 3	97 6	51 3	97	3 94	49 97
ENSG00000174865 ENSG00000230002	SNHG11 ALMS1-IT1	SNHG11 small nucleolar RNA host gene 11 ALMS1-IT1 ALMS1 intronic transcript 1	Other other Other other	1.09	0.47 1.12	0.11 -0.02	0.00	0.12	0.40 0.08	100 100	89 97	59 49	0	11 3	41 51
ENSG00000228327 ENSG00000259652	RP11-206L10.2 RP11-797A18.3			1.18 3.32	1.24	0.70	0.00	0.00	0.00	97 94	94	84	3	6	16
ENSG00000229512 ENSG00000237491	AC068580.5 RP11-206L10.9			-2.37 1.07	"-INF" 1.15	0.78 0.43	0.00	0.00	0.01	6 94	8 97	78 81	91 6	89 3	22 19
ENSG00000256576 ENSG00000260261	RP13-9770112	LOC100996246uncharacterized LOC100996246	Other other	1.09	0.02	-1.47	0.00	0.00	0.00	100	53	0	0	47	100
ENSG00000269906 ENSG00000245156	RP11-248/18.2 RP11-248/18.2 RP11-867G23.3	RAB18 RAB18, member RAS oncogene family	Cytoplasm other	-1.06 1.07	166	0.93 1.39	0.00	0.00	0.00	91 97	100	97 97	91 3	0	3
ENSG00000245156 ENSG00000266236 ENSG00000267096	NARF-IT1	RAS18 RAS18, member RAS oncogene family NARF-IT1 NARF intronic transcript 1	Other other	1.07 1.01 1.42	166 174 149	139 164 127	0.00	0.00	000	97 97 94	100 100 94	97 97 81	3 3 6	0	3 3 19
ENSG00000250889 ENSG00000270704	CTD-2537/9.13 LINC01336 SNORD64	UNC01336	Other other	1.42 1.36 1.66	1.49 0.67 1.76	022	0.00	0.00	0.00	94 100 91	94 78 94	57	0	6 22 6	19
ENSG00000270704 ENSG00000269942 ENSG00000267364	NA.			1.99	1.71		0.00	0.00		94	89		6	11	
ENSG000000240143	RP11-47L3.1 RP4-753P9.3			-1.09 -0.91	-0.84	-1.73 106	0.00	0.50	000	20	58	19 89	91 80	78	81 11
ENSG00000271869 ENSG00000265975	RP11-519.5 CTB-4116.2			1.00 -1.07	100 -108	-0.31 1.15	0.00	0.00	000	100 20	100 11	14 95	80	89	86 5
ENSG00000271725 ENSG00000259865	RP11-76114.A RP11-488.18.10			-0.59 0.85	-0.67 0.41	010 045	0.00	0.00	069 089	11 91	19 64	59 62	9	81 36	41 38
ENSG000000267481 ENSG000000239884	CTC-559E9.5 RN7SL608P	RN75L608P	Other other	0.97 1.20	0.58 1.62	-0.44 0.31	0.00	0.00	0.00 0.02	100 29	92 94	19 68	0 11	8 6	81 32
ENSG00000238164 ENSG000000225978	RP3-395M20.8 HAR1A	LOC115110 uncharacterized LOC115110 HAR1A highly accelerated region 1A (non-protein coding)	Other other	0.87	0.92	0.95 -1.25	0.00	0.00	000	97 97	100 86	97 3	3	0 14	3 97
ENSG000000260836 ENSG000000225948	RP11-39587.7 RP11-5548.1			0.85 1.84	0.52	0.42	0.00	0.00	0.07	97 94	81	62	3 6	19	38
ENSG00000270419 ENSG00000268205	CAHM CTC-444N24.11	CAHM colon a denocarcinoma hypermethylated (non-protein co-	Other other	-0.60 0.86	-1.24 0.56	0.50	0.00	0.00	0.08 0.23	11 94	6 81	78 57	89 6	94 19	22 43
ENSG00000222414 ENSG00000232412	RMU2-59P RP1-315G1.3	RNU2-59P LOC101928402uncharacterized LOC101928402	Other other Other other	-2.02 -0.93	-0.66 -0.74	0.41 0.03	0.00	0.00	0.03 0.36	20 23	28 22	76 54	80 77	72 78	24 46
ENSG00000246084 ENSG00000271347		LOC101929241uncharacterized LOC101929241	Other other	0.97 1.68	0.43 1.53	-1.69	0.00	0.53	0.00	97 29	75 92	5	3 11	25 8	95
ENSG00000269900 ENSG00000250950	RM RP RP11-3381.3	RMRP RNA component of mitochondrial RNA processing endoril	Cytoplasm other	0.60	0.85	-0.05 0.73	0.00	0.00	0.54	77 91	78 89	49 81	23 9	22 11	51 19
ENSG00000267475 ENSG00000261101	CTD-2538C1.2			-0.66 1.56	0.69 1.19	0.10	0.00	0.09	0.15	26 94	72 81	54 78	74	28 19	46 22
ENSG00000215447 ENSG00000266389	8X322557.10 CTB-4116.1			0.94 -0.86	0.10 -2.05	121	0.00	0.42	0.00	100	67	95	0 80	33	5
ENSG00000228485 ENSG00000243339	GRK5-IT1 RN7SL738P	GRKS-IT1 GRKS introvic transcript 1 RNTSL738P	Other other	-0.62 -0.57	-0.71 -0.80	-0.05 -0.01	0.00	0.00	0.24	20	22 19	49 49	80	78 81	51 51
ENSG00000271849 ENSG00000196559	CTC-332L22.1 LINC00610	not account	CORP CORP	-0.66	-0.93 0.78	-1.40 0.48	0.00	0.00	000	20	17	3	80	83	97
ENSG00000272140 ENSG00000273290				1.11	0.45	036	0.00	0.01	0.29	91 97	81	76	9	19	24
ENSG00000263990 ENSG00000273056				147	149	036	0.00	0.00	0.29	97 94 97	92	76	6	8	24
ENSG00000241217 ENSG00000251791	RN7SL809P SCARNA6	RN7SL809P RNA, 7SL, cytoplasmic 809, pseudogene	Other other	1.47	178 162	0.59 0.95	0.00	0.00	0.01	89 86	94 94	73 76	11 14	6	27 24
ENSG00000272994	RP11-332H14.2	SCARNA6 small Cajal body-specific RNA6 LOC100506473uncharacterized LOC100506473	Other other	0.84	0.83	-0.01	0.00	0.00	0.04	97 100	100	46	3	0	54
ENSG00000242086 ENSG00000261596 ENSG00000260534	CTB-31N19.3	SDHAP2 succinate dehydrogenase complex flavoprotein subunit A	Other other	-0.56	-0.42	0.82	0.00	0.00	0.00	26	100	97 76	74	83	3 24
ENSG00000260534 ENSG00000272645 ENSG00000272048	RP11-1006G14.A RP11-504P24.8	GTF 2920 general transcription factor III pseudogene 20	Other other	0.91	0.93 1.08 0.84	0.19	0.00	0.00	0.00	97 97	100	65 97	3	0	35 3
ENSG00000273190	RP11-255C15.4			1.18 -0.55	-0.30	-0.55 -0.64	0.00	0.00	000	97 23	78 31	24 8	3 77	22 69	76 92
ENSG00000214837 ENSG00000272574	RP11-359K18.4	IDD1 (includes dang intergenic non-protein coding RNA 1347	Other other	1.06 1.57	0.94 2.25	061 121	0.00	0.00	000	97 29	92 97	81 92	3 11	3	19 5
ENSG00000255455 ENSG00000257900	RP11-454K7.1	LOC103611081uncharacterized LOC103611081	Other other	0.97	106	0.15 0.82	0.00	0.41	0.18	100 89	61 92	62 92	0 11	39 8	38 8
ENSG00000236255 ENSG00000272432				0.96 -0.68	0.97 -0.67	081	0.00	0.00	0.00	23	94 31	89 51	77	69	11 49
ENSG00000270022 ENSG00000269044	RNU12 CTC-429P9.3	RNU12 RNA, U12 small nuclear	Nucleus other	0.93	0.86 0.85	0.97	0.00	0.00	0.00 0.43	29 100	94 100	84 70	11 0	6	16 30
ENSG000000269913 ENSG000000260404	NA RP11-384K6.6	LOC729218 uncharacterized LOC729218	Other other	1.11 0.81	0.49 0.93	0.22	0.00	0.70	0.26	89 97	67 97	73	11 3	33 3	27
ENSG000000269958 ENSG000000255933	RP11-49519.5			0.76 0.92	0.66 1.11	0.29 0.58	0.00	0.00	0.03	97 29	97 97	86 78	3 11	3	14 22
ENSG00000228107 ENSG00000230590	AP000692.9 FTX	FTX Transcript, XST regulator (non-protein coding)	Other other	0.90 0.75	0.87 0.46	0.30	0.00	0.00	0.09	100 97	89 83	76	0 3	11 17	24
ENSG000000257151 ENSG000000249614	PWAR6 RP11-703G6.1	PWAR6 Prader Willi/Angelman region RNA 6	Other other	0.79	0.80	0.69	0.00	0.00	0.00	91 94	92	86	9	8	14
ENSG00000270195 ENSG00000273142	RP11-458F8.4			1.02 0.85	0.89 0.72	0.72	0.00	0.00	0.00	94 91	94 97	84 57	6 9	6 3	16 43
ENSG00000272365 ENSG00000270015	RP11-389C8.3 RP11-54086.6	FAN1 FANCD 2 and FANCI a secciated nuclease 1	Nucleus enzyme	1.22 0.79	0.45	0.18	0.00	0.02	0.72	97 97	97	84	3	3	16
ENSG00000262251 ENSG00000262879	RP11-199F11.2 RP11-156P1.3		-	0.90	0.65 0.36	0.74 0.13	0.00	0.00	000	97 94	92 78	81 59	3	8 22	19 41
ENSG00000265625 ENSG00000272812	RP11-68(3.11 RP5-855021.3			0.84	0.25	0.89	0.00	0.64	0.00	80	69 86	86	11 11	31 14	14
ENSG00000236337 ENSG00000258441	FMR1-IT1 LINC00641	FMR1-IT1 FMR1 intronic transcript 1 UNC00641 long intergenic non-protein coding RNA641	Other other	1.70	1.14	-0.41	0.00	0.00	000	91 100	86 72	14	9	14	86
ENSG00000231560 ENSG00000223473	AC0918143 GS1-12485.3	LOC400002 uncharacterized LOC400002	Other other	0.86	114	0.63	0.00	0.00	0.01	94 94	94 86	76	6	6	24
ENSG00000237943 ENSG00000225975	PRKCQ-AS1 AC074138.3	PRIXCO_AS1 PRIXCO antisense RNA 1 UNC01534 long intergenic non-protein coding RNA 1534	Other other	0.79	0.54 1.03	-1.37	0.00	0.00	000	100 94	94 97	0	0	6	100
ENSG00000268568 ENSG0000020087	AC007228.9 SNORA738	SNORA738 small nucleolar RNA, H/ACA box 738	Other other	0.91	137 103	0.78 0.62	0.00	0.00	0.00	94 86 66	83 81	89 73	14 34	17 19	11 27
ENSG00000270108 ENSG00000242853		SNORA738 small nucleotae RNA, H _i ACA box 738 RNDS:7499	Other other	0.88	0.70 -0.66	034 014	0.00	0.00	059 059	86 26	81 81 22	65 54	34 14 74	19 19 78	27 35 46
ENSG00000242853 ENSG00000225880 ENSG00000252464	RN75L749P LINC00115 RN75XP70	LINC00115 long intergenic non-protein coding RNA115	Other other Other other	0.88	-0.66 0.85	1.06	0.00	0.00	0.59	91	97 81	97 65	74 9 14	78 3 19	3
ENSG000000207445	SNORD158	RN7SK970 RNA, 7SK small nuclear pseudogene 70 SNORD158 small nucleolar RNA, C/D box 158	Other other	1.39 2.18	1.05	0.79	0.00	0.00		86 89	75		11	22	35
ENSG00000264087 ENSG00000264673	CTC-429P9.2 RN7SL15P	RN75.15P	Other other	0.97 1.27	100 213	109	0.00	0.00	0.00	97 83	92 94	68 84	3 17	6	32 16
ENSG00000224078 ENSG00000267798	SNHG 14 NA	SNHG 14	Other other	1.08	0.72 1.41	-0.46 0.82	0.00	0.00	000	97 89	97 97	8 95	3 11	3	92 5
ENSG00000269688 ENSG00000252010	AC008982.2 SCARNA5	SCARNAS small Cajal body-specific RNAS	Other other	0.77	1.28 1.14	0.74	0.00	0.00	0.00	94 74	94 81	89	6 26	6 19	11
ENSG00000243015 ENSG00000265802	RN75L737P RN75L49P	RNTSL737P RNTSL48P	Other other Other other	1.34 1.74	102		0.00	0.02		91 91	78		9	22	
ENSG000000260257 ENSG000000252481	RPS-1085F17.3 SCARNA13	SCARNA13 small Cajal body-specific RNA13	Other other	0.67 1.54	0.65	-0.02	0.00	0.00	0.02	91 86	89	43	9 11	11	57
ENSG00000272799 ENSG00000264608	RP11-474N24.6 RP11-192H23.8			1.08 1.10	0.60 0.66	0.36	0.00	0.30	014	97 91	72 75	65	3 9	28 25	35
ENSG00000272947 ENSG000000271862	RP11-71H17.9 RP11-343L5.2			0.84 0.83	0.12 0.75	-0.41 0.02	0.00	0.16	0.00 0.17	94 97	58 81	27 51	6 3	42 19	73 49
ENSG00000262652 ENSG00000223768	LINC00205	LINC00205 long intergenic non-protein coding RNA 205	Other other	0.97 0.91	135	1.17	0.00	0.00	0.00	20 20	92	84	11 11	8	16
ENSG00000223525		RABGAP1L-IT1RABGAP1L intronic transcript 1 INE1 inactivation escape 1 (non-protein coding)	Other other	0.87 0.70	0.49 0.86	0.59 0.69	0.00	0.04	000	83 94	72 97	81 84	17 6	28 3	19 16
ENSG00000224975 ENSG00000268027	NE1 AC006129.2			0.68	0.16	-0.80	0.00	0.48	0.00	100	69	3	0	31	97

ENSG00000259821	₩11-468£2.5			1.03	0.89		0.00	0.00		91	81		9	19	
ENSG00000232300 ENSG00000235314	FAM2158 UNC00957	FAM2158 family with sequence similarity 215 member 8 (non-prot UNC00957 long intergenic non-protein coding RNA957	Other other	0.69	0.66	0.42	0.00	0.00	0.00	86 100	83 22	92	14 0	17	8 97
ENSG00000263202 ENSG0000026321	SNORDED	LINCOUSS / Tong intergence non-process coming NAA-957	Cour deser	-0.68 0.78	-0.85	0.60	0.00	0.00	000	31 86	17 89	81 76	60 14	83 11	19
ENSG00000269898 ENSG00000245164	NA SNHG8 LINCOO861	SNHS8 small nucleolar RNA host gene 8	Other other	0.53	0.32	-0.12 -1.52	0.00	0.37	000	100	86 36	41	0	14	59 97
ENSG00000245954 ENSG00000246898		UNC00861 long intergenic non-protein coding RNA861 LOC100996286uncharacterized LOC100996286	Other other	0.71	-0.26 -0.16	-2.00 -1.81	0.00	0.00	000	94	42 39	5	6	58	95
ENSG00000188185	LINC00265	UNC00920 long intergenic non-protein coding RNA 920 UNC00265 long intergenic non-protein coding RNA 265	Other other	0.63	0.66	1.02	0.00	0.00	0.00	91 97	97	97	3	61 3	3
ENSG00000262074 ENSG00000272382	SNORD38-2 CTD-2085E11.4	SNORD38-2 small nucleolar RNA, C/D box 38-2	Other other	-0.72 0.89	-0.99	0.64	0.00	0.00	0.00	31 91	22	89	9	78	11
ENSG00000259834 ENSG00000269063	NA NA			0.63	0.72	-1.40 0.55	0.00	0.00	0.00	94 91	22 89	0 73	9	78 11	100 27
ENSG00000273156 ENSG00000259880				0.80	0.62	0.44	0.00	0.14	0.00	83 86	92	84	17 14	53 8	16
ENSG00000273284 ENSG00000202538	RP11-888D10.4 RNU4-2	RNU4-2 RNA, U4 small nuclear 2	Other other	0.74 1.40	1.06 1.13	0.62 0.27	0.00	0.00	0.00	83 69	94 69	78 54	17 31	6 31	22 46
ENSG00000265206 ENSG00000263164	MIR142 RP11-333E1.2	mir-142 microRNA 142	Cytoplasm nicroRNA	0.68	1.05 0.46	147	0.00	0.00	0.00	83 80	86 75	89	17 20	14 25	11
ENSG00000261716 ENSG00000273353	RP11-196G18.22 CTA-268H5.12			1.09	0.35	-0.03	0.00	0.05	000	97 86	83	49	3 14	17	51
ENSG00000226029 ENSG00000262194	RP4798A10.2 CTD-319515.5	LINC01772	Other other	0.66	-0.14 1.12	-0.73 0.99	0.00	0.00	000	97 89	39 89	3 89	3 11	61 11	97 11
ENSG000000254911 ENSG000000267904	SCARNA9 CTC-429P9.5	SCARNA9 small Cajal body-specific RNA9	Other other	0.72 0.54	0.70	0.95 0.26	0.00	0.97	0.00 0.26	77 94	69 81	95 68	23 6	31 19	5 32
ENSG00000268471 ENSG00000267834	MIR4453 RP11-167N5.5			0.67 0.74	0.85	0.74	0.00	0.00	0.00	97 94	83	84	3 6	17	16
ENSG00000270083 ENSG00000232164	RP1-257020.14 AC092669.3	LINC01873 long intergenic non-protein coding RNA1873	Other other	0.59 0.58	1.18 0.54	0.60 0.42	0.00	0.00	0.00	86 91	97 78	78 78	14 9	3 22	22 22
ENSG00000268544 ENSG00000231125	NA AF129075.5			0.65	0.55	-1.23	0.00	0.00	0.00	94 80	92	0	6 20	8	100
ENSG000000272065 ENSG000000225528	U91328.20 RP3-370M22.8			0.69	0.34 1.30	0.07	0.00	0.97	0.23	83 80	69 100	51	17 20	31 0	49
ENSG00000267098 ENSG00000233016	NA SNHG7	SNHG7 small nucleolar RNA host gene 7	Other other	0.69	154 050	104 056	0.00	0.00	000	89 100	94 97	92 100	11 0	6 3	8
ENSG00000249731 ENSG00000264442	RP11-25902.3 NA			0.57 1.19	0.55 1.21	0.55 1.48	0.00	0.00	0.00	86 89	89 83	89 92	14 11	11 17	11 8
ENSG00000269952 ENSG00000273437	RP11-32422.3 RP11-434H6.7			1.06 1.04	1.47 0.74	0.31 -0.90	0.00	0.00	0.60	77 80	86 64	62 27	23 20	14 36	38 73
ENSG00000232686 ENSG00000267074	NA RP11-1094M14.5			0.70	0.89	0.01	0.00	0.00	0.12	80 74	86 89	51	20 26	14 11	49
ENSG00000270012 ENSG00000166770	LL0XNCD1-793.1 ZNF667-AS1	P9P1R3F protein phosphatase 1 regulatory subunit 3F ZNF667-AS1 ZNF667 antisense RNA1 (head to head)	Other other	0.55	0.15 1.40	-0.10 0.48	0.00	0.31	0.00	97 100	67 97	35 84	3	33	65 16
ENSG00000226328 ENSG00000234663	NUPSO-AS1 AC104820.2	NUPSOASI DUPSO antisense RNA I (head to head) UNC01984 long intergenic non-protein coding RNA 1984	Other other Other other	0.52	0.46	0.33	0.00	0.08	0.26	94 97	83	73	6	17	27
ENSG00000234663 ENSG00000233411 ENSG00000272777	RP11-104L21.2 RP11-571L19.8		June Other	1.09	0.10	-0.36	0.00	0.97	0.00	97 80 86	58	22	20	42	78
ENSG00000272777 ENSG00000239569 ENSG00000263607	RP11-571L19.8 KMT2E-AS1 NA	KMT2E-AS1 KMT2E antisense RNA1 (head to head)	Other other	0.62 0.54 0.78	0.10 0.47 1.31	0.93	0.00	0.48	000	86 86	78 86	97	14 14 14	42 22 14	3
ENSG00000244625 ENSG00000257410	NA CTA-211A9.5 RP11-2H8.2	MIATNB MIAT neighbor (non-protein coding)	Other other	0.78 0.54 0.59	-0.06 0.06	-0.36	0.01	0.00	000	97 89	86 44 56	11 16	3 11	14 56 44	89 84
ENSG00000260808	CTD-2007L18.5			0.62	1.05	-0.52	0.01	0.79	400	89	56 86	16	11	14	34
ENSG00000271927 ENSG00000269867				0.53	0.74		0.01	0.01		20	81		11	19	
ENSG00000213971 ENSG00000237989	AP001046.5	UNC01679 long intergenic non-protein coding RNA1679	Other other	0.57 0.53	0.71	0.52 -0.34	0.01	0.41	000	91 80	97 58	89 19	9 20	3 42	11 81
ENSG00000208772 ENSG00000272098	SNORD94 CTC 365E16.1	SNORD94 small nucleiclar RNA, C/D box 94	Other other	0.86	0.19		0.01	0.44		66 29	72		26 11	28	_
ENSG00000269940 ENSG00000256582	RP11-73M18.7 RP11-75L1.1			0.63	0.74 0.50	0.48 -0.43	0.02	0.02	0.00	77 94	83 92	78 19	23 6	17 8	22 81
ENSG00000214298 ENSG00000212443	APTR SNORAS3	APTR Alto-mediated CD KN1A/p21 transcriptional regulator (nor SNORA53 small nucleolar RNA, H/ACA box 53	Other other	0.59	0.51 1.09	036 083	0.02 0.08	0.02	020 015	91 71	97 67	81 62	9 29	3 33	19 38
ENSG00000178440 ENSG000000227403	LINC00843 AC009299.3	UNC00843 long intergenic non-protein coding RNA 843 UNC01806 long intergenic non-protein coding RNA 1806	Other other Other other	0.54 0.53	0.73	0.59 -0.70	0.08	0.01	0.07	83 94	78 58	76 11	17 6	22 42	24 89
ENSG00000272054 ENSG00000257499	RP11-423P10.2 NA	CEBP2 CCAAT/enhancer binding protein zeta	Nucleus iption regulator	0.51 0.63	0.85 0.84		0.04	0.00		80 86	86 94		20 14	6	
ENSG00000230732 ENSG00000269246	AC127904.2 CTC-246818.10			0.61	0.49 0.16	035 010	0.04	0.00	0.02 0.18	69 71	72 53	68 57	31 29	28 44	32 43
ENSG00000272933 ENSG00000271856	RP11-47A8.5 LINC01215	LINC01215 long intergenic non-protein coding RNA1215	Other other	-0.27 -0.25	-1.06 -0.87	0.08 0.09	0.00	0.00	0.26 0.24	31. 23	3	54 62	69 77	97 100	46 38
ENSG00000270069 ENSG00000229645	M R222HG NA	M R222HG	Other other	0.15	-1.47 -0.80	2.27 0.27	0.08	0.00	0.00	60	0	97 76	40	100 100	3 24
ENSG00000265150 ENSG00000266088	NA RP5-10281/7.2			0.13 -0.40	-0.59 -1.25	0.28 -0.77	0.07	0.00	0.64	54 17	25 3	59 8	46 83	75 97	41 92
ENSG00000238121 ENSG00000260979	LINC00426 RP11-77H9.8	UNC00426 long intergenic non-protein coding RNA426	Other other	-0.42 -0.44	-0.86 -0.90	-0.29 0.13	0.00	0.00	0.00	20 20	3 6	30 62	80 80	97 94	70 38
ENSG00000272005 ENSG00000268573	RP11-91J19.4 RP11-158H5.7	ZSCANBO zinc finger and SCAN domain containing 30	Other other	-0.46	-0.76 -0.70	-1.22 -1.12	0.01	0.00	0.00	60 14	11 6	3	40 86	89 94	97 97
ENSG00000267440 ENSG00000272091	CTC-501010.1 RP4-758124.5			-023	2.01	-1.13	0.00	0.00	0.00	14	100		86	0 94	100
ENSG00000261662 ENSG00000268855	RPS-104288.7 AC006129.1			-0.36 0.26	-0.81 -0.72	001	0.00	0.00	0.20	26 57	3 22	51 54	74 43	97	49
ENSG00000233721 ENSG00000272449	RP11-20516.1	LOC105376276	Other other	0.04	2.06	0.25	0.00	0.00	0.41	54	100	68	46	0 81	32
ENSG00000268947 ENSG00000235728	A0000684.2 AC007349.5				182 2.14		0.00	0.00	442		97 94		_	3	_
ENSG00000247134 ENSG00000272384	RP11-11N9.4 RP11-44N11.2			-0.47	-0.79	-0.44	0.00	0.00	0.00	40	11	32	60	89	68
ENSG00000272384 ENSG00000245060 ENSG00000272871	LINC00847	LINC00847 long intergenic non-protein coding RNA 847	Other other	-035	-0.51	0.12	0.00	0.00	0.45	11	6	59	89	94	41
ENSG00000272871 ENSG00000232233 ENSG00000229807	RP11-573015.2		Other other	-0.30	-0.76 1.23	036	0.00	0.00	0.27	20	97	68	80	86 3	32 16
ENSG00000249667	XST LINCO1259	XST X inactive specific transcript (non-protein coding) UNC01259 long intergenic non-protein coding RNA1259	Nucleus other Other other	0.48	0.52 -0.97	-2.00	0.00	0.00	000	54 71	75 11	49 5	17 29	3 89	95
ENSG00000267519 ENSG00000273344	PACIP1-AS1	PAXIP1-AS1 PAXIP1 antisense RNA 1 (head to head)	Other other	-031 002	0.70 -0.50	2.60 -0.29	0.00	0.00	000	34 54	89 17	100 14	66 46	11 83	0 86
ENSG00000262663 ENSG00000260260	RP11-497H17.1 SNHG19	SNHG19 small nucleolar RNA host gene 19	Other other	0.38	2.01 0.73	-0.36	0.97	0.00	0.00	77	78 100	14	23	0	86
ENSG00000267002 ENSG00000260868	RP11-34208.1 RP11-521/2.3			0.28	0.95 1.32	0.23	0.74	0.00	0.62	71	97 78	68	29	3 22	32
ENSG00000272583 ENSG00000271359	RP11-84C13.1			-050 -050	-0.97 -0.61	-1.01 -0.06	0.00	0.00 0.00	0.00	29 17	22 19	14 49	71 83	78 81	86 51
ENSG000000267143 ENSG000000232545	RP11-67704-6 KB-31888.7			0.39	0.95 1.45	0.43	0.08	0.00	0.01	74	86 83	78	26	14 17	22
ENSG000000264352 ENSG000000203620	RN75L6029 RP11-84A19.2	RN7SL6029 RNA, 7SL, cytoplasmic 602, pseudogene	Other other	0.63	1.27 0.71	0.67	0.17	0.00 0.00	0.01	74	86 92	78	26	14 8	22
ENSG00000238035 ENSG00000245532	AC138085.2 NEAT1			0.37	0.77 0.71	193	0.01	0.00	0.00	- 60	92 81	97	31	8 19	3
ENSG00000272556 ENSG00000251194	RP11-6388.1 RP1-68018.2	GTF 2IP13 general transcription factor III pseudogene 13	Other other	0.22	1.16 0.86	0.79	0.83	0.00	0.00	60	83 89	81	40	17 11	19
ENSG00000263874 ENSG00000258199	LINC00672 RP11-977G19.5	UNC00672 long intergenic non-protein coding RNA 672	Other other	0.56	0.76 0.88	-0.09 0.42	0.06 0.05	0.00	000	83 86	92 89	43 70	17 14	8	57 30
ENSG00000269899 ENSG00000244357	CTD-3222019.12 RN7SL145P	RN75L145P	Other other	0.47	0.73 1.42		0.08	0.00		91	94 81		9	6 17	
ENSG00000264756 ENSG00000262380	NA.			0.73	132 112	0.63	0.08	0.00	0.01	77	86 81	76	23	14 19	24
ENSG00000206612 ENSG00000231865	SNORAZA SIKS-IT1	SNORAZA small nucleolar RNA, H/ACA box 2A	Other other		179 059			0.00			81 83			17	-
ENSG00000270640 ENSG00000226067		UNC00623 long intergenic non-protein coding RNA623	Other other	-0.14 -0.34	0.91	1.48 -1.10	0.04	0.00	000	43 31	78 28	95 16	57 60	72	5 84
ENSG00000226091 ENSG00000269925	LINC00937 RP3-467L1.6	UNC00987 long intergenic non-protein coding RNA937	Other other	0.05	080	103	0.04	0.00	000	54 77	78 78	97 78	46 23	22	3 22
ENSG00000262758 ENSG00000232956	CTD-3195/5.1 SNHG15	SNHG15 small nucleolar RNA host gene 15	Other other	0.39	0.62 0.61	021	0.37	0.00	Q54 Q00	86 77	89 100	70 100	14 23	11 0	30 0
ENSG00000212607 ENSG00000231611	SNORA458 AP006216.11	SNORASB small nucleolar RNA, H/ACA box 38	Other other	0.39	136 065	0.38	0.29	0.00	0.12	91	75 97	78	9	19 3	22
ENSG00000245694 ENSG00000239868		LOC1 01 92 74 80 unch ar act or ked LOC 10 19 27 48 0 RN7 SL34 P	Other other		0.83 0.92	0.81 0.69	0.23	0.00	000 001		97 86 81	78 84 76		14 19	16 24
ENSG00000239868 ENSG00000232098 ENSG00000260023			ores other	0.46	0.61	0.19 -0.12	0.04	0.00	0.01 0.72	80 66	81 86 89	76 59 46	20 34	19 14 11	24 41 54
ENSG000000256092	MIR8072			0.51	0.62	0.38	0.11	0.00	0.02	86	86	81	14	14	19
ENSG00000254676 ENSG00000261061	RP11-308E16.2			0.24	0.55	-0.08 0.62	0.98	0.01	0.01	57	83 83	49 81	48	17	51 19
ENSG00000264469 ENSG00000259623	RP11-173M1.8 RP11-15666.1	KLHL11 kelch like family member 11	Other other	0.42	0.70 0.56	0.72 -0.22	0.10 0.52	0.01	000	83	83 92	95 22	37 17	17 8	78
ENSG00000243745 ENSG00000248360	NA LINCO0504	UNC00504	Other other	0.43	0.78 0.51	0.97 0.62	0.04	0.01	000	91	81 86	73 86	9	19 14	27 14
ENSG00000261468 ENSG00000223692	DP2A-IT1	DIP2A-IT1 DIP2A intronic transcript 1	Other other	0.44	0.58 0.70	-0.81 -0.35	0.08 0.31	0.01	0.00 0.01	94 60	92 78	0 43	6 40	8 22	100 57
ENSG000000245556 ENSG000000248323	SCAMP1-AS1 LUCAT1	SCAMP1-AS1 SCAMP1 antisense RNA1 LUCAT1 lung cancer associated transcript 1 (non-protein coding)	Other other	0.26	0.51	-0.37 2.43	0.73	0.02	000	83	97	100	17	3	92 0
ENSG00000241657 ENSG00000247774	TRBV11-2 PCED18-AS1	TRBV11-2 T cell receptor beta variable 11-2 PCED 18-AS1 PCED18 antisense RNA 1	Other other Other other	0.20	-0.08 0.27	-2.20 -1.48	0.29 0.58	0.01	000	71 29	44 78	0	29 11	56 22	100 100
ENSG00000271109 ENSG000000260822	GS1-35898.4	LOC102723540uncharacterized LOC102723540	Other other	0.51	0.43 -0.38	-1.38 -1.28	0.06 0.01	0.00	000	94 57	94 22	0	6 43	6 78	100 100
ENSG00000175061 ENSG00000273448	RP11-5407.18	L RRC75A-AS1 LRRC75A antisense RNA 1	Other other	-0.09	-0.16	-0.56 2.38	0.00	0.00	000	34	31	100	66	69	100
ENSG000000261888 ENSG000000260066	AC144831.1 RP11-690019.3			0.21	-0.23	2.04 -1.12	0.16	0.00	000	74	28	97 0	26	72	3 100
ENSG00000235999	NA.			-0.33	-0.49	-1.19	0.00	0.00	0.00	20	17	0	80	83	100

							_								
ENSG00000241014		LOC653160 uncharacterized LOC653160	Other other	0.46	0.18	-1.19	0.12	0.79	0.00	86	75	0	14	25	100
ENSG000000226380	MIR2981					133			0.00			100			0
ENSG00000273148 ENSG00000182165	RP5-1068E13.7 TP53TG1	TPS3TG1 TPS3 target 1 (non-protein coding)	Other other	-0.22	-0.22 -0.36	-1.01 -0.90	0.00	0.00	0.00	51 31	22	0	49 69	78 78	100 100
ENSG00000182168	AC007278.3	ing in a supple of the confidence of the confide	Coner coner	-0.22	-0.36	2.27	0.00	4.00	0.00	31	22	95	as	/8	5
ENSG00000231133	HAR1B	HAR1B highly accelerated region 18 (non-protein coding)	Other other	0.38	0.38	-1.89	0.30	0.25	0.00	80	78	3	20	22	97
ENSG000000247556	OIPS-AS1	CIPS-AS1 OIPS antikense RNA 1	Other other	0.21	-0.38	-0.77	0.08	0.00	0.00	71	14	0	29	86	100
ENSG000000260940				0.13	-0.31	-1.17	0.01	0.00	0.00	54	36	3	46	64	97
ENSG00000245937 ENSG00000235437	LINC01184 LINC01278	UNC01184 long intergenic non-protein coding RNA 1184 UNC01278 long intergenic non-protein coding RNA 1278	Other other	-0.13 0.14	-0.45 0.00	-0.91 -0.83	0.00	0.00	000	31 77	8 50	3	60 23	92 50	97 97
ENSG00000255437		LINCUI 278 long intergenic non-protein coding RNA 1278	Other other	0.38	0.23	-0.83 -0.91	0.13	0.65	0.00	91	64	3	9	36	97
ENSG00000251230	RP11-701P16.5	MIRS945HG MIR3945 hox gene	Other other			193	0.00		0.00		-	100			0
ENSG00000232324	AC008440.10			1		2.80			0.00	l		97			3
ENSG000000258929				1		1.46			0.00	l		100			0
ENSG000000270846				1		1.40			0.00			95			5
ENSG00000259976 ENSG00000264290	RP11-553L6.5 RP11-68B.4	mir-568 microRNA 568	Cytoplasm nicroRNA	0.47	0.04	-0.92 1.81	0.05	0.10	0.00	80	58	3	20	42	97
ENSG00000264290		LOC101928343uncharacterized LOC101928343	Other other	1		118			0.00	l		95 97			5 3
ENSG00000267350		COCTOS ELECTRICAL METER COCCO ESTADOS	COMP CENTER	-0.04	-0.44	-0.68	0.00	0.00	0.00	43	11	3	57	89	97
ENSG000000268713	CTC-444N24.8			-0.41	-0.16	-0.70	0.00	0.00	0.00	17	33	3	83	67	97
ENSG000000263941	RN75L32P	RN7SL32P RNA, 7SL, cytoplasmic 32, pseudogene	Other other	0.12	0.50	1.40	0.08	0.05	0.00	51	72	97	49	28	3
ENSG000000260805	RP11-61J19.5					131			0.00			97			3
ENSG00000257742 ENSG00000273008	RP11-350F4.2 RP11-351D16.3			0.35	-0.12	-0.72 130	0.72	0.00	0.00	91	33	95	9	67	100 S
ENSG00000273008				0.25	0.05	-1.01	1.00	0.21	0.00	74	56	95	26	44	92
ENSG00000255135				-0.30	0.08	-1.08	0.00	0.22	0.00	29	61	3	71	39	97
ENSG000000261026	CTD-3247F14.2	LOC286058 uncharacterized LOC286058	Other other	1		1.22			0.00	l		97			3
ENSG00000175701	LINC00116	UNC00116 long intergenic non-protein coding RNA116	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 ENSG00000272899		LOC100130705uncharacterized LOC100130705	Other other	-0.25	-0.04	-0.98 1.36	0.00	0.00	000	34	42	100	66	58	95 0
ENSG00000270101	NA NA	The state of the s	July dive	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
ENSG000000260563				0.06	-0.26	-0.66	0.00	0.00	0.00	51	25	11	49	75	89
ENSG00000248476	BACH1-IT1			1		156			0.00	l		95	l		5
ENSG00000271020		INCOMEN In a large of the large	Other		0.22	2.29			0.00		0.5	84	_	_	16
ENSG00000269220 ENSG00000273356	LINC00528 RP11-804H8.6	LINCOD528 long intergenic non-protein coding RNA 528	Other other	-0.17 -0.39	-0.50	0.86 1.03	0.00	0.75	0.00	37 34	94 17	100	63 66	83	0
ENSG00000273931	RP5-943/3.2			-0.40	-0.41	-0.95	0.00	0.00	0.00	17	14	5	83	86	95
ENSG000000244567	AC096772.6			-0.33	-0.19	-0.71	0.00	0.00	0.00	20	36	0	80	64	100
ENSG000000204272	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
ENSG000000264885				-0.07	-0.07	-0.65	0.00	0.00	0.00	43	44	0	57	56	100
ENSG00000215417 ENSG000002256950	MIR17HS DANCE	DINCO differentiales consendences and codes and	Other other	-0.04	-0.15	1.09 -0.61	0.00	0.00	0.00	43	39	89	57	61	11 100
ENSG00000273265		DANCR differentiation antagonizing non-protein coding RNA	Coner dener	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
ENSG000000224914	LINC00863	LINCOD863 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
ENSG000000261799		LOC283357 uncharacterized LOC283357	Other other	0.25	0.11	-0.62	0.89	0.22	0.00	74	56	5	26	44	95
ENSG000000260817	RP11-4883.4			-0.08	-0.08	-0.66	0.01	0.00	0.00	46	50 58	8	54 20	50 42	92 92
ENSG000000255328 ENSG000000253948		0.0106.0386666	Other other	0.62	-0.20	-0.76 -1.06	0.06	0.44	000	80 54	42	8 11	20 46	42 58	92
ENSG00000170846	AC098323.3	LOC93622 Morf 4 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
ENSG000000231507	LINC01353	LINCO1353 long intergenic non-protein coding RNA 1353	Other other	1		1.10			0.00	l		100			0
ENSG00000237310		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
ENSG000000259863	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 ENSG00000267521	RP11-166P13.3 RP11-87624.6			-0.02	-0.06	-0.88 1.40	0.11	0.03	0.00	46	42	97	54	58	97
ENSG00000230555				-0.16	-0.13	-0.76	0.00	0.00	0.00	40	33	5	60	67	95
ENSG000000229152	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
ENSG000000264456	8911-84891.2			1		0.98			0.00			95			5
ENSG00000237772	AC092620.3			-0.31		1.02	0.00		0.00	34		95	66		5
ENSG00000260997 ENSG00000273456	RP4-647121.1 RP11-68606.2	LOC285957 uncharacterized LOC285957	Other other	-0.46	-0.06	0.83	0.00	0.00	0.00	17 49	44 50	100	83 51	56 50	0
ENSG00000273450				0.38	-0.04	-0.83	0.00	0.00	000	80	47	14	20	53	84 86
ENSG00000273245				0.48	0.31	-0.98	0.20	0.97	0.00	77	72	14	23	28	86
ENSG000000272565				-0.12	0.22	0.67	0.00	0.70	0.00	46	64	100	54	36	0
ENSG000000224959	AC017002.2			1		1.22			0.00			84	l		16
ENSG000000273038			04	0.32	0.09	0.58	0.13	0.06	0.00	83	56	92	17	44	8
ENSG00000207501 ENSG000000257613	RNVUI-14 RP11-32097.1	RNVUI-14 RNA, variant UI small nuclear 14 UNC01481 long intergenic non-protein coding RNA 1481	Other other Other other	-0.33 0.27	-0.46 -0.26	-0.70	0.16	0.00	000	49 83	39 33	97 22	51 17	61 67	3 78
ENSG00000224376	AC017104.6	ARMC9 armadillo repeat containing 9	Cytoplasm other	427	-2.20	0.73	3.73	200	0.00	-		97	. "	37	3
ENSG00000241732	RP11-38P22.2			1		0.74			0.00	l		76	l		24
ENSG00000198106	SN029P2			-0.13	0.14	0.59	0.00	0.08	0.00	43	56	97	57	44	3
ENSG00000269951	No. 22-12 Inches			-0.08	0.07	0.61	0.00	0.01	0.00	43	58	100	57	42	0
ENSG00000226644 ENSG00000273272				1		160 161			0.00	l		86 97	l		14 3
ENSG00000273160				0.39	0.03	-1.11	0.41	0.42	0.00	71	50	14	29	47	86
ENSG00000271855	RP11-214N9.1			1	0.39	0.94		0.99	0.00		64	92		36	8
ENSG00000199568	RNUSA-1	RNUSA-1 RNA, USA small nuclear 1	Other other	1		2.61			0.00	l		78	l		11
ENSG000000223336	RNU2-6P	RNU2-6P RNA, U2 small nuclear 6, pseudogene	Other other	-0.19	-0.16	116	0.08	0.01	0.00	46	42	86	54	58	14
ENSG000000251580		LOC105374366	Other other	0.36	0.30	-1.08	0.73	0.86	0.00	66	67	19	34	33	81
ENSG00000273175 ENSG00000272716				-0.34	-0.45 0.24	-0.69 -0.77	0.00	0.00	0.00	26 54	67	22 11	74 46	86 33	78 89
ENSG00000269653	U62631.5				244	1.02	3.00		0.00		-	84	ı ~		16
ENSG00000273117				-0.08	0.15	0.69	0.00	0.24	0.00	43	67	89	57	33	11
ENSG000000207205		RNVUI-15 RNA, variant U1 small nuclear 15	Other other	1		2.27			0.00			73	l .		24
ENSG00000237892		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 ENSG00000236901		LOC105373098uncharacterized LOC105373098	Other other	1		0.82			0.00	l		84 84	l		16 16
ENSG00000234901		M R181A1HG MIR181A1 host gene	Other other	1		0.64			0.00	l		95	l		16 5
ENSG00000223401			June deller	1		126			0.00	l		78	l		22
ENSG00000229801	NA.			1		137			0.00	l		70	l		30
ENSG00000235908		RHOA-IT1	Other other	1		0.83			0.00			81	l		19
ENSG00000269930				0.27	0.00	0.73	0.18	0.01	0.00	60	50	84	31	50	16
ENSG00000269919 ENSG00000230138				1		0.96 0.70			0.00	l		76 81	l		24 19
ENSG00000230138 ENSG00000178977		UNC00324 long intergenic non-protein coding RNA324	Other other	-035	-0.45	0.70	0.00	0.00	000	29	28	81 81	71	72	19
ENSG00000197813				-0.02	-0.37	0.65	0.02	0.00	0.00	43	25	84	57	75	16
ENSG000000212456	NA.			0.51		1.01	0.43		0.00	60		76	40		24
ENSG00000235621		LINCOD494 long intergenic non-protein coding RNA494	Other other	1		0.61			0.00	I		78			22
ENSG00000263050		8075.2639	Other other	1		0.78			0.00	l		70 70	l		30 30
		THE PARTY AND ADDRESS OF THE PARTY AND ADDRESS	June Coner	1		485				ı		70			
ENSG00000240160 ENSG00000271914				0.16	0.14	056	0.29	0.51	0.04	60	58	73	40	42	27

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

				CD4+ v	s PBMC Re	esults							CD8+	vs PBMC Re	sults			
EnsemblGeneIds	GeneNames	logFC	logCPM	LR	Pvalue	FDR	MedianLogF	PercentDown	PercentUp	GeneNames	logFC	logCPM	LR .	Pvalue	FDR	MedianLogF	PercentDow	PercentUp
ENSG00000186815	TPCN1	0.57010976	4.62939163	74.3038222	6.70E-18	3 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	88.888889	11.1111111

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

				CD4+ v	s PBMC Re	sults							CD8+	vs PBMC Re	sults			
EnsemblGeneIds	GeneNames	logFC	logCPM	LR	Pvalue	FDR	MedianLogF	PercentDowr F	PercentUp	GeneNames	logFC	logCPM	LR	Pvalue	FDR	MedianLogF	PercentDown	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	5.5555556	94.444444
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	88.888889
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	30.555556	69.444444
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	97.222222
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	19.444444	80.555556
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	5.5555556	94.444444
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	97.222222
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	19.444444	80.555556

Genes Regulated in the same direction

				CD4+ v	vs PBMC R	esults						CD8+ v	vs PBMC Re	sults			
EnsemblGeneIds	GeneNames	logFC	logCPM	LR	Pvalue	FDR	MedianLogI	(PercentDowr PercentU	GeneNames	logFC	logCPM	LR	Pvalue	FDR	MedianLogF(PercentDowr	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	7 100	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	O 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	3 100	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	O TYROBP	-5.4830473	6.40434251	4341.5325	0	0	-5.6377018	100	0
ENSG00000019582	CD74	-4.0674413	10.4900897	3421.96946		0	0 -3.9721209	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	7 100	O TNFRSF1B	-1.9938727	7.65750881	741.113528	3.43E-163	4.71E-162	-1.9490992	97.222222	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	3 100	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	7 100	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	7 100	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	3 100	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	7 0 1	OO 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	2 100	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	3 100	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	3 100	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	7 100	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	5 100	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		0	0 -3.2729629	100	0 LGALS1	-3.1910265 5.98850798 1759.57402	0		-3.1096589	100	0
ENSG00000100292	HMOX1	-4.4713384 6.12084599		0	0 -4.3607943	100	0 HMOX1	-5.2236728 6.02370924 3974.91278	0		-5.1881408	100	0
ENSG00000100300	TSPO	-2.6696029 5.31473511		0	0 -2.5349352	100	0 TSPO	-2.9768844 5.27205723 1559.52331	0	0	-2.876872	100	0
ENSG00000100453	GZMB		2629.4526	0	0 -4.2741169	100	0 GZMB	-1.1585836 4.65493712 205.520107	1.30E-46				33.333333
ENSG00000100721	TCL1A	-6.2386888 1.79107689		0	0 -6.6974113	100	0 TCL1A	-4.6699522 1.71312441 1148.53693	9.33E-252		-4.6772239	100	0
ENSG00000101057	MYBL2	-3.7489304 4.16475426		0	0 -3.7838832	100	0 MYBL2	-2.5216153 4.15879847 916.138883	3.04E-201	4.95E-200		100	0
ENSG00000101160	CTSZ	-3.8854383 5.4100884		0	0 -3.8345332	100	0 CTSZ	-4.5957576 5.36617891 3189.69175	0		-4.6039543	100	0
ENSG00000101439	CST3		3597.0651	0	0 -4.1577047	100	0 CST3	-5.9255497 6.45520371 4751.42114	0		-5.9188171	100	0
ENSG00000101916	TLR8	-4.9050554 2.93122585		0	0 -4.8742291	100	0 TLR8	-6.7963648 2.99022251 2805.71476	0		-7.4129336	100	0
ENSG00000102007	PLP2	-2.6004319 5.66872403		0	0 -2.5815503	100	O PLP2	-2.2303805 5.71948365 977.727154	1.25E-214	2.15E-213		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		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		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		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		0	0 -3.985042	100	0 CD86	-5.7699358 5.0008114 4145.07808	0		-5.7378972	100	0
ENSG00000114450	GNB4	-4.2930321 3.40478661		0	0 -4.3340417	100	0 GNB4	-4.6338661 3.34035585 2049.73477	0		-4.6105721	100	0
ENSG00000115956	PLEK	-4.4850637 7.41051439		0	0 -4.1760174	100	O PLEK	-4.5996848 7.38692731 3247.43509	0		-4.4555316	100	0
ENSG00000116574	RHOU	-3.5262315 3.71159908		0	0 -3.4924518	100	0 RHOU	-4.2286718 3.677791 1992.43631	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		-5.6990073	100	0
ENSG00000117984	CTSD	-3.2659199 6.86956962		0	0 -3.1165516	100	0 CTSD	-3.3843619 6.89557164 2011.54122	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		-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		-6.3013252	100	0
ENSG00000121064	SCPEP1	-2.7970259 5.05460727		0	0 -2.6636559	100	0 SCPEP1	-2.6583607 5.10980842 1263.89857	7.92E-277		-2.6441696	100	0
ENSG00000121316	PLBD1	-5.1415 4.38021023		0	0 -5.1578093	100	0 PLBD1	-6.6949804 4.38820476 4336.56378	0		-7.132773	100	0
ENSG00000121552	CSTA	-4.5014977 3.97310946		0	0 -4.3862561	100	0 CSTA	-6.2854952 3.9236133 3598.2967	0		-6.4205715	100	0
ENSG00000123384	LRP1	-3.5861052 6.13377226		0	0 -3.4592486	100	0 LRP1	-4.7606223 6.07473281 3466.91478	0		-4.8453366	100	0
ENSG00000123689	GOS2	-4.7230788 7.60976584		0	0 -4.523553	100	0 G0S2	-6.5951731 7.5769061 5479.35349	0		-6.4538761	100	0
ENSG00000124145	SDC4	-3.5780521 3.33245925		0	0 -3.4834844	100	0 SDC4	-4.446691 3.293692 1829.18484	0		-4.6774305	100	0
ENSG00000125124	BBS2	2.70633163 4.90608514		0	0 2.84860099	0	100 BBS2	2.11941558 4.36532413 743.770031	-		2.00849502	0	100
ENSG00000125124	CFP	-2.6422581 5.30559208		0	0 -2.4464092	100	0 CFP	-3.9929189 5.21702656 2508.46346	0		-4.041528	100	0
ENSG00000127951	FGL2	-4.2533832 3.55065954		0	0 -4.0769357	100	0 FGL2	-5.4843786 3.67146127 2693.72755	0	0	-5.68742	100	0
ENSG00000127331	APOBEC3A	-4.5759645 4.96229936		0	0 -4.4872246	100	0 APOBEC3A	-6.123336 5.00833119 4088.85064	0	•	-6.3316709	100	ŏ
ENSG00000128383	PVRL2	-4.2700222 2.7037846		0	0 -4.4337513	100	0 PVRL2	-4.4602951 2.69182628 1551.26305	0		-4.5346694	100	ŏ
ENSG00000130202	LILRB2	-4.1071422 4.64725311		0	0 -4.0961087	100	O LILRB2	-5.8479082 4.59525897 3878.5205	0		-6.2199775	100	ŏ
ENSG00000131042	NAPSB	-4.1071422 4.64725311 -4.1320035 4.35578943		0	0 -4.0961087	100	O NAPSB	-5.4185456 4.31733953 3280.89062	0		-5.8285116	100	ŏ
ENSG00000131401	IL13RA1	-5.2358507 2.96592344		0	0 -5.2653224	100	0 IL13RA1	-5.5120323 2.92065457 2200.66929	0		-5.4985559	100	Ö
ENSG00000131724 ENSG00000133789	SWAP70	-2.9287854 5.63547599		0	0 -5.2653224	100	0 SWAP70	-3.1041637 5.53955202 1737.36081	0		-3.1247569	100	ď
	CD36	-2.9287854 5.63547599 -4.6546919 3.34816666		0	0 -4.4822188	100	0 CD36	-6.1043124 3.3110364 2637.52181	0		-6.7019896	100	ď
ENSG00000135218	CD36	-4.0346919 3.34816666	2207.24809	U	U -4.4822188	100	U CD36	-0.1045124 5.5110304 2037.52181	U	U	-0.7019896	100	U

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ENSG00000135363	LMO2	-4.3034024 3.49			0		-4.2270263	10		0 LMO2			3722 2920.66736	0		-6.2398194	100	0
ENSG00000135404	CD63 HLX	-3.710913 6.3			0		-3.6541088		00	0 CD63 0 HLX			5715 2137.96573	0		-3.5118053	100 100	0
ENSG00000136630		-4.8188179 3.10			0		-5.0653685			O TLR4			3994 2601.71477	0		-6.4449701		0
ENSG00000136869	TLR4 RAB20	-4.5468911 5.09			0		-4.2847766 -4.4828008		00	0 TLR4 0 RAB 20			5008 4588.98334	0	0	-6.5991547	100 100	0
ENSG00000139832	JDP2	-4.5410996 4.3				_					-6.0348653				0	-6.1375889		0
ENSG00000140044		-4.6957113 4.3			0					O JDP2			5683 3964.78114	0		-6.3668952	100	0
ENSG00000140379	BCL2A1	-2.6155408 5.			0	0	-2.524805		00	0 BCL2A1			5097 2013.32183	-	0	-3.4843256	100	0
ENSG00000141574	SECTM1	-3.1720754 3.9			0		-2.9480053		00	0 SECTM1			0923 2263.79546	0	0	-4.7872442	100	0
ENSG00000142512	SIGLEC10	-4.8460797 2.7			0		-4.8649128		00	0 SIGLEC10			9634 1569.46223	0	0	-4.5979935	100	0
ENSG 00000143878	RHOB	-3.1248683 5.70			0		-2.9596921		00	O RHOB	-1.7914263					-1.8542063	100	0
ENSG 00000146072	TNFRSF21	-3.4311061 4.8			0		-3.3542981		00	0 TNFRSF21			3596 1736.80512	0	0	-3.337885	100	0
ENSG00000150457	LATS2	-3.9673838 4.1			0		-4.0761419		00	0 LATS2			0458 609.701335			-1.7118199	100	0
ENSG00000151948	GLT1D1	-4.1516001 2.50			0		-3.9761135		00	0 GLT1D1			5394 2078.48718	0		-6.0596101	100	0
ENSG 00000153064	BANK1	-6.2344267 4.0			0		-6.0891458		00	0 BANK1			1075 2496.76828	0		-4.8597245	100	0
ENSG00000155130	NA	-4.5370806 6.7			0	0	-4.275207		00	0 NA			9124 4676.32351	0	0	-5.6417652	100	0
ENSG 00000155465	SLC7A7	-4.5777241 5.1			0		-4.4587986			0 SLC7A7			3996 4362.00789	0	0	-6.0295355	100	0
ENSG 00000155629	PIK3AP1	-4.2955145 4.9			0		-4.3706362		00	0 PIK3AP1			2797 515.519611			-1.4783289	100	0
ENSG00000156966	B3GNT7	-6.229367 4.20			0		-6.4960281		00	0 B3GNT7			9025 467.359128		1.16E-102	-1.666821	100	0
ENSG00000158457	TSPAN33	-5.2511245 5.3			0		-4.9956841		00	0 TSPAN33			3409 2580.74704	0		-4.0086914	100	0
ENSG 00000158825	CDA	-4.7225288 2.4			0		-4.6582444		00	O CDA			3584 2145.01813	0		-7.1451154	100	0
ENSG 00000158869	FCER1G	-4.4265612 5.0			0	0	-4.386564		00	0 FCER1G			1667 3815.02085	0		-5.2714181	100	0
ENSG 00000160991	ORAI2	-2.7667837 5.7			0		-2.6962876		00	O ORAI2			5287 650.351093			-1.8599992	100	0
ENSG00000161921	CXCL16	-2.9322946 6.69			0		-2.8026268		00	0 CXCL16			3421 1716.32735	0		-2.9332992	100	0
ENSG00000162444	RBP7	-4.8182409 1.8			0		-5.1065461		00	O RBP7			1425 1694.30445	0		-7.0055165	100	0
ENSG00000162734	PEA15	-3.1037953 5.0			0		-2.9820459		00	0 PEA15			9432 1328.9523		1.33E-289	-2.7475084	100	0
ENSG00000163131	CTSS	-3.3384352 7.79			0		-3.0549498		00	0 CTSS			1924 1894.9666	0		-3.2445121	100	0
ENSG00000163220	S100A9	-5.2609068 7.8			0		-5.1143898		00	0 S100A9			3382 5723.50158	0	0	-6.961067	100	0
ENSG00000163221	S100A12	-4.6669755 4.03			0		-4.5329815			0 S100A12			7229 3757.85917	0	0	-6.8865052	100	0
ENSG00000163534	FCRL1	-6.4069375 4.03			0		-6.4200116		00	0 FCRL1			7202 2038.86582	0		-4.1447586	100	0
ENSG 00000163563	MNDA	-4.9346449 3.4			0		-5.2535766		00	0 MNDA	-6.6341862			0		-7.3056619	100	0
ENSG 00000163694	RBM47	-4.2312358 4.0			0		-4.1906169		00	0 RBM47			2075 3474.57273	0	0	-6.1003861	100	0
ENSG 00000163823	CCR1	-5.1013947 5.1			0		-5.0616303			0 CCR1			5574 5048.40711	0	0	-7.0237088	100	0
ENSG00000165025	SYK	-4.6700227 4.8			0		-4.7161266		00	O SYK			9155 3393.50589	0	0 005 224	-5.102915	100	0
ENSG00000165030	NFIL3	-2.9975548 5.2			0		-2.7267562		00	0 NFIL3			7596 1057.81801			-2.39954	100	0
ENSG00000165140	FBP1	-3.6362522 3.0			0	0	-3.6435342		00	0 FBP1 0 CYBB			1025 2316.48463	0		-4.9879741	100	0
ENSG00000165168	CYBB	-4.9418555 5.13				•	-4.822201		00				3115 4068.74403	2 745 272	0 005 274	-5.6231666	100	0
ENSG00000165178 ENSG00000168081	NCF1C PNOC	-4.454762 1.99 -5.4574685 1.			0		-4.4446965 -5.7777662		00 00	0 NCF1C 0 PNOC			7677 1242.3928 5612 996.135003			-4.6724053 -4.9725571	100 100	0
					0		-4.9947255			0 RAB31				1.246-216				0
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ENSG00000168792	CLIC4	-4.6166447 5.7			0		-4.5519935		00	0 CLIC4			1043 3205.31023	1.02E-200		-4.5563744	100	0
ENSG00000169896	ITGAM	-4.4614764 5.2			0				00	0 ITGAM			7307 631.365039			-1.8354157	100	0
ENSG00000170458	CD14	-4.9072307 6.1		4192.7027	0		-4.6540953		00	0 CD14			1645 5168.7963	2.526-159		-6.4163477	100	0
ENSG00000170458 ENSG00000170866	NA	-4.6281127 3.2		1903.0959	0		-4.1360599			0 NA			0776 2558.10137	0				2.7777778
ENSG00000170866 ENSG00000171051	FPR1	-4.9727281 4.8			0		-5.1731573		00	O FPR1			3572 4671.29197	0		-6.9020934	100	2.7777770
ENSG00000171031	CXXC5	-4.6931696 5.89			0		-4.6660803		00	0 CXXC5			3985 2375.58207	0		-3.7073177	100	0
ENSG00000171804 ENSG00000171777	RASGRP4	-3.9658681 2.79			0		-3.8670802		00	0 RASGRP4			5652 2203.07069	0	0	-6.4780324	100	0
ENSG00000171777 ENSG00000173801	JUP	-3.0894523 4.10			0		-2.9985034		00	0 JUP			1328 1293.69589		5.93E-282	-3.0934293	100	0
ENSG00000173801	LRRC25	-5.0026983 4.6		3806.2395	0		-4.9979925		00	0 LRRC25			7854 4573.56913	2.03E-203 0		-6.8162167	100	Ö
ENSG00000175489	B3GNT5	-4.1996043 4.74			0		-4.1906971		00	0 B3GNT5			5327 3280.80576	0	0	-5.052696	100	0
ENSG00000178397	CD300LB	-4.1996043 4.74 -4.3045277 3.68			0		-4.1900971		00	0 CD300LB			2519 3060.92754	0	0	-6.1993766	100	0
ENSG00000178789	HLA-DQB1	-5.1114991 6.14			0	0	-4.2512094		00	0 HLA-DQB1			1636 3126.66109	0	0	-0.1993766 -4.5864298	100	0
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ENSG00000211660 GLV2-23 -7.9262171 2.11906667 2655.94997 0 0 -10000 100 0 GLV2-23 -6.3981224 2.1052319 1865.71409 0 0 -7.3963739 100 0 ENSG00000211663 GLV3-21 -7.6684607 2.67390184 3174.50302 0 0 -8.4822508 100 0 GLV3-21 -7.8204071 2.60897605 2688.66119 0 0 -8.2486336 100 0 ENSG00000211666 GLV2-14 -7.2007245 4.04068092 4963.54486 0 0 -7.6063428 100 0 GLV3-19 -6.3592337 2.25537278 2015.99837 0 0 -6.4975539 100 0 ENSG00000211666 GLV2-14 -7.2007245 4.04068092 4963.54486 0 0 -7.6063428 100 0 GLV2-14 -5.2100288 3.9609076 2887.90183 0 0 -5.2635439 100 0 ENSG00000211667 NA -7.4972125 1.9621919 2429.46159 0 0 -8.4113698 100 0 MA -6.4324792 1.93796475 1780.31501 0 0 -7.0029139 100 0 ENSG00000211677 GLC2 -7.0431384 4.32542491 4494.379 0 0 -7.037561 88.5714286 0 GLC2 -5.9386209 4.32532541 3191.8797 0 0 -5.733966 88.8888899 0 ENSG00000211897 GLC3 -7.1685688 4.24413216 5295.49761 0 0 -7.3145422 100 0 GLC2 -5.9386209 4.31371028 3556.7416 0 0 -5.7877776 100 0 ENSG0000211897 GHG3 -7.4735869 6.14713091 7098.54057 0 0 -7.8913194 100 0 GHG3 -7.6488646 3.18045998 3131.62586 0 0 -8.2522484 100 0 ENSG00000211897 GHG3 -6.6286815 3.48991934 3542.85329 0 0 -7.4379156 100 0 GHG3 -5.6930083 3.38071425 253.65755 0 0 -5.8251971 100 0 ENSG00000211899 GHM -7.2272283 318422588 807.21577 0 0 -7.2375308 100 0 GHM -4.8605318 9.1065279 3315.06488 0 0 -5.9831704 100 0 ENSG0000211893 GHW-1 -7.0621975 0.7814254 1551.38484 0 0 -7.2001668 100 0 GHW-1 -5.5931368 0.70075339 93.696857 4.21E-218 7.42E-217 5.7782628 100 0 ENSG0000211934 GHV-2 -7.5490701 2.7459310 234.06116 0 0 -7.9001168 100 0 GHW-2 -5.590155 2.67335719	ENSG00000211651	IGLV1-44	-8.0529669	2.11356698	2720.83174	0	0 -8.629	1364	100	0 IGLV1-44	-5.7030936	2.06941245 1	.647.97895	0	0	-6.3592425	100	0
ENSG00000211662 GLV3-21 -7.6086407 2.67390184 3174.50302 0 0 -8.4822508 100 0 GLV3-21 -7.8204071 2.60897606 2688.66119 0 0 -8.2486336 100 0 ENSG00000211666 GLV3-19 -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 ENSG00000211668 IGLV2-14 -7.2007245 4.04068092 4963.54486 0 0 -7.6063428 100 0 IGLV2-14 -5.2100288 3.9609076 2887.09183 0 0 -5.2836339 100 0 ENSG00000211668 IGLV2-11 -7.3655404 2.34383318 2744.43095 0 0 -8.0841068 100 0 IGLV2-14 -5.5879455 2.244158 1714.23486 0 0 -5.4880337 100 0 ENSG00000211671 NA -7.4972125 1.96219219 2429.6159 0 0 -8.48113698 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 2.9658498 2733.47539 0 0 -7.2301266 100 0 ENSG00000211679 IGLC2 -7.0431384 4.32542491 4494.379 0 0 -7.037561 88.5714286 0 IGLC2 -5.938609 4.32532541 3191.8797 0 0 -5.733966 88.888889 0 ENSG00000211897 IGLC3 -7.1685688 4.24413216 5295.49761 0 0 -7.3145422 100 0 IGLG3 -5.8976029 4.13771028 3556.7416 0 0 -5.7877776 100 0 ENSG00000211897 IGHG1 -7.4753869 6.14713091 7098.54057 0 0 -7.8921394 100 0 IGHG2 -7.6488646 3.18045998 3131.62586 0 0 -8.2522484 100 0 ENSG00000211898 IGHG1 -7.4753869 6.14713091 7098.54057 0 0 -7.2175308 100 0 IGHD -4.580132 6.42967996 3341.01718 0 0 -4.6051084 100 0 ENSG00000211898 IGHM -7.2272283 9.18422568 8072.31217 0 0 -7.22759073 100 0 IGHW -4.580132 6.42967996 3341.01718 0 0 -4.6051084 100 0 ENSG00000211934 IGHW -7.6261975 0 -7.5490701 2.74592174 3523.6016 0 0 -7.0901168 100 0 IGHW -7.599155 2.5735579 2.57.07555 0 0 -5.	ENSG00000211653	IGLV1-40	-6.9691907	2.54905941	2910.04971	0	0 -7.653	8457	100	0 IGLV1-40	-5.5560822	2.46399373 1	905.26285	0	0	-5.7815477	100	0
ENSGO0000211665 GLV3-19 -7.5634089 2.37407184 2910.43336 0 0 -8.4182559 100 0 GLV3-19 -6.3592337 2.25537278 2015.99837 0 0 -6.4975539 100 0 ENSGO00002116666 GLV2-14 -7.2007245 4.04068092 4963.54486 0 0 -7.6063428 100 0 GLV2-14 -5.2100288 3.96090776 2887.09183 0 0 -5.2635439 100 0 ENSGO0000211671 NA -7.4972125 1.96219219 2429.46159 0 0 -8.0841068 100 0 GLV2-14 -5.5879455 2.244186 0 0 -7.0029139 100 0 ENSGO0000211673 GLV2-1 -7.2897996 3.0536284 3490.24964 0 0 -7.8095481 100 0 GLV2-1 -6.8335602 2.96058498 2733.47539 0 0 -7.2301266 100 0 ENSGO0000211677 GLC2 -7.0431384 4.32542491 4494.379 0 0 -7.037561 88.5714286 0 GLC2 -5.9386209 4.32532541 3191.8797 0 0 -5.733966 88.8888889 0 ENSGO0000211893 GHG2 -7.7087566 3.31020407 3796.16706 0 0 -7.8095849 100 0 GHG2 -7.6488646 3.18045998 3131.62586 0 0 -7.8095828 100 0 ENSGO0000211898 GHG1 -7.4753869 6.14713091 7098.54057 0 0 -7.839136 100 0 GHG3 -5.6930083 3.38071425 2532.65755 0 0 -5.8251971 100 0 ENSGO0000211898 GHG1 -7.0867255 6.46670146 7328.22957 0 0 -7.2375308 100 0 GHG1 -7.489738 6.049670527 3341.0718 0 0 -5.8251971 100 0 ENSG00000211898 GHM -7.2272283 9.18422568 807.31217 0 0 -7.2579073 100 0 GHM -4.8605318 9.100535719 2157.07954 0 0 -5.9831704 100 0 ENSG00000211934 GHV1-2 -7.5490701 2.7459174 3234.06116 0 0 -7.9001168 100 0 GHV1-2 -5.910515 2.67335719 2157.07954 0 0 -5.9831704 100 0 ENSG00000211934 GHV1-2 -7.5490701 2.7459174 3234.06116 0 0 -7.9001168 100 0 GHV1-2 -5.910515 2.67335719 2157.07954 0 0 -5.9831704 100 0 ENSG00000211934 GHV1-2 -7.5490701 2.7459174 3234.06116 0 0 -7.9001168 100 0 GHV1-2 -5.910515 2.67335719 2157.07954 0 0 -5.9831704 100 0 ENSG00000211934	ENSG00000211660	IGLV2-23	-7.9262171	2.11906667	2655.94997	0	0 -1	0000	100	0 IGLV2-23	-6.3981224	2.1052319 1	.865.71409	0	0	-7.3963739	100	0
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ENSG00000211671	ENSG00000211663	IGLV3-19	-7.5634089	2.37407184	2910.43336	0	0 -8.418	2559	100	0 IGLV3-19	-6.3592337	2.25537278 2	015.99837	0	0	-6.4975539	100	0
ENSG0000211671 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 ENSG0000211673 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 ENSG0000211677 IGLC2 -7.0431384 4.32542491 4494.379 0 0 0 -7.037561 88.5714286 0 IGLC2 -5.9386209 4.32532541 3191.8797 0 0 -5.733966 88.8888889 0 ENSG0000211679 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 -7.0787566 3.31020407 3796.16706 0 0 -7.8921394 100 0 IGHG2 -7.6488646 3.18045998 3131.62586 0 0 -8.2522484 100 0 ENSG00000211899 IGHG1 -7.4753869 6.14713091 7098.54057 0 0 -7.8921394 100 0 IGHG1 -7.4179873 6.04347129 6072.68106 0 0 -5.8921971 100 0 IGHG2 ENSG00000211899 IGHD -7.0867255 6.46670146 7328.22957 0 0 -7.2175308 100 0 IGHD -4.580132 6.42967796 3341.01718 0 0 -4.6851084 100 0 IGHM -4.8605318 9.1005227 3315.06483 0 0 -4.8810891 100 0 IGHM -7.2272283 9.18422568 8072.31217 0 0 -7.2579073 100 0 IGHM -4.8605318 9.1005227 3315.06483 0 0 -4.8810891 100 0 IGHV-1 -7.0621975 0.7814254 1551.38484 0 0 0 -7.0001168 100 0 IGHV1-2 -5.991515 2.67335719 2157.07954 0 0 -5.9831704 100 0 IGHV -5.5931704 100 0 IGHV -5.5931704 100 0 IGHV -5.5931704 100 0 IGHV -5.5931704 IGHV -5.5931704 IGHV -7.5490701 2.74592174 3234.06116 0 0 -7.9001168 100 0 IGHV -5.5910515 2.67335719 2157.07954 0 0 -5.9831704 100 0 IGHV -5.5931704 IGHV -7.5490701 2.74592174 3234.06116 0 0 -7.9001168 100 0 IGHV -5.5931515 2.67335719 2157.07954 0 0 -5.9831704 100 0 IGHV -5.5931704 IGHV -5.	ENSG00000211666	IGLV2-14	-7.2007245	4.04068092	4963.54486	0	0 -7.606	3428	100	0 IGLV2-14	-5.2100288	3.96090776 2	887.09183	0	0	-5.2635439	100	0
ENSG0000211673 GLV3-1 -7.2897996 3.0536284 3490.24964 0 0 -7.8095481 100 0 GLV3-1 -6.8335602 2.96058498 2733.47539 0 0 -7.2301266 100 0 ENSG0000211677 GLC2 -7.0431384 4.32542491 4494.379 0 0 -7.037561 88.5714286 0 GLC2 -5.9386209 4.32532541 3191.8797 0 0 -5.733966 88.8888889 0 ENSG0000211679 GLC3 -7.1685688 4.24413216 5295.49761 0 0 -7.3145422 100 0 GLC3 -5.8976029 4.13771028 3556.7416 0 0 -5.7877776 100 0 ENSG0000211893 GHG2 -7.7087566 3.31020407 3796.16706 0 0 -7.8921394 100 0 GHG2 -7.6488646 3.18045998 3131.62586 0 0 -8.2522484 100 0 ENSG00000211896 GHG1 -7.4753869 6.14713091 7098.54057 0 0 -7.8921394 100 0 GHG1 -7.4179873 6.04347129 6072.68106 0 0 -7.8009828 100 0 ENSG00000211899 GHD -7.0867255 6.46670146 7328.22957 0 0 -7.2175308 100 0 GHHD -4.580132 6.42967796 3341.01718 0 0 -4.6801084 100 0 ENSG00000211893 GHW -7.2272283 9.18422568 8072.31217 0 0 -7.2579073 100 0 GHW -4.8605318 9.10065227 3315.06483 0 0 -4.8810891 100 0 ENSG00000211933 GHV6-1 -7.0621975 0.7814254 1551.38484 0 0 -10000 100 0 GHW -5.5931436 0.70273303 993.696857 4.21E-218 7.42E-217 -5.7782628 100 0 ENSG00000211934 GHV1-2 -7.5490701 2.74592174 3234.06116 0 0 -7.9001168 100 0 GHV1-2 -5.910515 2.67335719 2157.07954 0 0 -5.9831704 100 0 ENSG00000211934 GHV1-2 -7.5490701 2.74592174 3234.06116 0 0 -7.9001168 100 0 GHV1-2 -5.910515 2.67335719 2157.07954 0 0 -5.9831704 100 0 ENSG00000211934 GHV1-2 -7.5490701 2.74592174 3234.06116 0 0 -7.9001168 100 0 GHV1-2 -5.910515 2.67335719 2157.07954 0 0 -5.9831704 100 0 -5.9831704 100 0 -5.9831704 100 0 -5.9831704 100 0 -5.9831704 100 0 -5.9831704 100 0 -5.9831704 10	ENSG00000211668	IGLV2-11	-7.3655404	2.34383318	2744.43095	0	0 -8.084	1068	100	0 IGLV2-11	-5.5879455	2.244158 1	714.23486	0	0	-5.4880337	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 ENSG0000211679 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 ENSG0000211893 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 ENSG0000211896 IGHG1 -7.4753869 6.14713091 7098.54057 0 0 -7.8921394 100 0 IGHG1 -7.4179873 6.04347129 6072.68106 0 0 -7.8098282 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 ENSG00000211899 IGHM -7.2272283 9.18422568 8072.31217 0 0 -7.2579073 100 0 IGHM -4.8605318 9.1005227 3315.06483 0 0 -4.8801891 100 0 ENSG00000211933 IGHV6-1 -7.0621975 0.7814254 1551.38484 0 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 IGHV1-2	ENSG00000211671	NA	-7.4972125	1.96219219	2429.46159	0	0 -8.411	3698	100	0 NA	-6.4324792	1.93796475 1	780.31501	0	0	-7.0029139	100	0
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ENSG0000211896 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 ENSG0000211897 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 IGHD -4.580132 6.42967796 3341.01718 0 0 -4.6051084 100 0 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 IGHM -7.0621975 0.7814254 1551.38484 0 0 0 -7.000000211934 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			-7.7087566	3.31020407	3796.16706	0	0 -9.006	5849	100					0	0	-8.2522484	100	0
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ENSG0000211899 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	ENSG00000211897	IGHG3	-6.6286815	3.48991934	3542.85329	0	0 -7.437	9156	100	0 IGHG3	-5.6930083	3.38071425 2	532.65755	0	0	-5.8251971	100	0
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ENSGO0000240671 [KKV1-8] -7.3081332 0.76396608 IS87.15677 0 0 -8.1017741 100 0 KKV1-18] -5.3688837 0.71628703 956.385062 5.48E-210 9.26E-209 5.4787013 100 0 KKV1-200024084 KKV2-24] -7.7383575 1.30792025 R16.4053 0 0 -10000 100 0 KKV1-16] -5.604137 1.02003845 1108.98806 3.68E-243 7.04E-242 5.810118 100 0 KKV2-24] -7.7383575 1.30792025 R16.4053 0 0 -10000 100 0 KKV2-24] -6.429788 1.23648152 1275.08313 3.00E-279 6.68E-273 6.9567322 100 0 KKV2-24] -7.7383575 1.30792025 R16.4053 0 0 -10000 100 0 KKV2-24] -6.429788 1.23648152 1275.08313 3.00E-279 6.68E-278 6.9567322 100 0 KKV1-10 -7.4202088 3.43020924 R18.584928 0 0 -8.0842643 100 0 KKV2-24] -6.429788 1.23648152 1275.08313 3.00E-279 6.68E-278 6.9567322 100 0 KKV1-10 -7.4202088 3.43020924 R18.584928 0 0 -8.0842643 100 0 KKV1-15 -5.4126452 3.34083081 2504.444499 0 0 -3.2411737 100 0 KKV1-16 -7.6311309 3.28833214 A058.53015 0 0 -8.5913765 100 0 KKV1-15 -6.2787887 3.22528274 R18.9747 0 0 -3.241173 100 0 KKV1-15 -6.2787887 3.22528274 R18.9747 0 0 -6.5964442 100 0 KKV1-15 -7.116868 1.42633608 2007.3855 0 0 -8.0054371 100 0 KKV1-15 -5.3209004 2.25892108 R16.93266 0 0 -5.5515555 100 0 KKV1-15 -6.583603 3.3402094 R18.4042444 5.555555 100 0 KKV1-27 -5.1456024 1.35755904 1156.44989 1.78E-253 3.55E-252 5.411938 100 0 KKV1-27 -5.1456024 1.35755904 1156.44989 1.78E-253 3.55E-252 5.411938 100 0 KKV1-27 -5.1456024 1.35755904 1.564989 1.78E-253 3.55E-252 5.411938 100 0 KKV1-27 5.601566 2.6863608 2.978-138449 5.786000000000000000000000000000000000000		LILRA2				0	0	-4.7159109	10)	0 LILRA2				0	0	-7.2440622	100	0
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ENSG00000243466 GKV1-5	ENSG00000241351	IG KV3-11	-7.4202088	3.43020924	4185.84928	0	0	-8.0842643	10)	0 IGKV3-11	-5.4126452	3.34083081 2504	44499	0	0	-5.3827155	100	0
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ENSGO0000244734 HBB	ENSG00000244437	IGKV3-15	-6.9225786	2.35143725	2699.43982	0	0	-7.7286592	10)	0 IGKV3-15	-5.3209004	2.25892108 1661	.93266	0	0	-5.5515525	100	0
ENSGO0000254709 IGLLS	ENSG00000244575	IG KV1-27	-7.1168868	1.42633608	2007.3855	0	0	-8.0054371	10)	0 IGKV1-27	-5.1456024	1.35755904 1156	.44989	1.78E-253	3.55E-252	-5.411938	100	0
ENSG00000115902 SLC1A4	ENSG00000244734	HBB	-6.6334449	5.78001334	4635.01612	0	0	-6.9452619	10)	O HBB	-5.2346566	5.73725631 2449	.04824	0	0	-5.2299241	94.444444	5.5555556
ENSGO0000119900 OGFRL1	ENSG00000254709	IGLL5	-6.8583023	3.034072	3427.71156	0	0	-7.5120638	10)	0 IGLL5	-5.0601566	2.96356408 2019	.51653	0	0	-4.9420517	100	0
ENSGO000169413 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 ENSGO000172216 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 ENSGO0000161929 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 ENSGO000157851 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 -0.2463676 8.33333333 ENSGO000128245 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 -0.24636473 100 0 ENSGO0000067182 TNFRSF1A -2.4828717 5.30265915 1345.12565 1.77E-294 3.36E-293 -2.5179648 100 0 HBRS 1 -3.4670361 1.91000128 419.727895 2.80E-39 2.43E-92 -4.3203473 86.111111 11.1111111 ENSGO0000211936 NA -6.0464003 1.01075149 1341.09437 1.33E-293 2.51E-292 -6.6609182 100 0 NA -5.0968724 0.87823436 855.42399 4.31E-188 7.36E-187 -5.2168521 100 0 ENSG00000189319 FAM538 -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 94.444444 5.55555556	ENSG00000115902	SLC1A4	-2.8894123	4.09334084	1413.32458	0.00E+00	5.37E-308	-2.8125916	10)	0 SLC1A4	-1.5669356	4.30778784 396.1	52219	3.79E-88	3.17E-87	-1.4219178	97.222222	2.77777778
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 RIPN1 2.76842576 4.22510068 1358.63887 2.04E-297 3.93E-296 2.86587581 0 100 RIPN1 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 91.666667 8.33333333 ENSG00000128245 VWHAH -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 -2.46884717 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 86.111111 11.1111111 11.1111111 11.1111111	ENSG00000119900	OGFRL1	-2.4546942	5.90338473	1403.12549	4.40E-307	8.76E-306	-2.3383725	10)	0 OGFRL1	-1.6442227	6.01110125 561.7	96508	3.42E-124	3.81E-123	-1.6204332	100	0
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ENSG0000158106 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 VWHAH -2.7092628 4.26896879 1354.26493 1.82E-296 3.48E-295 -2.7447072 100 0 VWHAH -2.4019278 4.24839078 905.107551 7.61E-199 1.22E-197 -2.4368473 100 0 ENSG0000026172 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-294 -3.202473 86.1111111 11.1111111 ENSG00000189319 FAM538 -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 94.444444 5.55555556	ENSG00000172216	CEBPB	-2.4362218	6.07465393	1380.21318	4.19E-302	8.22E-301	-2.3236255	10)	O CEBPB	-2.0535036	6.10253802 833.3	883852	2.98E-183	4.47E-182	-2.0060425	100	0
ENSG0000167851 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 91.666667 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 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 86.111111 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 FAM538 -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 5.555555556	ENSG00000161929	SCIMP	-4.1262456	2.15980459	1374.6622	6.74E-301	1.32E-299	-4.1328367	10)	O SCIMP	-4.4571969	2.15095466 1257	25892	2.20E-275	4.78E-274	-4.522873	100	0
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 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 86.111111 11.1111111 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 5.555555556	ENSG00000158106	RHPN1	2.76842576	4.22510068	1358.63887	2.04E-297	3.93E-296	2.86587581) 1	00 RHPN1	2.2085345	3.68282393 654.4	183664	2.37E-144	3.01E-143	2.23372377	0	100
ENSG0000067182 TNFRSF1A	ENSG00000167851	CD300A	-3.301682	3.12542813	1355.39242	1.04E-296	1.98E-295	-3.2163668	10	0	0 CD300A	-0.9328543	3.57288924 121.4	190792	2.98E-28	1.01E-27	-0.9163276	91.6666667	8.33333333
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 86.111111 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 855.42399 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 5.555555556	ENSG00000128245	YWHAH	-2.7092628	4.26896879	1354.26493	1.82E-296	3.48E-295	-2.7447072	10)	0 YWHAH	-2.4019278	4.24839078 905.1	07551	7.61E-199	1.22E-197	-2.4368473	100	0
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-291 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	ENSG00000067182	TNFRSF1A	-2.4828717	5.30265915	1345.12565	1.77E-294	3.36E-293	-2.5179648	10	0	O TNFRSF1A	-2.6960405	5.27169777 1321	.06235	2.99E-289	6.83E-288	-2.7832826	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	ENSG00000206172	HBA1	-6.3638104	1.79888269	1342.05607	8.20E-294	1.55E-292	-8.5101988	10)	0 HBA1	-3.4670361	1.91000128 419.7	27895	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	10	0	0 NA	-5.0968724	0.87823436 855.4	23992	4.81E-188	7.36E-187	-5.2168521	100	0
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	ENSG00000189319	FAM53B	-2.3517318	6.9214198	1335.64766	2.03E-292	3.80E-291	-2.1691075	10)	0 FAM53B	-1.2308409	7.2194044 304.0	27735	4.37E-68	2.92E-67	-1.4493146	94.444444	5.5555556
	ENSG00000165175	MID1IP1	-2.4621918	5.11853096	1331.37286	1.72E-291	3.21E-290	-2.3612766	10)	0 MID1IP1	-2.9936789	4.9863489 1551	.37829	0	0	-3.0042019	100	0

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ENSG 00000205269	TMEM170B	-2.4273385 5.34328524 1322.13276	1.75E-289	3.26E-288 -2.405413		0 TMEM170B	-2.9595139 5.22923835 1562.71537	0		-2.8769353	100	0
ENSG00000163453	IGFBP7	-4.2629084 1.83648017 1321.04348	3.02E-289	5.62E-288 -4.47598		0 IGFBP7	-4.5707734 1.7607928 1151.25932	2.39E-252		-4.5515228	100	0
ENSG00000239855	IGKV1-6 ELF4	-7.8719001 0.25178684 1320.07594	4.90E-289	9.09E-288 -1000 1.14E-287 -2.221998		0 IGKV1-6	-6.8274383 0.13092716 919.779231	4.92E-202	8.06E-201	-10000	100	0
ENSG00000102034 ENSG00000213722	DDAH2	-2.3607764 6.17980689 1319.61724	6.17E-289 9.28E-288	1.14E-287 -2.221998 1.70E-286 -2.936121		0 ELF4 0 DDAH2	-2.2023124 6.20090712 951.100986 -2.9981597 3.59497753 1122.32668	7.65E-209 4.64E-246	1.27E-207 9.00E-245	-2.0353417 -3.0616081	100 100	0
ENSG00000213722	GLIPR2	-2.962895 3.59767157 1314.19828 -2.9098306 3.75908635 1312.38815	2.30E-287			0 GLIPR2		2.67E-187		-2.4925294	100	0
ENSG00000122694 ENSG00000187446	CHP1	-2.3970073 5.33885511 1311.73483	3.18E-287	4.20E-286 -2.750937 5.81E-286 -2.330743		0 CHP1	-2.4899127 3.81516527 852.003062 -1.4494131 5.50127488 428.851659	2.89E-95		-1.4183895	100	0
ENSG00000187446	S100A6	-2.3164217 7.63079463 1311.54318	3.51E-287	6.38E-286 -2.171789		0 S100A6	-2.2813087 7.64610868 1002.05273	6.43E-220	1.14E-218	-2.280579	100	0
ENSG00000197938	QPCT	-3.9994204 2.17839903 1310.3541	6.36E-287	1.15E-285 -3.889185		0 QPCT	-5.2640171 2.15466294 1555.74132	0.45E-220		-5.3239846	100	0
ENSG00000113828	RNF135	-3.4681649 2.73680775 1310.23957	6.73E-287	1.22E-285 -3.313836		0 RNF135	-3.4204126 2.76416183 1065.90955	8.48E-234	1.58E-232		100	0
ENSG00000101481	LYL1	-3.7565714 2.32317326 1306.70561	3.94E-286	7.11E-285 -3.743015		0 LYL1	-4.050482 2.25279276 1165.83967	1.62E-255		-4.2035188	100	0
ENSG0000015475	BID	-2.4652907 4.93431679 1306.0606	5.45E-286	9.78E-285 -2.397097		0 BID	-2.4169828 4.9451666 1058.44253	3.56E-232		-2.4403691	100	0
ENSG00000019169	MARCO	-4.5236498 1.70120997 1290.59652	1.25E-282	2.23E-281 -4.807414		0 MARCO	-6.2522989 1.74065562 1507.75698	0.302-232		-6.9016621	100	0
ENSG00000211974	IGHV2-70	-6.6421222 0.46550883 1290.37821	1.39E-282	2.48E-281 -1000		0 IGHV2-70	-7.1936178 0.39022648 1064.87026	1.43E-233	2.65E-232	-10000	100	0
ENSG00000211974	NA	-5.7400193 1.45845908 1283.25356	4.93E-281			5.71428571 NA	-5.4315017 1.42577465 980.791038	2.69E-215				2.7777778
ENSG00000172322	CLEC12A	-4.3728588 1.91703062 1280.91682	1.59E-280	2.80E-279 -4.078641		0 CLEC12A	-6.2017633 1.86585201 1554.64335	0		-6.3662806	100	0
ENSG00000172522	THEMIS2	-2.3192939 6.29958344 1276.57869	1.39E-279	2.45E-278 -2.22927		0 THEMIS2	-3.304792 6.21772936 1907.49781	0		-3.5465751	100	0
ENSG00000125505	MBOAT7	-2.5688188 4.41565309 1273.33918	7.03E-279	1.24E-277 -2.460614		0 MBOAT7	-2.9855613 4.38389445 1365.77579	5.75E-299		-2.9780413	100	0
ENSG00000158481	CD1C	-4.7000824 1.4943985 1269.66555	4.42E-278	7.75E-277 -4.798286		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 -2.268635	7 100	0 ST6GAL1	-2.4022017 5.78674859 1124.58513	1.50E-246	2.91F-245	-2.5131016	100	0
ENSG00000211950	IGHV1-24	-5.0983366 1.00644822 1267.63747	1.22E-277	2.13E-276 -5.166351		0 IGHV1-24	-5.578538 0.89412687 1066.20773	7.30E-234		-5.6407132	100	0
ENSG00000178719	GRINA	-2.3209554 5.81401763 1266.53272	2.12E-277	3.69E-276 -2.196813	1 100	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 -2.935439		0 FAM43A	-0.6117813 3.82600836 55.7548285	8.21E-14				22.222222
ENSG00000161944	ASGR2	-4.2295929 1.81304772 1263.10459	1.18E-276	2.04E-275 -4.283027	4 100	0 ASGR2	-6.0550993 1.78239754 1575.60882	0		-6.4632258	100	0
ENSG00000158470	B4GALT5	-2.3945377 5.1097461 1259.76389	6.27E-276	1.08E-274 -2.199550		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 -2.073836	5 100	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 -1000	0 100	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 -2.692546	1 100	0 FABP5	-1.2952234 4.34852522 277.789362	2.28E-62	1.38E-61	-1.246255	94.444444	5.5555556
ENSG00000167703	SLC43A2	-2.2682573 6.84026005 1244.19255	1.52E-272	2.59E-271 -2.246994	3 100	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 -2.285957	5 100	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 -3.270620	3 100	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 -2.323243	2 100	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 2.2736224	4 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 -2.169159	2 100	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 -2.994861	4 100	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 -3.373340	6 100	0 SPRY2	-0.7998757 2.9894848 71.9952151	2.16E-17	5.47E-17	-0.6922587	77.777778	22.222222
ENSG00000211976	IGHV3-73	-7.0471396 0.25297677 1225.87804	1.45E-268	2.42E-267 -1000	0 100	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 -2.711080		0 RHOC	-1.9795358 3.74187707 550.453641	1.00E-121		-2.0007932	100	0
ENSG00000163545	NUAK2	-2.2878767 5.67072172 1222.9962	6.13E-268	1.02E-266 -2.19208		0 NUAK2	-2.0144255 5.65508296 810.757938	2.47E-178		-2.0551723	100	0
ENSG00000143870	PDIA6	-2.3207653 5.23284855 1217.46225	9.78E-267	1.61E-265 -2.291327		0 PDIA6	-1.8276837 5.26845512 655.465306	1.45E-144		-1.8352158	100	0
ENSG00000104763	ASAH1	-2.2655539 6.02671129 1217.25435	1.09E-266	1.79E-265 -2.14814		0 ASAH1	-2.4170946 5.98754829 1143.70242	1.05E-250		-2.4803648	100	0
ENSG00000140406	MESDC1	-2.2903436 5.56063203 1208.97718	6.83E-265	1.12E-263 -2.236781		0 MESDC1	-2.3638225 5.47993544 1074.06214	1.43E-235		-2.3386347	100	0
ENSG 00000059377	TBXAS1	-3.1420607 3.07850416 1205.11608	4.71E-264	7.70E-263 -3.138367		0 TBXAS1	-5.158386 2.93473891 2018.17133	0		-5.2350864	100	0
ENSG00000211951	IGHV2-26	-7.3976983 0.01282831 1204.125	7.74E-264	1.26E-262 -1000		0 IGHV2-26	-5.9032877 -0.0416333 801.887017	2.10E-176	3.07E-175	-6.170188	100	0
ENSG 00000033327	GAB 2	-2.217093 6.94668897 1194.2067	1.11E-261	1.79E-260 -2.324092		0 GAB2	-2.0592807 6.94950708 849.633576	8.73E-187		-2.0839094	100	0
ENSG 00000188677	PARVB	-2.7951671 3.55918943 1182.13364	4.66E-259	7.51E-258 -2.672483		0 PARVB	-2.7755275 3.52444209 975.461932	3.87E-214		-2.8220721	100	0
ENSG00000146112	PPP1R18	-2.2355941 6.05610259 1175.90537	1.05E-257	1.69E-256 -2.104350		0 PPP1R18	-2.085121 6.08275539 864.319795	5.60E-190		-2.1005972	100	0
ENSG00000122877	EGR2	-2.5996551 4.14867641 1174.39478	2.24E-257	3.59E-256 -2.31355		0 EGR2	-2.7098479 4.19061595 1031.83164	2.16E-226		-2.8451942	100	0
ENSG00000156273	BACH1	-2.1727404 7.55793362 1171.35945	1.02E-256	1.64E-255 -1.996608		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 -2.105479		0 SNX30	-1.5998246 5.402761 508.755907	1.18E-112				2.7777778
ENSG00000243264	IGKV2D-29	-7.1388625 0.0368816 1160.20537	2.72E-254	4.31E-253 -1000		0 IGKV2D-29	-6.3069466 -0.044887 816.6697	1.28E-179	1.89E-178	-10000	100	0
ENSG00000137166	FOXP4 RHOQ	-2.2403813 5.46512243 1156.13701	2.08E-253	3.29E-252 -2.081980		0 FOXP4 0 RHOQ	-1.7696585 5.48934649 622.857034	1.79E-137		-1.7668045	100 100	0
ENSG00000119729	KHUU	-2.490149 4.19144439 1153.54944	7.59E-253	1.20E-251 -2.455154	2 100	UKHUU	-2.3046217 4.2042 847.709594	2.29E-186	3.45E-185	-2.3290524	100	U

ENSG00000159399	uva	2 2206107 E 86575420 1120 72722	7.675.350	1 205 249 2 10720	26 100	o uva	2 2719105 5 71265152 042 709576	E 10E 207	0 425 206	2.265000	100	ام
ENSG00000159399 ENSG00000127838	HK2 PNKD	-2.2206107 5.86575429 1139.72733 -2.4564459 4.28648146 1129.84175	7.67E-250 1.08E-247	1.20E-248 -2.10730 1.67E-246 -2.32252		0 HK2 0 PNKD	-2.2718195 5.71365152 942.708576 -2.863336 4.30860364 1245.1149	5.10E-207 9.57E-273	8.42E-206 2.07E-271	-2.265009 -2.958291	100 100	0
ENSG00000127838 ENSG00000184730	APOBR	-2.4519414 4.22428035 1124.86532	1.30E-247	2.02E-245 -2.32252		O APOBR	-2.863336 4.30860364 1243.1149	2.26E-138			100	0
ENSG00000184730	IFI6	-2.2606172 5.22508021 1123.51452	2.56E-246	3.96E-245 -2.15067		0 IFI6	-2.2466087 5.33642471 922.600094	1.20E-202		-2.2036148	100	0
ENSG00000126709	FTL	-2.1520899 10.3269411 1121.9873	5.50E-246	8.46E-245 -1.98820		0 FTL	-2.0994724 10.3366723 703.413964	5.41E-155		-2.2036148	100	0
ENSG00000087080	LRRC32	-2.71144 3.60823767 1120.55206	1.13E-245	1.73E-244 -2.60825		O LRRC32	-3.8230522 3.41070577 1566.29857	0.416-133		-3.8428056	100	0
ENSG00000137307 ENSG00000177989	ODF3B	-2.853315 3.33633237 1117.59225	4.96E-245	7.60E-244 -2.83229		0 ODF3B	-3.2654995 3.30124416 1154.71819	4.23E-253		-3.2121088	100	0
		-2.833313 3.33633237 1117.39223	1.44E-244			0 CHSY1		4.23E-233 3.53E-53			100	0
ENSG00000131873 ENSG00000177374	CHSY1 HIC1	-3.3551736 2.48773722 1103.44534	5.89E-242	2.20E-243 -2.24401 8.98E-241 -3.21895		0 HIC1	-1.0633407 5.52131632 235.631917 -2.3214255 2.67132626 493.959747	1.96E-109		-1.0643255 -2.5066914	100	0
												0
ENSG00000179388 ENSG00000186350	EGR3 RXRA	-2.652111 3.92806368 1102.27509 -2.4640786 4.15149936 1098.41554	1.06E-241 7.30E-241	1.61E-240 -2.64784 1.11E-239 -2.40950		2.85714286 EGR 3 0 RXRA	-1.9541431 4.00273288 548.239619 -2.0973826 4.22607851 684.304376	3.04E-121 7.74E-151		-1.9986179 -2.3490876	100 100	0
			1.34E-238			0 TPI1		3.43E-98				0
ENSG00000111669	TPI1	-2.1330086 5.89156095 1087.99974	6.49E-238	2.02E-237 -2.12100 9.73E-237 -100		-	-1.4588107 6.00753063 442.29409 -5.1813725 -0.1524849 616.271849	4.84E-136		-1.3992339	100	0
ENSG00000211638	IGLV8-61	-7.8665403 -0.0546704 1084.84889				0 IGLV8-61 100 GPRASP1		4.64E-136 4.45E-88		-6.1702063	100	100
ENSG00000198932 ENSG00000148834	GPRASP1 GSTO1	2.14596771 6.02392108 1084.69287 -2.3253079 4.48326438 1081.00207	7.01E-238 4.45E-237	1.05E-236 2.241946 6.63E-236 -2.10793		100 GPRASP1 0 GSTO1	1.40458613 5.42372915 395.833786 -2.5225873 4.41606599 1026.28446	4.45E-88 3.48E-225		1.38224891 -2.6155803	_	100
											100	0
ENSG00000104870	FCGRT	-2.1541767 5.73609798 1080.72298	5.11E-237 9.31E-237	7.61E-236 -2.10590		0 FCGRT	-2.9213789 5.59968875 1543.15784	0 9.40E-266		-2.9444996	100	0
ENSG00000143162	CREG1	-2.2941797 4.62406156 1079.52602		1.38E-235 -2.23217		0 CREG1	-2.7187184 4.59574723 1212.93885		1.97E-264	-2.938845	100	0
ENSG00000253276	CCDC71L	-2.6821097 3.50069125 1070.88021	7.05E-235	1.04E-233 -2.55614		0 CCDC71L	-2.4394978 3.51012486 764.920237	2.29E-168		-2.3796054	100	07 2222222
ENSG00000139631	CSAD	2.84393624 3.3651276 1070.71227	7.66E-235	1.13E-233 2.732467			1.80389477 2.46383616 292.955299	1.13E-65				97.222222
ENSG 00000086062	B4GALT1	-2.0489496 7.80166088 1065.34041	1.13E-233	1.65E-232 -1.91877		0 B4GALT1	-0.9078373 8.03607592 171.711559	3.13E-39		-0.9064827	100	0
ENSG00000140105	WARS	-2.1062832 6.14373723 1058.34318	3.74E-232	5.45E-231 -1.97759		0 WARS	-2.0721439 6.24607075 857.236034	1.94E-188		-2.0433954	100	0 2222222
ENSG00000175505	CLCF1	-3.7059396 1.74329151 1057.19503	6.64E-232	9.64E-231 -3.57047		0 CLCF1	-1.4183139 2.13803144 165.008956	9.11E-38				8.33333333
ENSG00000168961	LGALS9	-2.1003445 5.86134805 1056.89798	7.71E-232	1.12E-230 -2.00503		0 LGALS9	-2.4804064 5.76524251 1186.30173	5.79E-260	1.18E-258		100	0
ENSG00000178996	SNX18	-2.1076926 5.7580151 1054.46573		3.76E-230 -2.059679		0 SNX18	-1.969129 5.7576515 770.124377	1.69E-169	2.41E-168		100	0
ENSG00000111729	CLEC4A	-3.2235714 2.44446612 1052.23603	7.95E-231	1.15E-229 -3.05443		0 CLEC4A	-3.8720082 2.37635681 1116.04618	1.07E-244		-3.9826992	100	0
ENSG00000188820	FAM26F	-3.02537 2.92111327 1034.58036	5.47E-227	7.80E-226 -2.92290		0 FAM26F	-3.8292081 2.70508663 1208.38724	9.17E-265		-3.9580507	100	0
ENSG00000171700	RGS19	-2.4535987 3.88841467 1030.63941	3.93E-226	5.59E-225 -2.299530		0 RGS19	-2.4663442 3.90717472 872.703236	8.43E-192		-2.4706224	100	0
ENSG00000114738	MAPKAPK3 PGD	-2.0916255 5.43571073 1021.62644 -2.0921294 5.31661727 1014.26502	3.58E-224 1.42E-222	5.05E-223 -2.01130- 2.00E-221 -2.073359		0 MAPKAPK3 0 PGD	-2.3256966 5.41016242 1027.36401 -1.9564339 5.35470845 745.36441	2.02E-225 4.09E-164		-2.3980493 -2.0954734	100 100	0
ENSG00000142657			1.42E-222 1.86E-222					1.54E-146			100	100
ENSG00000124181	PLCG1	2.01924185 7.1845552 1013.72878 -2.2925749 4.42922373 1013.58623	2.00E-222	2.61E-221 2.067425 2.80E-221 -2.27243		100 PLCG1 0 AOAH	1.80451413 6.95044633 664.53819	1.76E-112		1.69643982		
ENSG00000136250	AOAH						-1.741859 4.50771625 507.963664					
ENSG00000187091	PLCD1 CPPED1	2.13750843 4.87573393 1004.86643 -3.1828923 2.4581609 999.998315	1.57E-220 1.80E-219	2.19E-219 2.242517 2.50E-218 -2.92847		100 PLCD1 0 CPPED1	1.63484761 4.46352717 473.742606 -2.9723066 2.4683745 726.657278	4.91E-105 4.78E-160		1.62825721 -3.0297507	0 100	100
ENSG00000103381 ENSG00000182287	AP1S2	-3.1828923 2.4581609 999.998315 -2.0841235 5.16614631 992.516591	7.60E-219	1.05E-216 -1.92110		0 AP1S2	-2.2006927 5.11270205 909.015532	1.08E-199		-3.0297507	100	0
ENSG00000182287 ENSG00000126247	CAPNS1	-2.0101281 6.36459917 991.371226	1.35E-217	1.87E-216 -1.90810		0 CAPNS1	-1.5247843 6.44768565 484.833799	1.90E-199	1.89E-106		100	0
ENSG00000128247 ENSG00000233429	HOTAIRM1	-2.9895647 2.67911603 984.860785	3.51E-216	4.84E-215 -2.86517		0 HOTAIRM1	-2.4992841 2.85818941 632.018006	1.82E-139	2.24E-138		100	0
ENSG00000233429 ENSG00000187840	EIF4EBP1	-3.2433077 2.16773492 980.588104	2.98E-215	4.09E-214 -3.2254		0 EIF4EBP1	-1.7464183 2.37160456 280.936295	4.69E-63		-1.7265323	100	0
ENSG00000187840	VASP	-2.0285571 6.05107363 976.204968	2.67E-214	3.65E-213 -2.06045		0 VASP	-1.4325717 6.15980346 423.495309	4.03E-03		-1.7203323	100	0
ENSG00000123733	GPX1P1	-3.0444031 2.48300557 974.236395	7.15E-214	9.76E-213 -2.91175		0 GPX1P1	-3.0744585 2.45498552 806.445574	2.14E-177		-3.1405094	100	0
ENSG00000137382 ENSG00000130489	SCO2	-2.5180479 3.57912493 973.683221	9.43E-214	1.28E-212 -2.51716		0 SCO2	-2.7596319 3.63792114 964.9515	7.46E-212		-2.8177685	100	0
ENSG00000130489	LSP1	-1.9617624 7.5489895 973.650057	9.59E-214	1.30E-212 -1.94648		0 LSP1	-1.8542218 7.53680571 685.474407	4.31E-151		-1.9685898	100	0
ENSG00000130332 ENSG00000211829	TRDC	-3.2810002 2.12521624 970.795297	4.00E-213	5.43E-212 -3.29379		0 TRDC	-2.6147249 2.10533236 528.55439	5.83E-117		-2.5697657	100	0
ENSG00000211823	ADAM15	-2.2796821 4.13010545 967.381404	2.21E-212	2.99E-211 -2.16309		0 ADAM15	-2.5952284 4.10135666 984.633763	3.93E-216		-2.4996931	100	0
ENSG00000143337	TPP1	-2.0239284 5.761538 959.634352	1.07E-210	1.43E-209 -1.94585		0 TPP1	-2.173143 5.72822135 908.065566	1.73E-199		-2.2565997	100	0
ENSG00000100340	RP2	-2.0790928 4.80260833 948.919428	2.28E-208	3.02E-207 -2.00001		0 RP2	-1.7157324 4.8448203 556.744598	4.29E-123		-1.7097244	100	o
ENSG00000102218 ENSG00000127947	PTPN12	-2.0790928 4.80260833 946.919428	3.92E-208	5.18E-207 -1.90984		0 PTPN12	-1.2983997 5.29142817 338.218379	1.56E-75		-1.7097244	100	ŏ
ENSG00000127947	SH3BGRL3	-1.9355845 7.48607592 944.809612	1.78E-207	2.35E-206 -1.76855		0 SH3BGRL3	-1.4341318 7.59620077 415.060908	2.90E-92		-1.4380244	100	0
ENSG00000142009 ENSG00000104918	RETN	-4.1949178 0.89922051 938.607134	3.97E-206	5.23E-205 -4.09005		O RETN	-4.8708927 0.94455675 901.442498	4.77E-198		-4.9206544	100	ő
ENSG00000104318	LCP1	-1.9187529 8.75870932 931.666833	1.28E-204	1.67E-203 -1.80573		0 LCP1	-1.599268 8.81425691 480.667614	1.53E-106		-1.5754183	100	ő
ENSG00000130107 ENSG00000189068	VSTM1	-4.5957486 0.81028379 930.732853	2.05E-204	2.67E-203 -4.84278		0 VSTM1	-6.2688302 0.77535257 1018.98731	1.34E-223	2.40E-222	-1.5754165	100	ŏ
ENSG00000185088	CHST10	-2.5806521 3.23225268 927.26491	1.16E-203	1.51E-202 -2.40135		0 CHST10	-0.7800726 3.57061244 88.8408221	4.28E-21			94.444444	5 5555556
ENSG00000115526 ENSG00000085514	PILRA	-2.561171 3.37203302 925.279702	3.14E-203	4.07E-202 -2.51258		0 PILRA	-3.0924011 3.3216625 1044.20299	4.43E-229	8.10E-228	-3.1965185	100	0.5555555
ENSG00000083314	ZYX	-1.9274122 7.16040117 925.123574		4.39E-202 -1.76093		O ZYX	-1.4595304 7.31912514 430.750792	1.12E-95			97.2222222	2 7777778
214355555555555	LIA	2.52/7122 /.1004011/ 525.1255/4	3.33E-203	202 -1.70033.	.5 100	LIN	1555504 7.51512514 450.750792	1.126-93	J.JUL-33	1.7031221	JIILLELLEL	2.7777770

FNC C 000000144570	1011/0.0	6.0700046	0.0000574		C 255 202	0.005.000	40000	400	o Louis	V 2 0	F 04 44 24 4	0.0740476	00 402705	4.075.400	2 275 420	F 6670477	400	
ENSG00000211670	IGLV3-9	-6.3789046 -0			6.36E-203	8.22E-202	-10000	100	0 IGLV			-0.3712476 5		1.97E-130	2.27E-129		100	0
ENSG00000057657	PRDM1	-2.0114874 5.			5.44E-201		-1.8600731	100	0 PRDI			5.20405403 1		1.24E-270	2.62E-269	-2.445149	100	0
ENSG00000170275	CRTAP	-1.9537289 5.			4.19E-200		-1.8242067	100	0 CRTA			5.42647547 1		6.06E-261	1.24E-259		100	0
ENSG00000138166	DUSP5	-1.9236688 6.			7.88E-200			100	0 DUS			6.33248192 6		4.80E-150		-1.8802379	100	0
ENSG00000164733	CTSB			907.387836	2.43E-199		-1.7006972	100	0 CTSE			6.50631878 1		0		-3.4205807	100	0
ENSG00000211445	GPX3	-3.377137 1			3.12E-198		-3.2417037	100	0 GPX			1.7938737 8		5.20E-185	7.83E-184		100	0
ENSG00000111796	KLRB1	-1.9757 5. -4.2854256 0.		900.253101	8.65E-198	1.10E-196	-1.894887	100 97.1428571	0 KLRE 2.85714286 IGHV			5.36283627 4		6.71E-98	6.13E-97	-1.490272	100	0 2222222
ENSG 00000211935 ENSG 00000105639	IGHV1-3 JAK3	1.88980477 7.		897.2417	3.90E-197 7.16E-197		1.87900757	97.1428571	100 JAK3			0.81269804 5 6.69224292 2		1.02E-111 2.09E-65				8.33333333 97.222222
ENSG00000103639	TIMP2	-1.9586807 5.			8.09E-196	1.02E-194	-1.885918	100	0 TIME			5.35106006 7		8.69E-167	1.33E-64 1.22E-165		100	97.222222
ENSG00000033862	KLF11	-1.9386807 5.			1.43E-195		-1.857716	100	0 KLF1			5.5454865 6		6.71E-151	8.74E-150		100	0
ENSG00000172033	AGPAT2	-2.7992967 2.			6.06E-194		-2.6909387	100	0 AGP			2.68682055 5		2.17E-132	2.54E-131		100	0
ENSG00000159128	IFNGR2	-1.9034518 6.			7.22E-194		-1.7875291	100	0 IFNG			5.79608512 1		0		-3.0649072	100	0
ENSG00000153120	LAPTM5	-1.8854842 11			4.32E-193		-1.8275737	100	0 LAPT			10.9266037 6		8.76E-140	1.08E-138		100	o
ENSG00000174125	TLR1	-2.1844517			1.62E-192		-2.1360667	100	O TLR1			3.91416328 1		1.01E-245	1.95E-244		100	0
ENSG00000174123	VOPP1	-1.8722879 6.			1.74E-192		-1.7909889	100	0 VOP			6.86257557		3.73E-162	5.09E-161		100	0
ENSG00000091490	SEL1L3	-1.9467262 5.			2.11E-191		-1.7564424	100	0 SEL1			5.20192248 5		3.50E-129		-1.8454909	100	0
ENSG00000088992	TESC	-2.8528469 2.			7.56E-190		-2.7660779	100	O TESO			2.59455327 3		2.28E-79		-1.9047653	100	0
ENSG00000075426	FOSL2	-1.8367068 8.			1.06E-189		-1.7875945	100	0 FOSI			9.01735702 5		1.03E-12	2.26E-12			8.33333333
ENSG00000213366	GSTM2	2.30701717 3.			6.38E-189		2.14450794	0	100 GSTI				127.74114	1.28E-29				80.555556
ENSG00000169385	RNASE2	-4.9338647 0.			1.64E-188		-5.7341684	100	0 RNA			0.37634242 8		8.53E-195	1.34E-193	-10000	100	0
ENSG00000232216	IGHV3-43	-6.1587434 -0	0.2988754	852.322638	2.27E-187	2.72E-186	-10000	100	0 IGHV	V3-43	-6.2228027	-0.3887244 6	47.714307	7.02E-143	8.85E-142	-10000	100	0
ENSG00000100365	NCF4	-2.737752 2.			2.51E-187		-2.7423353	100	0 NCF4			2.46705636 1		0		-4.6390466	100	0
ENSG00000142409	ZNF787	-2.0866585 4.	.27849102	850.964012	4.49E-187	5.34E-186	-2.113325	100	0 ZNF	787	-1.9909961	4.25726897 6	51.898973	8.63E-144	1.10E-142	-2.0115345	100	0
ENSG 00000244509	APOBEC3C	-2.2399935 3.	.79377967	845.568287	6.68E-186	7.94E-185	-2.1531126	100	0 APO	DBEC3C	-0.9086103	4.11654827 1	37.875429	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 GNG	G5	-1.729705	4.70604493 5	50.262681	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	O ZNF4	467	-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 GAP	PDH	-1.3122152	9.43848203 3	13.310201	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	O PRN	NP.	-1.1248018	7.46393128 2	67.566637	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	ŝ	-2.4643048	3.85635344 8	21.288629	1.27E-180	1.88E-179	-2.5021905	100	0
ENSG 00000108932	SLC16A6	-2.1837695 3.	.81144623	819.634588	2.91E-180	3.35E-179	-2.0869387	100	0 SLC1	16A6	-1.5560208	3.94773835 3	73.002075	4.15E-83	3.26E-82	-1.5768383	100	0
ENSG 00000065882	TBC1D1	-1.8227195 5.	.89520007	818.323313	5.60E-180	6.45E-179	-1.6868041	100	O TBC	C1D1	-1.1902136	5.98828704 3	04.157507	4.09E-68	2.74E-67	-1.2510562	100	0
ENSG 00000148429	USP6NL	-1.9706497 4.	.55988028	817.500907	8.45E-180	9.71E-179	-1.8644625	100	0 USP	P6NL	-1.5557319	4.58815751 4	40.028538	1.07E-97	9.74E-97	-1.5607566	100	0
ENSG00000128203	ASPHD2	-2.6479333 2.			4.11E-178	4.70E-177	-2.6038409	100	0 ASPI		-2.1469339	2.64123886 4		2.18E-102	2.07E-101		100	0
ENSG00000105963	ADAP1	-2.6626957 2.			1.41E-177		-2.5004123	100	0 ADA			2.85436611	248.9586	4.38E-56	2.46E-55			2.7777778
ENSG00000170677	SOCS6	-2.2717678 3.			1.43E-176		-2.2651375	100	0 SOC			3.42825874 9		1.28E-209		-2.7257569	100	0
ENSG 00000169756	LIMS1	-2.0748207 4.			3.97E-176		-2.0375564	100	0 LIMS			4.07901218 6		2.08E-135	2.47E-134		100	0
ENSG00000177105	RHOG	-1.7798743 6.			6.40E-176		-1.7043002	100	0 RHO			6.88548517		6.24E-89		-1.4320135	100	0
ENSG00000140030	GPR65	-2.0419788 4.			5.12E-174		-1.8735856	100	0 GPR				28.895111	1.67E-73		-1.3458771	100	0
ENSG00000196187	TMEM63A	1.8093388 5.			6.04E-174		1.83948455	0	100 TME			5.30345943 2		2.92E-66				97.222222
ENSG00000146540	C7orf50	-1.9760005 4			2.65E-172		-1.7341468	100	0 C7or			4.33260518 5		1.33E-131	1.54E-130		100	0
ENSG00000165527	ARF6	-1.7447768 7.			2.24E-171		-1.6763342	100	0 ARF			7.58222853 3		3.52E-83		-1.3764979	100	0
ENSG00000198833	UBE2J1	-1.7481491 7.			5.35E-171		-1.7201174	100	0 UBE				449.21261	1.07E-99 6.75E-163		-1.4813324	100	0
ENSG00000170296	GABARAP PRAM1	-1.8440591 5. -2.4504186 3			1.19E-170 1.84E-170		-1.6917727	100	0 GAB	BARAP		5.04022477 7 3.04648235 8		6.75E-163 2.02E-181	9.25E-162 3.01E-180		100 100	0
ENSG 00000133246 ENSG 00000130402	ACTN4	-1.7908134 5.			4.55E-169		-2.5011652 -1.7213221	100 100	0 ACTI			5.8199634 9		1.01E-22	3.01E-180 3.01E-22			13.8888889
ENSG00000130402	EMP3	-1.7319678 7			2.28E-168		-1.7213221	100	0 EMP			7.04412734 5		2.59E-130		-1.8087626	100	13.0000009
ENSG00000142227	CD151	-2.2538839 3.			2.54E-168	2.49E-167 2.77E-167	-2.169411	100	0 CD15			3.46887069 4		3.90E-102		-1.8087626	100	0
ENSG00000177697	IGLV9-49	-6.2118837 -0			1.32E-167	1.43E-166	-2.169411	100		V9-49		-0.4869072 6		1.23E-140	1.53E-139	-1.9894034	100	0
ENSG00000223330	KCTD12	-1.8276224 5.			1.83E-166		-1.8774749	100	0 KCTE			4.85604232 1		1.23E-140 0		-3.1314168	100	0
ENSG00000178693	ATP6V1F	-1.7503088 5.			6.38E-165		-1.7880296	100		26V1F		5.87188202 4		3.26E-94		-1.5179587	100	0
ENSG00000128324 ENSG00000074800	ENO1	-1.6997947 8.		748.416519	8.87E-165		-1.5793957	100	0 ENO		-1.4304636	7.9990363 5		1.81E-116		-1.6771766	100	0
ENSG00000074800	PYCARD	-2.6240584 2.			3.48E-164		-2.575912	100	0 PYCA			2.46352963 6		8.16E-138	9.90E-137		100	0
2.1.500000103430	··CAIND	2.0240304 2.	0132303	5.005050	3.70L 104	5.75E 103	2.373312	100	o Pio		2.0727333	2. 70332303 0	L 722732	5.10L 136	3.30E 137	2.3000700	100	3

Seconomic Seco	ENSG00000122862	CDCN	4 7222266	0.27242004	742 024020	0.005.164	0.435.463	1 (210220	100	OCDCN		1 2020510	0.20204202	05 205722	2 225 66	2 145 65	1 2465224	100	al
MSG60000014769 MSF15 1474219 45795727 75679336 278-162 2056142 20101496 0 0 MSF15 1.20104713 45050644 758-01548 2046-1077 27122222 27777777 27122222 278-0156000010120 0 0 0 0 0 0 0 0 0		SRGN				8.80E-164			100	0 SRGN					3.32E-66			100	0
MASSES MARROW APSEL 1,797033 4,00051511 73,795164 ASSEL 10 ASSE															•				07 222222
MAGRODOLISAD MARINE 1.867782 \$729775 7238254 3.86-1.07 \$7.075.000 3.96-1.07																			0
SECONOMICATION ORNER 1.827115 4.865489 73.222446 2.66719 2.76714737 100 ORNER 0.9313179 4.810313157 107.79151 5.01-39 1.48-28 0.9571002 1.267103 1.826390 100 ORNER 0.940171 1.867103 1.867																			97 222222
MSG0000017501 APTILOD APRISSEA 1567/1017 727-38002 4238-159 A18-159 A18-																			0
SASCONDOVINOS ARCIGE 1.7665078 ASSESTED 1.711531 SASCONDOVINOS ASSESTED 1.711531 SASCONDOVINOS ASSESTED ASS																			25
MSG0000005797 MCG																			0
SASSONODISOTA SOMIT 2011/8878 2000S288 70.881144 97.86154 1.99020781 0 100 FMRSONODISOTA 1711/10652 37.181645 57.581541 1.6155002 100 0 6TFF1 1.4617781 3.6080021 431.14149 3.14164 2.99169 5.1515709 100 0 0 0 0 0 0 0 0																			100
INSTOCOMORISSON FIFT 1.16978 3.4769.07 3.476																		•	
BSG00000012570 CORNIC -1.476178 5.3550787 703.4020 5.851-15 5.951-154 -1.615092 100 CORNIC -1.4862472 2.4220698 301-1975 8.615-74 6.01673 2.0103482 700.7007 700.7									_									•	0
MSCO0000129757 CRNIC -2,4671973 270089452 700.070070 2,141-154 2,191-153 2,3550599 100 0 CRNIC -1,000705566 ARAAAS1 -2,7237553 1981.39602 700.14767 2,781-154 2,861-153 2,6670648 100 0 RARAAS1 -2,0007993 2,03113953 336.283025 4,116-75 2,955-74 -1,9467173 100 0 0 0 0 0 0 0 0																			0
NSSCOROUSSESSES PART -1,7812566 471590838 700.39757 2.451-154 2.451-153 2.6516908 100 0.106811 0.7316358 4.9683602 107.662766 3.196-25 0.106-26773 0.106																			2.7777778
RNSCORDOOXSEGS ARRANS1																			0
NSCO000013527 NSF5198 1.88547																			0
INSCORDOUICISAR THE 1.652540 1.65254																			100
RNSCOROOUTZES CHAPPE 1.6527811 S.83116091 605.55889 185-153 187-152 1.5512236 100 0 0 0 0 0 0 0 0																		100	0
MSCO0000104582 Capacita Cap																			0
RNSCO0000019872 PUCA																			o
RNSCO000001085 TPK1		C19orf45				2.24E-152				100 C19orf					3.53E-63			0	100
ENSCORDOOTIONESIZE MAPPENS 1.65574109 6.42477000 6.26486780 6.26477000 6.264770000000 6.264770000 6.264770000 6.2647700000000000000000000000000000000000																		100	0
ENSCORDO00034152 MAPZN3	ENSG00000100605	ITPK1	-1.6965671	5.29653667	689.813624	4.91E-152	4.92E-151	-1.6072058	100	0 ITPK1	ı	-1.027753	5.44505692 2	19.733994	1.03E-49	5.31E-49	-1.088934	97.222222	2.7777778
ENSCO0000138804 MT-CO1 -1-6718649 12-690/177 682-845814 1.61E-150 1.60E-149 -1.556-849 100 0 MT-CO1 -1.0873559 12.8151788 165-786-498 6.1E-38 2.578-37 -1.1556-89 100 0 ENSCO0000179385 1.8129116 6868633 4.29E-150 4.2FE-149 2.476886 100 0 SLG30A1 -1.756135 46304199 677.07746 2.11E-149 2.0FE-148 1.7467-815 100 0 SLG30A1 -0.8594187 4.8889928 143.730932 4.0FE-33 1.54E-32 -0.8162489 100 0 ENSGO0001913 RAB34 -1.2500478 7.5700200 67.6864314 3.2E-149 3.9E-148 1.4709618 100 0 SHCBB -1.751888 7.47893848 613.75934 -1.7E-1518 -0.08162489 100 0 ENSGO0001913 RAB34 -2.3300474 2.82729312 676.79944 3.32E-149 3.9E-148 -2.2024717 100 0 FH3 -1.8525444 2.605239 4.0E-76 7.32E-76 -1.8461894 100 0 ENSGO00001839 -1.6512156 6.4961653 675.77177 3.7E-149 3.6FE-148 -2.515068 100 0 PFH3 -1.8525444 2.605239 4.866621 1.0E-76 7.32E-76 -1.8461894 -2.5107797 9.72E-2222 2.7777778 1.856500000189																			0
ENSCO00001938 SCAPE - 1,679318 SCAPE - 1	ENSG00000034152	MAP2K3	-1.6574109	6.24475062	682.846042	1.61E-150	1.60E-149	-1.5672346	100	0 MAP2	2K3	-0.9324747	6.38564946 1	87.031187	1.41E-42	6.43E-42	-0.9419847	100	0
ENSCOODOLITY 25 FINAL 1.776513	ENSG00000198804	MT-CO1	-1.6718649	12.6907177	682.845814	1.61E-150	1.60E-149	-1.556349	100	0 MT-CO	01	-1.0873559	12.8151788 1	65.786498	6.16E-38	2.57E-37	-1.1535689	100	0
ENSCO0000113252 ENSCO00001031306 FNL3	ENSG00000090013	BLVRB	-2.7307935	1.98129116	680.886233	4.29E-150	4.27E-149	-2.476886	100	0 BLVRB	В	-1.8581652	2.10800127 2	78.870945	1.32E-62	8.08E-62	-2.0048094	100	0
ENSGO000011313 RAB34	ENSG00000170385	SLC30A1	-1.7765135	4.63041949	677.707746	2.11E-149	2.09E-148	-1.7443852	100	0 SLC30	0A1	-0.8594187	4.88899283 1	43.730932	4.07E-33	1.54E-32	-0.8162489	100	0
ENSGO000128386 FHL3	ENSG00000111252	SH2B3	-1.6196887	7.57022002	676.864314	3.21E-149	3.19E-148	-1.4709618	100	0 SH2B3	3	-1.7316885	7.47963848 6	13.750349	1.71E-135	2.03E-134	-1.6606198	100	0
ENSGO000018319 PPIR8B	ENSG00000109113	RAB34	-2.3300474	2.82729312	676.79944	3.32E-149	3.29E-148	-2.2024717	100	0 RAB 34	34	-3.696272	2.69984712 1	169.32949	2.82E-256	5.71E-255	-3.7935524	100	0
ENSGO00017367 CHSTII	ENSG00000183386	FHL3	-2.4294465	2.544161	676.711488	3.47E-149	3.43E-148	-2.311795	100	0 FHL3		-1.8525444	2.605239 3	43.686612	1.00E-76	7.32E-76	-1.8461884	100	0
ENSGO0000173191	ENSG00000108819	PPP1R9B	-1.6321526	6.4961653	676.577177	3.71E-149	3.67E-148	-1.516068	100	0 PPP1R	R9B	-1.1461509	6.57117789 2	79.466924	9.81E-63	6.01E-62	-1.1776976	97.222222	2.7777778
ENSGOU000177879 AP351 AP	ENSG00000125657	TNFSF9	-2.7948315	1.78970946	675.768151	5.56E-149	5.49E-148	-2.6992246	100	0 TNFSF	F9	-1.3948181	2.10805478 1	57.683552	3.63E-36	1.46E-35	-1.3101112	94.444444	5.5555556
ENSGO0000142634 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 ENSGO000105738 SIPA113 -1.7095959 4.79940965 66.4410171 1.64E-148 1.5893799 100 0 SIPA113 -1.7095959 4.79940965 66.4410171 1.64E-148 1.5947399 100 0 SIPA113 -1.7095959 4.79940965 66.4410171 1.64E-148 1.5947399 100 0 SIPA113 -1.7095959 3.65257485 428.937397 2.77E-95 2.45E-94 -1.7076829 100 0 ENSGO00010978 ENSGO00010978 ENSGO00010978 ENSGO00010978 ENSGO00010978 ENSGO00010979 ENSGO000010979 ENSGO00010979 ENSGO00010979 ENSGO00010979 ENSGO000010979 ENSGO000000000000000000000000000000000000	ENSG00000171310	CHST11	-1.6660919	5.43574178	673.344852	1.87E-148	1.84E-147	-1.6174455	100	0 CHST1	11	-1.3797342	5.4775365 3	93.432493	1.48E-87	1.23E-86	-1.4263146	100	0
ENGO0000142634	ENSG00000177879	AP3S1	-1.6986214	5.06534489	671.87098	3.91E-148	3.84E-147	-1.6801534	100	0 AP3S1	1	-1.2427126	5.14798614 3	311.522361	1.02E-69	6.92E-69	-1.3013038	100	0
ENSGO000015738 SIPA1L3 -1.7095959 4.97490665 64.410171 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 0 0 0 0 0 0 0	ENSG00000005893	LAMP2	-1.6651177	5.47111481	667.492113	3.51E-147	3.42E-146	-1.5892304	100	0 LAMP2	P2	-1.6397824	5.46460647 5	47.208986	5.10E-121	5.53E-120	-1.6215108	100	0
ENSGO0000150403 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 ENSGO0000140749 ISSF6 -2.9053929 1.51566013 660.939832 9.33E-146 9.02E-145 -1.612688 100 0 ISSF6 -2.9053929 1.51566013 660.939832 9.33E-146 9.02E-145 -1.62631439 100 0 ISSF6 -3.334193 1.45763958 634.729285 4.68E-140 5.79E-139 -3.3627927 100 0 ENSGO000168516 ILHOC2 1.63389925 6.50552856 656.817935 7.35E-145 6.03E-144 1.5886092 0 100 ILHOC2 0.9950277 5.2233661 205.728237 1.17E-46 5.74E-46 0.99801408 2.77777778 97.2222222 ENSGO0000185334 ILHOC2 1.6389025 5.6634963 8.06E-145 7.72E-144 1.5301213 100 0 AKIRIN2 -1.3741166 5.9981649 399.18475 5.94E-455 -1.646555 9.7222222 2.7777778 97.2222222 ENSGO0000185334 ILHOC2 1.658025 5.4674267 654.15383 2.79E-144 1.5301213 100 0 AKIRIN2 -1.3741166 5.9981649 399.18475 5.94E-455 -1.6164655 9.7222222 2.7777778 97.222222 ENSGO000018525 ILHOC2 1.668025 5.4674267 654.15383 2.79E-144 1.5301213 100 0 AKIRIN2 -1.3741166 5.9981649 399.18475 8.28E-89 6.94E-88 -1.367188 100 0 ENSG00000185344 -1.624628 5.9941495 5.6634963 8.06E-145 7.72E-144 -1.5301213 100 0 AKIRIN2 -1.240212 5.3564196 51.516487 1.68E-70 1.5E-69 -1.2841449 100 0 ENSG0000018517 CD82 -1.6674654 5.3795102 654.15383 2.79E-143 -1.5144974 100 0 CD82 -2.798405 5.13790932 1.935.67176 4.52E-305 -1.076308 4.698163	ENSG00000142634	EFHD2	-1.6108102	7.28342576	665.540791	9.32E-147	9.06E-146	-1.6387966	100	0 EFHD2)2	-0.6898398	7.51689244 9	9.8390133	1.65E-23	5.00E-23	-0.7839614	91.6666667	8.33333333
ENSGO0000110987 BCL7A	ENSG00000105738	SIPA1L3	-1.7095959	4.97490665	664.410171	1.64E-146	1.59E-145	-1.5947399	100	0 SIPA1	1L3	-1.5633251	4.87675647 4	63.222851	9.56E-103	9.12E-102	-1.6560044	100	0
ENSGO0000140749 IGSF6	ENSG00000150403	TMCO3	-1.9971242	3.62470782	663.345726	2.80E-146	2.71E-145	-1.9382639	100	0 TMCO	03	-1.7297569	3.65257485 4	28.937397	2.77E-95	2.45E-94	-1.7076829	100	0
ENSGO0000188313 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 PLSCR1 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 97.222222	ENSG00000110987	BCL7A	-1.7018496	5.07706743	661.831068	5.97E-146	5.78E-145	-1.612688	100	0 BCL7A	Α	-1.4347793	5.02521678 4	01.088339	3.19E-89	2.69E-88	-1.471094	100	0
ENSGO0000165516 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 2.77777778 ENSGO0000172270 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 97.222222 2.77777778 ENSGO0000135334 AKIRIN2 -1.6524628 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 ENSGO0000185825 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 ENSGO0000085117 CD82 -1.6674654 5.37951023 651.899642 8.63E-144 8.25E-143 -1.5144974 100 0 CD82 -2.798405 5.13970932 1393.86717 4.52E-305 1.07E-303 -2.6937764 100 0 ENSGO0000072135 PTPN18 -1.6825737 4.96671983 650.515766 1.68E-143 1.60E-142 -5.5477346 97.1428571 2.85714286 IGHVVOR15-8 -4.6988652 -0.5856958 450.532149 5.52E-100 5.08E-114 5.384077205 100 0 ENSGO0000124570 SERPINB6 -2.155201 3.21178492 648.965487 3.75E-143 3.55E-142 -2.0652497 100 0 SERPINB6 -0.6275902 3.60620242 56.9335383 4.51E-14 1.04E-13 -0.730678 88.888889 11.111111 ENSGO000016484 MAPK7 -1.787776 4.34219926 648.81926 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 ENSG00000173457 PPP1R4B -1.781368 4.3178909 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 ENSG0000173457 PP1R14B -1.7813686 4.3178900 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 ENSG0000173457 PP1R14B -1.7813686 4.3178900 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 ENSG0000173457 PP1R14B -1.7813686 4.3178900 642.674873 8.75E-142 8.27E-141 1.7161489 100 0 PPP1R14B -1.514516 4.297	ENSG00000140749	IGSF6	-2.9053929	1.51566013	660.939832	9.33E-146	9.02E-145	-2.6631439	100	0 IGSF6	6	-3.3341934	1.45763958 6	34.729285	4.68E-140	5.79E-139		100	0
ENSGO0000172270 BSG	ENSG00000188313	PLSCR1	-1.8911815	4.04807113	659.627944	1.80E-145	1.74E-144	-1.7308978	100			-1.9664268	4.09867888 6	609.690171	1.31E-134	1.54E-133	-1.893248	100	0
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 1.50E-143 1.50E-1	ENSG00000165516	KLHDC2	1.62389925	6.02552856	657.13532	6.27E-145	6.03E-144	1.65850992	0	100 KLHDC	C2	0.99050277	5.52233661 2	05.728237	1.17E-46				97.222222
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ENSG00000259261 GHV4OR15-8 -4.9083217 -0.4831849 650.571766 1.68E-143 1.60E-142 -5.5477346 97.1428571 2.85714286 GHV4OR15-8 -4.6988652 -0.5856953 450.532149 5.52E-100 5.18E-99 -5.3840672 91.6666667 8.33333333333333333333333333333333333																			0
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ENSGO0000148175 STOM -1.5973405 4.92638675 575.584113 3.42E-127 2.92E-126 -1.6141493 100 10 STOM -0.7323504 5.185013 108.288451 2.32E-25 7.39E-25 0.6426165 97.222222 2.77777778 ENSGO0000127124 HVEP3 -1.6117777 4.65289902 571.731924 2.36E-126 1.99E-125 -1.5361385 100 0 HWEP3 -1.895643 4.54842115 626.298536 3.19E-138 3.89E-138 3.89E-133 1.85E-126 1.99E-125 -1.5361385 100 0 HWEP3 -1.895643 4.54842115 626.298536 3.19E-138 3.89E-138 3.89									-									0	100
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	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	97.222222

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ENSG 00000124783	SSR1		3 6.27652768		2.22E-120	1.78E-119 -		100	0 SSR1 0 RIT1			6.33443659 275.762383	6.30E-62		-1.1783604	100	0
ENSG 00000143622	RIT1			544.100154	2.42E-120	1.94E-119 -		100				6.45300333 278.049583	2.00E-62 2.71E-40		-1.1457752	100	0
ENSG00000147119 ENSG00000165312	CHST7 OTUD1		2 2.65563373 6 6.66445211		9.45E-120 1.77E-119	7.54E-119 1.41E-118 -	-2.119108	100 100	0 CHST7 0 OTUD1			2.82621836 176.575291 6.54863198 646.49446			-1.2529625 -1.8257405	100 100	0
	ZFP36L1				3.97E-119	3.16E-118 -		100	0 ZFP36L1				3.89E-82			100	0
ENSG00000185650 ENSG00000110911	SLC11A2			538.513608 537.116621	7.99E-119	6.34E-118 1		0	100 SLC11A2			8.15002228 368.542005 3.99558169 172.315331	2.31E-39		-1.3201425	2.7777778	07 222222
ENSG00000110911	NPHP3			537.110021	1.58E-118	1.25E-117 1		0	100 SECTIA2			4.26078892 254.789883	2.31E-39 2.35E-57		1.16429354	2.77777778	100
ENSG00000113971	LAT			534.892492	2.44E-118	1.93E-117 1		0	100 NPHPS			2.9078865 424.699331	2.33E-37 2.32E-94		1.9390286	0	100
ENSG00000213038	TRAF1		1 5.88961306		5.79E-118	4.56E-117 1		0	100 TRAF1			5.34199886 112.269005	3.12E-26			5.55555556	
ENSG00000030338	LIMK1			532.187278	9.44E-118	7.42E-117 -		100	0 LIMK1	-		4.56789915 218.031494	2.43E-49		-1.0765384	100	0
ENSG00000100003	ZNF512B		3 5.33179486		3.64E-117	2.86E-116 1		0	100 ZNF512B			4.76827861 97.1909111	6.30E-23			5.55555556	94 444444
ENSG00000177239	MAN1B1		7 5.55654603		4.69E-117	3.67E-116 1		0	100 MAN1B1			5.42261375 344.695473	6.06E-77		1.32404339	0.5555555	100
ENSG00000177233	IFIT2		1 3.63264286		2.25E-116	1.76E-115 -		100	0 IFIT2			3.7603885 347.91851	1.20E-77			97.2222222	
ENSG00000115322	CCDC64		7 5.43148434		2.74E-116	2.14E-115 1		0	100 CCDC64			5.33115969 413.600778	6.03E-92		1.39611507	0	100
ENSG00000133127	P4HTM		2 3.76867583		4.67E-116	3.63E-115 1		0	100 P4HTM			3.47928584 266.17109	7.75E-60		1.28196356	0	100
ENSG00000170407	REPIN1		8 5.55847961		9.35E-116	7.26E-115 -		100	0 REPIN1			5.51251639 406.79409	1.83E-90		-1.4799751	100	0
ENSG00000155252	PI4K2A		5 5.79411464		1.35E-115	1.05E-114 -		100	0 PI4K2A			5.91114335 164.575726	1.13E-37		-0.8858587	100	0
ENSG00000133232	ATM		4 7.40806929		5.52E-115	4.27E-114 1		0	100 ATM			7.08497298 235.292648					88.8888889
ENSG00000105519	CAPS			519.379702	5.77E-115	4.47E-114 1		0	100 CAPS			3.74963185 247.378888	9.68E-56				97.222222
ENSG00000180530	NRIP1			518.928822	7.24E-115	5.59E-114 -		100	0 NRIP1			7.24794843 377.080168	5.38E-84		-1.3412617	100	0
ENSG00000058600	POLR3E		3 6.53836801		8.21E-115	6.34E-114		0	100 POLR3E			6.34099086 364.88328	2.43E-81		1.19408608	0	100
ENSG00000163754	GYG1		6 3.85658377		8.27E-115	6.38E-114 -		100	0 GYG1			4.03260469 162.51204	3.20E-37		-0.9428228	100	0
ENSG00000215041	NEURL4		3 3.98739874		1.78E-114	1.37E-113 1		0	100 NEURL4			3.78167062 314.054085	2.86E-70			2.7777778	97.222222
ENSG00000168159	RNF187		3 4.90234802		4.60E-114	3.52E-113 -		100	0 RNF187			4.97076059 288.784902	9.15E-65	5.78E-64	-1.302288	100	0
ENSG00000105355	PLIN3		1 5.3495126		8.74E-114	6.67E-113 -		100	O PLIN3			5.27439897 627.60537	1.66E-138		-1.8973946	100	0
ENSG00000151748	SAV1		8 3.95705948		9.26E-114	7.05E-113 -		100	0 SAV1			3.86715157 437.137272	4.54E-97			97.222222	2.7777778
ENSG00000105717	PBX4	1.8863107	5 3.1861708	512.841547	1.53E-113	1.16E-112 1	1.91470386	0	100 PBX4	1.49	5798244	2.8483108 240.522189	3.03E-54	1.66E-53	1.38778261	0	100
ENSG00000223509	RP11-632K20.7		8 5.04654152		1.77E-113	1.34E-112 1		0				4.79630542 266.673551	6.02E-60	3.55E-59		2.77777778	97.222222
ENSG00000100092	SH3BP1	-1.479379	2 5.03177688	512.007019	2.32E-113	1.76E-112 -	1.4418377	100	0 SH3BP1	-1.0	.0645251	5.16687802 225.489785	5.74E-51	3.01E-50	-1.0786455	97.222222	2.7777778
ENSG00000135956	TMEM127		7 7.13652121		1.37E-112	1.03E-111 -		100	0 TMEM127			7.15032204 297.055265	1.44E-66	9.36E-66	-1.24937	100	0
ENSG00000002919	SNX11	-1.550576	1 4.39055084	507.918277	1.80E-112	1.35E-111 -	1.4296089	100	0 SNX11	-0.8	.8252764	4.56341549 129.273675	5.91E-30	2.09E-29	-0.8578553	100	0
ENSG00000101421	CHMP4B	-1.393964	4 7.14499865	504.008893	1.28E-111	9.54E-111 -	1.3402797	100	0 CHMP4B	-1.3	.1038262	7.18066254 259.899217	1.81E-58	1.05E-57	-1.1932909	100	0
ENSG00000066322	ELOVL1	-1.561378	3 4.30173624	503.715312	1.48E-111	1.10E-110 -	1.4611344	100	0 ELOVL1	-0.8	.8373381	4.49639367 131.092929	2.36E-30	8.40E-30	-0.8786324	100	0
ENSG00000175463	TBC1D10C	1.4105717	4 6.62199208	503.064333	2.05E-111	1.53E-110 1	1.44942674	0	100 TBC1D100	C 0.93	3667028	6.21555245 186.356716	1.98E-42	9.00E-42	0.81042135	0	100
ENSG00000082153	BZW1	-1.378422	5 8.08332461	501.991542	3.50E-111	2.61E-110 -	1.2524511	100	0 BZW1	-0.7	.7267148	8.22586206 108.582318	2.00E-25	6.39E-25	-0.7049773	100	0
ENSG00000134574	DDB2	1.6761182	3.81421645	501.12119	5.42E-111	4.03E-110 1	1.77581069	0	100 DDB 2	1.04	4715898	3.33329005 148.150376	4.40E-34	1.70E-33	0.99593828	0	100
ENSG00000215302	CTD-3092A11.1	1.8102313	4 3.32337799	500.486433	7.45E-111	5.54E-110 1	1.96609438	0	100 CTD-3092	2A11. 1.20	0203917	2.89160558 167.564411	2.52E-38	1.06E-37	1.11476066	0	100
ENSG00000181852	RNF41	-1.449262	3 5.12808429	500.329536	8.06E-111	5.98E-110 -	1.3194771	100	0 RNF41	-0.9	.9495396	5.20925812 186.274289	2.07E-42	9.37E-42	-0.9466207	100	0
ENSG00000157350	ST3GAL2	-1.684952	1 3.76718534	499.895433	1.00E-110	7.42E-110 -	1.5714884	100	0 ST3GAL2	-1.7	.7063396	3.74414883 427.008735	7.28E-95	6.42E-94	-1.7008813	100	0
ENSG00000111229	ARPC3	-1.391427	3 7.01581782	499.341376	1.32E-110	9.79E-110 -	1.3321226	100	0 ARPC3	-1.0	.0762195	7.05258629 246.99074	1.18E-55	6.58E-55	-1.1486092	100	0
ENSG00000106665	CLIP2	-1.734743	7 3.59759947	498.842748	1.70E-110	1.26E-109 -	1.7298115	100	0 CLIP2	-1.5	.5870466	3.61069536 359.265743	4.07E-80	3.07E-79	-1.6751845	100	0
ENSG00000134899	ERCC5	1.443148	1 5.12322142	498.100456	2.46E-110	1.82E-109 1	1.52329507	0	100 ERCC5	1.3	.1566601	4.89117092 263.637423	2.76E-59	1.61E-58	1.09524783	0	100
ENSG00000180376	CCDC66	1.4654072	1 4.85396992	495.244418	1.03E-109	7.57E-109 1	1.53072359	0	100 CCDC66	1.0	.0147191	4.47805058 189.105294	4.98E-43	2.29E-42	0.92448841	2.77777778	97.222222
ENSG00000162241	SLC25A45		4 4.40408461		2.28E-109	1.67E-108 1	1.61454431	0	100 SLC25A45	5 1.13	1477675	4.02563055 201.51949	9.73E-46	4.65E-45	0.96361221	2.77777778	97.222222
ENSG00000079616	KIF22		9 6.03544032		2.29E-109	1.68E-108 1		0	100 KIF22			6.0014604 434.65501	1.58E-96		1.29496404	0	100
ENSG00000137161	CNPY3		6 5.85661109		8.24E-109	6.03E-108 -		100	0 CNPY3			5.88965577 308.488964	4.66E-69		-1.3163462	100	0
ENSG00000143862	ARL8A		2 5.59766581		1.03E-108	7.50E-108 -		100	O ARL8A			5.62469883 277.10233	3.21E-62		-1.1619859	100	0
ENSG00000137404	NRM		3 2.08510568		2.35E-108	1.71E-107 -		100	0 NRM			2.02507787 427.823815	4.84E-95	4.27E-94	-2.414174	100	0
ENSG00000162408	NOL9		6 6.27820796		2.36E-108	1.71E-107 1		0	100 NOL9			6.02744053 282.792615	1.85E-63		1.02636837	0	100
ENSG00000160305	DIP2A		2 5.80140431		6.04E-108	4.37E-107		0	100 DIP2A			5.91573087 509.680598			1.44678201	0	100
ENSG00000137486	ARRB1		8 4.24864632		1.55E-107		1.3802865	100	0 ARRB1			4.09954737 795.983923	4.03E-175		-2.2176475	100	0
ENSG 00000126264	HCST	-1.462902	9 4.77488444	483.992043	2.89E-107	2.08E-106 -	-1.3237388	100	0 HCST	-0.4	.4434976	5.08338952 40.1007745	2.41E-10	4.84E-10	-0.546344	86.1111111	13.8888889

ENSGO0000117795 FINDS 1.44506129	100 1444444
ENSG00000184939 ZFP90	
ENSGO0000111712 C12cr489 -1.4509185 4.80957835 479.23277 3.14E-106 2.24E-105 -1.344752 100 0 C12cr489 -0.8374158 4.90627129 140.009677 2.65E-32 9.89E-32 -0.812503 100 0 ENSGO0000175055 (CDC57 1.39733379 5.93877818 473.199066 6.45E-105 3.14E-104 1.2325449 100 0 GNA13 -0.6613966 8.77796087 87.3390533 9.14E-21 2.58E-20 -0.600009 100 0 ENSGO0000176155 (CDC57 1.39733379 5.39877818 473.199066 6.45E-105 4.58E-104 1.52581977 0 100 CDC57 1.59666783 5.46064112 520.192545 3.84E-115 4.05E-114 1.46287147 0 ENSGO00001809002 ENSGO0000180902 ENSGO0000180902 ENSGO0000180902 ENSGO0000180902 ENSGO0000180902 ENSGO0000180902 ENSGO0000180902 ENSGO000018090 ENSGO000	0
ENSGO0000177595 PIDD1 1.44366629 4.79451272 476.12451 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 ENSGO0000175155 CCDC57 1.3933379 5.39877818 473.199066 6.42E-105 3.14E-104 1.125281497 0 100 CCDC57 1.59666788 5.46064112 520.192545 3.84E-114 0.65E-114 1.46287147 0 ENSGO000018902 D2HGDH 1.64156054 3.81356352 471.479472 1.53E-104 1.08E-103 1.66173363 0 100 D2HGDH 1.31967327 3.55552878 241.667427 1.70E-54 9.36E-54 1.12554571 0 ENSGO0000197586 ENTPD6 1.38922231 5.29214875 465.638485 2.85E-104 3.48E-103 1.25226673 100 0 LTAH - 1.2385417 5.76371015 319.639022 1.74E-72 1.4E-72 4.6E-72 0.725251 100 ENSGO0000197586 ENTPD6 1.38922231 5.29214875 465.638485 2.85E-104 3.20E-102 1.3420898 0 100 ENTPD6 0.70137208 4.77699961 95.547927 1.4E-72 1.4E-72 4.6E-72 0.725251 100 ENTPD6 0.70137208 4.77699961 95.547927 1.4E-72 1.4E-72 1.4E-72 1.70E-70 1.72754251 100 ENSGO0000195908 GRR183 - 1.3487561 6.42080603 465.38748 3.23E-103 2.26E-102 1.3850396 0 100 GLG1 1.02168853 6.1524891 223.689217 1.4E-50 7.36E-50 0.97997996 5.55555559 MENGGO000103245 NARFL 1.82434882 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 ENSGO0000103245 NARFL 1.82434882 3.05106891 463.448884 8.54E-103 5.96E-102 1.1240414 100 0 ECE1 -0.9936696 7.1291393 211.2838793 4.15E-48 2.08E-47 -0.9604076 100 ENSGO0000105554 PROSE -1.3315292 7.06273581 463.437385 8.59E-103 5.09E-102 -1.1545409 100 0 FNSGO0000105594 RARA -1.33358071 6.93355029 462.383005 1.46E-102 1.01E-101 -1.2845643 100 0 FNSGO0000106554 PROSE -1.3315297 7.06273581 461.616476 2.35660659 463.430778 8.62E-103 6.00E-102 -1.5455409 100 0 FNSGO0000106554 PROSE -1.3315297 7.06273581 461.616476 2.35660659 463.43078 8.62E-103 6.00E-102 -1.5455409 100 0 FNSGO000010660 PROSE -1.3385071 6.93355029 462.383005 1.46E-102 1.47E-101 1.48760054 0 100 PROSE -1.7382404 4.7725993 100 PROSE -1.2481010 PROSE -1.2481010 PROSE -1.2481010 PROSE -1.2481010 PROSE -1.2481010 PROSE -1.2481010 PROS	
ENSGO0000120063 CDCS7 1.39733379 5.3987818 473.199066 6.45E-105 3.14E-104 1.2352449 100 0 CDCS7 1.59666783 5.46064112 5.2012525 3.48E-114 1.6287147 0 ENSGO0000110144 1.64156054 3.81356352 471.479472 1.53E-104 1.08E-103 1.66173363 0 100 D2HGDH 1.31967327 3.555252878 241.667427 1.70E-54 9.36E-54 1.1255471 0 ENSGO0000111144 1.3728364 5.78697422 468.931334 5.47E-104 3.84E-103 1.61273663 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-71 1.20E-70 1.2754251 100 0 LTAHH 1.2388417 5.76371015 319.639022 1.74E-71 1.20E-70 1.2754251 100 0 LTAHH 1.2388417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.2754251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.75F4251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.7254251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.72574251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.72574251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.72574251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.72574251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.72574251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.72574251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.72574251 100 0 LTAHH 1.2385417 5.76371015 319.639022 1.74E-72 1.70E-70 1.72574	100
ENSGO0000176155 CCCCS7	0
ENSGO0000180902 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 0 0 0 0 0 0 0 0	100
ENSGO0000111144 LTA4H	100
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 91 91 91 91 91	0
ENSG00000169508 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 ENSG0000013245 FRIST 1.82E-483882 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 ENSG0000017298 ECE1 1.3315292 7.06273581 463.448884 8.54E-103 5.99E-102 1.2140414 100 0 ECE1 -0.9936696 7.1291938 212.383793 4.15E-48 2.08E-47 -0.9604076 100 ENSG00000131799 ENSG00000131799 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 97.222222 2. ENSG00000133079 ENSG0000013507 ENSG0000013507 ENSG0000013507 ENSG0000013507 ENSG0000013507 ENSG00000140931 ENSG00000140931 ENSG00000140931 FIRST 1.3524426 1.825668 2.56E-101 1.71E-102 1.48E-101 1.48E-101 1.48E-101 1.485603 100 ENSG00000140931 ENSG00000140931 FIRST 1.3524426 1.825682 3.58811873 456.724549 2.48E-101 1.71E-100 1.48F00753 0 100 ENSG0000014893	5666667
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ENSG0000076554 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 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 97.222222 2. ENSG000010401 ENSG0000016041 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 ENSG00000170322 NFRKB 1.35700296 5.69488714 461.144145 2.71E-102 1.48E-101 -1.3393855 100 0 CYB5R4 -1.0774164 4.73684161 224.141104 1.3E-50 5.88E-50 5.88E-50 1.00E-103.00E-10	0
ENSGO0000131759 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 0.7947323 97.222222 2. ENSGO000100401 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 ENSGO0000170322 NFRKB 1.35700296 5.69488714 461.144145 2.71E-102 1.48E-101 -1.3393855 100 0 CYB5R4 -1.0774164 4.73684161 224.141104 1.13E-50 5.88E-50 -1.0765696 100 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 NFRKB 1.35700296 5.69488714 459.855829 5.77E-102 3.57E-101 -1.8537347 100 0 BCKDK -1.3542421 2.794728221 196.233532 1.39E-44 6.47E-44 -1.3502838 100 ENSGO0000110660 SLC35F2 -1.6805802 3.53610473 458.774316 8.8E-102 6.12E-101 -1.6243101 100 0 SLC35F2 -1.6480337 3.4328262 358.75479 6.36E-80 4.78E-79 -1.5718061 100 ENSGO0000118503 TNFAIP3 1.35241426 11.8256087 456.681212 2.54E-101 1.71E-100 1.49407573 0 100 TNFAIP3 1.35241426 11.8256087 456.681212 2.54E-101 1.74E-100 1.49407573 0 100 TNFAIP3 1.35241426 11.8256087 456.681212 2.54E-101 1.74E-100 1.49407573 0 100 TNFAIP3 1.3524142 11.8256087 456.681212 2.54E-101 1.74E-100 1.49407573 0 100 TNFAIP3 1.70412188 1.0119239 418.515988 5.13E-93 4.46E-92 1.81816187 0 ENSGO0000121579 NAA50 -1.3207934 6.86683298 453.881288 1.03E-100 7.03E-100 -1.2346967 100 NAA50 -0.7636218 6.97305533 126.787448 2.07E-29 7.22E-29 -0.8047138 97.2222222 2. ENSGO000002586 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. ENSGO000002586 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. ENSGO000002586 CD99 -1.3360731 6.22918501 453.707493 1.13E-100 7.67E-100 -1.2812376 100 0 CD99 -1.0820046 6.3059876 246.001735 1.93E-55 1.08E-54 -1.1501606 97.2222222 2. EN	0
ENSGO00010401 RANGAP1 1.3331770 7.48899126 461.63968 2.11E-102 1.47E-101 1.48760054 0 100 RANGAP1 1.4716026 7.5147050 450.091269 6.89E-100 6.44E-99 1.26907408 0 ENSGO0000170322 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 5.5555555 94 ENSGO000103507 ENSGO0000103507 ENSGO0000110660 SLC35F2 -1.688020 3.53610473 458.774316 8.8E-102 6.12E-101 -1.6243101 100 0 SLC35F2 -1.6480337 3.4328262 358.375479 6.36E-80 4.78E-79 -1.5718061 100 ENSGO0000118503 TNFAIP3 1.35241426 11.8256087 456.681212 2.54E-101 1.71E-100 -1.3674731 100 0 RANGAP1 1.4716026 7.51470503 450.091269 6.89E-100 6.44E-99 1.26907408 0 100 NFRKB 0.69628618 5.18357949 100.685988 1.08E-23 3.28E-23 0.62955305 5.55555556 94 1.08E-24 1.2600000103507 ENSGO0000118503 TNFAIP3 1.35241426 11.8256087 456.681212 2.54E-101 1.71E-100 -1.3674731 100 0 CMTM3 -1.2679903 5.83750746 338.865318 1.23E-75 8.90E-75 -1.2195074 100 ENSGO00000148392 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 ENSGO0000121579 NAA50 -1.3360731 6.22918501 453.707493 1.13E-100 7.07E-100 -1.2812376 100 0 CD99 -1.0820046 6.3059876 246.001735 1.93E-55 1.08E-54 -1.1501606 97.2222222 2.	1777778
ENSG00000170322 NFRKB 1.35700296 5.69488714 461.1614745 2.71E-102 1.48E-101 1.41274695 0 100 NFRKB 0.69628618 5.18357949 100.685988 1.08E-23 3.28E-23 0.6295505 5.5555555 94 ENSG0000103507 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 ENSG00000110660 SLG35F2 -1.6805802 3.53610473 458.774316 8.88E-102 6.12E-101 -1.6243101 100 0 SLC35F2 -1.6805802 3.53610473 458.774316 8.88E-102 6.12E-101 -1.6243101 100 0 SLC35F2 -1.6805802 3.53610473 458.774316 8.88E-102 6.12E-101 -1.6243101 100 0 SLC35F2 -1.6805802 3.53610473 458.774316 8.88E-102 6.12E-101 -1.6243101 100 0 SLC35F2 -1.6805802 3.53610473 458.774316 8.88E-102 6.12E-101 -1.6243101 100 0 SLC35F2 -1.6805802 3.5350479 6.36E-80 4.78E-79 -1.5718061 100 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 -1.2950748 100 ENSG00000048392 RRM2B -1.4183322 4.76401627 456.118013 3.36E-101 2.31E-100 -1.3246967 100 0 NAA50 -0.7636218 6.97305533 126.787448 2.07E-29 7.22E-29 -0.8047138 97.222222 2. ENSG0000002586 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 97.222222 2.	100
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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 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 ENSG0000048392 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 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 97.222222 2. ENSG0000002586 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 97.222222 2.	0
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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 97.222222 2. 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 97.222222 2.	0
	1777778
ENCCOMMONICATAL TRAIN 1 2401007 E 02210127 AE1 76AE0 2 00E 100 2 02E 00 1 21EE200 400 AEDIN 1 400C022 E 020C027 20C E20C27 4 00E CC 4 24E CE 4 22C027 27 22C0222 2	1777778
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 97.222222 2.	1777778
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
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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
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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	222222
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
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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 97.222222 2.	/777778
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 97.222222 2.	/777778
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.	333333
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
	1111111
ENSG00000143110 Clorf162 -1.5520294 3.77910025 427.840266 4.80E-95 3.13E-94 -1.4612862 100 0 Clorf162 -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
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 8.3333333 91	5555556

ENSG00000090006	LTBP4	1.47964264 4.14176	714 424.53846	1 2.51E-94	1.63F-93	1.53273514	0	100	LTBP4	1.16234956	3.93633825 209.427506	1.83E-47	9.08F-47	1.07288966	2.77777778	97.2222222
ENSG00000198431	TXNRD1	-1.3099943 5.66248				-1.3857994	100	0	TXNRD1		5.77689716 139.840819				94,4444444	
ENSG00000139433	GLTP	-1.3130249 5.38626				-1.2734193	100	0	GLTP		5.5672141 92.0161336			-0.6587834	100	0
ENSG00000107317	PTGDS	-2.1597521 1.89445					97.1428571				2.24454315 144.443021				80.555556	19.444444
ENSG00000137509	PRCP	-1.4712276 4.10243				-1.2807987	100		PRCP		4.32988106 78.5100071				88.8888889	
ENSG00000262319	CTC-457L16.2	1.65007177 3.40934				1.64242983	0	_			2.75249251 59.7724536				13.8888889	
ENSG00000125731	SH2D3A	1.42246106 4.33586				1.51490454	0		SH2D3A		3.9633898 172.899469				2.77777778	
ENSG00000067225	PKM	-1.2661484 7.40935				-1.1624228	100		PKM		7.23871685 708.43757			-1.8322271	100	0
ENSG00000117500	TMED5	-1.2885398 5.73397				-1.1929699	100	0	TMED5		5.78342889 201.250496			-0.8975613	100	o
ENSG00000173991	TCAP	1.79485029 2.8162				1.76861392	0	100			2.50603299 204.979735			1.44542168	0	100
ENSG00000104904	OAZ1	-1.2716795 7.29958				-1.327834	100		OAZ1		7.27618991 348.119573			-1.4642622	100	0
ENSG00000023892	DEF6	1.27407194 6.30771				1.33002172	0		DEF6		6.20413979 300.379316				2.77777778	97.222222
ENSG00000122986	HVCN1	-1.671055 3.27207				-1.5027652	100		HVCN1		3.07198633 524.62573			-2.1786083	100	0
ENSG00000162909	CAPN2	-1,2678702 6,20816				-1.2329246	100	0	CAPN2		6.24912369 267.07374			-1.1440504	100	0
ENSG00000102503	CROCCP2	1.36951461 4.54720				1.35838431	0	100	CROCCP2		4.52746087 384.228983			1.39444905	0	100
ENSG00000215908	CROCCP2	1.36951461 4.54720				1.35838431	0		CROCCP2		4.45627587 203.913016			1.39444905	0	100
ENSG00000242372	EIF6	-1.3229723 4.90571				-1.3073026	100		EIF6		5.01537208 138.509618			-0.9214182	100	0
ENSG00000242372	SCRN1	-1.4489937 4.13483				-1.2860878	100	7	SCRN1		4.26834529 131.84353		5.79E-30		97.2222222	2 7777778
ENSG00000136133	CASP7	-1.4542701 4.00207				-1.3408262	100		CASP7		4.09242284 145.97584		5.04E-33		100	0
ENSG00000160404	TOR2A	-1.5757455 3.4928				-1.4470027	100		TOR2A		3.65447888 142.735625			-1.0168051	100	0
ENSG000001103454	SNX3	-1.2619066 6.06925				-1.2433538	100		SNX3		6.02728507 301.618848			-1.2448839	100	0
ENSG00000112333	AFF3	-1.3145681 5.01043				-1.1604951	100		AFF3		4.61729811 1071.38805			-2.4936975	100	0
ENSG00000144218	MAN2B1	-1.2487487 6.61140			4.03E-89		100	_	MAN2B1		6.55315428 407.213865			-1.4310731	100	0
ENSG00000104774	CBX7	1.32349007 4.88401				1.33649593	0		CBX7		4.45153048 88.467436				5.55555556	04 444444
ENSG00000100307	RNF216	1.24174987 6.7731				1.29772671	0		RNF216		6.76156279 351.354834			1.19681372	0.55555556	100
ENSG00000011273	SVIL	1.30738067 4.96550				1.39178345	0		SVIL		4.51233232 96.4003127				8.33333333	
ENSG00000197321 ENSG00000068831	RASGRP2	1.23025874 8.23844				1.27686705	0	100	RASGRP2		7.84013556 118.211984			0.59502214	0.33333333	
	ABTB1						0								_	100
ENSG 00000114626 ENSG 00000182158	CREB3L2	1.25999398 5.76427 -1.3848294 4.27911				1.32919883 -1.3064813	100	100	ABTB1 CREB3L2		5.44157659 145.465243 4.22017168 355.93437			-1.4217445	8.33333333 100	91.0000007
ENSG00000182138	STK38	1.27766869 5.35223					0	100	STK38						2.77777778	07 222222
ENSG00000112079	KIAA0247	-1.2280907 6.88383				1.27943694 -1.1216465	100	100	KIAA0247		4.97354469 141.651571 6.92889406 159.856944			-0.8197555	100	97.222222
ENSG00000100647	CCAR2	1.23442651 6.72826				1.21533247	0	100	CCAR2	1.22760833				1.0905944	0	100
ENSG00000138941	RGS1	1.24792258 9.70485				1.35763971	0		RGS1		9.41942573 151.73699				11.1111111	
ENSG00000030104	FBXO6	-2.0386879 1.78925				-1.9576968	100	100	FBXO6	-1.1824501				-1.1979345	100	00.000009
ENSG00000110003	ULK3	1.29623238 4.99599				1.28099907	0	100	ULK3		4.7255173 211.03721			0.90451542	0	100
ENSG00000140474	WBP1	1.49871978 3.71234				1.5198912	0		WBP1		3.25286389 108.752053			0.7883306	0	100
ENSG00000106868	SUSD1	-1.7671019 2.6604				-1.6212929	100		SUSD1		2.84715885 122.629791				97.2222222	
ENSG00000134590	FAM127A	-2.1089753 1.55971				-2.0764591	100	0	FAM127A		1.6701146 159.679643			-1.4599402	100	2.7777778
ENSG00000154550	CROCC	1.32579659 4.65137				1.35702436	0	100	CROCC		4.51927447 292.294431		1.01E-64		2.7777778	97 222222
ENSG00000038433	PPIE	1.32637365 4.66590				1.39408649	0		PPIE		4.59262093 302.23148			1.27278049	0	100
ENSG00000034072	ALOX5AP	-1.4940742 3.67644				-1.3770913	100		ALOX5AP		3.47940326 638.945366		7.05E-140		100	0
ENSG00000132905	ERP27	1.6243877 3.14704				1.67591033	0	_	ERP27		2.75684293 157.841907			1.08567198	0	100
ENSG00000150093	ITGB1	-1.2213479 6.44779				-1.1492372	100	100	ITGB1		6.41020357 260.232845			-1.0666477	100	
ENSG00000178498	DTX3	1.40241341 4.09751				1.40648012	0	100	DTX3		4.28368811 511.068979			1.72947782	0	100
ENSG00000178438	CYBA	-1.2239912 6.54853				-1.1520192	100		CYBA		6.80462007 44.1933369				72.222222	
ENSG00000031323	KIAA0319L	1.29687307 4.79233				1.3717067	0		KIAA0319L		4.40086958 111.990808				2.77777778	
ENSG00000142087	HMHA1	1.20527282 8.99779				1.28456416	0		HMHA1		8.83062119 203.831384				2.77777778	
ENSG00000171606	ZNF274	1.2266248 5.95423				1.21196823	0	100	ZNF274		5.57490465 109.095416				5.55555556	
ENSG00000171000 ENSG00000135905	DOCK10	1.20295947 7.34458				1.19045725	0		DOCK10	0.76060321					5.55555556	
ENSG00000133303	DUSP1	-1.2347549 9.90484					94.2857143		DUSP1		10.0796048 85.7500265		5.70E-20		83.3333333	
ENSG00000120129	RRAGC	-1.2479865 5.30611				-1.0761202	100		RRAGC		5.30307235 220.323592			-1.0234865	100	0.0000007
ENSG00000116954	MAPK6	-1.2479865 5.30611			5.35E-84		100	0	MAPK6		6.08232226 376.016482		7.24E-83		100	č
ENSG00000069849	ATP1B3	-1.3185972 4.6256					97.1428571	2 8571/1296			4.93862725 24.3906512				77.777778	22 222222
EN300000003649	AIF103	-1.3103372 4.0230	JJ4 J00.101000	3 1.130-04	3.73E-64	-1.3321090	37.14203/1	2.03/14200	ATT 103	-0.5510515	4.55002725 24.5900512	7.00E-07	1.346-00	-0.3033039	11.1111110	LL. LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL

ENSG00000154845	PPP4R1	1 2476250 5 17020070 270 072112	2.005.04	1 225 92 1 1001144	100	0 000401	0.7050007 5.26722227 122 501506	1 125 20	4.015.30	0.7020604	100	ام
ENSG00000134845 ENSG00000137076	TLN1	-1.2476359 5.17828979 378.972112 -1.2010647 7.13414186 377.810038		1.22E-83 -1.1901144 2.19E-83 -1.0574214	100 100	O PPP4R1 O TLN1	-0.7950807 5.26723337 132.581586 -1.0065422 7.16304435 215.956704	1.12E-30 6.89E-49		-0.7828684 -1.0396366	100 100	0
ENSG00000137078	ERMARD	1.64920644 2.96846173 374.721557		1.03E-82 1.68271497	0	100 ERMARD	1.44546412 2.75347706 226.66668	3.18E-51		1.41149408	0	100
ENSG00000130023	IMPDH1	-1.2824334 4.75894672 374.47675		1.16E-82 -1.1615853	100	0 IMPDH1	-1.5503204 4.66758568 439.315236	1.53E-97		-1.5292158	100	100
ENSG00000164039	BDH2	1.48996301 3.54352315 372.864627		2.60E-82 1.48723158	0	100 BDH2	1.32577231 3.32991349 233.968096	8.13E-53			2.77777778	97 222222
ENSG00000104033	COG1	1.24603511 5.04082992 371.730079		4.58E-82 1.30667686	0	100 COG1	1.16866821 4.95942508 272.533693	3.18E-61		1.09848555	0	100
ENSG00000100083	ABHD4	-1.7891382 2.37164587 371.073785		6.35E-82 -1.6813255	100	0 ABHD4	-0.5750613 2.70511461 36.9521646	1.21E-09			94.4444444	
ENSG00000155640	C10orf12	-1.4444065 3.76862282 370.18842		9.90E-82 -1.4038519	100	0 C10orf12	-0.8626555 3.90816442 118.507088	1.34E-27			97.2222222	
ENSG00000193040	POLRMT	1.2775596 4.72909788 369.592896		1.33E-81 1.29009216	0	100 POLRMT	1.02946431 4.49701983 193.793483	4.72E-44			2.77777778	
ENSG00000033321	EHMT2	1.24081295 5.0715193 369.236038		1.59E-81 1.34269009	0	100 EHMT2	1.26891361 5.02083148 319.076706	2.30E-71			2.77777778	
ENSG00000099991	CABIN1	1.20556437 5.77148677 368.493792		2.30E-81 1.33358424	0	100 CABIN1	1.30660791 5.79667804 360.221993	2.52E-80		1.22063854	0	100
ENSG00000232533	AC093673.5	-2.1871138 1.13379707 368.364549		2.45E-81 -2.0965804	100	0 AC093673.5	-1.3149813 1.26797998 113.971519	1.32E-26		-1.3228422	100	0
ENSG00000164896	FASTK	1.25026359 4.92129317 368.186402		2.68E-81 1.27946904	0	100 FASTK	0.9339783 4.66248594 166.93057	3.46E-38		0.84918565	0	100
ENSG00000136238	RAC1	-1.1879367 6.59262472 366.334834		6.75E-81 -1.1937466	100	0 RAC1	-1.0485134 6.59139534 238.343835	9.03E-54		-1.088647	100	0
ENSG00000103966	EHD4	-1.2064423 5.97337831 365.49081		1.03E-80 -1.2244064	100	0 EHD4	-1.0842844 5.96413835 245.87013	2.06E-55			97.222222	2.7777778
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	5.5555556	94.444444
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			2.77777778	
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	88.888889
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	5.5555556	94.444444
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	97.222222	2.7777778
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	97.222222
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	8.3333333
ENSG00000213281	NRAS	-1.1526138 7.25555266 351.571997		1.07E-77 -1.1370569	100	0 NRAS	-0.6492083 7.3436859 91.1259345	1.35E-21		-0.6364057	100	0
ENSG00000008282	SYPL1	-1.1841919 5.4868062 351.094734		1.36E-77 -1.1022633	100	0 SYPL1	-1.0833883 5.45236951 244.514061	4.08E-55		-1.0210551	100	0
ENSG00000162302	RPS6KA4	-1.3945274 3.79036421 350.934408		1.47E-77 -1.3732819	100	0 RPS6KA4	-1.4777979 3.76304304 321.758514	6.00E-72		-1.5928393	100	0
ENSG00000160213	CSTB	-1.3550032 4.00823229 350.251066		2.07E-77 -1.3512442	100	0 CSTB	-1.5248949 3.91173732 357.514565	9.79E-80		-1.5467949	100	0
ENSG00000172671	ZFAND4	1.24209132 4.70713901 350.196539		2.12E-77 1.2712629	0	100 ZFAND4	1.01252975 4.50512529 188.67438	6.19E-43			5.5555556	
ENSG00000131797	CLUHP3	1.2087334 5.13693349 348.456227		5.06E-77 1.16928186	0	100 CLUHP3	1.04176139 4.87086534 211.849473	5.42E-48			2.77777778	
ENSG00000174227	PIGG	1.2180416 4.90285832 348.279685		5.52E-77 1.37021676	0	100 PIGG	1.01366974 4.72823714 199.089281	3.30E-45		0.94662946	0	100
ENSG00000182541	LIMK2	1.14724641 7.1048261 346.934867		1.08E-76 1.17732602	0	100 LIMK2	0.91851932 6.93449257 182.836624	1.16E-41		0.83575479	0	100
ENSG00000176871	WSB2	-1.2764971 4.38757681 346.607232		1.27E-76 -1.1489043	100	0 WSB2	-0.9697818 4.46096422 172.973395	1.66E-39		-0.983996	100	0
ENSG00000159461	AMFR	-1.1430585 7.14686139 345.685503		2.02E-76 -1.0864339	100	0 AMFR	-0.9766104 7.13923952 205.993245	1.03E-46		-1.0388822	100	0
ENSG00000197150	ABCB8	1.44070761 3.56499848 345.641251		2.06E-76 1.50948652	0	100 ABCB8	1.32799397 3.40745537 236.338743	2.47E-53			2.77777778	97.222222
ENSG00000140612	SEC11A	-1.1680207 5.78185035 344.891039		3.00E-76 -1.1417933	100	0 SEC11A	-1.1275749 5.76239054 270.927038	7.13E-61		-1.2033137	100	0
ENSG00000187742	SECISBP2	1.14893765 6.58080239 344.680752		3.32E-76 1.1652253	0	100 SECISBP2	0.74605947 6.25728236 122.137823	2.15E-28		0.65105126	0	100
ENSG00000114353	GNAI2	-1.1421408 7.72081645 343.82482		5.10E-76 -1.0251978	100	0 GNAI2	-0.9769614 7.75956893 198.586718	4.25E-45		-1.0188545	100	0
ENSG00000182199	SHMT2	-1.2627817 4.44538074 343.746309		5.30E-76 -1.1340621	100	0 SHMT2	-1.3040758 4.35320765 299.819212	3.61E-67		-1.3728789	100	0
ENSG00000120992	LYPLA1	-1.2096745 4.86263067 342.158281		1.17E-75 -1.0177125	100	0 LYPLA1	-1.183218 4.81584228 273.201401	2.28E-61		-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	97.222222	2.7777778

ENCCOOCOOTECAA	ACTD	1 1 400 400 10 4222472 240 527675	4.075.76	2.645.75 1.0510562	100	O ACTD	0.5400024 40.5750707 50.7442500	C 755 17	1 005 10 0 0700224 04 444444 5 5555555
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 7.94E-14	1.69E-16 -0.6700234 94.4444444 5.55555556
ENSG 00000198624 ENSG 00000197694	CCDC69 SPTAN1	-1.1311051 7.39449554 340.062266 1.13120418 7.28851939 339.569072	6.18E-76 7.92E-76	3.34E-75 -1.0584481 4.28E-75 1.1734927	100 0	0 CCDC69 100 SPTAN1	-0.5082992 7.58900026 55.820406 1.17577815 7.25107669 294.664717	7.94E-14 4.79E-66	1.81E-13 -0.5573053 97.2222222 2.77777778 3.08E-65 1.15337953 0 100
ENSG00000197694 ENSG00000110274	CEP164	1.34912162 3.93085895 338.822671	1.15E-75	6.22E-75 1.36349534	0	100 SPTAN1 100 CEP164	1.10159187 3.68832467 178.627028	9.67E-41	3.08E-65 1.15337953 0 100 4.28E-40 1.04230173 2.77777778 97.2222222
ENSG00000110274 ENSG00000136068	FLNB	1.13833465 7.13719989 338.182725	1.15E-75 1.59E-75	8.56E-75 1.21901756	0	100 CEP164 100 FLNB	1.33171633 7.28927132 371.596736	8.40E-83	6.56E-82 1.26895341 0 100
ENSG00000130008	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 2.7777778
ENSG00000227300	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 2.7777778
ENSG00000012232	BCL6	-1.1402581 6.47159049 335.656232	5.63E-75	3.02E-74 -1.0763625	100	0 BCL6	-1.1500884 6.35841074 282.054119	2.43E-13 2.68E-63	1.65E-62 -1.0820269 100 0
ENSG00000113916	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
ENSG00000042733	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
ENSG00000104142	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
ENSG00000171332	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
ENSG00000162980	VPS28	1.144716 6.06708509 334.519062	9.80E-75 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 VF328	1.2693172 3.09534948 200.766401	1.42E-45	6.77E-45 1.23689666 0 100
ENSG00000119723 ENSG00000185883	ATP6V0C	-1.1719455 5.19826672 334.262524	1.02E-74 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
ENSG00000183883		-1.7185619 2.49297403 333.874637	1.13E-74 1.38E-74	7.34E-74 -1.5930351		5.71428571 HLA-DOB		1.69E-61	1.01E-60 -1.9281322 97.2222222 2.77777778
ENSG00000241106 ENSG00000197969	HLA-DOB VPS13A	1.16667393 5.36522607 333.741844	1.36E-74 1.47E-74	7.84E-74 1.26991982	94.265/145	100 VPS13A	-1.7748435 2.36609973 273.795905 1.32490917 5.405364 356.657166	1.50E-79	1.13E-78 1.18579232 0 100
					100			1.70E-80	
ENSG00000133318	RTN3 SP1	-1.2105862 4.7647847 333.67966 -1.1425211 6.00402569 333.507107	1.52E-74 1.66E-74	8.08E-74 -1.1079081	100	0 RTN3 0 SP1	-1.3919202 4.69406394 361.008487 -1.0292541 5.98023229 227.989103	1.70E-80 1.64E-51	1.29E-79 -1.4252726 100 0 8.64E-51 -1.0822413 100 0
ENSG00000185591				8.80E-74 -1.0743276					
ENSG00000136720	HS6ST1 LRRC37B	-1.2597572 4.35364412 333.277868 1.14179756 5.83194388 332.550751	1.86E-74 2.67E-74	9.87E-74 -1.2386483	100	0 HS6ST1 100 LRRC37B	-1.3379641 4.29151353 307.429522	7.93E-69 1.82E-38	5.34E-68 -1.4002836 100 0 7.68E-38 0.80659522 0 100
ENSG00000185158				1.42E-73 1.24327961	0		0.8870512 5.60313062 168.211096		
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 9.67E-43	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		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 2.28E-200 2.12577161 0 100
ENSG00000169710	FASN	1.13326787 7.31141873 329.661422	1.14E-73	5.99E-73 1.04448813	_	100 FASN	2.19237761 7.99645594 917.694674	1.40E-201	2.202 200 2.12377101
ENSG00000103091	WDR59	1.29770732 4.06270508 329.159848	1.46E-73 1.77E-73	7.70E-73 1.43838439	0	100 WDR59 0 GCA	1.0617621 3.79922151 174.23538	8.79E-40 1.06E-123	3.82E-39 1.07872802 2.77777778 97.2222222
ENSG00000115271	GCA	-1.624431 2.58850021 328.783144		9.28E-73 -1.647737	100		-2.4815324 2.44363938 559.536069		1.17E-122 -2.5307749 100 0
ENSG 00000159720 ENSG 00000168297	ATP6V0D1 PXK	-1.1319967 5.98899556 328.307224 -1.2278986 4.47470752 327.983492	2.25E-73 2.64E-73	1.18E-72 -1.0063832 1.38E-72 -1.1441475	100 100	0 ATP6V0D1 0 PXK	-0.7647416 6.08946951 126.84128 -0.5873607 4.66467414 66.7209958	2.01E-29 3.13E-16	7.03E-29 -0.8470332 100 0 7.70E-16 -0.7138414 94.4444444 5.55555556
					100			1.05E-88	
ENSG 00000140853 ENSG 00000108771	NLRC5 DHX58	1.10983594 7.78413125 327.94326 1.3638414 3.6828541 327.190558	2.70E-73 3.93E-73	1.41E-72 1.19689166 2.06E-72 1.45426347	0	100 NLRC5 100 DHX58	1.39730036 7.95158454 398.709878 0.7496616 3.24266893 74.4603243	6.19E-18	8.81E-88 1.34859041 0 100 1.59E-17 0.6985661 8.33333333 91.6666667
ENSG00000108771	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
ENSG00000131378	TCOF1	1.15476864 5.42898497 327.006428	4.12E-73 4.31E-73	2.25E-72 1.27116547		97.1428571 TCOF1	1.13865894 5.36402638 265.374589	1.16E-59	6.77E-59 1.13338878 2.77777778 97.2222222
ENSG00000070814	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
ENSG00000137333	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
ENSG00000023302	NA 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
ENSG00000165508	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
ENSG00000137303	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
ENSG00000131748	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 8.333333333
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
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	O 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		-2.0882363 0.99716145 245.438651	2.56E-55	1.43E-54 -2.1452531 100 0
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ENSGO0000132824 SERING3 1.10342253 6.21043474 314.177399 2.69E-70 1.36E-69 1.17849494 0 100 SERING3 0.8617855 5.98295754 161.038406 6.71E-37 2.74E-36 0.84450588 5.55555556 94.4444 ENSGO0000110429 FBXO3 1.10389985 6.19863475 312.308989 6.14E-70 3.10E-69 1.17962566 0 100 MPHOSPH9 1.10850038 5.12190088 250.081346 2.49E-47 1.23E-46 0.9105333 2.7777777777777777777777777777777777	100 222222 100
ENSG00000110429 FBXO3	222222 100
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 ENSG0000040199 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 97.222222 2.77777 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 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 97.222222 2.77777 ENSG0000025828 FAM229A 1.31647686 3.7249336 308.219061 5.34E-69 2.66E-68 1.40478269 0 100 FAM229A 0.82379434 3.3712163 93.62781 3.81E-22 1.11E-21 0.75568204 0 ENSG00000171791 BCL2 -1.104023 5.64685996 304.671041 3.16E-68 1.57E-67 -0.9896708 100 0 BCL2 -1.476033 5.43298412 441.39247 5.39E-98 4.94E-97 -1.541815 100 ENSG00000184678 HIST2H2BE -1.3623143 3.49981213 303.917084 4.62E-68 2.28E-67 -1.3066991 97.1428571 2.85714286 HIST2H2BE -0.7109864 3.58468594 73.3311568 1.10E-17 2.80E-17 -0.7708101 94.4444444 5.555555	100
ENSG0000040199 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 97.222222 2.77777 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 ENSG00000156639 EAND -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 ENSG00000178741 COXSA -1.1624844 4.70350908 308.880035 3.83E-69 1.91E-68 -1.0443205 100 0 COXSA -0.6925932 4.8203158 94.9533851 1.95E-22 5.74E-22 -0.813076 97.222222 2.77777 ENSG0000025828 FAM229A 1.31647686 3.7249336 308.219061 5.34E-69 2.66E-68 1.40478269 0 100 FAM229A 0.8237943 3.3712163 93.62781 3.81E-22 1.11E-21 0.75368204 0 ENSG00000171791 BCL2 -1.104023 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 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 5.555551	
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 PPP3CA -0.098436 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 PPP3CA -0.098436 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 PPP3CA -0.098593849 67.3887496 2.23E-16 5.52E-16 -0.6193049 100 PPP3CA -0.0985934	/7/778
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 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 97.222222 2.77777 ENSG0000025828 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 ENSG00000171791 BCL2 -1.104023 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 ENSG00000184678 HIST2H2BE -1.3623143 3.49981213 303.917084 4.62E-68 2.28E-67 -1.306691 97.1428571 2.85714286 HIST2H2BE -0.7109864 3.58468594 73.3311568 1.10E-17 2.80E-17 -0.7708101 94.4444444 5.555559	0
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 ENSG0000105656 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 11.1112 ENSG00000171791 BCL2 -1.104023 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 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 5.555559	0
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 ENSG0000105656 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 11.1112 ENSG00000171791 BCL2 -1.104023 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 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 5.555559	177778
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 11.1111 ENSG00000171791 BCL2 -1.104023 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 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 5.555559	100
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 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 5.55555	111111
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 5.55555	0
	555556
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 97.2222	222222
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 97.2223	
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 FBX044 1.34337672 3.57262012 301.890879 1.28E-67 6.28E-67 1.32407187 0 100 FBX044 0.76639953 3.12693574 73.1763067 1.19E-17 3.03E-17 0.57551157 11.1111111 88.8881	388889
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 97.2222	
ENSG00000160712 ILGR -1.1416015 4.95532057 300.839987 2.16E-67 1.06E-66 -1.0844786 100 0 ILGR -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 94.444	144444
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 94.4444	
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 97.2222	222222
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 2.77777	777778
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 8.33333	333333
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 RP11-573D15.5 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 97.2222	22222
ENSG00000164823 OSGIN2 -1.1375366 4.65587823 293.509828 8.55E-66 4.12E-65 -1.0681489 100 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 3.5958779 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 97.222	22222
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 97.222	222222
ENSG00000148384 INPPSE 1.30842664 3.58333589 290.882073 3.19E-65 1.53E-64 1.36624402 0 100 INPPSE 0.77960451 3.14529391 78.1590446 9.51E-19 2.52E-18 0.69147243 2.77777778 97.2223	222222
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 97.222	222222
ENSG00000102580 DNAJC3 -1.0577363 6.17353294 290.366809 4.14E-65 1.97E-64 -0.9735319 100 0 DNAJC3 -0.4959978 6.3092030 54.1526318 1.86E-13 4.18E-13 -0.5071632 97.222222 2.77777	177778
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 97.222	222222
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 97.2223	22222
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 IF127L2 -1.5445461 2.49204727 288.526077 1.04E-64 4.93E-64 -1.4716642 100 0 IF127L2 -1.0303102 2.62133871 111.166577 5.44E-26 1.75E-25 -0.9985406 97.2222222 2.77777	
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 97.222222 2.77777	/77778

ENSG00000091527	CDV3	1 0221111	8.33009233	206 200600	3.35E-64	1 EQE 63	-0.9609476	100	ام	CDV3	0.5710796	8.42880447	67 1667901	2.49E-16	6 16E 16	-0.5681671	100	ام
ENSG00000031327	P4HB		7.17046538		3.37E-64		-0.9835277	100		P4HB		7.29048859		2.43E-20			97.2222222	2 7777779
ENSG00000164338			4.6911816		6.61E-64		1.17913245	0	_	UTP15		4.4345288		1.60E-31		0.76812486	0	100
ENSG00000173281	PPP1R3B		4.25071437		7.52E-64		-1.0031404	100	100	PPP1R3B		4.06943814		2.41E-101		-1.6728569	100	0
ENSG00000173201	NR4A1		6.45922856		1.14E-63				11.4285714			6.3829689		6.28E-39			91.6666667	8 33333333
ENSG00000125338	SSH1		6.46356108		1.83E-63		-0.9731236	100		SSH1		6.49202379		3.10E-32		-0.7334738	100	0.5555555
ENSG00000004112	PELP1		4.90663303		3.53E-63		1.11830314	0		PELP1		4.80527923		3.05E-40			2.77777778	97.222222
ENSG00000141430	TMEM164		4.23951686		4.81E-63		-1.0698885	100	0	TMEM164		4.18553437		1.98E-55		-1.2287581	100	0
ENSG00000137642	SORL1		8.03160906		5.57E-63		1.11045777	0	100	SORL1		7.76654999		3.04E-22			8.33333333	91 6666667
ENSG00000137642	PQLC1		5.73916485		6.75E-63		-0.9688259	100		PQLC1		5.81709641		1.77E-30			97.2222222	
ENSG00000122430	UBR2		5.57607042		1.01E-62		1.03040647	0		UBR2		5.46633862		7.02E-37		0.79733234	0	100
ENSG00000024048	PCM1		7.10762411		1.09E-62		1.08106646	0		PCM1		7.00244708		3.55E-44			5.5555556	
ENSG0000007047	MARK4	-1.2299997		279.165879	1.14E-62		-1.2000082	100	0	MARK4		3.96336015		8.53E-20			97.2222222	
ENSG00000156931	VPS8		4.72313529		2.81E-62		1.14188027	0	100	VPS8		4.37178074		3.79E-21			8.33333333	
ENSG00000035403	VCL		3.84417614		3.11E-62		-1.1223127	100	0	VCL		3.73705583		5.14E-67		-1.5504243	100	0
ENSG00000140264	SERF2		6.83170503	275.7784	6.25E-62		-0.9662161	100	0	SERF2		6.79796698		5.24E-45			97.2222222	2 7777778
ENSG00000198736	MSRB1		1.69775104		6.38E-62		-1.480843	100		MSRB1		1.71690697		1.13E-54		-1.7651515	100	0
ENSG00000125746	EML2		3.30016955		8.49E-62		1.48571391	0		EML2		2.96802943		3.03E-25			8.33333333	91 6666667
ENSG00000125748	APPL2		5.75075319		1.09E-61		1.09137176	0		APPL2		5.62422126		3.85E-43		0.84574342	0.5555555	100
ENSG00000157500	APPL1		5.29430419		1.37E-61		-0.9891075	100		APPL1		5.27155846		1.47E-40		-0.9422305	100	0
ENSG00000137500	PICK1	1.43939092	2.743737		1.93E-61		1.45510024	0	_	PICK1		2.62583622		8.01E-46		1.32996654	0	100
ENSG00000113719	ERGIC1		6.15447828		2.33E-61		-0.9934342	100		ERGIC1		6.2469932		2.21E-22		-0.6711252	100	0
ENSG00000188725	SMIM15		4.24855384	273.02741	2.48E-61	1.13E-60	-1.06932	100		SMIM15		4.19098751		1.15E-49	5.92E-49	-1.104339	100	0
ENSG00000164808	SPIDR		3.95267848		2.56E-61		-1.1740113	100		SPIDR		3.87232972		1.20E-57	6.90E-57	-1.285689	100	0
ENSG00000108518	PFN1		8.38636456		3.75E-61		-0.9526975	100	-	PFN1		8.42487737		2.39E-27			97.2222222	2.7777778
ENSG00000140545	MFGE8		3.64932377		1.26E-60		1.2708296	0		MFGE8		3.73026409		8.43E-74		1.36265614	0	100
ENSG00000186660	ZFP91		7.17855248		1.50E-60		-0.9373357	100		ZFP91		7.1848717		7.79E-29		-0.7850387	100	0
ENSG00000025156	HSF2		5.43090002		2.24E-60		1.05921644	0	100	HSF2		5.33096791		3.84E-47			2.77777778	97.222222
ENSG00000125827	TMX4		6.71582184		2.94E-60		-0.9034241	100	0	TMX4		6.78844125		1.71E-19			97.222222	
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	97.222222
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	5.5555556	94.444444
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	97.222222
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	97.222222
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	97.222222	2.7777778
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	97.222222
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	97.222222
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	97.222222
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		2.98130404		1.65E-57				97.1428571	ZNF700		2.77391093		5.53E-30			5.5555556	94.444444
ENSG00000172301	COPRS		1.44849776		2.34E-57		-1.6313013	100	0	COPRS		1.38374217		2.32E-39		-1.5737131	100	0
ENSG00000167785			3.45801767		2.41E-57		1.16445207	0		ZNF558		3.0828414		7.79E-18			8.33333333	
ENSG00000196839	ADA		4.41291474		2.71E-57				97.1428571	ADA		4.12463526		9.17E-22			8.33333333	91.6666667
ENSG00000166887			6.68787787		3.32E-57		1.05060713	0	100	VPS39	0.90630866			8.00E-41		0.86886335	0	100
ENSG00000107341	UBE2R2	-0.9934108	5.9292875	253.85408	3.75E-57		-0.9169522	100	0	UBE2R2		5.88627825		1.82E-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

PROSECURIOSISPAY PROB 0,977,2223 57,744602 25,357,713 47,657 26,575,756,736 20,575,756 20,5	ENC C 00000100004	DVCD	0.0072220	1 5 72444602	252 207242	4 745 57	2.055.56	0.07056306		100	DVCD	0.73530544	E E2062242	111 000701	2 705 26	1 225 25	0.00411071		100
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ENSGO000157520 LPPR2 -1.2547024 3.3625807 241.468019 1.88E-54 7.82E-54 -1.282318 88.571428 11.4285714 LPPR2 -2.0983669 3.19326984 499.37094 1.30E-110 1.33E-109 -2.2512157 94.444444 5.55555556 ENSGO000018294 APHIA -0.9511876 7.20194163 241.456041 1.98E-54 7.88E-54 -0.8574797 100 0 APHIA -0.6671235 7.26297117 96.7757046 7.76E-23 2.31E-22 0.77757785 ENSGO000018290 COXBA -0.9781842 5.48642857 240.223123 3.52E-54 1.45E-53 -0.9888457 100 0 NA -0.66783755 5.04318142 93.5523868 3.59E-22 1.15E-5555556 ENSGO0000176340 COXBA -0.9781842 5.48642857 240.223123 3.52E-54 1.45E-53 -0.9888457 100 0 COXBA -0.701191 5.5630325 10.4742003 1.39E-24 4.32E-24 -0.7545266 94.444444 5.55555556 ENSGO000017555 CKLF -1.5199763 1.95825428 238.94129 6.69E-54 2.75E-53 1.2891039 0 0 CKLF -1.8091284 1.88376923 259.015964 2.81E-58 1.63E-79 1.00 0 ENSGO0000141429 GAINT1 -0.9592316 6.30446747 248.887763 6.69E-54 2.75E-53 1.054718 100 0 SMS -1.261827 24.252886 6.8884107 2.44E-59 1.42E-58 -1.381593 1.0154718 100 0 SMS -1.261827 24.252886 6.8884107 2.44E-59 1.42E-58 -1.381593 1.0154718 100 0 SMS -1.261827 24.252886 6.8884107 2.44E-59 1.42E-58 -1.381593 1.0154718 100 0 SMS -1.261827 24.252886 6.8884107 2.44E-59 1.42E-58 -1.381593 1.00 0 ENSGO0000148803 FUOM -1.7332201 1.08476736 236.994507 7.18E-53 9.93E-53 1.05501477 100 0 SERPINBB -1.1533329 4.33849639 234.039428 7.84E-53 4.22E-53 -0.988673 100 0 SERPINBB -1.1533329 4.33849639 234.039428 7.84E-59 4.22E-58 -1.3150555556 ENSGO0000125245 GPR1B -1.0999277 4.04718816 235.91569 3.05E-53 1.21E-52 0.9901654 100 0 GED1A 0.90525095 4.06723158 13.3701312 6.35E-51 1.60E-50 -2.0158132 100 0 ENSGO0000125245 GPR1B -1.0999277 4.04718816 235.91569 3.05E-53 1.21E-52 0.9901654 100 0 GYSTM1 -1.5993228 1.68148022 24375302 23.34F525 23.34F525 2.59.93829 100 0 STRSIMA -1.119714 4.1476002 4.0666979 1.77E-54 1.52E-53 -1.1765977 97.222222 2.77777778 ENSGO000016615 RHE -0.9068575 2.4483059 23.34F525 2.345063 23.34F525 2.5555556 2.098927 97.1428571 1.00900014254 5.00960001621 24.546600001621 24.546600001621 24.546600001621 24.54										0								100	0
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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																			
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																			97.222222
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																			0
									_	100									97.222222
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										0									0
	ENSG00000187650	VMAC	1.2755215	4 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	5.5555556	94.444444

ENSG00000176624	MEX3C	-0.9273303 7.	1770204E	220 666011	7.05E-52	2 0/15 51	-0.8232212	100	0	MEX3C	0.62407	7 10127200	88.2604441	5.74E-21	1.63E-20	-0.667225	100	al
ENSG00000176624	MBTPS1	0.92795662 6.			7.05E-52 7.34E-52		1.00751377	0		MBTPS1			141.450974	1.28E-32		0.78443289	100	100
ENSG00000140943	HPS4	0.95041533 5.			7.54E-52 7.52E-52		0.9968479	0		HPS4			155.870623	9.04E-36		0.7506516	0	100
ENSG00000100099	CTSA	-0.9876803 5.			1.21E-51			•		CTSA			76.9506276	1.75E-18		-0.8394418	75	25
ENSG000000101452	DHX35	1.00941381 4.			1.21E-51 1.29E-51		1.06040432	0		DHX35			219.616402	1.10E-49		0.92341901	73	100
ENSG00000101432	TMX3	1.00341381 4.			1.35E-51		1.06063642	0		TMX3			144.612145	2.61E-33	9.95E-33		2.77777778	
ENSG00000100479	GIGYF2	0.94526689 5.		227.8688	1.74E-51		0.93956336	0		GIGYF2		5.42923398		7.47E-25			2.77777778	
ENSG00000204120	TBC1D5	-1.0011862 4.			2.09E-51		-0.8136261	100		TBC1D5			266.92468	5.31E-60	3.13E-59	-1.220931	100	0
ENSG00000131374	DDOST	-0.936821 6.			2.39E-51		-0.8130201	100		DDOST			92.8832272	5.55E-22			97.2222222	2 7777778
ENSG00000244038	HKR1	1.00246733 4.			2.47E-51		0.99880961	0	100				243.111509	8.25E-55		1.09528147	0	100
ENSG00000131236	CAP1	-0.926705 7.			2.72E-51		-0.7784789	100		CAP1			122.75636	1.58E-28		-0.8090483	100	100
ENSG00000131230	PBXIP1	0.9178039 7.			3.67E-51		0.97577709	0		PBXIP1		7.59430867		1.08E-33		0.72983498	100	100
ENSG00000103340	DCHS1	0.94761171 5.			4.51E-51		0.96007127	0		DCHS1			314.402182	2.40E-70			2.77777778	
ENSG00000100341	RP11-285F7.2	1.82285142 0.			4.71E-51		1.92003849	0		RP11-285F7.2				4.15E-15			5.55555556	
ENSG00000242801	HN1	-1.1130408 3.			4.71E-51 4.86E-51			97.1428571		HN1		3.94982733		2.40E-12			88.8888889	
ENSG00000162971	TYW5	0.97742656 4.			6.10E-51			2.85714286		TYW5		4.85451234		2.40E-12 2.08E-40			5.5555556	
ENSG00000182971	NA	-1.2911949 2.		224.86035	7.88E-51		-1.2552981	100		NA .		2.90961866		7.06E-10	1.39E-09			
ENSG00000184880	SNX10	-1.1076878 3.			8.95E-51				5.71428571			3.7509824		3.75E-69		-1.4308383	100	11.1111111
ENSG00000088300	RAB1A	-0.9239202			1.00E-50		-0.8614102	100		RAB1A			148.951825	2.94E-34		-0.8622492	100	0
ENSG00000138009	TSPYL4	0.93388965 5.			1.00E-50		0.98154964	0		TSPYL4			274.313918	1.30E-61		1.09189783	0	100
ENSG00000187189	PAFAH1B2	-0.9305759			1.00E-50 1.09E-50		-0.9309513	100		PAFAH1B2		5.98819992		2.94E-23		-0.7191134	100	100
ENSG00000108032	GTF3C3	1.02789432 4.			1.31E-50		1.10827782	0		GTF3C3			133.921785	5.68E-31			2.7777778	07 222222
ENSG00000119041 ENSG00000171608	PIK3CD	0.91040444 8.		223.82164	1.33E-50		0.94799397	0		PIK3CD		7.92670729		6.36E-19			2.77777778	
ENSG00000171008	COMMD5	-1.1389803			1.39E-50		-1.005337	100		COMMD5			76.5720602	2.12E-18		-0.7528527	100	0
ENSG00000170819	GUCD1	-0.9195036 6.			1.39E-30 1.44E-50		-0.8633881	100		GUCD1		6.61195108		1.20E-32		-0.7328327	100	0
ENSG00000138867 ENSG00000235655	H3F3AP4	-1.011468 4.			1.54E-50		-0.9911011	100		H3F3AP4			77.0860998	1.64E-18	4.31E-32 4.31E-18		97.2222222	2 7777770
ENSG00000233633	FAM118A	0.93989078 5.			1.54E-50 1.56E-50		0.97638454	0		FAM118A			162.020272	4.10E-37	1.68E-36	0.8658728	0	100
ENSG00000100370	WDR45B	-0.9268131 6.			2.24E-50		-0.8118652	100		WDR45B			48.3262119	3.61E-12			91.6666667	
ENSG00000141380	TBC1D10B	-1.041003 4.			3.32E-50		-0.9419395	100		TBC1D10B			45.4588573	1.56E-11	3.27E-11		94.444444	
ENSG00000103221	AVPI1	-1.3137209 2.			3.92E-50				2.85714286				59.9734955	9.61E-15			88.8888889	
ENSG00000119988	DYNLT1	0.97589883 4.			4.35E-50		1.01320133	0		DYNLT1		4.54890782		5.07E-19			13.8888889	
ENSG00000140423	SPAST	-1.020595 4.			4.85E-50		-0.8157973	100		SPAST			81.6868603	1.59E-19			94.444444	
ENSG00000021574	DENND1A	-0.9676624 4.			4.90E-50		-0.8321548	100		DENND1A		4.87151665		8.81E-43		-1.0030283	100	0.55555550
ENSG00000115322	ATG16L1	0.9212464 6.			5.15E-50		0.96996593	0		ATG 16L1			226.960098	2.74E-51	1.45E-50	0.9357809	0	100
ENSG00000135926	TMBIM1	-0.9207173 6.			6.19E-50		-0.8385814	100		TMBIM1		6.17959205		2.35E-59		-1.1051468	100	0
ENSG00000133320	SNN	-0.9171823 6.			6.20E-50		-0.7360965	100		SNN		6.92433369		1.90E-27		-0.8292792	100	0
ENSG00000103342	GSPT1	0.90632705 7.			7.89E-50		0.94054609	0	-	GSPT1			277.019099	3.35E-62			2.77777778	97 222222
ENSG00000115977	AAK1	0.93733659 5.			8.45E-50		1.01355298	0		AAK1			85.2996035	2.56E-20			2.77777778	
ENSG00000169032	MAP2K1	-0.9462511 5.		219.93332	9.35E-50		-0.8884452	100		MAP2K1			68.4016706	1.33E-16		-0.5874134	100	0
ENSG00000256525	POLG2	1.36491333 2.			1.18E-49		1.17711244	0		POLG2			106.110286	6.97E-25			2.77777778	97.222222
ENSG00000185324	CDK10	1.12466447 3.		218.46433	1.96E-49		1.10190686	0		CDK10		3.34638581		1.91E-29		0.90587013	0	100
ENSG00000023041	ZDHHC6	0.9945873 4.			2.77E-49		1.02726383	0		ZDHHC6			139.027723	4.34E-32		0.84464701	0	100
ENSG00000134250	NOTCH2	-0.9066431 6.			4.07E-49	1.57E-48		-	2.85714286				271.727288	4.77E-61		-1.1559027	100	0
ENSG00000170242	USP47		7.3139436		4.32E-49		0.96178669	0		USP47		7.20746537		2.02E-34				97.2222222
ENSG00000205302	SNX2			216.860265	4.38E-49	1.69E-48	-0.843577	100		SNX2		5.89652647		3.91E-22		-0.6558142	100	0
ENSG00000182952	HMGN4		4.0439774		8.97E-49		-0.9694841	100		HMGN4			78.5808929	7.68E-19		-0.6806919	100	0
ENSG00000014123	UFL1	0.93094677 5.			1.55E-48		0.93365257	0	100				91.8827258	9.20E-22				88.8888889
ENSG000000172936	MYD88	-0.9150672 5.			1.77E-48		-0.8237352	100		MYD88			86.7151846	1.25E-20				2.7777778
ENSG000000172550	NDUFAF7	1.18509569 3.			2.05E-48		1.26612019	0		NDUFAF7			88.9874355	3.97E-21		0.77312576	0	100
ENSG00000130559	CAMSAP1	-0.9429127 5.			2.27E-48		-0.8047964	100		CAMSAP1			183.200716	9.70E-42		-0.8520876	100	0
ENSG00000189077	TMEM120A	-1.3498645 2.			2.56E-48				2.85714286				255.917038	1.33E-57			97.2222222	2.77777778
ENSG00000185946	RNPC3	1.00945908 4.			3.14E-48		1.03019281	0		RNPC3		4.06179226		3.02E-20				91.6666667
ENSG00000163041	H3F3A	-0.8867021 8.			5.91E-48		-0.8631726	100		H3F3A			65.7574211	5.10E-16		-0.6008785	100	0
									-								300	-1

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 0.57499	102 11 1111111	00 0000000
ENSG00000130024	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 -0.7977		
ENSG00000104219	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 0.90328		
ENSG00000177303	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 -0.8191		
ENSG00000102702	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 0.52989		
ENSG00000102910	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 -0.8344		
ENSG00000108091	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		712 97.2222222	
ENSG00000197500	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 -0.5193		
ENSG00000196934	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 0.83623		
ENSG00000094880	C9orf89	-0.9164756 5.51258885 210.337257	1.15E-47 1.16E-47	4.36E-47 -0.7940537	_		-0.805851 5.55351814 136.502144	1.17E-31 1.55E-31			
	TMED7		1.16E-47 1.64E-47		100	0 TMED7		7.24E-30	2.55E-29 -0.711	407 97.2222222	
ENSG00000134970	CTDSP1	-0.9029143 5.78211868 209.648809	1.94E-47	6.15E-47 -0.8381183			-0.7777974 5.79125774 128.869986	3.10E-48			
ENSG 00000144579 ENSG 00000069399	BCL3	-0.9250452 5.14319077 209.31664 -0.8894937 6.58132755 208.862726	2.43E-47	7.26E-47 -0.8642611 9.10E-47 -0.8384494	100 100	0 CTDSP1 0 BCL3	-1.0314236 5.07002006 212.96444 -0.8992312 6.54063386 175.133722	5.60E-40	1.55E-47 -1.1289 2.44E-39 -0.8933		
ENSG00000118454	ANKR D13C RP11-73E17.2	0.90911494 5.40037591 208.77356	2.54E-47	9.52E-47 0.98287297	0 100	100 ANKRD13C 0 RP11-73E17.2	0.83909553 5.30801312 148.17817	4.34E-34	1.68E-33 0.71750		
ENSG00000258738		-1.1843995 3.05433175 208.437461	3.01E-47	1.13E-46 -1.0693017			-1.0319678 3.02909782 131.367292	2.06E-30	7.34E-30 -0.9805		
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 -1.2654		
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 -1.6799		
ENSG00000231025	RP11-175019.4 TTC14	-1.0956004 3.55287043 207.373962	5.14E-47	1.91E-46 -1.0065737	100	0 RP11-175019.	-0.5374273 3.70791092 44.6303752	2.38E-11 2.59E-37	4.96E-11 -0.5417		
ENSG00000163728		0.97479289 4.46099864 207.286765	5.37E-47	2.00E-46 1.10932209	0	100 TTC14	0.95564813 4.37623148 162.933184		1.06E-36 0.93128		
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 1.03E-87	8.17E-25 -0.7402		
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		8.56E-87 -1.4542		
ENSG00000112303	VNN2	-1.1604566 3.30327442 206.215848	9.19E-47	3.41E-46 -0.9042949			-1.1145509 3.28761604 155.947809	8.69E-36	3.48E-35 -1.2517		
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 -1.0234		
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 -1.4438		
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 1.74156		
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 -1.2052		
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 0.87819		
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 0.69071		
ENSG00000170471	RALGAPB	0.88573889 5.9807294 203.129518	4.33E-46	1.59E-45 0.95299702		100 RALGAPB	1.00017189 6.01885861 215.721119	7.76E-49	3.93E-48 0.97913		
ENSG 00000161920 ENSG 00000161981	MED11 SNRNP25	-1.4797049 1.54523539 202.716138 -1.3263764 2.23416796 201.383591	5.33E-46	1.96E-45 -1.3840595	100 100	0 MED11 0 SNRNP25	-1.2628381 1.58553111 118.788757 -0.6165898 2.3767459 37.9093378	1.16E-27 7.41E-10	3.91E-27 -1.3396	573 100 964 88.8888889	
			1.04E-45	3.81E-45 -1.1712432							
ENSG00000204397	CARD16	-1.2717008 2.55275598 201.241616	1.12E-45 1.15E-45	4.09E-45 -1.2034557	100 0	0 CARD16	-1.6357414 2.45540115 258.633784	3.41E-58 2.23E-25	1.97E-57 -1.5865		
ENSG 00000131876 ENSG 00000154589	SNRPA1 LY96	0.87392034 6.47061953 201.180722 -1.4241843 1.78369276 200.949536	1.15E-45 1.30E-45	4.21E-45 0.88840822 4.73E-45 -1.3799172	100	100 SNRPA1 0 LY96	0.70228735 6.27582775 108.369057 -2.470539 1.55807195 402.559766	1.53E-25	7.10E-25 0.59471 1.29E-88 -2.4321		
ENSG00000134389	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 -1.0772		
ENSG00000223347	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 -0.7932		
ENSG00000140992	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 -1.077		
ENSG00000243078	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 0.91043		
ENSG00000130433	GANAB	0.87175847 6.7245598 199.754841	2.36E-45		_	97.1428571 GANAB	0.78957949 6.61373157 135.154614	3.05E-31	1.11E-30 0.74727		
ENSG000000112297	AIM1	0.87965694 6.08179225 199.27775	3.00E-45	1.09E-44 0.88756022	2.03/14200	100 AIM1	0.70678197 5.87273533 108.078203	2.58E-25	8.21E-25 0.67372		
ENSG00000112237	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 -0.7878		
ENSG00000166273	FBXW2	0.88962457 5.39355399 199.001361	3.45E-45	1.25E-44 0.9523057	0	100 FBXW2	0.59242325 5.18521536 73.2787635	1.30E-23 1.13E-17	2.88E-17 0.54233		
ENSG00000115402	PPIB	-0.8730355 6.26867398 198.945601	3.55E-45	1.29E-44 -0.7815997	100	O PPIB	-0.6780716 6.29856778 100.360578	1.27E-23	3.86E-23 -0.7719		
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 0.92578		
ENSG00000133835	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 0.79651		
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 -0.6668		
ENSG00000130043	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 0.73169		
ENSG00000132234 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 -0.6678		
ENSG000000110074	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 1.10324		
ENSG00000110074	ARFGEF1	0.87311064 5.74378908 196.295077	1.34E-44	4.83E-44 0.93363985	0	100 POXICEDI 100 ARFGEF1	0.86292417 5.68632279 159.913119	1.18E-36	4.81E-36 0.84471		
ENSG000000072501	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 0.7772		
ENSG00000072301	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 0.84100		
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 -1.0872		
5000001.5545		3.3.470300	1.002 77	0.7024031	200	o d iiiii.Eb	2.55557 1.55105012 255.742020	3.112 33			•

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ENSG00000112146	FBXO9		4.77110167		2.19E-44		1.01291885	0		FBXO9		4.55249551		2.16E-17			8.33333333	91.6666667
ENSG 00000060762	MPC1		3.99769501		2.38E-44	8.51E-44	-0.903878	100		MPC1		4.03694499		1.51E-23		-0.8356968	100	0
ENSG 00000139679	LPAR6		3.41962941		2.40E-44				2.85714286 l			3.05677259		1.75E-195		-2.9388513	100	0
ENSG00000159388	BTG2		8.50347168		3.91E-44				2.85714286			8.47664914		3.28E-29		-0.7685296	100	0
ENSG00000213903	LTB4R		4.08388581		3.97E-44		0.99368983	0	100 (4.04480335		9.82E-36				97.222222
ENSG00000142192	APP		6.20055703		4.60E-44				2.85714286			5.82407349		6.43E-195		-2.1151144	100	0
ENSG00000136003	ISCU		7.08783562		1.04E-43		0.84509104	0		SCU		7.13903819		7.72E-47		0.89925027	0	100
ENSG00000161203	AP2M1		6.07639606		1.10E-43		-0.7708662	100		AP2M1		6.14799242		3.87E-17		-0.6137578	100	0
ENSG00000102317	RBM3		9.06109549		1.29E-43		-0.7732121	100		RBM3		9.09879732		1.38E-15		-0.5972867	100	0
ENSG00000122971	ACADS		2.24752707		1.32E-43		1.32769669	0		ACADS		2.1244509		8.09E-27			2.77777778	97.222222
ENSG00000142230	SAE1		4.00254461		1.39E-43		-0.8912745	100		SAE1		4.12212352		2.57E-11		-0.5042273	100	0
ENSG00000119760	SUPT7L		5.50920571		1.49E-43		0.93864819	0		SUPT7L		5.43835355		1.52E-37		0.81959031	0	100
ENSG00000120725	SIL1		3.06050202		1.86E-43		-1.0810708	100		SIL1		3.01018512		7.16E-39		-1.3168302	100	0
ENSG00000141644	MBD1		6.01813681		1.91E-43		0.90943993	0	100			5.89486571		1.38E-23			2.77777778	-
ENSG00000126088	UROD		4.25675284		1.92E-43		0.95752264	0		UROD		4.03297426		6.63E-19			5.5555556	94.444444
ENSG00000243646	IL10RB		3.77279645		2.16E-43		-0.9365946	100		L10RB		3.69440362		1.54E-62		-1.452891	100	0
ENSG00000131368	MRPS25		4.46689607		2.25E-43		0.93900757	0		MRPS25		4.33489838		1.32E-30		0.74010905	0	100
ENSG00000101856	PGRMC1		4.42471211		2.35E-43		-0.8723269	100		PGRMC1		4.36492307		1.17E-37		-1.0112447	100	0
ENSG00000128739	SNRPN		2.18466385		2.40E-43		1.33870151	0		SNRPN		2.23149214		3.91E-43		1.41513917	0	100
ENSG00000148399	DPH7		4.64184088		3.37E-43		0.97389533	0	100			4.55735065		7.22E-32		0.70246683	0	100
ENSG00000167394	ZNF668		2.92659488		3.44E-43		-1.2711322	100		ZNF668		3.02351763		3.54E-16			94.444444	
ENSG00000104969	SGTA		5.53134345		3.78E-43		-0.864006	100		SGTA		5.64342156		2.18E-12			97.2222222	
ENSG00000176953	NFATC2IP		5.29571627		4.57E-43		0.85999733	0		NFATC2IP		5.16631767		5.07E-29			2.77777778	
ENSG00000101040	ZMYND8		4.19255969		5.37E-43		1.01972202	0		ZMYND8		3.85684659		6.67E-14			5.5555556	
ENSG00000031698	SARS		5.60801956		5.51E-43		0.96186539		100 5			5.63496258		1.58E-44		0.92325022	0	100
ENSG00000130313 ENSG00000172354	PGLS GNB2		4.41691106 6.27476403		5.74E-43 7.24E-43		-0.9071576	100 97.1428571		PGLS		4.39009402 6.34904804		9.19E-35 3.14E-19			97.222222 91.6666667	
ENSG00000172334 ENSG00000100564	PIGH		4.19436905		7.24E-43 7.27E-43		1.04152315	97.1428571	100			4.14098513		5.14E-19 5.13E-37		0.89490217	91.0000007	
ENSG00000100364 ENSG00000120662	MTRF1		2.82855827		7.27E-43 7.72E-43		1.19765301	0		MTRF1		2.47023625		4.25E-17			2.77777778	100
ENSG00000120662 ENSG00000121691	CAT		4.14351422		7.72E-43 7.76E-43			-	2.85714286			4.12661871		2.70E-28		-0.8782642	100	91.222222
ENSG00000121691	TET3		6.97989149		7.76E-43 7.88E-43		-0.9157421	100		TET3		6.99469732		4.15E-20			94.4444444	5 5555556
ENSG00000187003	COG4		3.30254008		9.49E-43		1.16006161	0	100			3.11141772		9.06E-21			5.55555556	
ENSG00000103031	RARS2		4.11645033		9.49E-43 9.66E-43		1.0248067	0		RARS2		3.89787052		1.68E-18		0.63777643	0.55555556	100
ENSG00000140282	KIAA2013		4.31082869		1.03E-42			97.1428571		KIAA2013		4.35461536		3.11E-22			97.2222222	
ENSG00000110003	KDM1B		3.72353701		1.23E-42		-0.8656984	100		KDM1B		3.68036598		2.12E-37		-1.1058953	100	0
ENSG00000105097	S100PBP		3.72968928		1.34E-42		1.09591569	0		S100PBP		3.48671853		3.94E-18		0.55348493	100	100
ENSG00000110437	CTB-31O20.4		4.04057424		1.80E-42		0.91340094	0		CTB-31O20.4				3.14E-48			2.77777778	
ENSG00000272501	XXbac-BPG299		3.11942232		2.49E-42		1.13960004	0				2.8188319		7.20E-16			5.55555556	
ENSG00000152127	MGAT5		6.45802229		3.81E-42		-0.7865191	100		MGAT5		6.40383066		1.17E-29		-0.8292408	100	0
ENSG00000132127	TRIM28		7.69403402		4.19E-42		0.86623864	0		TRIM28		7.7370206		4.84E-51		0.93510714	0	100
ENSG00000048471	SNX29		6.4684337		4.41E-42			-	2.85714286			6.21915656		1.65E-75		-1.3133469	100	0
ENSG00000042445	RETSAT		2.96268344		4.53E-42		1.13793824	0		RETSAT		2.97259196		2.50E-45		1.26354709	0	100
ENSG00000160588	MPZL3		4.40178828		4.95E-42			-	97.1428571			4.47562158		5.97E-49			2.77777778	
ENSG00000092010	PSME1		6.84513984		5.03E-42		-0.7789526	100		PSME1		6.9340204		2.29E-15				2.7777778
ENSG00000170266	GLB1		3.15370634		5.10E-42		-1.0001908	100		GLB1		2.99366825		1.71E-94		-2.0953747	100	0
ENSG00000007923	DNAJC11		3.9433131		5.38E-42		1.03108176	0		DNAJC11		3.85476398		3.14E-27		0.78217495	0	100
ENSG00000184900	SUMO3		6.92576228		5.93E-42		-0.8298961	100		SUMO3		6.93794241		3.30E-22		-0.6911452	100	0
ENSG00000100528	CNIH1		5.24208903		8.24E-42		-0.8597432	100		CNIH1		5.15292152		2.14E-41		-0.9330935	100	o
ENSG00000129933	MAU2		6.84783747		8.93E-42		0.89706961	0		MAU2		6.81899151		6.54E-35		0.75091064	0	100
ENSG00000156804	FBXO32		4.94636734		9.07E-42		0.85301994	0		FBXO32		4.97693774		6.93E-43			2.77777778	
ENSG00000163510	CWC22		4.94088323		9.75E-42		0.95139288	0		CWC22		4.80600234		1.97E-27		0.67175799	0	100
ENSG00000143761	ARF1		8.52710798		1.16E-41		-0.8309242	100		ARF1		8.58960672		3.00E-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
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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
ENSG00000178188	NDUFV1	0.84592227 5.78338134 181.62524	2.14E-41	7.29E-41 0.82348423		100 SH2B1	0.83650847 5.72843329 147.488121	6.14E-34	2.36E-33 0.78144444 2.77777778 97.2222222
ENSG00000107732	MT-ATP8	-0.8235457 8.93973567 181.539202	2.14E-41 2.24E-41			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		100 C1orf228	0.92210799 4.75750645 163.396876	2.05E-37	8.45E-37 0.72860979 0 100
ENSG00000138320	RBM26	0.82788944 6.48502949 180.880948	3.11E-41	1.06E-40 0.92400139		100 C10/1228	0.58429709 6.28511645 74.9827663	4.75E-18	1.23E-17 0.51550012 8.33333333 91.6666667
ENSG00000139746	ANKR D52	0.83829309 5.79985207 180.606725	3.57E-41	1.21E-40 0.93680498		100 KBM26 100 ANKRD52	0.93793329 5.79870118 187.968259	8.83E-43	4.03E-42 0.85046829 5.5555556 94.4444444
ENSG00000139643	CDK2	1.14096591 2.8725816 179.508788	6.20E-41	2.10E-40 0.93680498		100 AN KND52 100 CDK2	1.00321156 2.68911975 110.161911	9.03E-26	2.90E-25 0.84364664 0 100
ENSG00000146066	HIGD2A HAUS6	-0.8550355 5.08544242 178.783011	8.94E-41	3.02E-40 -0.7755568		0 HIGD2A 100 HAUS6	-0.4840229 5.18604987 48.738472	2.92E-12 1.92E-24	6.32E-12 -0.5764251 91.6666667 8.33333333 5.94E-24 0.68046608 2.77777778 97.2222222
ENSG00000147874		0.8408796 5.42310163 178.765608	9.01E-41	3.05E-40 0.87603977			0.70606191 5.28447126 104.103009		
ENSG 00000105677 ENSG 00000134686	TMEM147 PHC2	-1.0123885 3.57849952 178.754595	9.06E-41 1.04E-40	3.06E-40 -0.95345 3.51E-40 -0.7066528		0 TMEM147 0 PHC2	-0.5391567 3.69528996 44.4278338 -0.6892343 6.32133466 103.77109	2.64E-11 2.27E-24	5.49E-11 -0.614103 91.6666667 8.33333333 7.01E-24 -0.7040086 100 0
		-0.8264782 6.2982076 178.479963							
ENSG00000154889	MPPE1	0.90237036 4.42811873 178.459439	1.05E-40	3.55E-40 0.95838523		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		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		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		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		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		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		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		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		100 MTA1	0.6824417 5.1505723 94.8311692	2.07E-22	6.09E-22 0.50813103 5.5555556 94.4444444
ENSG00000103197	TSC2	0.85772788 5.00886107 176.541277	2.76E-40	9.22E-40 0.94655931		100 TSC2	0.77569088 4.86775908 117.713613	2.00E-27	6.68E-27 0.68321635 5.5555556 94.4444444
ENSG00000149554	CHEK1	1.0236714 3.45962151 176.363207	3.02E-40	1.01E-39 1.0591546		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			-0.8708546 4.2483781 132.283446	1.30E-30	4.66E-30 -0.9000678 97.2222222 2.77777778
ENSG 00000166188	ZNF319	-0.973282 3.7844872 175.764412	4.08E-40	1.36E-39 -0.8686533		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		0 PAPSS1	-1.359853 2.8324201 208.665049	2.69E-47	1.33E-46 -1.3870773 100 0
ENSG 00000169100	SLC25A6	-0.8081571 9.33432306 175.031519	5.89E-40	1.96E-39 -0.7315602		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		0 MBD2	-0.9377712 6.02214148 190.026171	3.14E-43	1.44E-42 -0.9250012 100 0
ENSG 00000031823	RANBP3	0.81052435 6.51552061 173.95343	1.01E-39	3.36E-39 0.85386536		100 RANBP3	1.07688866 6.64797183 251.372928	1.30E-56	7.37E-56 0.98826032 0 100
ENSG 00000113732	ATP6V0E1	-0.886003 4.50946273 173.823284	1.08E-39	3.58E-39 -0.6978166		0 ATP6V0E1	-0.5468427 4.61943077 56.9602218	4.45E-14	1.03E-13 -0.6156739 94.4444444 5.55555556
ENSG 00000125834	STK35	0.83580306 5.26171755 173.600165	1.21E-39	4.00E-39 0.84006433		100 STK35	0.81096668 5.16557506 135.116252	3.11E-31	1.13E-30 0.67182377 5.5555556 94.4444444
ENSG 00000122674	CCZ1	1.04948132 3.23169324 173.099671	1.56E-39	5.14E-39 1.05714429		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		0 MAGT1	-0.6419325 5.49249646 88.052956	6.37E-21	1.81E-20 -0.6591264 100 0
ENSG 00000254909	RP11-110I1.5	2.17860958 -1.1543375 172.865913	1.75E-39	5.78E-39 2.29967065			2.19634746 -1.2348556 129.322365	5.77E-30	2.04E-29 2.34135689 2.77777778 97.2222222
ENSG 00000100580	TMED8	-0.8669578 4.6705192 172.789397	1.82E-39	6.00E-39 -0.7013707		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		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		0 ZNF687	-0.7643784 5.99014613 127.402836	1.52E-29	5.31E-29 -0.8692494 100 0
ENSG 00000040633	PHF23	-1.2132719 2.33900982 172.045541	2.64E-39	8.71E-39 -1.1278035			-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		100 ZNF266	0.8985501 5.77159081 173.156778	1.51E-39	6.54E-39 0.81895038 2.77777778 97.2222222
ENSG 00000142082	SIRT3	1.14184647 2.66390308 170.725821	5.14E-39	1.69E-38 1.12269884		100 SIRT3	1.17922666 2.65495841 148.844764	3.10E-34	1.20E-33 1.01531596 2.77777778 97.2222222
ENSG 00000083535	PIBF1	1.00718977 3.45455498 170.575448	5.54E-39	1.82E-38 1.04199338		100 PIBF1	0.59523962 3.17888926 46.011515	1.18E-11	2.48E-11 0.56404261 8.33333333 91.6666667
ENSG 00000181915	ADO	-0.8956077 4.29422365 170.440212	5.93E-39	1.94E-38 -0.8077583			-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			0.91890821 5.1773428 170.472493	5.83E-39	2.49E-38 0.99471589 2.77777778 97.2222222
ENSG 00000076513	ANKR D13A	-0.8090886 5.88382887 170.029465	7.29E-39	2.39E-38 -0.7116433		0 ANKRD13A	-0.7905111 5.8609024 135.763662	2.25E-31	8.19E-31 -0.8410741 100 0
ENSG 00000226479	TMEM185B	-0.9361878 3.93489308 169.965101	7.53E-39	2.46E-38 -0.8618959		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		100 DG KZ	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		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		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		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		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			-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			1.35026056 5.60915093 371.97927	6.94E-83	5.43E-82 1.27835322 5.5555556 94.4444444
ENSG00000111203	ITFG2	0.8766386 4.44896238 167.757277	2.29E-38	7.41E-38 0.89577203		100 ITFG2	0.77475887 4.33101595 107.694788	3.14E-25	9.92E-25 0.69824807 2.77777778 97.2222222
ENSG 00000270589	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 -0.517993	5 94 444444	5 5555556
ENSG0000003322	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 0.9363506		
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 -1.111267		0
ENSG000001725898	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		2 7777778
ENSG00000123856	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 0.647786		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		
ENSG00000170104	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		
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 0.8732690		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 -0.781996		
ENSG00000090905	TNRC6A	0.79372597 6.23520654 164.572036	1.13E-37	3.64E-37 0.86256826	0	100 TNR C6A	0.74572484 6.18289088 121.008067	3.81E-28		7 2.77777778	
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 -1.064167		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 0.8573934		100
ENSG00000113546	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 0.6306827		
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		
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		9 5.5555556	
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 0.6586142		
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		
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		
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 0.6809561		
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		
ENSG00000135506	OS9	-0.7973349 6.09754671 163.846657	1.63E-37		97.1428571	2.85714286 OS9	-0.8881362 6.04786392 166.671949	3.95E-38	1.65E-37 -1.034109:		
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		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 -1.490530		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 -1.340440	7 100	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 0.7812011		100
ENSG00000123329	ARHG AP9	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		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	5 100	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 0.8234552	3 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	2 100	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 0.5899556	3 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	97.222222	2.7777778
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	5 2.77777778	97.222222
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 -1.070163	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	1 100	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 0.6573912	5 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	9 66.6666667	33.333333
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 -0.617588	2 100	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 0.6929262	5 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 -0.689859		
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		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		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		
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 0.5458020		
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		
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		100
ENSG00000184596	NA	1.34824301 1.34228984 157.563831	3.85E-36	1.20E-35 1.33290344			1.65912995 1.53208722 192.024038	1.15E-43	5.32E-43 1.6444373		
ENSG00000071894	CPSF1	0.79190408 5.60104381 157.539875	3.90E-36	1.21E-35 0.87815268		94.2857143 CPSF1	1.00161138 5.65862412 204.469042	2.21E-46	1.07E-45 0.8107436		
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		5 97.2222222	
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		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 0.66305030		
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		100
ENSG00000130939	UBE4B	0.79965953 5.05114041 156.425498	6.83E-36	2.11E-35 0.89433703	0	100 UB E4B	0.83451112 5.00875252 141.815388	1.07E-32	4.01E-32 0.8268048	5 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 -0.68	4372 100 0
ENSG00000115703	SDHAF1	-1.2368095 1.79324928 155.754349	9.58E-36	2.96E-35 -1.162927		0 SDHAF1	-0.7661973 1.89054076 50.0664983	1.49E-12		3626 97.2222222 2.77777778
ENSG00000203136	SURF6	0.82785561 4.5894729 155.739393	9.65E-36	2.98E-35 0.82131408		100 SURF6	0.89223224 4.58730579 151.053975	1.02E-34	4.00E-34 0.7490	
ENSG00000111679	PTPN6	-0.7793808 5.80413474 155.497852	1.09E-35	3.36E-35 -0.6557265			-1.5243002 5.58281274 469.267445	4.63E-104	4.48E-103 -1.489	
ENSG00000111075	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 -0.772	
ENSG00000122008	TMEM205	-1.1087439 2.53537838 154.502532	1.80E-35	5.55E-35 -0.9471848		0 TMEM205	-1.3158031 2.42705356 169.816971	8.11E-39	3.44E-38 -1.392	
ENSG00000103318	C4orf48	-1.3323059 1.2763562 154.371152	1.92E-35	5.92E-35 -1.34101		0 C4orf48	-0.8149332 1.42406913 47.3687267	5.88E-12		9666 88.8888889 11.1111111
ENSG00000243449	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		1473 97.2222222 2.77777778
ENSG00000144303	NDUFB7	-0.9417245 3.59378928 153.385472	3.16E-35	9.66E-35 -0.8739294			-0.6984656 3.63234841 73.1945287	1.17E-17		8744 91.6666667 8.33333333
ENSG00000033733	CPEB4	-0.7775961 5.69665422 153.358112	3.20E-35	9.79E-35 -0.6909706			-0.7170555 5.69773001 108.91159	1.70E-25		2999 94.4444444 5.55555556
ENSG00000113742	BLOC1S1	-1.0297786 2.97673351 153.186016	3.49E-35	1.07E-34 -1.0013327		0 BLOC1S1	-0.7971694 3.03630146 78.1281607	9.66E-19		7382 94.4444444 5.55555556
ENSG00000171522	PTGER4	0.76386517 8.728633 153.168666	3.52E-35	1.08E-34 0.93242876			0.64326196 8.59681005 81.6773799	1.60E-19		2098 16.6666667 83.3333333
ENSG00000171322	RNF20	0.84550309 4.31068558 153.0498	3.74E-35	1.14E-34 0.871798		100 RNF20	0.6168375 4.10819916 65.752716	5.11E-16	1.25E-15 0.5609	
ENSG00000119392	GLE1	0.81834548 4.59198419 152.676523	4.51E-35	1.38E-34 0.8649259		100 GLE1	0.64370979 4.45652834 77.342788	1.44E-18	3.79E-18 0.5806	
ENSG00000115352	PSENEN	-1.2244567 1.82772974 152.365186	5.27E-35	1.61E-34 -1.2580722		0 PSENEN	-0.7789226 1.94587874 51.8514788	5.99E-13		8514 94.4444444 5.55555556
ENSG00000203133	ARHGEF1	0.753145 8.69494799 152.273663	5.52E-35	1.68E-34 0.79019501		100 ARHGEF1	0.72274911 8.58696946 103.574252	2.51E-24		5509 5.55555556 94.4444444
ENSG00000070328	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 -1.009	
ENSG00000125071	ZNF76	0.85089623 4.25776864 151.502103	8.14E-35	2.47E-34 0.93599673			0.76896528 4.12286721 100.903281	9.66E-24		6652 2.77777778 97.2222222
ENSG 000000167685	ZNF444	0.87388768 4.01889339 151.306951	8.98E-35	2.73E-34 0.9985201		100 ZNF444	0.68853423 3.8675776 76.4443961	2.27E-18		2011 5.55555556 94.4444444
ENSG00000186480	INSIG1	-0.7570254 6.48206408 151.17603	9.59E-35	2.91E-34 -0.6289153		0 INSIG1	-0.8425325 6.39327498 153.102348	3.64E-35	1.44E-34 -0.812	
ENSG00000180480	RFC1	0.75718522 6.29409836 151.119233	9.87E-35	2.99E-34 0.80759179		100 RFC1	0.6136345 6.11616154 82.4176733	1.10E-19		7181 5.55555556 94.4444444
ENSG00000117448	AKR1A1	-0.8864142 3.92036852 150.969475	1.06E-34	3.23E-34 -0.7495648		0 AKR1A1	-0.669937 3.93523253 72.7981787	1.44E-17		0262 94.4444444 5.55555556
ENSG0000017448	PHPT1	-1.0947736 2.51870686 150.480889	1.36E-34	4.12E-34 -1.1254135		0 PHPT1	-0.6951291 2.62874694 51.4650647	7.29E-13		0475 91.6666667 8.33333333
ENSG00000054148	SLK	-0.7581262 6.08977204 150.395493	1.42E-34	4.30E-34 -0.6422777		O SLK	-0.5551639 6.11181369 67.4852159	2.12E-16		0667 94.4444444 5.55555556
ENSG00000157800	SLC37A3	0.90086026 3.77785519 150.326582	1.47E-34	4.45E-34 0.95687839		100 SLC37A3	0.74565561 3.61181319 83.5971024	6.07E-20	1.67E-19 0.6714	
ENSG00000141985	SH3GL1	-0.7788726 5.21112941 150.294468	1.49E-34	4.52E-34 -0.7385813		0 SH3GL1	-0.5013077 5.26534578 52.5942679	4.10E-13		5511 97.2222222 2.7777778
ENSG00000141303	TBC1D10A	0.80067463 4.73554412 150.100401	1.65E-34	4.98E-34 0.82623418		100 TBC1D10A	0.95302194 4.78911477 178.252511	1.17E-40	5.16E-40 0.8588	
ENSG00000196182	STK40	-0.7724187 5.44118965 149.98472	1.75E-34	5.28E-34 -0.587416	_	0 STK40	-1.0184779 5.37198055 215.387765	9.17E-49	4.64E-48 -1.017	
ENSG00000104388	RAB2A	-0.758261 6.02589405 149.854026	1.87E-34	5.63E-34 -0.6998655		2.85714286 RAB2A	-0.4830437 6.05958247 51.2866401	7.98E-13		2728 94.4444444 5.55555556
ENSG00000085511	MAP3K4	0.83553469 4.30129398 149.687459	2.03E-34	6.12E-34 0.87982536		100 MAP3K4	0.74510557 4.18183564 97.3318065	5.86E-23	1.75E-22 0.6847	
ENSG00000170348	TMED10	-0.7515132 6.44698126 149.420148	2.32E-34	7.00E-34 -0.7477305		0 TMED10	-0.5301356 6.49142696 61.7035713	3.99E-15	9.52E-15 -0.569	
ENSG00000156471	PTDSS1	-0.7538728 6.04969864 148.963297	2.92E-34	8.79E-34 -0.6719498		0 PTDSS1	-0.5659484 6.06068517 70.4529055	4.71E-17	1.19E-16 -0.639	3982 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 0.6454	5043 5.55555556 94.4444444
ENSG00000138600	SPPL2A	-0.7854131 4.93284104 147.766003	5.34E-34	1.60E-33 -0.6806405	100	O SPPL2A	-0.549031 4.99325866 61.1822554	5.20E-15	1.23E-14 -0.59	3174 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 0.709	3801 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 1.2035	8612 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 0.8582	9915 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 -0.553	3813 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 0.5812	0415 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 1.2858	2512 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 -1.165	5293 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 -0.861	9012 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 1.0684	5173 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 -0.773	5128 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 0.8997	1075 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 0.6387	5056 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		8232 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 0.7765	9283 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 0.728	4172 2.77777778 97.2222222
ENSG00000100263	RHBDD3	1.07506753 2.47056139 145.112173	2.03E-33	6.02E-33 1.08096392		100 RHB DD3	0.94449476 2.33685 88.0570218	6.36E-21	1.80E-20 0.7786	
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 1.0870	
ENSG00000188186	LAMTOR4	-0.7767087 4.92712835 144.701128	2.50E-33	7.39E-33 -0.6882303		0 LAMTOR4	-0.9616798 4.83700984 180.310901	4.15E-41		3647 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 0.6212	8138 0 100

ENSG00000092140	G2E3	0.70272010	4.77239273	142 274627	5.12E-33	1 E1E 22	0.80497605	0	100	G2E3	0.57111400	A 612A1616	62.0689333	3.32E-15	7 01E 1E	0.57419042	11.1111111	00 0000000
ENSG00000092140 ENSG00000137312	FLOT1		5.09220524		5.12E-33 5.42E-33			94.2857143					443.804909	1.61E-98		-1.4989757	100	00.0000009
ENSG00000137312 ENSG00000120875	DUSP4		6.67389989		5.44E-33			91.4285714		DUSP4			96.7305357	7.94E-23			88.8888889	11 1111111
ENSG00000120875	WASH2P		3.49584935		6.69E-33		0.92406521	0		WASH2P			107.967744	2.73E-25		0.74136305	00.0000000	100
ENSG00000146556 ENSG00000126001	CEP250		4.79022314		7.96E-33		0.84126475	0		CEP250			177.504346	1.70E-40		0.74136303	0	100
ENSG00000126001	VHL		6.33441902		7.98E-33		-0.6303682	100	100	VHL			107.268883	3.89E-25	1.23E-24	-0.728792	100	100
ENSG00000134086 ENSG00000131467	PSME3		6.22789745		9.28E-33		-0.6522798	100	0	PSME3			39.549992	3.20E-25	6.40E-10		97.2222222	2 7777779
ENSG00000131467 ENSG00000125734	GPR108		3.82143853		1.03E-32		-0.0522798			GPR 108			76.4183485	2.30E-10	6.40E-10 6.00E-18	-0.7903553	100	2.7777770
ENSG00000125734 ENSG00000148730	EIF4EBP2		6.23713208		1.03E-32 1.59E-32		-0.7581355	100 100		EIF4EBP2			61.6091615	4.19E-15	9.96E-15	-0.7903553	100	0
ENSG00000148730	HPRT1		3.4922976		1.64E-32		-0.832319	100	0	HPRT1			83.5984491	6.06E-20	1.66E-19	-0.7635849	100	0
ENSG00000163704 ENSG00000152240	HAUS1		1.79205436		2.30E-32		-1.1128401	100	0	HAUS1			38.2321559	6.28E-10			94.4444444	C EEEEEEE
ENSG00000132240	MED13L		8.34339577		2.55E-32		-0.6104874		0	MED13L			94.9354585	1.97E-22			97.2222222	
ENSG00000123066 ENSG00000100599	RIN3		7.18745986		2.55E-32 2.59E-32			100 94.2857143		RIN3			191.50504	1.97E-22 1.49E-43		-1.0059398	100	2.7777778
	DVL1		4.44042971		2.83E-32			94.2857145	-	DVL1			90.4453014	1.49E-43 1.90E-21		0.61802019	0	100
ENSG 00000107404 ENSG 00000168256	NKIRAS2		4.94996764		3.03E-32		0.78919573 -0.699063	100		NKIRAS2			130.386786	3.37E-30		-0.9078901	100	100
ENSG00000188258	PJA2		7.23236906		3.51E-32		-0.677483	100		PJA2			80.8518273	2.43E-19			97.2222222	2 7777770
ENSG00000198961 ENSG00000196498	NCOR2		7.29483187		3.84E-32		-0.5943004	100		NCOR2			185.829889	2.43E-19 2.59E-42			97.2222222	
ENSG00000196438	KDELR1		3.99611717		3.87E-32		-0.7319541	100		KDELR1			99.0656328	2.44E-23	7.36E-23	-0.8648579	100	2.7777770
ENSG00000103438 ENSG00000173273	TNKS		5.31507635		4.33E-32		0.76271247	0		TNKS			109.426442	1.31E-25	4.19E-25		2.77777778	07 222222
										_				1.31E-23 1.27E-12			91.6666667	
ENSG 00000108061 ENSG 00000213246	SHOC2 SUPT4H1		6.40133137 5.58762375		4.91E-32 5.58E-32		-0.6418086 -0.6531396	100 100		SHOC2 SUPT4H1			50.3723316 137.87879	7.75E-32	2.79E-12 2.86E-31	-0.5022458 -0.8851218	100	8.3333333
			3.74376159		5.76E-32			100	100	ESF1				3.29E-15			2.7777778	07 222222
ENSG 00000089048 ENSG 00000131844	ESF1 MCCC2		4.08277344		5.76E-32 5.99E-32		0.97585475 0.91748616	0		MCCC2			62.0820999 57.6286852	3.29E-15 3.17E-14	7.86E-15		5.5555556	
	SERPINB1				7.75E-32			_		SERPINB1	0.59295114		174.567714	7.44E-40		-0.9404664		94.4444444
ENSG00000021355 ENSG00000137996	RTCA		5.94117965 4.35260643		8.13E-32		0.87025182	97.1428571		RTCA			165.220902	8.19E-38		0.91272955	100 0	100
ENSG00000137936 ENSG00000198874	TYW1		4.15039833		1.09E-31		0.88208964	0	100	TYW1			120.811566	4.20E-28		0.75567501	0	100
ENSG00000198874 ENSG00000147324	MFHAS1		4.71856663		1.19E-31			91.4285714		MFHAS1			890.595039	1.09E-195		-2.4331916	100	100
ENSG00000147524 ENSG00000063587	ZNF275		4.65879764		1.74E-31		0.75266555	0		ZNF275			80.3666625	3.11E-19			5.5555556	04 4444444
ENSG00000005387	DNASE2		3.31574959		1.84E-31			94.2857143		DNASE2			139.226633	3.93E-32		-1.1144524	100	0
ENSG00000103012	TMEM167B		6.68709053		1.97E-31		-0.6434381	100	0.71428371	TMEM167B			96.146544	1.07E-22		-0.6962564	100	0
ENSG00000215717 ENSG00000185947	ZNF267		5.49190683		2.31E-31		-0.6320972	100	0	ZNF267			114.406653	1.06E-26		-0.7482646	100	0
ENSG00000141873	SLC39A3		3.89005601		2.59E-31		-0.7858231	100		SLC39A3			50.5311456	1.17E-12		-0.5048642	100	0
ENSG00000141875	UNKL		3.83224842		2.70E-31		0.91651704	0	_	UNKL			112.787253	2.40E-26			2.77777778	97 222222
ENSG00000099917	MED15		7.08993816		3.28E-31		0.7859679	0		MED15			257.605922	5.71E-58		1.0881729	0	100
ENSG00000108829	LRRC59		6.04427005		4.13E-31		-0.6818201	100	0	LRRC59			52.8683667	3.57E-13		-0.5291203	100	0
ENSG00000167315	ACAA2		3.52516979		4.56E-31		-0.8518627	100	0	ACAA2			32.3014522	1.32E-08	2.46E-08		86.1111111	13.8888889
ENSG00000182247	UBE2E2		2.87178595		5.52E-31		-0.8308801	100		UBE2E2			83.2857281	7.10E-20		-0.8778762	100	0
ENSG00000172869	DMXL1		5.34337782		6.52E-31		-0.6159143	100		DMXL1			70.8498891	3.85E-17		-0.5826794	100	0
ENSG00000270184	RP11-568J23.5		0.80982233		7.48E-31		1.42643732	0		RP11-568J23.5				1.53E-34			2.7777778	97.222222
ENSG00000147130	ZMYM3		3.81476644		9.13E-31		0.88465561	0		ZMYM3			147.992069	4.76E-34			2.77777778	
ENSG00000172493	AFF1		6.12090642		1.46E-30			88.5714286	11.4285714	AFF1			148.791616	3.18E-34		-0.8388788	100	0
ENSG00000148688	RPP30		4.29936856		1.51E-30		0.81241032	0		RPP30			77.8476996	1.11E-18			2.7777778	97.222222
ENSG00000197858	GPAA1		4.37496845		2.29E-30		-0.7298905	100		GPAA1			52.0358536	5.45E-13			91.6666667	
ENSG00000078043	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	97.222222
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		5.88275013		2.97E-30		0.75669004	0		AQR			147.968534	4.82E-34			5.5555556	
ENSG00000138071	ACTR2		7.95745124		3.17E-30		-0.6368756	100	0	ACTR2			84.3915111	4.06E-20			97.2222222	
ENSG00000136146	MED4		5.28265943		3.31E-30		0.78044703	0	100	MED4			94.6027238	2.33E-22			5.5555556	
ENSG00000130749	ZC3H4		4.87808219		4.92E-30			2.85714286		ZC3H4			71.118088	3.36E-17			8.33333333	
ENSG00000108654	DDX5		10.389261		6.45E-30		0.72270037	0		DDX5			44.0137886	3.26E-11			13.8888889	
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		-0.6550636	100	0	TRAF6			70.3100465	5.07E-17	1.28E-16	-0.531544	100	0
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ENSG 00000166913	YWHAB	-0.6903634 7.02392539 128.0		3.04E-29 -0.6569578		0 YWHAB	-0.647448 6.9741095 92.0600394	8.41E-22	2.43E-21 -0.6628		
ENSG00000146083	RNF44	0.68932013 7.00932735 127.8		3.39E-29 0.77807567		100 RNF44	0.61928251 6.89891705 83.9662525	5.03E-20	1.39E-19 0.59118		
ENSG 00000254635	WAC-AS1	-0.8757338 3.40809837 127.6		3.69E-29 -0.7296575			-0.8697174 3.37033869 104.331285	1.71E-24	5.30E-24 -0.9960		
ENSG00000150961	SEC24D	-0.833101 3.73316775 127		4.43E-29 -0.8123508		0 SEC24D	-0.5822409 3.80594358 53.3737373	2.76E-13	6.18E-13 -0.5954		
ENSG00000102531	FNDC3A	0.72771566 4.89696459 127.1		4.79E-29 0.76328271		100 FNDC3A	0.88080952 4.95802788 155.683154	9.93E-36	3.96E-35 0.87619		
ENSG00000003056	M6PR	-0.800641 4.02113359 126.7		5.82E-29 -0.6997759			-0.7363273 4.03400421 90.5694485	1.79E-21	5.13E-21 -0.8035		
ENSG00000198382	UVRAG	-0.7244231 4.95648568 126.5		6.27E-29 -0.6148359		0 UVRAG	-0.6956651 4.87459662 96.6660868	8.21E-23	2.44E-22 -0.7135		
ENSG00000015285	WAS	-0.7114087 5.30738177 126.1		7.70E-29 -0.6140249			-0.7159075 5.28719533 105.941753	7.59E-25	2.38E-24 -0.8299		
ENSG00000116906	GNPAT	0.85809895 3.51511395 126.0		8.36E-29 0.94289905			0.54680764 3.29850842 40.4584214	2.01E-10	4.05E-10 0.65801		
ENSG00000100911	PSME2	-0.7052182 5.42664578 125.5		1.07E-28 -0.534308		0 PSME2	-0.6265546 5.43711497 82.7284182	9.41E-20	2.57E-19 -0.6498		
ENSG00000095261	PSMD5	0.73266971 4.73291204 125.1		1.27E-28 0.78210205		100 PSMD5	0.63089914 4.63038024 76.6666232	2.02E-18	5.30E-18 0.60107		
ENSG00000170445	HARS	0.72120505 4.90950472 125.1		1.27E-28 0.80596081		100 HARS	1.01863774 5.02952212 210.294023	1.19E-47	5.89E-47 0.96586		200
ENSG00000163348	PYGO2	0.74372972 4.53975022 125		1.34E-28 0.77954511		100 PYGO2	0.76079387 4.53213978 109.562737	1.22E-25	3.91E-25 0.6911		
ENSG00000180917	CMTR2	-0.797791 3.95533454 124.8		1.49E-28 -0.8103517		0 CMTR2	-0.7832904 3.87995063 99.3622712	2.10E-23	6.34E-23 -0.8411		
ENSG00000079739	PGM1	-0.9221763 2.97016679 124.8	802695 5.62E-29	1.53E-28 -0.8357123	100	0 PGM1	-0.5845041 3.08307303 43.881003	3.49E-11	7.22E-11 -0.5990	773 100	0
ENSG00000122965	RBM19	0.72802003 4.77834844 124.5		1.76E-28 0.79155567	0	100 RBM19	0.80151033 4.75899277 125.513549	3.93E-29	1.36E-28 0.74508		
ENSG00000124151	NCOA3	-0.6781541 7.40403996 124.2	259345 7.39E-29	2.01E-28 -0.5270338	100	0 NCOA3	-0.6619324 7.35029337 94.874092	2.03E-22	5.97E-22 -0.6586	736 97.2222222	2.7777778
ENSG0000001497	LAS1L	0.71418933 4.99789956 124.2	245243 7.44E-29	2.03E-28 0.80389425	0	100 LAS1L	0.62451818 4.87142687 78.5550353	7.78E-19	2.07E-18 0.53177	202 0	100
ENSG00000164983	TMEM65	-0.9199509 2.9774233 124.1	138106 7.86E-29	2.14E-28 -0.7217627	100	0 TMEM65	-1.2764608 2.85080777 187.168876	1.32E-42	6.01E-42 -1.2266	474 100	0
ENSG00000067248	DHX29	0.70399041 5.22267831 124.1	114005 7.95E-29	2.17E-28 0.78169554	0	100 DHX29	0.63919442 5.10831922 84.6494849	3.56E-20	9.85E-20 0.63176	913 0	100
ENSG00000144357	UBR3	0.71748262 4.9222066 124.1	101325 8.00E-29	2.18E-28 0.77266544	0	100 UBR3	0.50302997 4.74751952 49.9228941	1.60E-12	3.48E-12 0.50584	607 11.1111111	88.888889
ENSG00000172831	CES2	0.74770937 4.4786056 124.0	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 0.71594	598 2.77777778	97.222222
ENSG00000103174	NAGPA	0.75642974 4.34407535 124.0	025336 8.32E-29	2.26E-28 0.8590549	0	100 NAGPA	0.66271291 4.21787351 77.7853796	1.15E-18	3.04E-18 0.60721	196 0	100
ENSG00000135040	NAA35	0.855344 3.44747237 123	3.56083 1.05E-28	2.86E-28 0.87778916	0	100 NAA35	0.77345218 3.36805325 83.1664235	7.54E-20	2.07E-19 0.67670	396 5.5555556	94.444444
ENSG00000105708	ZNF14	0.74476974 4.57997338 123.3	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 0.91948	357 13.8888889	86.1111111
ENSG00000131871	VIMP	-0.7678172 4.1886738 122.8	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 -0.5697	468 97.222222	2.7777778
ENSG00000204282	TNRC6C-AS1	0.81436605 3.79261421 122.6	587729 1.63E-28	4.42E-28 0.88911442	2.85714286	97.1428571 TNR C6C-AS1	0.72646455 3.64106836 78.3839149	8.48E-19	2.26E-18 0.5928	691 2.7777778	97.222222
ENSG00000160888	IER2	-0.680922 7.84852024 122.6	570287 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 -0.5647	715 86.1111111	13.8888889
ENSG00000196642	RABL6	0.69158547 5.65846563 12	2.3321 1.95E-28	5.28E-28 0.74493541	. 0	100 RABL6	0.77726246 5.6852963 127.73929	1.28E-29	4.49E-29 0.69560	337 5.5555556	94.444444
ENSG00000092439	TRPM7	0.67737219 6.64504044 122.2	286678 2.00E-28	5.40E-28 0.71502303	0	100 TRPM7	0.64347686 6.56580462 90.4316667	1.91E-21	5.49E-21 0.56883	024 5.5555556	94.444444
ENSG00000113300	CNOT6	0.72423799 4.70508523 122.2	273496 2.01E-28	5.43E-28 0.83429046	0	100 CNOT6	0.82064477 4.74573842 131.920907	1.56E-30	5.58E-30 0.76640	744 0	100
ENSG00000110851	PRDM4	-0.6778111 6.48857447 121.4	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 -0.6985	357 100	0
ENSG00000122224	LY9	-0.6932685 5.86352314 120.9	956321 3.91E-28	1.05E-27 -0.6133798	8 85.7142857	14.2857143 LY9	-0.9817042 5.66975194 199.398783	2.83E-45	1.34E-44 -0.9966	397 97.222222	2.7777778
ENSG00000075785	RAB7A	-0.6719847 6.92610958 120.7	792077 4.24E-28	1.14E-27 -0.6454385	100	O RAB7A	-0.7581622 6.84467784 125.651589	3.66E-29	1.27E-28 -0.812	288 100	0
ENSG00000130703	OSBPL2	0.69368456 5.23199208 120.5	598951 4.68E-28	1.26E-27 0.75357718	0	100 OSBPL2	0.68017465 5.16945026 96.3281558	9.73E-23	2.89E-22 0.63013	917 2.7777778	97.222222
ENSG00000112893	MAN2A1	0.67395767 6.35282132 120.2	220501 5.66E-28	1.52E-27 0.74405753	0	100 MAN2A1	0.67845422 6.2929971 100.559459	1.15E-23	3.49E-23 0.59486	524 5.5555556	94.444444
ENSG00000121892	PDS5A	0.67445979 6.33935772 120.1	125241 5.94E-28	1.59E-27 0.75899699	0	100 PDS5A	0.60792496 6.21858523 81.1381866	2.10E-19	5.70E-19 0.62160	275 8.33333333	91.6666667
ENSG00000187514	PTMA	-0.6738378 10.5897394 120.0	074312 6.09E-28	1.63E-27 -0.5901153	100	O PTMA	-0.5222025 10.560058 47.3104824	6.06E-12	1.30E-11 -0.5552	592 100	0
ENSG00000224078	SNHG14	0.74310785 4.38766554 119.9	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 0.72284	319 2.7777778	97.222222
ENSG00000132549	VPS13B	0.68113314 5.86312479 119.6	594894 7.38E-28	1.98E-27 0.61829612	2 0	100 VPS13B	0.59286552 5.73536618 75.3979641	3.85E-18	9.98E-18 0.55475	478 5.5555556	94.444444
ENSG00000205413	SAMD9	-0.7172004 4.73994501 119.6	582738 7.42E-28	1.99E-27 -0.563122	100	0 SAMD9	-0.5186084 4.79699707 52.4625394	4.39E-13	9.76E-13 -0.5220	553 86.1111111	13.8888889
ENSG00000103363	TCEB2	-0.6830024 5.65714169 118.8	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 -0.6171	937 94.444444	5.5555556
ENSG00000105953	OGDH	-0.8342464 3.50234509 118.7	758874 1.18E-27	3.15E-27 -0.7203855	100	0 OG DH	-0.4591821 3.53925774 30.7922107	2.87E-08	5.26E-08 -0.506	447 88.8888889	11.1111111
ENSG00000127463	EMC1	0.7007889 4.93162205 118	3.57655 1.30E-27	3.46E-27 0.77687832	2 0	100 EMC1	0.84797414 4.97574492 145.634932	1.56E-33	5.97E-33 0.72632	538 0	100
ENSG00000155115	GTF3C6	-0.7849393 3.87840338 118.2	261193 1.52E-27	4.05E-27 -0.7311024	100	0 GTF3C6	-0.4940542 3.93463957 40.2875702	2.19E-10	4.41E-10 -0.5476	234 97.2222222	2.7777778
ENSG00000213024	NUP62	-0.6852373 5.33257579 118.2	254569 1.53E-27	4.06E-27 -0.5890684	100	0 NUP62	-0.5995753 5.29151172 75.8713412	3.03E-18	7.88E-18 -0.6313	023 97.2222222	2.7777778
ENSG00000164105	SAP30	-1.1427463 1.37985345 118.0	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 -0.5144	808 94.444444	5.5555556
ENSG00000163349	HIPK1	0.66126101 8.49417125 117.8	865942 1.86E-27	4.93E-27 0.70796512	0	100 HIPK1	1.02894216 8.63971688 210.078603	1.32E-47	6.56E-47 1.02872	219 2.77777778	97.222222
ENSG00000108854	SMURF2	0.68599083 5.22361417 117.6		5.38E-27 0.68363867		100 SMURF2	0.75012414 5.22406878 117.683976	2.03E-27	6.78E-27 0.62078		
ENSG00000089737	DDX24	0.65721742 8.45336667 117.5		5.86E-27 0.65653861		100 DDX24	0.85129343 8.48763953 147.862588	5.08E-34	1.96E-33 0.80044		
ENSG00000159110	IFNAR2	-0.7604386 4.08613703 117.3		6.25E-27 -0.7051442		0 IFNAR2	-1.3551996 3.88943174 288.699404	9.55E-65	6.02E-64 -1.3631		
ENSG00000182117	NOP10	-0.7294102 4.46397106 116.9				11.4285714 NOP10	-0.7308837 4.42678143 97.0825273	6.65E-23	1.98E-22 -0.8482		_
ENSG00000204946	ZNF783	0.72552896 4.45690719 116.6		8.97E-27 0.80265616			0.68278485 4.35699268 84.7513209	3.38E-20	9.36E-20 0.58498		

ENSG00000105607	GCDH	0.94728304			3.74E-27		1.04563707	0	100	GCDH		2.44925923 68.47		29E-16			2.77777778	97.222222
ENSG00000239672	NME1	-1.0174349			3.89E-27		-0.9550745	100	(NME1		2.06380454 65.98		4E-16		-0.9472766	100	0
ENSG00000174231	PRPF8	0.65494234			4.14E-27		0.65792592	0	100	PRPF8		8.77720182 152.3		20E-35			2.77777778	97.222222
ENSG00000141627	DYM	-0.7228324			4.52E-27		-0.6230177	100	(DYM		4.38333968 99.45		00E-23		-0.7118239	100	0
ENSG 00000117523	PRRC2C	0.65561911			5.37E-27		0.63349342	0	100			9.36850537 126.5		38E-29			2.77777778	
ENSG00000113649	TCERG1	0.65778794			5.90E-27		0.68462332	0	100					51E-21			2.77777778	97.222222
ENSG 00000236104	ZBTB22		3.67038838		6.02E-27			94.2857143	5.71428571			3.59789384 125.0		04E-29		-1.0764988	100	0
ENSG 00000026508	CD44	-0.6541368			6.36E-27		-0.5898623	100	(CD44		9.34331229 56.6		L8E-14		-0.5542006	100	0
ENSG 00000246451	RP11-894P9.1	1.0784023			6.72E-27	1.77E-26	1.17162588	5.71428571		RP11-894P9.1		1.82232682 117.2		57E-27			2.77777778	
ENSG00000168228	ZCCHC4	0.89473169			7.39E-27		1.01970286	0	100	ZCCHC4		2.8138964 77.58		27E-18			2.77777778	97.222222
ENSG00000068323	TFE3	-0.6615995	6.05448579	114.820281	8.62E-27		-0.5526744	100	(TFE3	-0.6942871	5.99768261 105.2	21297 1.0	09E-24	3.40E-24	-0.7564063	100	0
ENSG00000151806	GUF1	0.72787508			9.13E-27		0.84729515	0	100	GUF1		4.21975517 67.3		25E-16			5.5555556	
ENSG 00000126005	MMP24-AS1	-0.7173338	4.47939383	114.668516	9.30E-27	2.44E-26	-0.6680912	100	(MMP24-AS1	-0.5522329	4.52048591 57.19	69175 3.9	94E-14	9.12E-14	-0.6755692	91.6666667	8.3333333
ENSG00000099940	SNAP29	-0.6769867	5.22367369	114.652033	9.38E-27	2.46E-26	-0.5680165	100	(SNAP29	-0.4740079	5.26216465 47.43		57E-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	(F11R	-0.6241502	4.02958347 65.98	44915 4.5	54E-16	1.11E-15	-0.6522442	100	0
ENSG 00000074695	LMAN1	0.68185448	5.07184077	114.240115	1.15E-26	3.02E-26	0.68879208	0	100	LMAN1	0.79278576	5.10509762 128.7	28503 7.7	78E-30	2.74E-29	0.75747328	2.77777778	97.222222
ENSG 00000175602	CCDC85B	-0.7198475	4.49972384	114.174634	1.19E-26	3.12E-26	-0.6522824	85.7142857	14.2857143	CCDC85B	-0.5121924	4.49771345 48.58	47607 3.1	L6E-12	6.82E-12	-0.5595095	88.888889	11.1111111
ENSG 00000100888	CHD8	0.64872496	7.63271175	114.106274	1.24E-26	3.23E-26	0.71496389	0	100	CHD8	0.74699002	7.6316707 119.1	84928 9.5	4E-28	3.21E-27	0.63322284	2.77777778	97.222222
ENSG 00000099910	KLHL22	0.82949398	3.36750277	114.091115	1.24E-26	3.26E-26	0.91413268	0	100	KLHL22	0.7926697	3.3270722 86.51	41195 1.3	39E-20	3.89E-20	0.78480344	2.77777778	97.222222
ENSG00000128534	LSM8	0.67486526	5.21060494	113.898136	1.37E-26	3.58E-26	0.70945732	0	100	LSM8	0.74617161	5.20370381 116.0	56834 4.6	52E-27	1.53E-26	0.69317714	0	100
ENSG 00000176108	CHMP6	-0.9934439	2.2139851	113.866557	1.39E-26	3.64E-26	-0.8934878	100	(CHMP6	-0.9085634	2.21944265 76.45	65765 2.2	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 195.5	96151 1.9	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	(UTP3	-0.5134228	4.44637216 49.21	07977 2.3	30E-12	4.97E-12	-0.5243114	97.222222	2.7777778
ENSG00000101558	VAPA	-0.6485123	7.17241319	113.682828	1.53E-26	3.99E-26	-0.5404285	100	(VAPA	-0.6587851	7.08764071 94.74	01182 2.1	L7E-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 117.9	75579 1.7	76E-27	5.87E-27	0.68591276	2.77777778	97.222222
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 2.8	33E-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 170.0	99062 7.0	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 98.53	11429 3.2	20E-23	9.60E-23	0.58767099	5.5555556	94.444444
ENSG00000156170	NDUFAF6	0.80594676	3.48398362	111.280405	5.14E-26	1.33E-25	0.85867141	0	100	NDUFAF6	0.6458723	3.29149728 57.17	07303 4.0	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	(TBCB	-0.4562138	4.50330569 38.94	71358 4.3	35E-10	8.65E-10	-0.5357498	91.6666667	8.3333333
ENSG00000104671	DCTN6	0.7050292	4.54502612	111.251686	5.21E-26	1.35E-25	0.68241342	0	100	DCTN6	0.80219858	4.54868628 120.3	84172 5.2	21E-28	1.76E-27	0.77584483	5.5555556	94.444444
ENSG 00000188647	PTAR1	0.64900424	6.36579368	110.896034	6.24E-26	1.61E-25	0.66051981	0	100	PTAR1	0.54299913	6.24716844 64.11	94607 1.1	L7E-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	(MRGBP	-0.7751558	3.32502125 82.46	17726 1.0	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	(CINP	-0.5269296	2.94270761 34.07	13473 5.3	31E-09	1.01E-08	-0.5309153	100	0
ENSG00000126945	HNR NPH2	-0.6496032	6.24715209	110.71946	6.82E-26	1.76E-25	-0.5714828	97.1428571	2.85714286	HNRNPH2	-0.8010623	6.13520843 139.8	69003 2.8	34E-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 84.46	06007 3.9	92E-20	1.08E-19	0.53208207	2.77777778	97.222222
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 103.2	54922 2.9	95E-24	9.06E-24	-0.902413	97.222222	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 124.7	06166 5.9	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 76.97	54719 1.7	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 116.9	52878 2.9	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 107.9	45601 2.7	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 97.08	21169 6.6	55E-23	1.98E-22	0.79081861	2.77777778	97.222222
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 115.3	33889 6.6	55E-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 67.23	49646 2.4	11E-16	5.96E-16	0.64621778	5.5555556	94.444444
ENSG 00000168172	ноокз	-0.6512502	5.49590078	108.567448	2.02E-25	5.16E-25	-0.6465868	100	(НООК3	-0.6683567	5.42527227 95.20	81384 1.7	71E-22	5.05E-22	-0.6846382	97.222222	2.7777778
ENSG00000173511	VEGFB	-0.7698274	3.69985768	108.556453	2.03E-25	5.19E-25	-0.6840635	100	0	VEGFB		3.6346148 83.80		16E-20			97.222222	
ENSG00000131653	TRAF7	-0.6839172	4.67037215	108.552478	2.03E-25	5.19E-25	-0.6325913	100	(TRAF7	-0.4839095	4.70676465 45.6	56608 1.4	11E-11	2.97E-11	-0.53922	88.888889	11.1111111
ENSG 00000068366	ACSL4	-0.6572967	5.32571471	108.458282	2.13E-25	5.44E-25	-0.6202548	97.1428571	2.85714286	ACSL4	-0.6939412	5.30883922 101.1	10858 8.7	70E-24	2.66E-23	-0.7129626	100	0
ENSG00000174373	RALGAPA1	0.65200394			2.25E-25	5.73E-25	0.72103294	0	100	RALGAPA1		5.40786992 97.90		38E-23	1.31E-22	0.71891079	5.5555556	94.444444
ENSG 00000017260	ATP2C1	0.65894229	5.17561879	108.31365	2.29E-25	5.85E-25	0.64131721	0	100	ATP2C1	0.64747211	5.10187328 86.53	72318 1.3	37E-20	3.85E-20	0.68081958	5.5555556	94.444444
ENSG00000181026	AEN	-0.6708557	4.95409935	107.86362	2.88E-25	7.33E-25	-0.5602927	94.2857143	5.71428571			4.8590187 92.02		55E-22	2.47E-21	-0.7613857	100	o
ENSG00000115524	SF3B1	0.63243297	9.33304591	107.577276	3.33E-25	8.45E-25	0.66452245	0	100	SF3B1	0.62829516	9.24589582 75.79	96399 3.1	L4E-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 88.29	26737 5.6	55E-21	1.60E-20	0.61644089	8.3333333	91.6666667
								_										

FNCC00000073434	7510 (506	0.00703053 4.57300057 407.533547	2 425 25	0.000.00.00.000.00		400 7510 /525	0.75244455 4.52055445 444 522455	4 5 4 5 9 5	4 475 25 2 6 65705475
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			-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			-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			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 DES12	-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		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		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 5.5555556 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			-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	01.4205714	100 CEP85L	0.57779317 5.85949368 72.2427715	1.90E-17	4.84E-17 0.5017139 5.5555556 94.4444444
ENSG00000004399	PLXND1	-0.645265 5.17955412 100.92606	9.55E-24	2.35E-23 -0.5177073			-0.7760118 5.18882946 115.68249	5.58E-27	1.84E-26 -0.8624324 77.7777778 22.2222222
ENSG00000106268	NUDT1 TAB1	-0.9098009 2.36235906 100.789554 0.73744888 3.73398662 100.35623	1.02E-23 1.27E-23	2.52E-23 -0.7593509 3.13E-23 0.82156825	100 0	0 NUDT1 100 TAB1	-0.6472465 2.41189897 42.4438264 0.7529812 3.69511396 86.84539	7.27E-11 1.17E-20	1.49E-10 -0.7555663 94.4444444 5.55555556
ENSG00000100324 ENSG00000225973	PIGBOS1		1.27E-23 1.33E-23		100	0 PIGBOS1	0.7529812 3.69511396 86.84539 -0.794026 1.61397171 48.9403488	2.64E-12	3.30E-20 0.66246963 2.77777778 97.2222222 5.70E-12 -0.8311908 97.2222222 2.77777778
ENSG00000223973	CRY1	-1.0173646 1.57716651 100.270674 0.62280688 5.73232749 100.239228	1.35E-23	3.27E-23 -0.884798 3.32E-23 0.65896208	100	100 CRY1	0.92656338 5.83008218 184.281818	5.63E-42	2.54E-41 0.84670774 0 100
ENSG00000008405	CK41 CKAP2	0.63281808 5.2457255 100.122699	1.43E-23	3.52E-23 0.65896208 3.52E-23 0.73752085	•		0.717319 5.21911121 106.414533	5.98E-25	1.88E-24 0.69414739 5.55555556 94.4444444
ENSG00000130108	HCFC2	0.68805477 4.210046 99.4464467	2.02E-23	4.94E-23 0.78150489			0.70543104 4.119757 85.7066489	2.09E-20	5.82E-20 0.64305458 2.77777778 97.2222222
ENSG00000111727 ENSG00000198898	CAPZA2	-0.6136631 6.33822849 99.410229	2.02E-23 2.05E-23	5.03E-23 -0.6047125			-0.5883952 6.28085815 75.2664949	4.11E-18	1.07E-17 -0.6096928 97.2222222 2.7777778
ENSG00000138838	GEMIN7	-0.9317946 2.13475765 99.1394184	2.35E-23	5.76E-23 -0.9595128			-0.6992225 2.15171133 45.625005	1.43E-11	3.01E-11 -0.7650789 94.4444444 5.55555556
ENSG00000142252	CHCHD2	-0.6069498 7.18227975 99.1244835	2.33E-23 2.37E-23	5.80E-23 -0.5443005			-0.4750606 7.17279324 49.3367058	2.16E-12	4.67E-12 -0.7630769 94.4444444 5.55555556
ENSG00000106133	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
ENSG00000116108	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-37	3.44E-13 -0.5951274 97.2222222 2.77777778
ENSG00000110433	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
ENSG00000214307	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	_		-0.5367279 3.94294135 47.4199321	5.73E-12	1.23E-11 -0.5206056 94.4444444 5.55555556
ENSG00000133002	SDF4	-0.6205844 5.55516376 98.2137241	3.76E-23	9.13E-23 -0.6325995			-0.4976861 5.57619398 52.705068	3.88E-13	8.65E-13 -0.6195318 86.1111111 13.8888889
ENSG00000078829	EIF2AK4	-0.6400451 4.88134534 97.998223	4.19E-23	1.02E-22 -0.6394716			-0.8803586 4.76452786 151.306283	8.98E-35	3.53E-34 -0.9433341 97.2222222 2.77777778
ENSG00000128829	ABCD3	0.69264383 4.08972365 97.9559698	4.19E-23 4.28E-23	1.04E-22 0.70102404	94.203/143	100 ABCD3	0.7232346 4.07365949 89.0027401	3.94E-21	1.12E-20
ENSG00000117528	CAND1	0.6045986 6.841015 97.9546247	4.28E-23	1.04E-22 0.70102404 1.04E-22 0.65183027	0	100 ABCD3	0.621773 6.7557852 84.6273921	3.60E-20	9.95E-20 0.5753434 5.55555556 94.4444444
ENSG00000111330	PTRHD1	-0.7797387 3.28992758 97.9447832	4.20E-23	1.04E-22 -0.7211778	-		-0.4178291 3.38529754 24.3087851	8.21E-07	1.40E-06 -0.5044262 86.1111111 13.8888889
ENSG00000184924	DDX28	-0.7168298 3.86425331 97.8753319	4.46E-23	1.08E-22 -0.6343187			-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	4.40E-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
ENSG00000153337	SHKBP1	-0.6180519 5.61551949 97.2510565	6.11E-23	1.48E-22 -0.6341787			-0.6056707 5.61121297 76.6421036	2.05E-18	5.37E-18 -0.8556567 80.5555556 19.4444444
55555555555	Jimor I	1.1100313 3.01331343 37.2310303	J.11L 23	U.UJ-1707	23.7.2.42.037	1.1.2037 2 13 31 IKBI 1	5.555707 5.01121257 70.0421050	2.052 10	5.5.2.20 0.055050, 00.5555550 15.444444

I				
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 8.3333333
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 10
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 80.555555
ENSG00000198406	BZW1P2	-1.0231587 1.45759031 96.6972651	8.08E-23	1.95F-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 94.444444 5.5555555
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 19.444444
ENSG00000129355	CDKN2D	-0.6091456 6.04708219 96.426938	9.26E-23	2.23E-22 -0.5418183 91.4285714 8.57142857 COKN2D -0.7920375 5.93247849 134.769764 3.71E-31 1.34E-30 -0.7871722 100
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 2.7777777
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 97.222222
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
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 2.777777778 97.222222
ENSG00000006530	AGK	0.72125071 3.72861134 95.6439318	1.38E-22	3.30E-22 0.83280723
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
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 10
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 8.3333333 91.666666
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 8.3333333 91.666666
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 97.222222
ENSG00000137364	TPMT	-0.7662255 3.29656522 94.5888713	2.34E-22	5.61E-22 -0.6847788 100 0TPMT -0.4850867 3.37038733 32.9717006 9.35E-09 1.75E-08 -0.5281579 97.2222222 2.7777777
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
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 2.777777778 97.222222
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 97.222222
ENSG 00000138495	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 2.7777777
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 10
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 97.222222
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
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 86.111111
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 10
ENSG 00000049245	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 2.7777777
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 97.222222
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 10
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 10
ENSG 00000099385	BCL7C	-0.658167 4.2267444 91.1591544	1.33E-21	3.13E-21 -0.5648274 97.1428571 2.85714286 BCI7C -0.6618348 4.17146244 76.2131225 2.55E-18 6.64E-18 -0.7259067 97.2222222 2.7777777
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 97.222222
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 13.888888
ENSG 00000070831	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 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
ENSG00000163840	DTX3L	-0.6213936 4.75557224 90.8800037	1.53E-21	
ENSG00000172578 ENSG00000101882	KLHL6 NKAP	0.60481754 5.13898828 90.8737182	1.53E-21 1.60E-21	3.012 22 0.003 200 3.200
	HIST3H2A	0.67880312 3.96313163 90.7873572		
ENSG00000181218 ENSG00000023191	RNH1	-1.0715154 0.96445442 90.7557771 -0.5862194 6.32326503 90.558124	1.63E-21 1.80E-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 30.555555 4.22E-21 -0.5055481 91.4285714 8.57142857 RNH1 -0.4370146 6.33810592 41.7589699 1.03E-10 -0.5603032 88.8888889 11.1111111
ENSG00000023191	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 10
ENSG00000104888	GRAMD3	0.73125378 3.4124716 89.8323423	2.47E-21 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 91.666666
ENSG00000135324	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 2.7777777
ENSG00000075142	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 97.222222
ENSG00000182130	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 94.444444 5.5555555
ENSG00000101888	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 8.3333333 91.666666
ENSG00000214415	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
ENSG00000028116	CISD2	-0.814138 2.86103034 88.2961774 -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
ENSG00000143334 ENSG00000047621	C12orf4	0.71352574 3.49499665 88.1151094	6.18E-21	1.36E-20 -0.360467 97.1426371 2.63714266 USD2 -0.4341599 4.34424033 44.6036048 2.41E-11 5.02E-11 -0.307613 100 1.43E-20 0.82665344 0 100 C12orf4 0.62214474 3.39558118 54.5194595 1.54E-13 3.48E-13 0.60455681 2.77777778 97.222222
ENSG00000047621	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
ENSG00000164219	TAF11	0.61085836 4.75084825 87.9023922	6.74E-21 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 8.3333333 91.666666
ENSG00000064993	REEP4	-0.7254192 3.41671224 87.8346612	7.12E-21	1.59E-20 0.00010424 0 100 1AF11 0.57/40253 4.67057607 64.8752028 7.90E-16 1.94E-15 0.52440405 8.5555555 91.000000 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 2.7777777
ENSG00000100239	PPP6R2	0.59919484 5.0310025 87.5116815	8.38E-21	1.05E-20 -0.7550905 94.2857145 5.71428571 PPP6R2 0.73704313 5.02584732 108.809324 1.79E-25 5.70E-25 0.60559389 5.55555556 94.444444
211300000100239	TTFUNZ	0.55515404 5.0510025 67.5110015	0.30L-21	2.72 2.0 0.700273 2.722071 2.722071 3.722071 2.00020712 2.000000000 2.7220 2.70023 0.00000000 3.0000000 34.444444

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SEGEO-CORDISION-19 CAPPOLI CAP	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
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ENS-00000154913 MAIS 0.58869019 6.2006807 8.1959308 3.667.0 8.11-20 0.60706893 7.1428571 8.181 0.75908022 6.24959139 122.281742 2.06.28 6.887.28 0.7751709 8.3333333 3.66666667 ENS-0000015955 PMAIS 0.5595867 7.1020581 8.1438502 3.987.2 0.987.2 0.5595867 7.1020581 8.1438502 3.987.2 0.987			0.79632448 2.67621782 84.769518	3.35E-20	7.63E-20 0.89010646 0	100 NUDT22		4.26E-10	
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ENGCOOD0012838 ENCCOOD0012839 ENCCOOD0012839 ENCCOOD0012839 ENGCOOD0012839 ENGC	ENSG 00000198355	PIM3	-0.5599357 8.28716649 84.4308502	3.98E-20	9.04E-20 -0.5513871 85.7142857 14.2857	143 PIM3	-0.6554278 8.15001073 89.1723243	3.62E-21	1.03E-20 -0.6134087 97.2222222 2.77777778
ENSCORDOOULS CONTINUE CONT	ENSG 00000160741	CRTC2	0.55955866 7.12065837 84.3879852	4.07E-20	9.23E-20 0.6692472 2.85714286 97.1428	571 CRTC2		2.15E-24	6.63E-24 0.61758651 0 100
ENSCO000027539 KAALIAF 0.5588024 6.652-9415 83.734128 5.662-00 1.05674057 0.100 KNANLTY 0.5598024 6.015555 6.66440868 83.44264 5.5555555 9.444444 ENSCO00001579 KAALIAF 0.5588024 6.01555 3.5590705 8.4279842 6.612-00 1.05674057 0.100 KNANLTY 0.597808 6.011457 0.5588024 6.011555 3.656408 8.6484011 4.725-1 1.345-20 0.6166763 2.7777778 97.222222 ENSCO000015867 END 0.5602375 6.4166248 8.15861718 83.171693 7.527-20 1.585-10 0.5283864 0.100 FNMM 0.5787269 6.35115649 4.728440 1.315-12 2.885171.05112 7.288517 1.355-20 0.5585555 9.4444444 ENSCO00015748 SVNE3 0.4656599 1.617560 8.0151714 7.9657719 1.000 0	ENSG 00000093183	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 5.5555556 94.4444444
ENSG00000257093 KNALIAF7 0.55580224 6.94840888 83.4422664 6.5652-00 1.865-19 0.70408676 0.100 ZNRS 0.5040768 6.9014269 6.4111555 3.666-15 8.986-16 0.55050705 83.2777777777777777777777777777777777777	ENSG 00000013563	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
ENSCO000015291 ENSCO0000152921 ENSCO0000152930 ENSCO00000152930 ENSCO000001529	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
ENSGO000015478 ENSGO000017648 ENSGO000017648 ENSGO000017648 ENSGO000017649 ENSGO000017648 ENSGO000017654 ENSGO000017656 ENSGO000017676 ENSGO0000176776 ENSGO0000176776 ENSGO0000176776 ENSGO0000176776 ENSGO0000176776 ENSGO0000176776 ENSGO0000176776 ENSGO0000176776 ENSGO0000176776 ENSGO0000176777777778 ENSGO000017677777778 ENSGO000017677777778 ENSGO000017677777778 ENSGO000017677777778 ENSGO000017677777778 ENSGO000017677777778 ENSGO000017677777778 ENSGO000017677777778 ENSGO000017677777778 ENSGO00001767787777778 ENSGO0000176787 ENSGO00	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 5.5555556 94.4444444
ENSG0000015291 ENSG00000154548 SPHAP	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
ENSG00000127848 ENSG00000127848 ENSG00000127848 ENSG00000127849 ENSG000000127849 ENSG000000127849 ENSG000000127849 ENSG000000127849 ENSG000000127849 ENSG000000127849 ENSG000000127849 ENSG000000127849 ENSG000000127849 ENSG0000000127849 ENSG0000000127849 ENSG000000000000000000000000000000000000	ENSG 00000163636	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 5.5555556 94.4444444
ENSG00000127884 ECHS1	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
RYSGO000015948 RYSGO000015947 RYSGO0000015947 RYSGO0000015940 RYSGO0000015947 RYSGO00000015947 RYSGO00000015940 RYSGO00000015940 RYSGO00000015940 RYSGO000000000000000000000000000000000000	ENSG 00000176438	SYNE3	-0.6365959 4.11676562 83.0751724	7.90E-20	1.78E-19 -0.5684601 97.1428571 2.85714	286 SYNE3	-1.4300149 3.82656132 314.014033	2.92E-70	2.00E-69 -1.4359406 100 0
ROSGO0000115947 CRC4	ENSG 00000127884	ECHS1	-0.7678977 2.84450162 82.6567045	9.76E-20	2.19E-19 -0.7561492 97.1428571 2.85714	286 ECHS1	-0.6580213 2.87719501 50.9315074	9.56E-13	2.11E-12 -0.7195019 94.4444444 5.55555556
ENGGOU00115947 CRC4 0.61651353 4.27935271 81.6545593 1.62E-19 3.62E-19 3.6	ENSG 00000168488	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
ENSGO0000112796 ELK1	ENSG 00000204186	ZDBF2	0.5547028 6.74040955 81.7760154	1.52E-19	3.41E-19 0.59341622 2.85714286 97.1428	571 ZDBF2	0.67748653 6.70154656 98.6873749	2.96E-23	8.89E-23 0.76086613 8.33333333 91.6666667
ENSGO000012994 (PAPE 2)	ENSG 00000115947	ORC4	0.61651353 4.27935271 81.6545593	1.62E-19	3.62E-19 0.68136189 0	100 OR C4	0.6512107 4.23810807 75.4429149	3.76E-18	9.76E-18 0.64283311 2.77777778 97.2222222
FGR10P2 0.5587669 5.6772381 81.0258675 2.3E-19 4.95E-19 0.5234024 100 0 FGR10P2 0.4713993 5.65355119 48.2952279 3.67E-12 7.89E-12 0.5027321 100 0 0 0 0 0 0 0 0									
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ENSG0000181274 FRAT2 -0.6385684 3.87744062 77.6444198 1.23E-18 2.69E-18 -0.6304814 88.5714286 11.4285714 FRAT2 -0.580903 3.8419499 53.6241246 2.43E-13 5.45E-13 -0.6526023 94.444444 5.55555556 ENSG0000267352 SH3GLIP3 0.90118192 1.51793708 77.3569323 1.43E-18 3.11E-18 0.90476308 0 100 SH3GLIP3 1.01357107 1.56908216 77.0866251 1.64E-18 4.31E-18 0.78808177 0 100 ENSG00000138614 VWA9 0.59700431 4.30790636 76.8866325 1.81E-18 3.93E-18 0.65287771 0 100 ENSG00000128191 ENSG00000196459 TRAPPC2 0.6214746 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 5.5555556 94.4444444									
ENSG0000267352 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 SH3G00000146007 2MAT2 -0.553934 5.24522509 77.2180319 1.53E-18 3.33E-18 -0.5075817 97.1428571 2.85714286 2MAT2 -0.4876589 5.22895368 50.0438701 1.50E-12 3.28E-12 -0.5269785 97.222222 2.77777778 ENSG0000138614 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 0.6894784 2.85714286 97.1428571 TRAPPC2 0.70754074 3.9543622 82.4619073 1.08E-19 2.94E-19 0.63033039 5.55555556 94.44444444									
ENSG0000146007 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 97.222222 2.77777778 ENSG0000138614 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 0.68947884 2.85714286 97.1428571 TRAPPC2 0.70754074 3.9543622 82.4619073 1.08E-19 2.94E-19 0.63033039 5.55555556 94.44444444									
ENSG0000138614 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 94.44444444									
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									
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									

ENSG00000214026	MRPL23	-0.6247098 3.93346209 75.9739498	2.87E-18	6.21E-18 -0.6171124	01 4205714	0 E71420E7 MDDI 22	-0.6442908 3.89884958 66.9669664	2.76E-16	6.81E-16 -0.7613122 94.4444444 5.55555556
ENSG00000214026 ENSG00000133884	DPF2	0.54323513 5.4990645 75.8452396	3.07E-18	6.63E-18 0.57752524	91.4285/14	100 DPF2	0.78353147 5.58879496 132.007803	1.49E-30	
ENSG00000133884 ENSG00000158019	BRE	-0.6652395 3.48547503 75.8139429	3.12E-18	6.73E-18 -0.5658455				2.02E-10	5.34E-30 0.67008318 0 100 4.06E-10 -0.5290766 100 0
ENSG00000138019	RP11-47I22.3	0.7570251 2.53094331 74.4336242	6.27E-18	1.35E-17 0.80933544	0 0	100 RP11-47I22.3	-0.5291696 3.48655047 40.45063 0.71334845 2.44870575 52.63011	4.03E-13	8.98E-13 0.70200926 2.77777778 97.2222222
ENSG00000232774 ENSG00000127540	UQCR11	-0.5977651 4.18276252 74.4240489	6.27E-18 6.30E-18	1.36E-17 -0.5196691	•		-0.5813178 4.15700166 58.567335	1.96E-14	4.58E-14 -0.7053501 94.444444 5.55555556
ENSG00000127340	OXCT1	0.60523288 4.0689948 74.0986459	7.43E-18	1.60E-17 0.67859174			0.63407221 4.00445642 67.4233319	2.19E-16	5.42E-16
ENSG00000083720	ZNF776	-0.5443649 5.16372645 74.0286397	7.43E-18 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
ENSG 00000168014 ENSG 00000164080	C2CD3 RAD54L2	0.569792 4.57642702 73.8863186	8.27E-18 1.06E-17	1.77E-17 0.66154412 2.27E-17 0.56448216	2.85/14286	100 RAD54L2	0.69151911 4.58202243 91.178325	1.31E-21 5.54E-22	3.78E-21 0.68854397 8.33333333 91.6666667 1.61E-21 0.61818336 5.55555556 94.4444444
		0.5322697 5.70238786 73.3960076			•		0.65696792 5.74298591 92.8862199		
ENSG00000101413	RPRD1B	0.54563381 5.17662076 73.3817714	1.07E-17	2.28E-17 0.5233996			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			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		2.85714286		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			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 5.5555556 94.4444444
ENSG00000167969	ECI1	-0.7866177 2.15551749 71.3444344	3.00E-17	6.34E-17 -0.7440806			-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				0.61699989 6.36060107 83.3799058	6.77E-20	1.86E-19 0.52115767 5.5555556 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			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			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			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 5.5555556 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 5.5555556 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 5.5555556 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 5.5555556 94.4444444
ENSG00000069493	CLEC2D	0.54995402 4.42354559 66.3254599	3.82E-16	7.86E-16 0.6185501			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			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			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			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			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 5.5555556 94.4444444
ENSG00000235677	NPM1P26	0.8449057 1.29734785 63.7005812	1.45E-15	2.93E-15 0.86117827			1.01954153 1.23005188 69.8976239	6.25E-17	1.57E-16 1.05195566 5.5555556 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			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			0.75353614 5.29196082 118.524749	1.33E-27	4.47E-27 0.71105309 5.5555556 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 5.5555556 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			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			-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 5.5555556 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

ENGG 000004 53543	04 (50	0.54005050	4.530.43000	F0 F7050F0	4.475.44	2 245 44	0.55220454		400	C4 (F2)	0.53000453	4.55404007	75 2724047	2 005 40	4 045 47	0.5303055		400
ENSG00000162642	C1orf52		4.57047083		1.17E-14		0.56329451	0		C1orf52		4.56134227		3.88E-18		0.5392855	0	100
ENSG00000092929 ENSG00000151612	UNC13D ZNF827		5.44208617 5.13468455		1.34E-14 1.90E-14		0.52199311	11.4285/14	88.5714286	ZNF827		5.52432736		3.91E-26 5.85E-57		1.01453982	8.33333333	100
	SBDS							•				5.47503877		1.73E-14			•	
ENSG00000126524 ENSG00000261416	RP11-455F5.5		7.67980024 1.30115943		2.09E-14 2.18E-14				97.1428571	RP11-455F5.5		7.62927929	53.7972054	1.73E-14 2.22E-13			5.5555556 2.7777778	
ENSG00000261416 ENSG00000068971	PPP2R5B		3.07958203		2.16E-14 2.43E-14			2.65/14260		PPP2R5B		2.92329402		2.22E-13 2.91E-10			8.33333333	
	PSMC5		5.47545431		2.43E-14 2.59E-14		0.66276014 0.51385398	0	100	PSMC5			106.791068	4.95E-25		0.63322097	0.33333333	100
ENSG00000087191	SNRNP40		4.90550368		3.59E-14			2.85714286		SNR NP40			117.469768	4.95E-25 2.27E-27		0.68124834	0	100
ENSG00000060688	NUDC				3.63E-14									3.58E-20			•	
ENSG00000090273	CCDC101		5.39736319 4.00407406		4.35E-14				97.1428571 97.1428571			5.44026129 4.03950401		5.57E-19			2.77777778	
ENSG00000176476	RNF25				4.35E-14 4.45E-14			2.85/14286		RNF25				8.19E-18		0.58381413	2.77777778	100
ENSG00000163481 ENSG00000273271	AP000254.8		3.83022181 1.45383817		4.45E-14 5.16E-14		0.60256842	0		AP000254.8		1.35151796	73.905459	2.13E-08			5.55555556	
	NELFA				5.16E-14 5.32E-14		0.80985708	0		NELFA				1.98E-18		0.50000346	5.55555556	
ENSG00000185049	EP400		5.1871779				0.51533723	0		EP400			76.7056516	3.29E-25			0	100
ENSG00000183495 ENSG00000092931			6.07561465		5.35E-14 5.86E-14		0.55276326	0		MFSD11		6.17208863		3.29E-25 2.01E-15		0.55286943	5.55555556	100
	MFSD11		3.95314298		6.09E-14		0.61585351	0		SUCLA2		3.98791953		4.92E-11				
ENSG00000136143	SUCLA2 TCEAL4		2.86187623 2.29451867		7.21E-14		0.71355049	_				2.32698912	43.2075134	4.92E-11 8.99E-08			2.77777778 94.4444444	
ENSG00000133142								97.1426571	2.85714286									
ENSG00000110925 ENSG00000008710	CSRNP2 PKD1		3.49040006 5.82540672		9.35E-14 2.48E-13		0.65503512	5.71428571		CSRNP2 PKD1			77.3527789 77.2410086	1.43E-18 1.51E-18			2.77777778 8.33333333	
ENSG00000169738	DCXR AKTIP		3.75282526 3.21800433		4.48E-13 7.07E-13				97.1428571 97.1428571			3.94823019 3.34798742		8.67E-33 4.76E-27			2.77777778 2.77777778	
ENSG00000166971																		
ENSG00000163541	SUCLG1		4.26662238 4.67731146		7.29E-13 1.01E-12				97.1428571	SLC35A3			43.5334548	4.17E-11 1.47E-14			5.5555556	
ENSG00000117620	SLC35A3						0.51116004	0				4.66978568					8.33333333	
ENSG00000131351	HAUS8		3.36979695		1.67E-12 2.55E-12			2.85/14286	97.1428571			3.30343422		1.90E-10 9.83E-36			2.77777778	
ENSG00000204564	C6orf136		3.53620537				0.55640212	•		C6orf136		3.77134985				0.88314163	•	100
ENSG00000139546	TARBP2		3.21556095 2.4918599		2.87E-12 3.38E-12		0.5907589	0 5.71428571	100	TARBP2		3.20283994		7.85E-15 2.74E-17			2.77777778 5.55555556	
ENSG00000172613	RAD9A									RAD9A		2.5592357						
ENSG00000250539 ENSG00000154451	KRT8P33 GBP5		1.91936569 5.29850157		4.41E-12 9.15E-12		0.50500171	2.85/14286	97.1428571	GBP5		1.89041811 5.63540713		1.58E-09 1.46E-40			5.5555556 2.7777778	
ENSG00000103145 ENSG00000272779	HCFC1R1 LL22NC03-80A:		2.3833633 1.81996408		9.33E-12 1.03E-11		-0.5988343	94.2857143 100		HCFC1R1 LL22NC03-80A		2.3303536		7.92E-10 2.23E-07			91.6666667 91.6666667	
ENSG00000272779	NA		1.05581607		1.03E-11 1.08E-11		0.77863773	0	100			1.12180995		3.34E-13			8.33333333	
ENSG00000236883	UNK		4.99081657		1.06E-11 1.15E-11		0.77863773	0		UNK		4.99303209		1.64E-14		0.5038688	0.33333333	100
ENSG00000132478	ZNF384		5.96891185		1.23E-11		0.50182555	0		ZNF384		6.02527609		1.04E-14 1.01E-19		0.52483039	0	100
ENSG00000120740	NPDC1		2.66862594		1.25E-11		0.5965989	20		NPDC1		3.03222842		2.09E-49			2.7777778	
ENSG00000107281	TIMM13		3.02755048		1.32E-11				5.71428571		-0.5764539		40.5182657	1.95E-10	3.93E-10		91.6666667	
ENSG00000150779	TIMM8B		2.16287346		1.99E-11				11.4285714				26.755116	2.31E-07			91.6666667	
ENSG00000150775	NA		0.07683486		2.06E-11			14.2857143		NA		-0.0309657		8.27E-08			16.6666667	
ENSG00000266156	ATRIP		3.23750551		3.27E-11				97.1428571			3.15748534		7.10E-09	1.34E-08		11.1111111	
ENSG00000104033	C1orf174		4.44911278		3.35E-11		0.56395775	0		C1orf174		4.44788909		1.53E-14		0.50132984	0	100
ENSG00000156512	SYTL3		4.46473539		1.25E-10		0.5960556	20		SYTL3		4.69124879		2.17E-31			5.5555556	
ENSG00000134674	CCDC53		2.50209294		1.60E-10				97.1428571			2.44815762		7.00E-08			13.8888889	
ENSG00000167775	CD320		3.28211076		1.64E-10				97.1428571			3.29785408		2.67E-14			5.5555556	
ENSG00000197536	C5orf56		2.82849932		3.75E-10				94.2857143			2.81300933		2.40E-09			11.1111111	
ENSG00000100601	ALKBH1		3.12587728		1.31E-09		0.58188452	0.77.2037.2		ALKBH1		3.16104337		2.12E-12			2.77777778	
ENSG00000138303	ASCC1		2.77738547		1.51E-09			2.85714286		ASCC1		2.82342932		1.04E-12			2.77777778	
ENSG00000182973	CNOT10		3.81136539		1.57E-09				97.1428571				46.2528748	1.04E-11			5.55555556	
ENSG00000166477	LEO1		2.67413221		1.93E-09		0.53840821	0		LEO1		2.73440873		5.98E-15		0.66606193	0	100
ENSG00000213443	CLEC2D		2.5129769		2.32E-09			_	94.2857143				37.554718	8.89E-10			8.33333333	
ENSG000000213443	METTL22		3.27602678		3.27E-09		0.53211002	0.71420371		METTL22		3.31342632		1.69E-10			2.77777778	
ENSG00000007503	TRPV2		3.69723667		1.20E-08			_	88.5714286			3.69509157		3.97E-11			11.1111111	
ENSG00000267906	NA V2		0.18695682		1.94E-08				94.2857143			0.22091824		2.82E-08			11.1111111	
	RP11-326C3.7				2.19E-08					RP11-326C3.7				2.23E-06			5.5555556	
	22 020007			32.02.2070	3.202 00					12 020 30.7				3.202.00				

I																		
ENSG00000065559	MAP2K4		3.41950364		2.87E-08			5.71428571				3.53826665		8.69E-16			2.77777778	
ENSG00000264577	SNORD4A		1.86964161		1.06E-07			8.57142857		SNORD4A		1.85717202		6.09E-09			11.1111111	
ENSG00000156500	FAM122C		2.74250784		7.68E-07			8.57142857				2.75471679		7.59E-09			8.33333333	
ENSG00000251578	TRBV21-1		0.24888698		1.11E-05			5.71428571	94.285/143	TRBV21-1				0.00033306				83.333333
ENSG00000224137	AC079767.4		0.42707887		0		-7.1098029	100	0	AC079767.4		0.38651391				-4.9561328	100	0
ENSG00000224397	LINC01272		1.60834762		0	0	-4.1032442	100	0	LINC01272		1.54756902		0		-6.5586175	100	0
ENSG00000253701	AL928768.3		-0.1549888		0	0	-10000	100	0	AL928768.3		-0.1260765			5.04E-275	-10000	100	0
ENSG00000269728	RP11-145M9.4		1.92315933		0	0	0.00200.0	100	0	RP11-145M9.4		1.87419804			1.92E-291	-3.901069	100	0
ENSG00000234184	RP5-887A10.1		-0.2443392		6.42E-302	2.96E-300	-10000	100	0	RP5-887A10.1		-0.2655509			1.60E-210	-5.2494327	100	0
ENSG00000211459	MT-RNR1			1231.26838	9.77E-270			100	0	MT-RNR1		10.4699443				-1.1449902	100	0
ENSG00000267174	CTC-510F12.4		-0.1435735		4.48E-221			97.1428571	0	CTC-510F12.4		-0.1509149				-6.1929431	100	0
ENSG00000272523	LINC01023	-3.3236581		763.125318	5.62E-168		-3.3245239	100	0	LINC01023		0.02224949				-2.0701364	100	0
ENSG00000253364	RP11-731F5.2	-6.1493045		665.448564	9.76E-147	1.95E-145	-10000	100	0	RP11-731F5.2					6.62E-127			
ENSG00000260359	NA		1.16163457		1.10E-144		-2.2024773	100	0	NA		1.32657088		6.81E-51	7.73E-50			
ENSG00000180422	LIN C00304		1.04129814		6.31E-137		2.97747543	0	100	LIN C00304	1.8506121		266.518781	6.51E-60		2.08639522	0	100
ENSG00000272077	RP11-348P10.2				9.94E-125		-2.3589464	100	0	RP11-348P10.				1.68E-45			94.444444	5.5555556
ENSG00000172965	MIR4435-1HG		1.80458339		4.62E-121			100	0	MIR4435-1HG		1.86064093		2.64E-92		-1.7061829	100	0
ENSG00000233901	RP11-65J3.1			520.447266	3.38E-115	5.48E-114		100	0	RP11-65J3.1		-1.0716429				-4.2950207	100	0
ENSG00000175898	CTD-2369P2.2		2.19404545		4.57E-109		-1.6215094	100	0	CTD-2369P2.2		2.04226277				-2.0339457	100	0
ENSG00000268913	AC026806.2		-0.6658963		1.78E-107		-2.5875749	100	0	AC026806.2		-0.6145388		8.25E-95		-2.6641038	100	0
ENSG00000259004	RP11-8L8.2			453.037486	1.57E-100		-3.7183709	100	0	RP11-8L8.2		-1.4831157		1.29E-96	3.00E-95	-3.987525	100	0
ENSG00000272053	RP11-367G6.3		1.23959025		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	97.222222	2.7777778
ENSG00000188070	C11orf95		3.02141062		7.93E-87		-1.6765277	100	0	C11orf95		3.21393278		5.54E-35			91.6666667	8.33333333
ENSG00000270055	CTD-3092A11.2				1.86E-86		1.70314396	0	100	CTD-3092A11.				8.33E-41	7.42E-40	1.29918104	0	100
ENSG 00000261455	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		0.11917588		7.79E-78	7.91E-77	-1.5449377	100	0	AP001055.6		0.00906469				-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	LIN C00152		2.17978088		1.30E-73			97.1428571		LIN C00152		2.28894992		1.26E-61			94.444444	
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	88.888889
ENSG 00000260006	RP11-469M7.1		4.23900225		5.84E-67		-1.4665234	100	0	RP11-469M7.1		4.39113748		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	LIN C00565	1.49034348	2.1117465	297.549968	1.13E-66	9.78E-66	1.65872027	0	100	LIN C00565	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	5.5555556	94.444444
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		1.00E-116	-2.4509473	100	0
ENSG00000237438	CECR7		0.28353166		1.16E-59		-1.3658024	100	0	CECR7		0.41856942		4.98E-38	4.01E-37		97.222222	
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	97.222222
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		2.23E-26	-0.7053929	97.222222	2.7777778
ENSG 00000261560	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				1.06E-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	8.3333333
ENSG 00000272849	RP11-347I19.8	1.55851293	0.60526796	225.883012	4.71E-51	3.21E-50	1.80634141	2.85714286	97.1428571	RP11-347I19.8	1.34903944	0.37653884	147.661069	5.63E-34	3.92E-33	1.8042685	2.77777778	97.222222
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	RP11-108M9.4	-1.4315255	-0.6691416	121.183741	3.48E-28	1.94E-27	-1.1510664	94.444444	5.5555556
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		0.00019821	0.55968221	5.5555556	94.444444
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			1.88E-25	9.48E-25	1.5321372	5.5555556	94.444444
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	94.444444	5.5555556
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	5.5555556	94.444444
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	88.888889
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
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ENSG00000233261	LIN C00264	1 25240135	0.06219516	140 11679	2.51E-32	1 25F-31	1 67914567	2.85714286	97 1428571	LINC00264	1.01658055	-0.1063059	75 4173231	3.81E-18	1 35F-17	1.32745927	0	100
ENSG00000233201	DLEU2		0.97112681		1.71E-31		-0.7678532	100		DLEU2		0.82666073		8.79E-50		-1.2414152	100	0
ENSG00000269996	NA		1.50434968		1.77E-30			91.4285714				1.34766848		4.47E-61		-1.2474216	100	0
ENSG00000267701	RP11-28F1.2		-1.8306119		8.71E-30		-1.7786211	100	(RP11-28F1.2		-1.8523306		3.26E-24			91.6666667	8.33333333
ENSG00000261824	LIN C00662		0.3149384		4.67E-29		-0.7635914	100	Č	LINC00662		0.23116184		1.48E-30		-0.9952785	100	0
ENSG00000273352	RP11-61L19.3		-1.0431036		1.71E-28				8.57142857	RP11-61L19.3		-0.9234789		2.60E-16			83.3333333	16.6666667
ENSG00000215908	CROCCP2		4.50095522		2.33E-28		1.35838431	0		CROCCP2		4.52746087		1.49E-85		1.39444905	0	100
ENSG00000215908	CROCCP2		4.50095522		2.33E-28		1.35838431	0	100			4.45627587		2.92E-46		1.39444905	0	100
ENSG00000232470	RP11-313D6.3				2.50E-26		2.2543504	0	100					1.73E-17		1.97710821	0	100
ENSG00000259715	CTD-3110H11.1				4.88E-26			2.85714286					53.9019648	2.11E-13			11.1111111	
ENSG00000271938	RP11-589C21.6				6.39E-26					RP11-589C21.				1.96E-33		1.7636302	0	100
ENSG00000255989	NA		-0.1638419		3.06E-25			91.4285714			-0.9709911			9.93E-17			88.8888889	11.1111111
ENSG00000270972	RP11-326C3.15				2.87E-24					RP11-326C3.1				2.74E-09			11.1111111	
ENSG00000271843	RP11-245J9.5				1.39E-23					RP11-245J9.5				1.19E-13			8.33333333	
ENSG00000227486	RP13-188A5.1		-1.1106149		6.10E-23					RP13-188A5.1			99.2121972	2.27E-23			91.6666667	
ENSG00000271975	RP11-383J24.6		1.35552564		5.27E-22					RP11-383J24.6				1.71E-46		-1.1431123	100	0
ENSG00000264112	RP11-159D12.2		4.66520381		8.91E-22					RP11-159D12.				7.12E-34			2.7777778	97.222222
ENSG00000260539	GLG1		0.93214257		1.15E-21		1.26600723	0	100			0.64479745		5.18E-06			16.6666667	
ENSG00000222375	RN7SKP127		-2.5941428		1.73E-21		2.88156798	0	100	RN7SKP127		-2.8490724		3.99E-16			2.77777778	
ENSG00000152487	ARL5B-AS1		-1.5854301		4.14E-21			2.85714286	97.1428571		1.40494802			2.54E-16			2.77777778	
ENSG00000269086	CTC-523E23.5		1.08862501		9.99E-21		1.23867548	0	100			1.12338928		1.45E-18		1.20220481	0	100
ENSG00000270066	SCARNA2		-1.2787625		1.30E-20			2.85714286	97.1428571			-1.8573902		2.86E-07			13.8888889	
ENSG00000273033	RP11-67L2.2		3.82525915		9.62E-20					RP11-67L2.2		3.68528862		2.34E-57	3.00E-56		100	0
ENSG00000204261	PSMB8-AS1		3.09354211		4.01E-19			94.2857143		PSMB8-AS1		3.05898101		1.21E-23		-0.5163391	100	0
ENSG00000261526	CTB-31O20.2		4.30779858		9.18E-18		1.22381845	0	100			4.18284686		2.24E-22			2.77777778	97.2222222
ENSG00000230002	ALMS1-IT1		1.03970337		1.36E-17		1.09138517	0	100			1.01609807		1.41E-16			2.77777778	
ENSG00000237491	RP11-206L10.9				4.33E-16			5.71428571						4.03E-18			2.77777778	
ENSG00000270704	SNORD64		-1.5442355		1.06E-14			8.57142857				-1.5119706		1.40E-14			5.5555556	
ENSG00000269942	NA		-1.8507047		1.41E-14			5.71428571			1.24034205			2.47E-11			11.1111111	
ENSG00000271869	RP11-51J9.5		3.05414844		6.10E-14		1.00245913	0		RP11-51J9.5		3.04630366		9.75E-19		1.00429901	0	100
ENSG00000271725	RP11-761I4.4		-0.6740512		1.51E-13			_		RP11-761I4.4	-0.9547284			3.42E-13			80.555556	
ENSG00000267481	CTC-559E9.5		0.64223774		3.57E-13		0.96563225	0	100	CTC-559E9.5		0.43550431					8.33333333	
ENSG00000239884	RN7SL608P		-1.2478128		4.02E-13			11.4285714				-1.1336359		7.18E-17			5.5555556	
ENSG00000260336	RP11-395B7.7		2.72544557		9.45E-13					RP11-395B7.7							19.444444	
ENSG00000270419	CAHM		-1.1951761		3.28E-12	8.55E-12		88.5714286		CAHM	-1.635266			7.13E-25			94.444444	
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	19.444444	80.555556
ENSG00000222414	RNU2-59P		-2.3062229		6.70E-12	1.72E-11		80	20		-0.9679482			1.79E-06	3.27E-06		72.222222	
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		77.777778	
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		0.46842308		2.92E-11			22.8571429			0.68527739		24.2629906	8.40E-07			22.222222	
ENSG00000228485	GRK5-IT1		-1.3931038		5.53E-11		-0.6154948	80	20		-1.075295			3.46E-11			77.777778	
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	80.555556	19.444444
ENSG00000196559	LIN C00610	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	5.5555556	94.444444
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				8.61E-10					RP11-1006G14				1.98E-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	69.444444	30.555556
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	97.222222
ENSG00000269958	RP11-73M18.8	0.48864053	1.83090548	33.6848716	6.48E-09	1.35E-08	0.76065349	2.85714286	97.1428571	RP11-73M18.8	0.47306515	1.78145605	23.6279858	1.17E-06	2.16E-06	0.65971792	2.77777778	97.222222
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	88.888889
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	97.222222
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
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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	5.5555556	94.444444
ENSG00000225975	AC074138.3	0.59218485	-0.7525362	25.9941895	3.42E-07			5.71428571			0.81529481	-0.6881691	40.0919824	2.42E-10	5.57E-10	1.03400343	2.77777778	97.222222
ENSG00000270108	RP11-73M18.6	0.54260167	-0.3090027	25.4906956	4.45E-07	8.17E-07	0.87950444	14.2857143	85.7142857	RP11-73M18.6	0.48458829	-0.3620723	16.0128096	6.29E-05	0.00010147	0.70075436	19.444444	80.555556
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	77.777778	22.222222
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	19.444444	80.555556
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	22.222222	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	97.222222
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	19.444444	80.555556
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	22.222222	77.777778
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	88.888889
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	19.444444	80.555556
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	19.444444	80.555556
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	88.888889
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	30.555556	69.444444
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	19.444444	80.555556
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	22.222222	77.777778
ENSG00000225528	RP3-370M22.8	0.35764184	-0.2569858	11.3854856	0.0007402	0.00107617	0.80627553	20	80	RP3-370M22.8	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	RP11-324I22.3	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	88.888889
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	97.222222
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-2007L18.5	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	19.444444	80.555556
ENSG00000269940	RP11-73M18.7	0.28382722	-0.6105158	6.38870776	0.01148486	0.01515293	0.63198088	22.8571429	77.1428571	RP11-73M18.7	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	97.222222
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	LIN C00843	0.26290097	-0.8387798	4.93349849	0.02634094	0.03342844	0.53561429	17.1428571	82.8571429	LIN C00843	0.37224284	-0.8308246	7.95574067	0.00479351	0.00653045	0.73115464	22.222222	77.777778
ENSG00000272054	RP11-423P10.2	0.21131912					0.51355966	20		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	5.5555556	94.444444

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:	Œ	04+	CI	08+	CD4	CD8-	PE	вмс
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 t	akes place before filtering ste	ferential expression analysis t	akes place before filtering ste	ferential expression analysis t	akes place before filtering ste	erential expression analysis	takes place before filtering st
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 48. Protein coding DE genes between Cases and Controls samh i Gan e iDs CDS+ CD4-CDS- PRA CDS+ CD4-CDS- PRM THE COSE COACOS PRAY CD4+ CD8+ CD4-CD8- PR TOLL CORE COLUCIE, PRIM m4+ m8+ m4-m8- P8 NA+ COS+ COA-COS+ PS N CDS+ CD4-CDS- PS NSGMOM245543 -1.95 ENGCODOM TOTAL 000 400 0 000 ... 0.00 29 18 33 173 .098 .090 ENSG0000181404 XXIac. VRM 2039 MANCE WASH complex subunit 1 Cytonlasm 207 -165 -133 14 11 10 25 0.00 0.00 18 25 ENSG00000129925 TMEMSA MEM 8A transmembrane protein 84 Plasma Membrane other 0.90 0.52 0.30 0.65 0.77 0.40 0.51 19 21 ENSG00000008517 L 32 Extracellular Space cytokin 1.26 1.09 0.00 0.00 0.00 17 ribosomal protein SA pseuc Other ENSG00000237506 RPSAP15 NSG00000186470 butyrophilin subfamily 3 m Plasma M-FN9500000188820 FAM26F family with sequence simil Other allionpää et al. 2014 0.20 0.05 -0.19 0.09 0.15 100 1.00 58 0.62 0.70 0.47 0.40 ENSG00000137801 THRS thrombospondin 1 Extracellular Space 0.71 0.37 0.28 0.63 0.00 0.00 0.00 0.07 0.13 0.00 69 54 61 58 42 ENCOMOMOGGG 17752 17153 leurine zimer tumor sunor Cytonlasm 0.62 0.42 0.27 0.20 .0.16 .0.10 .0.05 010 0.06 0.01 1.00 0.95 1.00 1.00 25 ENSG00000138706 LARS louryl, IRNA cynthetase Cytonlasm oravmo 0.50 0.82 00.00 ENSG00000160598 junction adhesion molecule Plasma Membrane 00 0.00 0.00 0.01 0.08 0.00 1.00 11 AMICA1 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 ENSG00000090857 POPR pyrtuvate dehydrogenase piCytoplasm allionpää et al. 2014 ergyme ENSG00000130222 6400456 growth arrest and DNA dar Nucleus .0.23 .0.14 0.09 0.12 0.00 0.10 100 0.68 1.00 100 22 19 40 36 ATP binding cassette subfar Plasma Membrane -0.23 -036 1.00 0.40 33 ENSG00000226210 WASH7P 0010028877 WAS protein family homolcOther 0.45 0.64 0.88 10.0 0.00 100 0.17 0.57 0.31 22 18 17 diacylglycerol kinase theta Cytoplasm ENSG00000145214 nsko 0.54 047 031 0.84 000 0.47 0.00 0.00 0.24 0.07 ENSCMOM149220 DICC14 0.0014 regulator of G-protein sign Cytoplasm other 0.85 0.39 0.60 0.68 1.06 0.27 0.63 00 0.01 0.00 0.00 100 0.00 1.00 0.32 67 65 60 82 75 33 35 18 0.17 0.16 0.00 0.47 0.55 0.27 ENSGMOM1@440 CD52 CDS2 CDS2 melacula Phoma Membrane other ounier et al. 2010 0.49 -011 0.25 060 049 068 011 100 100 75 68 58 73 42 50 5.0 0.20 1.00 1.00 22 30 ENSG00000160179 ABCG1 A BCG1 ATP binding cassette subfai Plasma Membrane - transporter -035 0.13 -0.14 -0.22 -0.23 0.00 0.00 100 0.97 60 36 0.21 0.43 -0.29 0.07 00 0.31 0.08 1.00 69 59 ENSG00000110090 CPT1A camitine palmitoyltransfer Cytoplasm 0.29 erzyme sorting nexin 25 Cytoplasm ENSG00000178927 C17orf62 17ar162 chromosome 17 open read Other 0.47 0.49 0.89 0.30 0.53 0.68 030 58 1.00 ENSG00000189060 H1 histone family member Nucleus -011 -001 0.01 -0.18 0.85 0.91 1.00 50 -0.72 -0.65 ENSG00000254912 RPI1.632K20.2 -0.88 -0.52 0.07 100 0.01 20 ENSCMONTATE 12 NAGO TI nicetinate aberateriberate Oderland .052 -047 -021 -0.85 0.54 0.02 0.49 0.14 1.00 30 ENSGM000100092 SHRRP1 HRRPI SH3 domain binding proteir Other other 0.51 0.32 -001 0.32 0.25 0.29 -0.32 0.11 0.00 0.66 0.97 0.21 100 0.15 1.00 1.00 69 57 63 60 33 31 43 50 36 67 ENSG00000211710 TRRV4.1 RRV4.1 Ticell recentor heta variabi@ther other 1.11 1.23 1.18 0.01 0.08 030 72 59 64 41 20 ENSG00000164056 SPRY1 PRY1 scrouty RTK signaling antai Cytoplasm other -050 -0.24 -012 -041 -0.42 -0.12 -0.13 -0.15 00 0.44 0.45 0.03 100 0.92 1.00 1.00 17 35 33 65 0.68 0.87 1.00 1.00 31 49 30 36 42 -0.05 0.75 -0.07 -0.06 0.06 00 0.80 0.98 ENSG00000215302 CTD-3092A11.1 -0.56 -0.02 ee 51 53 58 0.55 0.37 ENSG00000188290 -0.65 0.69 100 1.00 HPS4 has family bHLH transcript Other glycerophosphodiester pho Plasma Membrane ENSG00000158555 GDP05 Biompää et al. 2014 -064 -071 -008 00 0.00 0.08 1.00 ENSG00000128383 APORECRA BUBEC31 apolipogrotein B mRNA edi Cvt colorm Bornas et al. 2014 Forreira et al. Nahetec 2014 0.59 0.28 1.24 0.00 0.11 0.23 1.00 1.00 1.00 58 55 SO. 42 ENSG0000111848 TMEMIAC MEM 140 transmembrane motein 14 Plasma Membrane other 051 0.44 0.55 0.58 0.56 Q45 Q41 0.58 0.00 0.37 0.02 100 026 100 100 27 24 25 0.00 0.01 1.00 0.15 1.00 1.00 ENSG00000188690 UROS uroparphyrinagen III syntha Cytaplasm erevme 0.46 0.51 0.49 060 053 0.48 0.45 0.29 33 -0.86 -0.59 -0.41 -0.50 ENSG00000095370 SH2D3C 4203C SH2 domain containing 3C Cytoplasm other -050 -032 -0.14 -031 0.00 0.31 0.38 0.15 0.50 038 28 32 42 32 10 18 17 58 0.37 0.57 1.00 0.59 25 30 CTA-29F11.1 -058 -031 -0.42 -0.73 -0.26 -0.43 -0.43 0.18 0.02 0.00 20 27 42 63 ENSG00000260708 58 0.48 0.21 0.60 0.28 0.86 0.00 0.00 1.00 0.67 0.35 0.39 ENSG00000145649 lionpää et al. 2014 0.66 0.19 0.40 0.45 43 33 GZ MA granzyme A Cytoplasm growth factor -0.02 0.23 0.18 1.00 ENSG00000025708 thymidine phosphorylase Extracellular Space -127 -0.08 0.69 0.00 0.58 0.34 1.00 0.00 50 ENSG00000115523 Cytoplasm -0.28 0.17 1.00 granulysin -0.57 0.00 0.07 ENSG00000100302 RASD family member 2 Cytoplasm .0.92 ENSG00000115414 FN1 Shoner tin 1 Extracellular Sna envene 0.80 0.55 0.00 0.07 1.00 45 ENSG00000073861 TBX21 T-box 21 Nucleus transcription regulator alliompää et al. 2014. Heninger et al. 2017 -0.74 0.13 -0.78 0.27 0.19 0.00 0.33 0.95 0.00 1.00 1.00 16 58 42 032 -0.31 -0.08 -0.10 0.83 0.00 0.16 0.09 1.00 0.00 1.00 1.00 42 19 ENSG00000176845 METRNL METRNL meteorin like, glial cell diff Cytoplasm other -019 -0.78 -0.19 -0.30 50 55 50 -0.48 -0.65 -1.19 -0.36 -0.54 16 30 17 ENSG00000152492 CCDC 50 CCDC50 coiled-coil domain containi Cytoplasm other -045 -110 -0.26 0.00 0.00 0.00 0.00 0.11 0.00 0.91 020 25 22 18 0.01 0.02 100 0.00 1.00 100 ENSG00000135114 Z-S-oligoadenylate synthe Cytoplasm -0.26 0.53 -0.54 -0.35 -0.14 25 63 OASL erzyme lionpăă et al. 2014, Reynier et al. 2010, Ferreira et al. 20 -0.03 ENSG00000107317 prostaglandin D2 synthase Cytoplasm erzyme -013 0.00 0.83 0.18 1.00 1.00 ENSG00000211689 TCR gamma alternate reacCytoplasm ENSG00000075234 tetratric opeptide repeat de Cytoplasm -0.73 0.86 ENSGMOM135047 0.29 -0.25 -0.05 0.38 0.89 0.17 0.80 1.00 0.52 50 CISI cathepsin L Cytoplasm peptidas ENSG00000158747 NRI1 BL1 neuroblastoma 1 DAN fam Nucleus -036 -0.37 0.27 ENSG00000065989 POE4A phosphodiesterase 4A Cytoplasm -072 -013 -033 0.06 0.07 -033 0.07 0.05 0.56 1.00 1.00 019 100 0.00 1.00 1.00 ENSG00000188404 SELL selectin L Plasma Mombrane transmembrane receptor Floet al. 2010 0.38 0.59 0.80 0.81 0.48 0.24 0.00 0.00 32 42 0.00 0.00 1.00 1.00 -0.73 -0.29 -011 -1.02 -0.42 -0.43 0.74 0.99 33 55 ENSG00000111537 FNG Extracellular Space cytokine erreira et al. Diabetes 2014. Reinert-Hartwall et al. 2015 32 interferon gamma ENSG00000158869 FCER1G Fc fragment of igE recepto Plasma Membrane transmembrane recepto 0.97 0.11 111 096 -0.29 0.10 0.10 1.00 0.07 1.00 FCER 1G ENSG00000073605 GSDMB gasdermin B Cytoplasm zinc finger protein 683 Other ENSG00000105374 natural killer cell granule p Plasma Memb -086 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 53 60 58 NKG7 AAEDI 0.00 ENSG00000158122 A AED 4 AhpC/TSA antioxidant enzy Other -0.08 0.27 -0.28 0.02 0.09 0.82 0.20 0.11 1.00 1.00 50 50 101 0.00 ENGGM000177211 un e DNA believes B Mudaue erzyme referent at Disherter 2014 022 0.49 012 027 0.42 100 0.28 072 64 18 SO. 60 ENSGM000148878 RHOR RHOR rac homolog family memb Odoolacm omumo -0.29 -059 0.21 0.00 012 -0.09 0.03 014 011 000 037 013 100 0.62 1.00 1.00 44 30 ENSG0000131149 GSE1 GSE1 God collected notein. Extracellular Space other -077 -032 -035 -1.03 -O 32 -038 0.00 0.00 0.00 0.00 1.00 090 16 -0.21 -0.86 -0.23 0.00 0.00 100 0.02 0.60 030 39 40 -042 -033 011 0.00 33 ENSG00000196126 HLA-DRB1 HLA-DRB1 major histocomestibility c cPlasma Membrane - transmembrane receptor loet at 2010 -040 32 immediate early response Other NSG00000188483 -0.01 -0.58 -0.11 -0.03 039 0.00 0.60 0.78 1.00 0.08 1.00 1.00 50 ENSG00000147448 Plasma Membrane -0.04 58 ENSG00000117318 inhibitor of DNA binding 3, Nucleus -022 -115 -019 -037 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 ENSG00000223745 RP4-717123.3 COCLO ACI CCDC18 artisense RNA 1 Other 0.09 0.59 0.45 -0.52 0.17 0.81 0.08 0.00 0.05 100 0.00 0.42 40 64 32 29 36 17 ENSCM000134530 KIRD4 RD4 killer cell lectin like recept Plasma Membrane - transmembrane receptor Borns Set at 2014 -059 0.41 0.38 0.30 0.47 0.00 0.00 0.01 0.42 0.76 24 0.30 ENSG0000211694 TRGV10 TRGVIO Total recentor gamma var Other other -061 -0.05 0.20 0.01 0.77 100 24 -0.07 0.19 0.17 1.00 1.00 33 ENSG00000169554 ZFR 2 zinc finger F. box binding h-Nucleus transcription regulator .053 -016 -015 -0.92 -0.05 0.01 0.00 27 0.13 -0.55 ENSG00000134107 BHLHE40 BHLHE40 basic helix-loco-helix famil Nucleus transcription regulator -021 -0.63 -014 -023 -0.07 0.10 0.74 0.01 0.69 0.19 100 0.01 1.00 1.00 39 24 37 42 63 58 XCL2 -0.66 0.27 0.46 0.01 0.97 0.90 1.00 1.00 30 55 45 33 ENSG00000148185 XCL2 X-C motif chemokine ligan/Extracellular Space cytokine 0.14 0.63 ENSG00000145882 PCYOXL 013

0.00 037 0.41

PCYOX1L

prenylcysteine oxidase 1 iii Other

Elo et al. 2010. Kalliongia et al. 2014

		_				
NSG00000148484	RSU1	R SLIL	Ras suppressor protein 1		other	
ENSG00000114812	VIPR1	VPR1			G-protein coupled recept or	
ENSG00000186810 ENSG00000189735	CXCR3 TRK1	CXCR3 TBK1	C-X-C motif chemokine re TANK binding kinese 1		G-protein coupled receptor	
ENSG00000188736 ENSG00000077585	GPR 137B	GPR137B	G protein-coupled recepts			
ENSG00000110665	C11orf21	C11orf21	chromosome 11 open rea		other	
ENSG00000179588	ZFPM1	ZFPM1	zinc finger protein, FOG fi		transcription regulator	
ENSG00000185112	FAM 43A	FAM43A	family with sequence simi	il Other	other	
ENSG00000160223	ICOSLG	ICOSLG/LOC 1027239	Minducible T-cell costimula	t: Plasma Membrane	other	
ENSG00000136213	CHST12					
ENSG00000184939	2F P90	ZFP90	ZFP90 zinc finger protein		transcription regulator	
ENSG00000179344	HLA-DQB1	HLA-DQ81	major histocompatibility of			Eloet al. 2010
ENSG00000101057	MYB L2	MYBL2	MYB proto-oncogene like	2 Nucleus	transcription regulator	
ENSG00000211940 ENSG00000091409	NA ITGA6	ITGA6			transmembrane receptor	
ENSG00000196735	HLA-DOA1	HIA-DOAL			transmembrane receptor	Kalliomää et al. 2014
ENSG00000168685	L78	IL78			transmembrane receptor	Kanorpas et at 2014
ENSG00000113263	ITK	ITK	IL2 inducible T-cell kinese		kinase	
ENSG00000138795	LEF1	LEF1	lymphoid enhancer bindir		transcription regulator	Kallionpää et al. 2014
ENSG00000182866	LCK	LCK	LCK proto-oncogene, Src f	a Cytoplasm	kinase	1
ENSG00000229164	NA					1
ENSG00000082074	FYB	FYB	PYN binding protein	Nucleus	other	1
ENSG00000117602	RCANB	RCANB	RCAN family member 3	Other	other	1
ENSG00000211953	NA					1
ENSG00000111913	FAM 658	FAM65B	family with sequence simi		other	1
ENSG00000184613	NELL2	NELL2		Extracellular Space		L
ENSG00000167286 ENSG00000205268	CD3D	CDSD PDE7A	CD3d molecule		transmembrane receptor	Reynier et al. 2010
ENSG00000205268 ENSG00000162894	PDE7A FAIM3	PDE7A FCMR	phosphodiesterase 7A Fc fragment of igM recep		erzyme	I
ENSG00000162894 ENSG00000172005	MAL.	MAL	mal, T-cell differentiation			Eloet al. 2010
ENSGODOOT7200B	APRA2	APBA2	amybid beta precursor p		transporter	Kalliomää et al. 2014
ENSG00000186854	TR ABDIA	- Tana	any broses pecusion p	· cpcpiani	a map da m	Antiopartiti 2014
ENSG00000189339	SLC3SE28	SLC3SE2B	solute carrier family 35 m	«Other	other	
ENSG00000196329	GIMAPS	GIMAP5	GTPase, IMAP family mer		other	
ENSG0000015730B	SUSD3	SUSD3	sushi domain containing		other	
ENSG00000111817	DSE	DSE	dermatan sulfate epimer		erzyme	
ENSG00000175352	NRIP3	NRIP3	nuclear receptor interact		other	
ENSG00000148515	ATP882	ATP882	ATPase phospholipid trans	sį Plasma Membrane	transporter	
ENSG00000147408	CSGALNACT1	CSGALNACT1	chondroitin sulfate Nace		erzyme	Kallionpää et al. 2014
ENSG00000178562	CD28	C D28	CD28 malecule		transmembrane receptor	
ENSG00000165929	TC2N	TC2N	tandem C2 domains, nucl		transporter	
ENSG00000111801	BTNBA3 FCGR2C	BTN3A3	butyrophilin subfamily 3 r			
ENSG00000244682 ENSG00000105483	FCGR2C CARDS	FCGR2C CARD8	Fc fragment of igG recept caspase recruitment dom		transmembrane receptor other	
ENSG0000105488	SYNGAP1	CARUS	caspase recruitment dom	a Nucleus	other	
ENSG00000197288 ENSG00000135426	TESPA1	TESPAL	thymocyte expressed, pos	it Cytonlasm	other	Kallionpää et al. 2014
ENSG00000135426	TURRS	TUBB6	tubulin beta 6 class V		other	2014
ENSG0000152056	AP1S3	APIS3	adaptor related protein o		transporter	1
ENSG00000065675	PRKCQ	PRKCQ	protein kinase C theta		kinase	I
ENSG00000127152	BCL11B	BCL11B	B-cell CLL/lymphoma 118		transcription regulator	I
ENSG00000116824	CD2	C 02	CD2 molecule	Plasma Membrane	transmembrane receptor	I
ENSG00000176749	CDISR1	CDKSR1	cyclin dependent kinase 5	rNucleus	kinase	Kalliorpää et al. 2014
ENSG00000160654	CD3G	CDBG			transmembrane receptor	I
ENSG00000179144	GMAP7	GIMAP7	GTPase, IMAP family men		erzyme	I
ENSG00000157978	LDL RAP1	LDLRAPI	low density lipoprotein re		transporter	I
ENSG00000196187	ТМЕМ63А	ТМЕМВА	transmembrane protein 6		other	I
ENSG00000225217	HSPA7	HSPA7	heat shock protein family		other	I
ENSG00000122877	EGR2	EGR2	early growth response 2		transcription regulator	Heninger et al. 2017
ENSG00000184384	MAML2	MAML2	mastermind like transcrip		transcription regulator	L
ENSG00000074966 ENSG00000110208	TXX FOLR3	TXX FOLR3		Cytoplasm Extracellular Space	kinase	Kaliorpää et al. 2014 Kaliorpää et al. 2014
ENSG00000110208 ENSG00000177575	FOLR3 CD163	FOLR3 CD163	folate receptor 3 CD 163 molecule		other transmembrane receptor	Kallionpää et al. 2014 Ferreira et al. Diabetes 2014
ENSG00000177575	LRRC32	LRRC32	CD 163 morecuse leucine rich repeat contai			draws at one property 2014
ENSG00000137507	GEN1	GEN1	GEN1. Holliday junction S		erzyme	I
ENSG00000167664	TMIGD2	TMIGD2	transmembrane and imm		other	1
ENSG00000159674	SPON2	SPON2	spondin 2	Extracellular Space		Kalliorpää et al. 2014
ENSG00000081059	TCF7	TCF7	transcription factor 7 (T-c		transcription regulator	l .
ENSG00000119487	MARKAP1	MAPKAP1	mitogen-activated protein		other	I
	DIP2A	DIP2A	disco interacting protein	2 Nucleus	transcription regulator	I
ENSG00000160305	DDX11	DOXL1	DEAD/H-box helicase 11		erzyme	I
ENSG00000160305 ENSG00000013573	DUXII		Interded to Secure of	u Plasma Membrane	transmembrane receptor	I
ENSG00000013573 ENSG00000100385	IL2RB	IL2RB	interleuen 2 receptor sub			
ENSG00000013573 ENSG00000100385 ENSG00000215788	IL2RB TNFRSF25	TNFRSF25	TNF receptor superfamily		transmembrane receptor	
ENSG0000013573 ENSG00000100385 ENSG00000215788 ENSG00000160185	IL2RB TNFRSF25 LIBASHBA	TNFRSF25 UBASH3A	TNF receptor superfamily ubiquitin associated and S	S-Cytoplasm	enzyme	
ENSG0000013573 ENSG00000100385 ENSG00000215788 ENSG00000160185 ENSG00000110448	IL2RB TNFRSF25 LIBASHBA CD5	TNFRSF25 UBASH3A CD5	TNF receptor superfamily ubiquitin associated and S CDS molecule	Plasma Membrane	enzyme transmembrane receptor	
ENSG00000013573 ENSG00000100385 ENSG00000215788 ENSG00000160185 ENSG00000110448 ENSG00000197540	IL2RB TNFRSF25 UBASHBA CD6 GZMM	TNFRSF2S UBASH3A CDS GZMM	TNF receptor superfamily ubiquitin associated and S CDS molecule granzyme M	9-Cytoplasm Plasma Membrane Cytoplasm	enzyme transmembrane receptor peptidase	
ENGG0000013573 ENGG00000100385 ENGG00000215788 ENGG00000160185 ENGG00000110448 ENGG00000197540 ENGG00000145287	IL2RB TNFRSF2S UBASHBA CDS GZMM PLACB	TNFRSF2S UBASH3A CD5 GZMM PLAC8	TNF receptor superfamily ubiquitin associated and S CDS molecule granzyme M placenta specific 8	PCytoplasm Plasma Membrane Cytoplasm Nucleus	enzyme transmembrane receptor poptidase other	
ENSG0000013573 ENSG00000100385 ENSG00000215788 ENSG00000160185 ENSG00000110448 ENSG00000197540	IL2RB TNFRSF25 UBASHBA CD6 GZMM	TNFRSF2S UBASH3A CDS GZMM	TNF receptor superfamily ubiquitin associated and S CDS molecule granzyme M	P Cytoplasm Plasma Membrane Cytoplasm Nucleus ny Nucleus	enzyme transmembrane receptor peptidase	

									_																					
ENSG00000148484	RSU1 VIPR1	RSU1 VPR1	Ras suppressor protein 1 Cytoplasm vaspactive intestinal peptid Plasma Membrane	other			0.63			0.05 0.85 0.35 0.98	051	0.60	0.00 0.02			LOO 0.00 LOO 0.00	0.93	0.45 58	68 73		68 50 84 70		75 6	7 42	32 27	24 3	2 50	27 9	25 33	
ENSG0000134812 ENSG00000186810	CXCR3	CXCR3	C.X.C motif chemokine rec Plasma Membrane				-0.73		-0.06	-0.44		0.43	0.00 0.00		0.00	0.60	1.00	082			84 /U 50	36	58 6		70	58 90	- 1 -		42 33	
ENSG00000183735	TBK1	TBK1		kinase			-0.52		-033	-	-0.23	-0.35		0.02		0.00		100	27		34	-	33 4		7.0	74 66	6		67 58	1
ENSG00000077585	GPR 1378	GPR137B		other			-054		-0.14		0.08	-0.07	0.08	0.25				1.00	22		42		58 4			58 5	8		42 58	1
ENSG00000110665	C11arf21	C 11 or f 21	chromosome 11 open read Cytoplasm	other			0.51			0.25 0.51	032	0.31	0.19 0.08			L00 0.00	1.00	100 53	73	66	58 40	73	58 6	7 47	27	34 40	2 60	27	42 33	1
ENSG00000179588	ZFPM1	ZFPM1		transcription regulator			-055		0.25	-0.16			0.08		0.79	0.81			30		61	36			70	3	9	64		1
ENSG00000185112	FAM43A	FAM43A		other			-0.70		-013	-0.69		0.33	0.04		0.97	0.25		1.00	30		47	27	67 6	7	70	45 5			33 33	1
ENSG00000160223	ICOSLG	ICOSLG/LOC 1027239	Sinducible T-cell costimulats Plasma Membrane	other			-0.66			001 -0.11		-0.09	0.11 0.04			L00 0.88		1.00 28			29 50	36	58 4		70	68 7	1 50		42 58	1
ENSG00000136213 ENSG00000184939	CHST12 ZFP90	ZFP90	ZFP90 zinc finger protein Nucleus	transcription regulator			-0.64 0.56		0.09	037 010	0.02	0.03	0.04		0.39	100 0.39		1.00 0.97 58	73		53 76 70	-	50 50		76 27	42 40		45	50 50 17	1
ENSG0000179344	HLA-DQB1	HLA-DQB1	major histocompatibility ccPlasma Membrane		Eloet al. 2010	u32	0.56		-0.42	037 010	-0.32	0.29	0.16 0.05		0.00	100 0.39		037 58	/3		76 70 37	20	33 5		2/	68 6	3 30	45	67 50	
ENSG00000101057	MYBL2	MYB12		transcription regulator					-0.98		-0.50	-051			0.00			0.02			21		33 2			79 75	9		67 75	4
ENSG00000211940	NA		,					0.76	1.04		1.27	1.08			0.00		0.00	000			68		75 6			21 3	2		25 33	1
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	067 61	62	76	63 60	55	67 5	8 39	38	24 3	7 40	45	33 42	
ENSG00000196735	HLA-DQA1	HLA-DQA1	major histocompatibility ccPlasma Membrane		Kallionpää et al. 2014				-033		-0.43	-0.06			0.00			1.00			39		25 5			66 6			75 50	I
ENSG00000168685	L7R	IL7R	interleukin 7 receptor Plasma Membrane							0.04 0.14	0.45	0.12	0.29 0.71			L00 0.91		100 53			66 50 74 50		58 5			26 3			42 42	I
ENSG00000113263 ENSG00000138795	ITK LEF1	LEF1		kinase	Voltage III at al 2014		0.25			0.06 0.06 0.12 0.10		0.11	0.07 0.61 0.51 0.84			L00 0.72 L00 0.91		0.99 61 1.00 53		79	74 50 76 30		75 75 67 6		30 38	21 2	6 50		25 25 33 33	I
ENSG00000138795 ENSG00000182866	LCK	LOX	, , , , , , , , , , , , , , , , , , , ,	transcription regulator kinase	Kalliorpää et al. 2014		0.12			0.12 0.10 0.19 -0.01		0.18	0.51 0.84			LOO 0.91 LOO 0.79		068 44		79	76 30 74 30		67 7		38 49	21 2	70		33 25	I
ENSG00000229164	NA.		tex prote-one against, sie ra cyrepiasm	Minde						0.11 -0.09		0.13	0.53 0.91			100 0.79		100 53		82	74 40	_	67 5		46	18 2	6 60		33 42	I
ENSG00000082074	FYB	FYB	PYN binding protein Nucleus	other			0.33	0.62	0.39	0.07 0.33	0.18	0.38	0.29 0.32	0.00	0.00	L00 0.19	1.00	100 47	76	76	74 40	82	67 7	5 53	24	24 26	6 60	18	33 25	I
ENSG00000117602	RCANB	RCANB		other	1		0.12			0.02 0.00	0.20	-0.02	0.39 0.70			L00 0.97		1.00 56	62	84	66 30	55	67 4		38	16 3	4 70		33 58	1
ENSG00000211953	NA	I			1	l		0.82	0.48		0.64	0.19		0.00	0.00		0.14	030		68	68		75 6	7		32 3	2		25 33	1
ENSG00000111913	FAM 658	FAM658		other	1		0.19			022 019		0.39	0.00 0.07			L00 0.08		0.55 69	73	74	74 70	73	58 7		27	26 26	_		42 25	1
ENSG00000184613	NELL2	NELL2	neural EGFL like 2 Extracellular Space		1					0.11 0.20		0.39	0.84 0.87			L00 0.91		097 44		71	68 20		67 6			29 3			33 33	1
ENSG00000167286 ENSG00000205268	CD3D PDF7A	C 080 PD F7 A		transmembrane receptor enzyme	Reynier et al. 2010					012 Q03 011 Q27	0.63 0.64	0.22	0.19 0.76			L00 0.63		1.00 56	57 68	79	79 60 68 60		67 8: 83 5		43	21 21	1 40		33 17 17 42	1
ENSG00000205268 ENSG00000162894	FAM3	FCMR	phosphodiesterase /A Cytoplasm Fc fragment of kM recept Plasma Membrane				0.24			011 U2/ 003 016		0.30	0.06 0.29			L00 0.08		0.80 56			68 50		58 6		32	29 3			1/ 42 42 33	I
ENSG0000172005	MAL	MAL	mal, T-cell differentiation; Plasma Membrane		Floet al. 2010		0.07			005 005	066	0.16	0.22 0.98			L00 0.08 L00 0.94		100 64	57		74 60		67 5		43	29 3	6 40	36	33 42	1
ENSG00000034053	APBA2	APBA2		transporter	Kalionpää et al. 2014		0.22			0.25 0.22		0.21	0.80 0.67			L00 0.30		0.87 47		76	74 30		75 6	_	41	24 26	6 70	36	25 33	
ENSG00000186854	TRABD2A				· .		0.21			0.04 0.31	0.54	0.34	0.03 0.45	0.00		L00 0.09	0.73	100 61	68	71	74 50	73	67 6		32	29 26	6 50	27	33 33	1
ENSG00000189339	SLC35E28	SLC3SE2B	solute carrier family 35 mcOther	other		0.20	0.24	0.52	0.37	014 018	0.39	0.41	0.00 0.02	0.00	0.00	L00 0.01	0.44	0.18 58	68	68	68 60	73	67 8	3 42	32	32 3	2 40	27	33 17	1
ENSG00000196329	GIMAPS	GIMAPS		other						0.08 0.35		0.31	0.02 0.33			L00 0.01		100 61	68		68 40		58 5		32	26 3	2 60		42 42	1
ENSG0000015730B	SUSD3	SUSD3		other		0.39	0.34			0.17 0.52		0.62	0.00 0.08			LOO 0.00		019 69	84		71 80	100	75 8	_	16	18 2	9 20	0	25 17	
ENSG00000111817	DSE	DSE NRIP3		enzyme					-0.62 -0.41		-0.64 -0.51	-0.52 0.00		0.00	0.00		0.42	0.75			29		33 3: 42 5:	·		71 7	1		67 67	4
ENSG00000175352 ENSG00000148515	NRIP3 ATP882	ATP882	nuclear receptor interactinOther ATPase phospholigid transpPlasma Membrane			0.36	0.41			032 048		0.00	0.00 0.06		0.00	100 0.00	0.46	1.00 0.02 58	70		37 61 60	91	75 6		30	76 6 26 3			58 50 25 33	
ENSG00000147408	CSGALNACT1	CSGAL NACT1		erzyme	Kaliomää et al. 2014		0.72			032 048		0.24	0.00 0.14			LOO 0.00		0.82 69			74 70		75 7	_	35	18 2			25 25	1
ENSG00000178562	CD28	CD28		transmembrane receptor	and participation of the second					0.09 0.04		0.25	0.76 0.72			L00 0.31		100 58			71 50		67 5			21 25			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	L00 0.84	0.91	1.00 39	62	82	68 20	45	75 50	0 61	38	18 3	2 80	55	25 50	1
ENSG00000111801	BTNBA3	BTN3A3		other		0.42	0.49		0.79	0.40 0.50		0.83	0.00 0.02		0.00	L00 0.00		0.08 78	73	76	74 90	91	83	3 22	27	24 26	6 10	9	17	1
ENSG00000244682	FCGR2C	FCGR2C	Fc fragment of igG receptoPlasma Membrane					-0.83	_		-1.16			0.00			0.00			32			33			68	1		67	
ENSG00000105483	CARDS	C ARD8	caspase recruitment doma Nucleus	other			0.32			010 039		0.58	10.0 00.0			0.00		021 61			71 50		7			26 25		18	25	I
ENSG00000197283 ENSG00000135426	SYNGAP1 TESPA1	TESPAL	thymocyte expressed, posit Cytoplasm	other	Kallionpää et al. 2014		0.34			0.27 0.48 0.18 0.12		0.46	0.11 0.50 0.73 0.48			L00 0.01 L00 0.62		0.67 56 1.00 53			74 70 71 30	82 64	75 6: 67 5 8		35 32	24 25 24 25	_		25 33 33 42	
ENSG00000176014	TUBB6	TUBB6		other	Kallonpaa et at. 2014	401	0.1/		-0.68	0.18 0.12	-0.42	0.05	0.73 0.48		0.03	100 0.62		100 53	68		71 30 29	64	33 5		32	79 7	1		67 50	
ENSG00000152056	AP1S3	APIS3		transporter				-0.69			-0.02	0.01		0.00	0.00		0.83			26			42	Ĭ		74			58	I
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	L00 0.97	1.00	100 47	51	74	63 40	36	67 5	8 53	49	26 3	7 60	64	33 42	I
ENSG00000127152	BCL11B	BCL11B	B-cell CLL/lymphoma 11B Nucleus	transcription regulator		0.04	0.01	0.60	0.25	0.09 0.00	031	0.02	0.99 0.98	0.00		1.00 0.99	0.72	100 50	54		68 30	45	58 50	0 50	46	29 3	2 70	SS	42 50	I
ENSG00000116824	CD2	CD2		transmembrane receptor			0.06			0.06 0.23		0.35	0.89 0.78			L00 0.41		1.00 53		76	74 70	73	67 6		41	24 2	6 30		33 33	I
ENSG00000176749	CDISR1	CDKSR1	-	kinase	Kalionpää et al. 2014		0.42			0.57 0.45		0.66	0.00 0.06			0.05		031 83	84	82	71 80	82	83 8		16	18 2	9 20		17 17	1
ENSG00000160654 ENSG00000179144	CD3G GMA97	CD8G GIMAP7		transmembrane receptor			-0.12 0.37			0.09 -0.27 0.37 0.58		-001	0.30 0.90			L00 0.86 L00 0.15		1.00 50			61 30 66 60		67 43 58 63		54 35	24 3	9 70		33 58 42 33	1
ENSG00000179144 ENSG00000157978	GIMAP7 LDLRAP1	GIMAP7		erzyme transporter	1					0.37 0.58 0.02 0.15		0.17	0.09 0.76			100 0.15		1.00 67			66 60 71 40		58 6	_		29 34		27 45	42 33 33	1
ENSG00000196187	TMEM63A	TMEMERA		other	1		0.35			0.14 0.35		0.33	0.09 0.04			100 0.02		0.96 58			68 40		75 6			26 3			25 33	1
ENSG00000225217	HSPA7	HSPA7		other				-091			-1.50			0.00			0.02			34	-		42	1		66		-	58	
ENSG00000122877	EGR2	EGR2		transcription regulator	Heninger et al. 2017	I _		-0.57	-031		-0.28	-033		0.00	0.00		0.94	0.53		24	29		33 2	5		76 75	1		67 75	4
ENSG00000184384	MAML2	MAML2		transcription regulator	1					016 0.79		0.37	0.17 0.06			LOO 0.00		100 64			66 70		75 5	_		24 3			25 42	1
ENSG00000074966	TXX	TXX		kinase	Kalionpää et al. 2014	-010	0.30			0.31 0.41		0.36	0.57 0.18			L00 0.01		0.41 42	62		68 30	73	75 6	7 58	38	26 3			25 33	1
ENSG00000110208 ENSG00000177575	FOLR3 CD163	FOLR3 CD163	folate receptor 3 Extracellular Space CD 163 molecule Plasma Membrane	other transmembrane receptor	Kallionpää et al. 2014 Formina et al. Diabetes 2014	I			0.89		1.19 0.64	0.83			0.00			1.00 0.78			68		67 6 67 6	7		32 33			33 33 33 33	1
ENSG00000177575 ENSG00000137507	CD163 LRRC32	LRRC32	CD 163 molecule Plasma Membrane leucine rich repeat contain Plasma Membrane		rerretra et al. Diabetes 2014	l			-0.67		-0.36	-0.41			0.00			0.78			71 24		25 2			71 7	6		33 33 75 75	1
ENSG0000137507 ENSG00000178295	GEN1	GENI.		erzyme	1	l		-051	-433		-0.43	-430		0.00	0.00		1.00			26			42	1		74			/5 /5 58	1
ENSG00000167664	TMIGD2	TMIGD2		other	1	0.24	0.31		0.44	0.05 0.62		0.50	0.19 0.45		0.00	LOO 0.03		021 56	65	71	68 50	91	67 7	5 44	35	29 3	2 50		33 25	1
ENSG00000159674	SPON2	SPON2		other	Kallionpää et al. 2014			0.51	0.43	-0.18		0.31	0.38		0.00	1.00		0.03	41		66	45	67 5			32 3	4		33 42	1
ENSG00000081059	TCF7	TCF7		transcription regulator			0.06			0.07 0.06	0.42	0.23	0.58 0.96	0.00		L00 0.89		1.00 53			71 30	-	83 5		38	18 2	9 70		17 42	1
ENSG00000119487	MARKAP1	MAPKAP1		other	1		0.45			039 083	0.72	0.48	0.02 0.36			0.00		0.44 58			61 60		75 6	7 42	41	34 3	9 40		25 33	1
ENSG00000160305	DIP2A	DIP2A		transcription regulator	1		0.40			000 044		0.35	0.35 0.65			L00 0.27		0.15 50			74 50		75 8		35	34 2	6 50		25 17	1
ENSG00000013573	DDX11	DDX11		erzyme	1		-041	-0.66		1.15 -0.95		I	10.0 00.01	0.00		0.00	0.68	39		34	20	~	42	61	62	66	80		58	1
ENSG00000100385	IL2RB TNFRSF25	IL2RB		transmembrane receptor	1					0.12 0.08 0.12 0.00		0.33	0.75 0.44 0.85 0.75			100 0.91		017 47 100 50			61 50 61 50		67 7: 75 6:	5 53	62 41	26 ¥	9 50		33 25	1
ENSG00000215788	TNFRSF25 UBASHBA	TNFRSF25 UBASH3A	TNF receptor superfamily rPlasma Membrane ubiquitin associated and SrCytoplasm	transmembrane receptor enzyme						0.12 0.00 0.06 0.06	0.76	0.29	0.85 0.75 0.87 0.99			L00 0.75 L00 0.99		100 50 100 42			61 50 63 30		75 6			32 ¥		45	25 33 42	1
ENSG00000160185	COLUMN TO SERVE	CD5		transmembrane receptor	1	-400	0.00			0.06 0.04	0.53	0.18	0.36 0.85			LOO 0.98		100 31			50 30		67 5		59	24 50			33 42	1
ENSG00000160185 ENSG00000110448	CD5						0.10				041	0.75									co 00	73	58 7		49	34 30	2 20		42 25	1
	CDS GZMM	GZMM	granzyme M Cytoplasm	peptidase		0.17	0.10	0.51	0.39	036 027	441	0.75	0.11 0.89	0.00	0.01	L00 0.28	0.42	0.05 64	51	66	68 80	/3	58 /:	35	49	34 3	2 20	27	42 25	
ENSG00000110448		GZMM PLAC8		peptidase other			0.10			036 027 001 019		0.75	0.11 0.89			L00 0.28 L00 0.62		0.05 64 1.00 58		76	68 50		58 5		35	24 3			42 42	
ENSG00000110448 ENSG00000197540 ENSG00000145287 ENSG00000163516	GZMM PLAC8 ANKZF1	PLAC8 ANKZF1	placenta specific 8 Nucleus ankyrin repeat and zinc fin Nucleus	other transcription regulator		011 012	0.29 0.30	0.55 0.51	0.29	0.01 0.19 0.30 0.25	010 040	0.14	0.11 0.65 0.05 0.28	0.00	0.01	L00 0.62 L00 0.43	1.00 0.83	1.00 58 56	65 68	76	76 30	55 64	58 58 75	8 42 44	35 32	24 32 24 24	2 50 4 70	45 36	42 42 25	
ENSG00000110448 ENSG00000197540 ENSG00000145287	GZMM PLAC8 ANKZF1	PLAC8	placenta specific 8 Nucleus ankyrin repeat and zinc fin Nucleus	other		011 012	0.29 0.30	0.55 0.51	0.29	0.01 0.19	010 040		0.11 0.65 0.05 0.28	0.00	0.01	L00 0.62	1.00 0.83	1.00 58	65 68	76		55 64	58 5	8 42 44	35 32	24 32 24 24	2 50	45 36	42 42	

ENSG00000162729	IGSF8	IGSF8	immunoglobulin superfami Plasma Membrane other				0.57		-0.11 0.25		0.36	026 0.45			.00 0.67			5 79	-	50 64			39 35	21 32	- -	36	25
ENSG00000172340	SUCLG2	SUCL 62	succinate-CoA ligase GDP-I Cytoplasm enzyme		0.14	0.50	0.61		027 079		0.62	0.08 0.35					0.99 56 5		61	50 73			44 41	29 39		27 25	33
ENSG00000183019	MCEMP1	MCEMP1	mast cell expressed memb Cytoplasm other					-0.23	002 033		-0.27			0.09			100 47	32	42		25	33	SI 27	68 58		75	67
ENSG00000162892	L24 CDSS	IL24	interleukin 24 Extracellular Space cytokine CDSh molecule Plasma Membrane other		-0.02		0.63			0.37	0.18	0.23 0.04					120	3 76	71	50 73	67			24 29		27 33	33
ENSG00000172116 ENSG00000163823	CD88 CCR1	CD88 CCR1	CD8b malecule Plasma Membrane other C-C motif chemokine reces Plasma Membrane G-protein coupled:		1	0.08	0.53 -0.56	0.68 -0.40	0.13	-0.78	0.73 -0.15	0.76		0.00	0.45		0.05	4 71	66 47	73	58	67 50	46	29 34 68 53	1	27 42 75	33 50
ENSG00000140398	NBL1	NEL1	nei like DNA glycosylase 1 Nucleus enzyme	copt d	010	-011	-055	-034	-0.38		-0.19	0.98 0.41		0.00	0.51		100 42		26	27			58 62	66 74		73 42	58
ENSG0000140398	CD27	CD27	CD27 molecule Plasma Membrane transmembrane re	mine	0.13		0.70		021 004	0.52	0.39	022 0.87					100 58 5		66	70 55			40 43	29 34		45 33	33
ENSG00000137070	IL11RA	IL11RA	interleukin 11 receptor sub Plasma Membrane transmembrane re		0.20		0.55		-0.21 020	0.55	0.39	011 0.27	0.00			0.60	56		00	40 55		67	42 43 44 41	29 34		45 25	33
ENSG00000211734	TRBV5-1	TRBV5-1	T cell receptor beta variabl Other other	apar .	0.19	0.40	0.86		019 002	0.38	0.04	0.15 0.76					1.00 53		63	50 55		67	47 43	26 37		45 25	33
ENSG0000035115	SH3YL1	SHBYL1	SH3 and SYLF domain conti Plasma Membrane other	Kalliorpää et al. 2014	021	0.26	0.55		041 002	0.42	0.28	0.07 0.72					100 61		63	60 64			ay as	24 37		36 25	42
ENSG0000231475	IGHV4.31	IGHV4-31	immunoglobulin heavy vari Other other	namosparat at 2004	-	0.10	0.62	0.36	041 401	0.20	0.46	0.72		0.01			0.82	68	63		58	75		32 37		42	25
ENSG00000226660	TRBV2	TRBV2	T cell receptor beta variabl Other other		022	0.22	0.85		-0.14 0.22		0.10	0.22 0.53	0.00		.00 0.51		1.00 58	3 84	71	40 91			42 27	16 29	9 60	9	42
ENSG00000106560	GIMAP2	GIMAP2	GTPase, IMAP family mem Cytoplasm other		0.18	0.33	0.78		033 060	0.58	0.46	0.14 0.68						9 71	61	60 64	83		42 41	29 39		36 17	33
ENSG00000166825	ANPEP	ANPEP	alanyl aminopeptidase, me Plasma Membrane peptidase	Kaliomää et al. 2014	0.08		-0.55		016	-0.40	-0.73	096			.00		100 56	34	37	60	33		44	66 63		67	58
ENSG00000181035	9.035442	SLC25M2	solute carrier family 25 ms Cytoplasm transporter		015	0.16	0.54		.0.32 0.16			022 0.66	0.00		00 0.47		56			40 64			44 43	29		36	
ENSG00000013725	CD6	CD6	CD6 molecule Plasma Membrane transmembrane re	aptor	-0.07	-0.10	0.51	0.14	-0.02 0.12	051	0.18	0.19 0.87	0.00	0.41 1	.00 0.95	0.84	100 36	6 68	61	50 55	75	67	64 54	32 39	9 50	45 25	33
ENSG00000064886	CH3L2	CH3L2	chitinese 3 like 2 Extracellular Space erzyme		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	100 56	6 68	55	60 36	58	42	44 54	32 45	5 40	64 42	58
ENSG00000026950	BTNBA1	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 5	9 68	76	40 55	75		39 41	32 24	4 60	45 25	25
ENSG00000226752	PSM D5-AS 1	PSM D5-AS1	PSMD5 antisense RNA 1 (h/Other other		0.33	0.36	0.52	0.59	016 011		0.30	0.10 0.66	0.00	0.00 1	.00 0.97		1.00 58 5	9 68	74	60 55		75	42 41	32 26	6 40	45	25
ENSG00000211747	TRBV20-1	TR8V20-1	T cell receptor beta variabl Other other		0.02	-0.03	0.53	0.28	002 029	0.16	0.38	0.76 0.98	0.00	0.07 1	.00 0.98	1.00	100 53	9 68	66	60 55	58	67	47 51	32 34	4 40	45 42	33
ENSG00000232869	TRBV29-1	TRBV29-1	T cell receptor beta variabl Other other		-017	-0.02	0.57	0.14	-0.30 -0.10	036	-0.07	0.73 0.84	0.01	0.67 1	.00 0.96	1.00	100 47	6 71	61	40 45	58	50 5	53 54	29 39	9 60	55 42	50
ENSG00000130598	TNN2	TNN2	troponin I2, fast skeletal by Cytoplasm enzyme	1	1		-053	-0.48		-0.48	-037		0.01	0.05		0.69	1.00	29	32		33	42		71 68		67	58
ENSG00000166681	NGFRAP1	BEG	brain expressed X-linked 3 Cytoplasm other	1	0.27	0.26	0.65	0.47	-0.06 0.18	0.59	0.10	0.00 0.72	0.01	0.00	.00 0.70	1.00	100 64 6	8 79	76	50 55	75	75	36 32	21 24	4 50	45 25	25
ENSG00000213930	GALT	GALT	galactose-1-phosphate urid Cytoplasm enzyme	1	0.33	0.24	0.53		0.05 0.42	0.53		0.08 0.24	0.01			1.00		3 68		60 91	58		31 27	32	40	9 42	- 1
ENSG00000176171	BNP3	B NIP3	BCL2 interacting protein 3 Cytoplasm other	1	0.07	0.13	0.60	0.32	-0.08 0.10	0.19	0.32	0.76 0.84	0.01			1.00	100 64 6	2 71	66	50 64	58	58	36 38	29 34	4 50	36 42	42
ENSG00000090554	RLT3LG	FLTBLG	fms related tyrosine kinase Extracellular Space cytokine	1	0.15	0.26	0.50	0.30	031 057	0.68	0.40	0.31 0.85		0.09		0.99	058 64 6	8 71	71	90 82	75	100	36 32	29 29	9 10	18 25	0
ENSG00000198937	CCDC167	CCDC167	coiled-coil domain containi Other other	1	0.12	0.22	0.75	0.60	018 002	0.64	0.79	0.35 0.86		0.04	.00 0.94	1.00	100 56 5	9 68	66	60 55	67	75	44 41	32 34	4 40	45 33	25
ENSG00000136630	HLX	HLX	H2.0 like homeobox Nucleus transcription regul	or	1		-054			-0.51	-020		0.02				1.00	32	39		33	42		68 61	1	67	58
ENSG00000227191	TRGC2	TRGC2	T cell receptor gamma con Other other	1	1	-021	0.61	0.39	-0.06		0.35	0.41	0.02		0.84			1 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	035 056	0.52	0.10	0.27 0.75	0.02	0.09 1	.00 0.62	1.00	100 64 6	2 68	61	60 64	67	67	36 38	32 39	9 40	36 33	33
ENSG00000123342	MMP19	MMP19	matrix metallopeptidase 1/Extracellular Space poptidase				-0.54			0.11			0.02			1.00		34			50			66		50	
ENSG00000211677	IGLC2	IGLC2	immunoglobulin lambda c c Extrac ellular Space other				-0.60	-0.48		-0.34	-051		0.02	0.13		1.00	1.00	34	37		33	33		66 63	ž.	67	67
ENSG00000104951	L41	IL4I1	interleukin 4 induced 1 Cytoplasm enzyme	Ferreira et al. Diabetes 2014			0.54			0.69			0.08			1.00		66			67			34		33	
ENSG00000115263	GCG	GCG	glucagon Plasma Membrane other					0.57			0.39			0.00			000		74			75		26	i		25
ENSG00000118785	SPP1	SPP1	secreted phosphoprotein 1 Extracellular Space cytokine					1.62						0.00					76			- 1		20	i.		
ENSG00000074706	IPCEF1	IPCEF1	interaction protein for cyto Cytoplasm enzyme		0.41	0.30			022 009		0.31	0.00 0.07			.00 0.50			6	71	60 73			33 24	29		27	42
ENSG00000254647	INS	INS	insulin Extracellular Space other					0.74			0.51			0.00			0.06		74			67		26			33
ENSG00000150867	RP4K2A	PIP4K2A	phosphatidylinositol-5-phorCytoplasm kinase		0.35		0.33		0.45 0.78	0.28	0.72	0.00 0.04						0 74	68	70 73	67		36 30	26 32		27 33	25
ENSG00000180357	ZNF609	ZNF609	zinc finger protein 609 Nucleus other		0.39				0.40		0.74	0.00 0.00			.00			8	68	70			36 32	32			25
ENSG00000151702	RJ1	FU1	Ri-1 proto-oncogene, ETS t Nucleus transcription regul	or Kallionpää et al. 2014	0.49	0.43	0.38		0.56 0.43	0.22	0.85	0.00 0.02			0.00			8 66	66	60 82	67		36 32	34 34	4 40	18 33	25
ENSG00000115386	REG1A	R EG 1A	regenerating family memb Extracellular Space growth factor					0.52			0.38			0.00			036		66			58		34	<i>i</i>		42
ENSG00000101017	CD40	CD40	CD40 molecule Plasma Membrane transmembrane re				-0.43	-0.68		-0.31	-047			0.00			0.07	13	18		8	17		87 82	£ .	92	83
ENSG00000198502	HLA-DR85	HLA-DRBS	major histocompatibility ccPlasma Membrane transmembrane re	aptor Elo et al. 2010			-039	-0.87		-0.10	-0.93			0.00			0.90	29	32		50	42		71 68	<u> </u>	50	58
ENSG00000197043	ANXA6	A NKA6	annexin A6 Plasma Membrane ion channel		0.25	0.35	0.49		029 056	0.49	0.69	0.00 0.65			.00 0.11	0.75	0.25 64 5	9 66	68	80 73	75	75	36 41	34 32	2 20	27 25	25
ENSG00000111331 ENSG00000204642	OAS3 HLA.F	OAS3 HLA-F	Z-5'-oligoa danylate synthe Cytoplasm enzyme	Kallionpää et al. 2014, Reynier et al. 2010, Ferreira et al. 20	14	0.47		0.53						0.00					66					34	1		
ENSG00000204642 ENSG00000214078	CPNE1	CPNF1	major histocompatibility ccPlasma Membrane transmembrane re codine 1 Nucleus transporter	aptor Elo et al. 2010	0.49	0.47	0.44		0.43 0.60	0.27	0.34	0.00 0.18 0.00 0.25					021 75 7	3 74 5 76	74 68	80 82 70 73			25 27 31 35	26 26 24 32		18 33 27 17	17 33
ENSG00000171130	ATR6V0E2	ATP6V0E2			037		0.39		036 077	u39	0.67	0.00 0.27			.00 0.01			5	68	80 82			31 35 28 35	24 32	_	18	
ENSG00000171130	CST7	CST7	ATPase H+transporting V0 Cytoplasm enzyme cvstatin F Extracellular Space other	Kalliomää et al. 2014		-0.51	0.46	0.52	-0.36	0.69	0.72	0.14 0.08		0.00			0.01 61		66	80 82		75	26 35 39 59	21 34		64 42	25 25
ENSG0000017984	TURM	CSI/	cystatin F Extracellular space other	Kalionpaa et al. 2014	014		0.46		0.36		0.70	0.14 0.08			0.15			5 82	82	70 64		75	25 35	18 18		64 42 36 17	25
ENSG00000105953	OGDH	обри	oxoglutarate dahydrogena:Cytoplasm enzyme		ula	0.40	0.27	0.63	029 026	434	0.75	0.61		0.00	.00 0.33			9 66	68	70 04	8.3	75	41	34 32		30 17	25
ENSG00000147955	SIGMARI	SIGMAR1	sigma non-opioid intracelli Plasma Membrane transmembrane re	mtor	030		U.27		-0.01		0.73	0.01 0.31			.00			2	71	50		75	39 38	34 32			25
ENSG0000147935	FAMILIR	FAM111B	family with sequence simil Other other		4.50	0.40	-050	-0.58		-0.72	-0.63	0.31		0.00			012	34	26	30	33	25		66 74	<u> </u>	67	75
ENSG00000010292	NCAPD2	NCAP02	non-SMC condensin I come Nucleus other	1	012	0.23			000		0.59	0.18 0.48			.00		0.74 58		68	50			42 32	32	2 50		33
ENSG00000154229	PRICA	PRKCA	protein kinase C alpha Cytoplasm kinase	1	011				004 004		0.10	031 0.56			.00 0.27			8	68	70 64			33 32	32	_	36	42
ENSG00000136266	FFAR1	FFAR1	free fatty acid receptor 1 Plasma Membrane G-grotein coupled:	ceator	1		-034	-0.53		-0.37	-0.20			0.00			100	34	34		42	50	-	66 H	<u> </u>	58	50
ENSG00000153406	NMRAL1	NMR AL1	NmrA like redox sensor 1 Nucleus other		0.17	0.31	-		-0.05 0.52		0.61	0.17 0.25			.00 0.19		0.76 64 6		74	40 64			36 35	26	6 60	36	25
ENSG00000131634	TMEM 204	TMEM 204	transmembrane protein 20 Plasma Membrane other	1		0.62			025 071		0.35	0.01 0.07			.00 0.07		100 69		66	60 82			31 30	34		18	42
ENSG00000083454	P2R05	P2RXS	purinergic receptor PZX 5 Plasma Membrane ion channel	1	1		0.50	0.55		0.55	0.27			0.00			1.00	71	74		67	58		29 26		33	42
ENSG00000188191	PRKAR1B	PRKAR1B	protein kinase cAMP-deper Cytoplasm kinase	1	011	0.39			-0.07 0.41		0.24	0.27 0.59			.00 0.06		0.98 69 6	8	82	50 82			31 32	18		18	17
ENSG00000211746	TRBV19	TRBV19	T cell receptor beta variabl Other other	Eloet al. 2010		0.15			0.43 0.07		0.47	0.10 0.61			.00 0.94			5	74	70 55			33 35	26		45	25
ENSG00000181754	AMIG01	AMIGO1	adhesion molecule with Ig Plasma Membrane other	1	-0.04	0.16		0.52	-0.31		-0.05	0.30 0.55		0.00 1	.00		100 47 5	9	71	10		50 9	53 41	25	90		50
ENSG00000122694	GLIPR2	GUPR2	GLI pathogenesis related 2 Cytoplasm other	1	1		0.12	0.57		0.06	0.38		0.02	0.00		1.00	1.00	58	68		50	83		42 32	2	50	17
ENSG00000167815	PRDX2	PRDX2	peroxinedaxin 2 Cytoplasm enzyme	1	0.43	0.44	0.61	0.55	0.47 0.71	0.62	1.00	0.03 0.81		0.00 1	.00 0.19	1.00	0.63 61 9	9 61	68	70 73	67	75	39 41	39 32	2 30	27 33	25
ENSG00000149531	FRG1B	FRG1BP	FSHD region gene 1 family Other other	1	-0.66	-0.69	-030	-0.61	-0.70 -0.79	-0.52	-077	0.01 0.05	0.10	0.01 1	.00 0.13	0.48	030 39 3	0 37	34	30 27	25	25	61 70	63 66	6 70	73 75	75
ENSG00000106397	PLOOS	PLOD3	procollagen-lysine, 2-oxogls Cytoplasm enzyme	1			0.25	0.52		021	0.35		0.01	0.01		1.00	1.00	68	74		58	67		32 26	ă .	42	33
ENSG00000137959	IR44L	IR44L	interferon induced protein Nucleus other	Kalliorpää 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	14 0.00	0.48	0.68 56 9	9 58	66	30 18	33	42	44 41	42 34	70	82 67	58
ENSG00000223350	IGLV9-49	IGLV9-49	immunoglobulin lambda v: Other other	1	1			0.67		0.67	0.89			0.02			0.86	71	71		75	75		29 29	a l	25	25
	NAGA	NAGA	alpha-Nacetylgalactosami-Cytoplasm enzyme	1	1		0.42	0.57		0.19	0.42		0.00	0.02		1.00	100	63	68		67	75		37 32	ž.	33	25
ENSG00000198951		TMEM 106C	transmembrane protein 10 Other other	1	0.18	0.27		0.50	-0.12		0.48	0.23 0.49		0.03 1	.00		100 67 6	2	68	40		67	33 38	30	2 60		33
ENSG00000198951 ENSG00000134291	TMEM106C		annex in AS Plasma Membrane transporter	I	035	-019	0.22	0.56	024 -0.19	0.25	0.34	0.09 0.78	0.55	0.04 1	.00 0.64	1.00	100 61	1 58	66	60 27	58	67	39 59	42 34	4 40	73 42	33
ENSG00000134291 ENSG00000164111	ANXAS	ANKAS					0.17	0.61					0.14	0.04				55	66								- 1
ENSG00000134291 ENSG00000164111 ENSG00000104974	ANXAS LILRA1	LERA1	leukocyte immunoglobulin Plasma Membrane - transmembrane re	aptor																				45 34	١.		
ENSG00000134291 ENSG00000164111 ENSG00000104974 ENSG00000225630	ANXAS LILRA1 MTND2P28	LERA1 MTND2928	leukocyte immunoglobulin Plasma Membrane transmembrane re 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 61 9	7 63	53	80 64	67		39 43	37 47		36 33	50
ENSG0000134291 ENSG00000164111 ENSG00000104974 ENSG00000225630 ENSG00000124882	ANXAS UILRA1 MTND2P28 EREG	LLRA1 MTND2P28 EREG	leukocyte immunoglobulin Plasma Membrane transmembrane re mitochondrially encoded N Other other epiregulin Extracellular Space growth factor	Ferreira et al. Diabetes 2014	0.46	0.75	0.19 0.36	0.06 0.19	1.19	033	0.86	10.0 00.01	0.00	0.00 0	.00	0.88	0.00 67	7 63 2 68	53 58	80 61 70	67 58	75	33 38	37 47 32 42	2 30	42	25
ENSG0000134291 ENSG00000164111 ENSG00000104974 ENSG00000225630 ENSG00000124882 ENSG00000134531	ANXAS LILRA1 MTND2P28 EREG EMP1	LLRA1 MTND2928 EREG EMP1	leukocyte immunoglobulin Plasma Membrane i transmembrane re mitochondrially encodel N Other other opting ulin. Et ac ellular Space growth factor optitudial membrane prote Plasma Membrane other	Ferreira et al. Diabetes 2034	0.46 -0.08	0.75	0.19 0.36 -0.25	0.06 0.19 -0.27	119 080 088	033 006	0.86	0.00 0.01 0.97 0.77	0.00 0.01 0.12	0.00 0 0.01 0 0.20 0	00 0.08	0.88 1.00	0.00 67 6 0.89 47	7 63 2 68 1 42	53 58 39	80 64	58	75 50	33 38 53 49	37 47 32 42 58 61	2 30	42 36 42	25 50
ENSG0000134291 ENSG0000164111 ENSG0000104974 ENSG0000225630 ENSG0000124882 ENSG0000134531 ENSG0000060138	ANXAS UILRA1 MTND2P28 EREG EMP1 YBX3	LLRA1 MTND2928 EREG EMP1 YBX3	Toutocyte immunoglobulin Plasma Membrane imitochondrially encoded N Other other other opingulin springulin sprindu springulin springulin springulin springulin springulin spring	Ferreira et al. Diabetes 2034	0.46 -0.08 0.20	0.75 0.00 0.35	0.19 0.36 -0.25 0.01	0.06 0.19 -0.27 0.00	119 080 088 077 044	033 006 017	0.86 0.41 0.26	0.00 0.01 0.97 0.77 0.02 0.55	0.00 0.01 0.12 0.72	0.00 0 0.01 0 0.20 0 0.67 0	000 0.08 000 0.00	0.88 1.00 1.00	0.00 67 6 0.89 47 5 1.00 56 6	7 63 2 68 3 42 8 50	53 58 39 50	80 64 80 82	58 58	75 50 67	33 38	37 47 32 42 58 61 50 50	2 30 1 20 0 20	42 36 42 18 42	25
ENSG0000134291 ENSG00000164111 ENSG00000104974 ENSG00000225630 ENSG00000124882 ENSG00000134531	ANXAS LILRA1 MTND2P28 EREG EMP1	LLRA1 MTND2928 EREG EMP1	leukocyte immunoglobulin Plasma Membrane i transmembrane re mitochondrially encodel N Other other opting ulin. Et ac ellular Space growth factor optitudial membrane prote Plasma Membrane other	Ferreira et al. Diabetes 2034	0.46 -0.08	0.75	0.19 0.36 -0.25	0.06 0.19 -0.27 0.00	119 080 088	033 006 017	0.86 0.41 0.26	0.00 0.01 0.97 0.77	0.00 0.01 0.12 0.72	0.00 0 0.01 0 0.20 0 0.67 0	000 0.08 000 0.00	0.88 1.00 1.00	0.00 67 6 0.89 47 5 1.00 56 6	7 63 2 68 1 42	53 58 39	80 64	58 58	75 50	33 38 53 49	37 47 32 42 58 61	2 30 1 20 0 20	42 36 42	25 50

ENSG00000186407	CD300E	C 0300E	CD300e molecule Plasma Membrane other		0.49		0.10		1.28	0.43	0.92	000	0.76		00		100 6			70		58 58	36	50	_	30	42 42	
ENSG00000124942	AHNAK	AHNAK	AHNAK nucleoprotein Nucleus other		0.24		-0.20		0.67 0.61	0.07		0.34 0.9			0.77		100 5			3 70		50 67	42	49 5		30 36	50 33	
ENSG00000078804	TP53INP2	TPS3INP2	tumor protein p53 inducibl Nucleus other		0.13		-0.10		0.55 0.25	-0.02		0.56 0.7			0.77		100 5			82 80		42 58	42	49 63		20 36	58 42	_
ENSG00000154451	GBP5	GBP5	guanylate binding protein !Plasma Membrane enzyme	Kallionpää et al. 2014, Reynier et al. 2010, Ferreira et al. 2			0.00		-0.39 -0.85	-0.15	-021	0.02 0.0	8 0.97		76 0.00		1.00 4			12 30		42 33	58	70 50	_	70 91	58 67	4
ENSG00000132386	SERPINF1	SERPINF1	serpin family Fmember 1 Extracellular Space other	Kallionpää et al. 2014	0.31		-026	0.29	0.64 1.21	-0.37		0.0 00.0			0.00		1.00 5		37	6 60	73	33 67	42	46 63		40 27	67 33	1
ENSG00000163013	FBX041	FBXD41	F-box protein 41 Cytoplasm enzyme		0.40		0.40	0.38	051 087		0.79	0.00	0.00		0.00		0.10 7	78		74 70	73	67	25	22 16	5 26	30 27	33	1
ENSG00000136997	MYC	MYC	v-myc avian myelocytomat Nucleus transcript	regulator	0.22	0.28	-0.04	0.13	0.44 0.60	-0.11	0.14	0.13 0.8	3 0.89	0.18 0.	0.00	1.00	1.00 5	57	45	3 70	82	42 50	44	43 55	5 47	30 18	58 50	1
ENSG00000071073	MGAT4A	MGAT4A	mannosyl (alpha-1,3-)-glyo Cytoplasm enzyme		0.39	0.35	0.43	0.48	0.43 0.68	0.43	0.51	0.00 0.2	9 0.00	0.00	0.00	0.28	0.30 7	70	84 1	84 90	91	83 100	28	30 16	5 16	10 9	17 0	1
ENSG00000026297	RNASET2	R NASET2	ribonuclease T2 Cytoplasm enzyme		0.07	0.37	0.01	0.11	0.48 0.85	0.01	80.0	0.26 0.6	6 0.62	0.51 1	00.00	1.00	1.00 5	59	58	8 60	73	58 58	44	41 43	2 42	40 27	42 42	1
ENSG00000040938	INPP4A	INPP4A	inositol polyphosphate-4pl Cytoplasm phosphate		0.10	0.20		0.42	0.07 0.54		0.50	0.21 0.1	8	0.00 1	0.00		0.00	59		6 50	73	75	47	41	34	50 27	25	1
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	0.0 00.0	5 0.00	0.00	0.00	1.00	0.29 8	70	68	82 80	100	58 92	17	30 33	2 18	20 0	42 8	1
ENSG00000178199	2C3H12D	ZC3H12D	zinc finger CCCH-type cont Cytoplasm other		-0.04	0.04	0.17	0.20	010 086	0.37	0.34	0.49 0.9	8 0.43	0.56 1	0.00	1.00	1.00 4	51	63	1 60	73	67 75	56	49 37	7 39	40 27	33 25	1
ENSG00000127663	KDM48	KDM48	lysine demethylase 48 Nucleus erzyme		0.16	0.25	0.07	0.15	030 056	0.50	0.64	0.48 0.8	3 0.82	0.42 0	0.00	0.84	0.22 5	62	55	3 70	82	83 83	44	38 49	5 37	30 18	17 17	1
ENSG00000130775	THEM52	THEMIS2	thymocyte selection associ Other other		0.50	0.57	0.00	-014	0.53 0.57	-0.32	-0.09	0.0 0.0	0.98	0.74 0	0.00	1.00	1.00 7	62	50	12 70	73	33 50	22	38 50	58	30 27	67 50	. 1
ENSG00000117648	MANIC1	MANICI	mannosidase alphe class 1/Cytoplasm enzyme		0.11			0.48	0.22 0.52		0.54	0.21 0.2	0	0.00 1	0.00		0.08 5	68		74 70	82	83	42	32	26	30 18	17	1
ENSG00000121281	ADCY7	ADCY7	adenylate cyclase 7 Plasma Membrane enzyme		0.23		0.44		-0.06 0.77	0.48	0.58	0.0 0.0			00.00		016 6		74	71 50	82	67 83	39	27 26	5 29	50 18	33 17	1
ENSG00000167261	DPEP2	DPEP2	dpeptidase 2 Plasma Membrane peptidase		0.29		0.26		0.27 0.56	0.20	0.09	0.0 0.0			00.00		1.00 6			55 60	91	75 58	33	24 3	2 45	40 9	25 42	
ENSG00000148466	NA		-,		0.21				0.06 0.69		0.44	0.02 0.0	2		0.00		0.82 6	70		51 50	82	75	36	30	39	50 18	25	
ENSG00000172543	CTSW	CTSW	cathepsin W Cytoplasm peptidase		0.46		0.30		012 -0.57	0.35		0.49 0.2	0 0.12		00.00	1.00	100 6			17 60	27	67 42	36	59 34	. 9	40 73	33 58	
ENSG00000120875	DUSP4	DUSP4	dual specificity phosphatas Nucleus phosphata	1	-030		-0.13		-0.10 -0.80	-0.05		0.08 0.0			0.00		100 4			7 50		50 50	58	73 5		90 73	50 50	. 1
ENSG00000162777	DENND2D	DENND2D	DENN domain containing 2 Cytoplasm other		0.28		0.48	0.49	0.59 0.64	0.45	0.85	0.00 0.0			0.00		018 6		79	4 70		75 83	36	35 2	-	30 18	25 17	
ENSG00000113319	RASGRF2	R ASGR F2			0.44		0.46		0.45 0.66	445	0.85	0.00 0.4			1 0.01	0.55	6		/9	60		/5 83	31	33 2		40 27	25 17	1
ENSG00000099326	MZF1	MZF1			0.27				0.10 0.58			0.03 0.0			0.01		7			80	100		28	19		20 0		1
ENSG00000137478		FCH502		regulator	022				034 058										61			58 58	42	38 39			42 42	
	FCHSD2		FCH and double SH3 domai Other other		0.22		0.44			0.35	0.37	0.01 0.1								-			42		-	30 27		1
ENSG00000169896	ITGAM	ITGAM		ne receptor		-045	-0.08	-0.02	-0.67	-0.08	-0.02	0.0	1 0.82	0.67	0.01		100	30		60		42 50	1	70 5	_	73	58 50	
ENSG00000055332	EIF2AK2	EIF2AK2	eukaryotic translation initi: Cytoplasm kinase		-0.22		-0.10		-0.28 -0.59	-0.41		0.19 0.7			0.01		0.96 3			30		25 33	61	57 6		70 91	75 67	4
ENSG00000178035	MPDH2	IMPOH2	inosine monophosphate de Cytoplasm enzyme		0.15		0.23		0.15 0.50	0.23		0.31 0.8			0.01		0.99 5			50		67 75	42	38 3	-	50 18	33 25	
ENSG00000107819	SEXNB	SFIN3	sideroffexin 3 Cytoplasm transport		0.37		0.08	0.19	0.66 0.61	0.48		0.16 0.4			0.01		100 6			3 70		67 67	36	27 39	37	30 18	33 33	1
ENSG00000185504	C17arf70	FAAP100	Fanconi anemia core comp Nucleus other		0.36		0.36		0.43 0.52	0.46	0.59	0.00 0.6			0.01		031 6		76	6 70		83 75	31	35 24		30 9	17 25	1
ENSG00000010295	IFFO1	IFF01	intermediate filament famiOther other		0.38		0.38		0.22 0.58	0.51		0.03 0.1			0.02	1.00	65	70	68	70		67	31	30 33		30 9	33	_
ENSG00000181896	ZNF101	ZNF101	zinc finger protein 101 Nucleus other		-0.04		0.13		-0.43 -0.59	-0.05		0.21 0.7			0.02		0.69			0 10		50 25	50	65 37	_	90 100	50 75	-
ENSG00000130164	LDLR	l			0.23		-0.02		0.56 0.68	0.08		0.78 0.9		0.14 0.			0.07 5			8 70		50 67	47	41 5		30 27	50 33	
ENSG00000137312	FLOT1	FLOT1	flotilin 1 Plasma Membrane other		0.17	0.37	0.06	0.20	0.09 0.51	-0.12	0.20	0.00 0.1	6 0.90	0.15 1	0.02	1.00	1.00 6	62	53	60	73	50 67	33	38 47	7 39	40 27	50 33	1
ENSG00000225138	CTD-2228K2.7	l						- 1	0.53						0.02						91		1			9		1
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 0.3	6 0.58	0.96 1	0.02	1.00	1.00 5	62	50	55 50	73	58 50	50	38 50	45	50 27	42 50	1
ENSG00000161381	PLXDC1	PLXDC1	plexin domain containing 1Plasma Membrane other		-0.22	0.44		- 1	0.26 0.70			0.79 0.4	1	1	0.03		4	59		60	73		58	41		40 27		1
ENSG00000198771	RCSD1	R CSD1	RCSD domain containing 1 Other other		0.34	0.48	0.40	0.41	0.33 0.64	0.47	0.53	0.0 00.0	0.00	0.00 1	0.03	1.00	0.86 64	68	76	6 70	73	75 75	36	32 24	4 34	30 27	25 25	1
ENSG0000010600B	LFNG	LFNG	LFNG O- fuz osylpeptide 3-bi Cytoplasm enzyme		0.18	0.33	0.15	0.15	-0.08 0.61	0.10	0.21	0.06 0.6	5 0.33	0.15	0.04	1.00	1.00 5	59	58	50	73	50 58	42	41 43	2 39	50 27	50 42	_
ENSG00000068878	PSME4	PSM 64	proteasome activator subu Cytoplasm other		-0.34	-0.54	-0.24	-0.29	-0.38 -0.63	-0.17	-0.29	0.00 0.1	8 0.00	0.04	0.04	1.00	1.00 1	30	21	26 20	18	25 25	81	70 79	74	80 82	75 75	4
ENSG00000128185	DGCR6L	DGCR6L	DiGeorge syndrome critica Nucleus other		0.32	0.28	0.34	0.26	030 066	0.22	0.54	0.13 0.7	8 0.08	0.04 1	0.04	1.00	0.99 64	59	71	60	73	58 75	36	41 29	34	40 27	42 25	1
ENSG00000160271	RALGDS	RALGOS	ral guanine nucleotide diss Cytoplasm other		-0.05	0.10	-0.16	-0.09	032 054	0.24	0.04	0.97 0.9	7 0.36	0.79 1	0.04	1.00	1.00 4	51	42	17 60	73	58 50	53	49 58	3 53	40 27	42 50	1
ENSG00000142089	IRTM3	IRTMB	interferon induced transmoPlasma Membrane other	Kalliorpää et al 2014	0.42	-0.04	-0.07	0.20	-0.37 -0.32	-0.51	-061	0.23 0.8	7 0.74	0.44 1	0.98	0.00	0.00	49	42	5 40	45	17 33	42	51 58	8 45	60 55	83 67	4
ENSG00000126709	IR6	IR6	interferon alpha inducible ¡Cytoplasm other	Kalliorpää et al 2014	031	0.38	0.12	0.38	-0.31 0.15	-1.16	-095	0.42 0.8	5 0.99	0.86 1	0.94	0.00	0.05 6	62	55	5 50	55	25 33	33	38 49	5 45	50 45	75 67	4
ENSG00000131401	NA PSB	NAPS8	rapsin B aspartic peptidass Other other		- 1		-034	-037		-0.73	-0.43		0.00	0.00		0.01	000		37	32		25 25	1	63	68		75 75	4
ENSG00000085265	FCN1	FCNL	ficolin 1 Extracellular Space peptidase	1	-0.14	-0.08	-051		101 -0.08	-0.88		0.69 0.9	5 0.00		0 0.97		0.01 4	49	39	19 60		25 25	56	51 6	1 61	40 55	75 75	4
ENSG00000244734	HBB	нвв	hemoglobin subunit beta Cytoplasm transport			-0.14	-0.43	-0.97	0.10	-1.28	-146	0.2	7 0.00	0.00	0.99	0.01	0.00	43	45	12		33 42		54 55	5 58	45	67 58	1
ENSG00000110077	MS4A6A	MS4A6A	membrane spanning 4-don Other other				-0.25	0.04		-0.72	-0.13		0.55	0.70			0.29	-		10		33 42	1	5	3 50		67 58	
ENSG00000157933	SIG	SM	SKI proto-oncogene Nucleus transcript	regulator	0.18	0.29	0.31		025 043	0.75		0.17 0.9			3 0.00		011 6	57		8 80		83 83	*	43 37	_	20 9	17 17	
ENSG00000121316	PLBD1	PLBD1	phospholipase B domain or Extracellular Space enzyme	THE COLUMN TO TH		0.23	-0.42	-0.16	023 043	-0.51	-061	0.27	0.01	0.00	0.00	0.03	0.01			19		25 33	1	6/			75 67	4
ENSG00000173762	C07	C07	CD7 molecule Plasma Membrane other		0.00	-011	0.27		014 -0.03	0.55		090 0.7	0.00	0.00	0 0.72		030 5	35		71 60		100 92	90	65 1		40 55	0 8	1
ENSG00000188536	HBA2	HBA1/HBA2	hemoglobin subunit alpha :Extracellular Space transport		400	-127	-0.62	-152	0.03	-0.76	-1.64	0.0		0.00	0.72	0.26	000	38		12		42 33		59 5		-U 33	58 67	4
ENSG00000206172	HBA1	HBA1/HBA2	hemoglobin subunit alpha : Extrac ellular Space transport		- 1	-22/	0.04	-0.78		-0.55	-159	0.0	0.21	0.00		0.70	0.00	30		12		42 33 50 33	1	39 30	_		50 67	4
ENSG00000196565	HBG2	HBG2		Kalliomää et al. 2014	- 1		-0.30	-4176		-0.31	-2.12		0.22	0.00		0.70	0.00		45			33 33	1	51	_		67 67	4
	HBG2 HLA-H	HBG2 HLA-H	hemoglobin suburit gamm Cytoplasm other	nationpas et al. 2014	0.14	0.27	-0.30 0.43		0.07 0.98	-0.31	0.81	0.00 0.4		0.00			0.00	57		8 50		33 33 67 75	40	43 37		50 45	07 07	4
ENSG00000206341			major histocompatibility ccPlasma Membrane other		014	0.27	0.48	0.29	u98		0.81	0.00 0.4	0.00	0.00 1	0.01	0.33	0.01 5	57	63	a 50		67 75 58 75	42	45 37	42	au 45	33 25 42 25	
ENSG00000221957	KIR2DS4		fiskiller cell immunoglobulin Plasma Membrane - transmen	ine receptor	- 1					155	1.06					0.03	0.02											
ENSG00000167680	SEMA 6B	SEM AGB	semaphorin 68 Plasma Membrane other				0.19	0.61		0.61	0.95		0.80	0.53		0.91	0.02			5		58 67		4	-		42 33	
ENSG00000188486	H2AFX	H2AFX	H2A histone family membe Nucleus transcript	regulator	-016	-0.25	0.15	0.03	0.25 0.03	0.45	0.57	034 0.4	9 0.27	0.85 1	00 0.88	0.83	0.05	38	66	60 50	64	83 83	61	62 34	\$ 50	50 36	17 17	_

Supplementary Table	e 4C. Non-codin	DE genes be	etween Cases and Controls			1				Median I	ogFC						FDR						Percent	Up				-	Percent I	lown		$\overline{}$
			IPA ANNOTATION		Previously	Human IncRNA ATLAS Hon et al. Nature 2017:548;199-20-		Over All T	imepoin ts			2 mo bafore :	SC .	Ov	er All Tim	ep oints		12 mo b	efore SC		Over All	Timepoints			before SC		Over A	All Timepoint			no before SC	_
Ensembil Gene IDs	Gene Names	Symbol	Entrez Gene Name Locatio	on Type(s)		FANTOM CAT tool CAT gene class CAT gene category											MC C		D4-CD8- PBA									CD4 CD8-				
ENSG00000228463	AP0062222	57				on give one on great and	0.83							0.00						78						2	2					
ENSG00000260711	RP11-747H7.3						0.71			- 1				0.00						69			- 1				11					
ENSG00000260065	CTA-445C9.15					No implications in coexilncRNA intergene_IncRNA	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 0.9	9 69	54	66	63	45	58	58 3	1 46	34	37	55	42	42
ENSG00000249667	LINC01259	UNC01259	long intergenic non-protein coding RNA 12990 ther	other		No implications in coex IncRNA intergenothers	0.55	0.55		0.80	0.65		0.76	0.00	0.02	0	.00 0.	.73	0.6	0 67	65		68	80		67 3	3 35		32	20		33
ENSG00000271938	RP11-589C21.6					1 eQTL linked co-expre IncRNA intergenp_IncRNA_intergen	-0.59	-0.72	-0.27	-036	0.12 -0.	45 -0.12	-0.29	0.01	0.00	0.07 0	.07 0.	99 0.50	0.99 0.8	1 33	24	26	26	50 36	33	33 6	76	74	74	50 64	67	67
ENSG00000234449	RP11-7060 15.3						0.64	0.82			0.0	85		0.01	0.01			0.33		69	73			73		3	1 27			27		
ENSG00000235576	AC092580.4					No implications in coex; IncRNA intergene_IncRNA	1.08	-0.18	0.77	0.10	1.08 -0.	51 1.72	0.06	0.01	0.38	0.00	.15 0.	56 0.70	0.66 0.9	9 75	46	66	58	90 27	58	58 2	15 54	34	42	10 73	42	42
ENSG00000269996	NA.					No implications in coex/IncRNA intergenothers	0.63	0.41	0.06	0.29	0.74 0.	43 -0.21	0.08	0.01	0.32	0.99 0	54 0.	65 0.75	0.99 1.0	0 81	70	55	61	80 73	42	50 1	19 30	45	39	20 27	58	50
ENSG00000232677	LINC00665	UNC00665	long intergenic nan-protein coding RNA 665 Other	other		6 eQTL linked co-expre IncRNA divergerp_IncRNA_diverger	-0.67	-0.50	-0.17	-022	0.94 -0.	.50 -0.18	-0.50	0.02	0.04	0.80	.98 0.	.04 0.55	0.99 0.7	8 28	30	39	37	10 18	25	17 7	72 70	61	8	90 82	75	83
ENSG00000223692	DP2A-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 0.9	9 28	32	34	42	50 36	33	58 7	2 68	66	58	50 64	67	42
ENSG00000270127	PRIORP1						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		2	8 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	0.5	8 61	73		68	60 64		75 3	9 27		32	40 36		25
ENSG00000259715	CTD-3110H11.1						0.29	0.96	0.40	ŀ		.08 0.50				0.52		.99 0.95	1.00	64	81	63	- 1	40 45	Ø		19			60 55		
ENSG00000273038	RP11-479G22.8						-0.15	-0.66	-0.45		0.30 -0.					0.01 0		99 0.10	0.99 0.6		27	29	39	40 18	50		73		61	60 82		58
ENSG00000254419	RP11-261P9.4						0.37	0.68	041		0.12 0/	47 0.73				0.25		.99 0.33	0.80	61	73	63		60 73	모		9 27	37		40 27	8	
ENSG00000235532	LINC00402	LINC00402	long intergenic non-protein coding RNA 402 Other			No implications in coexilncRNA intergenothers	0.35	0.87		0.38					0.01		.00			58	70		71				12 30		29			
ENSG0000022740B	AC009299.3	LINC01806	long intergenic non-protein coding RNA 18050 ther	other		No implications in coexylncRNA intergenp_IncRNA_intergen			0.73		0.41 05	59 0.85							0.25 0.1			79	84	70 91	Ø		12 14	21	16	30 9	33	17
ENSG00000260461	RP11-541N10.3					No implications in coexilncRNA intergene_IncRNA	0.16	0.68			0.05		-0.08		0.01			.99	0.9		70		58	50			31 30		42	50		58
ENSG00000223745	RP4717123.3		CCDC18 antisense RNA 1 Other			4 eQTL linked co-expre IncRNA divergerp_IncRNA_diverger	0.09	0.59	1.45	0.17	0.5	17 0.81	0.15	0.40	0.02	0.11 0	.14 0.	99 026	0.33 0.9	9 50	68	71	63	40 64	83	58 5	60 32	29	37	60 36	17	42
ENSG00000265185	SNORD3B-1	SNORD3B-1	small nucleolar RNA, C/D box 38-1 Other	other		No implications in coexilincRNA intergenothers	0.63	0.22		0.80	0.73 15		1.28	0.06	0.08	0.00	00 0	99 001	0.09 0.2	4 58		76	58	60 73	75	67 4	12 41	92	42	40 27	25	33
ENSG00000245164	LINCOOB61	UNC00861	long intergenic non-protein coding RNA 861 Other PRKCO antisense RNA 1 Other			No implications in coexilnoRNA intergenothers		0.33	1.10 0.77												59 59	76 82	58		-			24 18	34		_	33
ENSG00000237948 ENSG00000202198	PRICQASI RN7SK	PRKCQ-AS1 RN7SK		s other		1 eQTL linked co-expresincRNA divergerp_incRNA_diverger	0.14	0.29	-0.61	0.29 -0.20	0.24 0.							99 0.77 89 0.83	0.66 0.9		57	24	42	40 73 80 55	25		41 14 43		58	60 27 20 45	25	58
ENSG00000256576	RP13-977J11.2		6 uncharacterized LOC100996246 Other			No implications in coexilorRNA divergerp_IncRNA_diverger	0.05	0.08	0.61	0.34	0.08 0					0.00			0.66 0.9		57	84	74	40 55	-		ia 43	16	26	60 45	25	25
ENSG00000272282	RP13-97/311.2 RP11-222K16.2	10/10/09/624	6 uncharacterized LOC100996246 Other	other		1 eQTL linked co-expresIncRNA intergenp_IncRNA_interger No implications in cœx;IncRNA intergenp_IncRNA_intergen		-0.13	052	0.52	0.08 01	0.62	0.30			0.00 0		99 100	0.86 0.9	9 53	43	76	74	40 55	D	/5 4	17 43 57	24	29	60 45	25	25
ENSG00000261574	RP1-168P16.2					no impricatorism custimoner mangerip_money_manger	ì	0.55	-0.59	-0.65	-0.	.67 -027	-0.35			0.00		0.62	0.80 0.9	۰	38	18	29	27	25	25	62		71	77	75	75
ENSG00000235437	LINC01278	UNC01278	long intergenic non-protein coding RNA 1278Other	other		1 eQTL linked co-expresincRNA intergenp_incRNA_intergen	0.18		050		0.18 0			0.24		0.00 0		.99 0.42	0.80 0.5	-	62	79	63	70 73	75		16 38		37	30 27		33
ENSG00000212232	SNORD17	SNOR D17	small nucleolar RNA, C/D box 17 Other			Best associated with hir small RNA others		-0.28	-1.07	0.02		50 -147						99 0.77	0.25 0.9		38	32	50	70 18	33		3 62		50	30 82	67	42
ENSG00000245937	LINC01184	UNC01184	long intergenic non-protein coding RNA 1184Other			No implications in coex IncRNA divergerp_IncRNA_diverger			054		0.22 0/					0.00 0		99 0.77	0.99 0.9		57	68	66	70 64	67		12 43		34	30 36	33	25
ENSG00000272048	NA					No implications in coexilncRNA intergenothers		0.27	0.79		0.13 0		-0.03		0.57	0.00 0		99 0.77	0.80 0.9		65	84	66	60 73	75		16 35	16	34	40 27	25	50
ENSG00000237772	AC092620.3								-0.61	-0.52		-0.62				0.00			0.34			24	39		17			76	61.		83	
ENSG00000273272	CTA-384D8.34					No implications in coex; IncRNA intergene_IncRNA	l		-0.59			-0.63				0.00			0.32	1		29			17			71			83	
ENSG00000212694	LINC01089	UNC01089	long intergenic non-protein coding RNA 10890 ther	other		1 eQTL linked co-expresincRNA sense intothers	0.04	0.28	051	0.31	0.07 0.	21 0.53	0.39	0.50	0.59	0.00	47 0.	99 0.85	0.83 0.9	9 58	68	79	74	30 73	75	75 4	12 32	21	26	70 27	25	25
ENSG00000272849	RP11-347(19.8					No implications in coex/IncRNA antisensothers	0.21	0.39	0.70	0.41	0.07 01	0.52	0.06	0.39	0.20	0.00	45 1.	.00 0.77	0.80 0.9	9 58	76	74	63	40 64	67	50 4	12 24	26	37	60 36	33	50
ENSG00000235314	LINC00957	LINC00957	long intergenic non-protein coding RNA 957 Other	other			0.12	0.50	052	0.38	0.25 0.	14 0.19	-0.01	0.48	0.48	0.00	.07 0.	.99 0.88	1.00 0.9	9 58	76	76	71	20 73	67	50 4	12 24	24	29	80 27	33	50
ENSG00000255135	RP11-111M72.3					1 eQTL linked co-expresincRNA divergerp_incRNA_diverger	0.18	0.37	0.82	0.05	0.07 03	31 0.82	0.00	0.35	0.76	0.01 0	34 0.	99 096	0.99 0.9	9 64	62	68	55	50 55	58	50 3	16 38	32	45	50 45	42	50
ENSG00000240905	R N7SL798P	RN7SL798P	Other	other			l		-0.91	-001		-0.95	-0.28			0.01 0	.81		0.59 0.9	9		24	50		33	42		76	50		67	58
ENSG00000225978	HAR1A	HAR1A	highly accelerated region 1A (non-protein co/Other	other		No implications in coexilncRNA intergenp_IncRNA_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 0.9	9 50	49	68	63	30 55	67	75 5	50 51	32	37	70 45	33	25
ENSG00000266274	RN7SL138P	RN75L138P	Other	other			l		-0.58	-065		-0.86	-1.48	l		0.01 0	.07		0.66 0.6	8		32	37		33	33		68	8		67	67
ENSG00000269900	RMRP	RMRP	RNA component of mitochondrial RNA proce/Cytopla	asrother		No implications in coexilncRNA divergerp_IncRNA_diverger	0.13	-0.41	40.66	+0.34	1.00 -0.	41 -1.14	-0.35	030	0.12	0.01 0	.14 0.	.77 0.93	0.14 0.9	9 50	30	32	32	70 36	25	33 5	70	68	68	30 64	75	67
ENSG00000260910	LINCO0565	UNC00565	long intergenic non-protein coding RNA 565 Other	other		2 eQTL linked co-expresincRNA intergene_incRNA	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 0.9	9 53	54	74	66	60 64	83	67 4	7 46	26	34	40 36	17	33
ENSG00000271948	RP11-242F4.2	I						0.16	0.67	0.16	0.51 0.							76 081	0.66 0.9		62	76	55	90 73	75		19 38	24	45	10 27	25	50
ENSG00000253948	RP11-410L14.2	LO C10537566	66 Other	other		No implications in coexilncRNA divergerp_IncRNA_diverger	0.36	0.61	0.74	0.59	0.34 0	69 0.72	0.49		0.33	0.03 0	.04 0.	.99 0.55	1.00 0.9		57	66	71	60 64	67		12 43	34	29	40 36	33	25
ENSG00000272812	RPS-855D213					No implications in coexilncRNA divergerp_IncRNA_diverger	0.27	0.33	0.57		0.17 0.					0.03		.99 0.55	0.80 0.9		68	68		70 73	75		86 32			30 27		25
ENSG00000262074	SNORD3B-2		small nucleolar RNA, C/D box 38-2 Other	other		No implications in coexilncRNA intergenp_IncRNA_intergen	-0.49		-0.58	-0.69		-0.32		0.14		0.03 0			0.80 0.3			34	26		33		4	66	74		67	83
ENSG00000257613	RP11-320P7.1	UNC01481	long intergenic non-protein coding RNA 14810 ther	other					0.58		0.03 -0.								1.00 0.9			76	63	50 45	83		41		37	50 55		25
ENSG00000260539	GLGI					No implications in coexilncRNA intergene_IncRNA			0.36	0.84	0.36 0.5	54 0.59						.99 0.50	0.30 0.2		68	66	68	70 73	67	67 2	15 32	34	32	30 27	33	33
ENSG00000223891	OSER 1-AS1	OSER1-AS1	OSER 1 antisense RNA 1 (head to head) Other	other		1 eQTL linked co-expresincRNA divergenp_incRNA_divergen	f	0.58		0.68			0.54	l '	0.27		.00		0.6	5	59		79			92	41		21			8
ENSG00000260804	PKI55	UNC01963	long intergenic non-protein coding RNA 19630 ther	other		No implications in coexilncRNA intergene_IncRNA	l			0.63				l			.00			1			68			- 1			32			- 1
ENSG00000270091	RP11-7807.2	L						0.44		0.57			0.08		0.33	0			0.8	_	59		66		_	58 4	7 41		34		-	42
ENSG00000203875	SNHGS	SNHGS	small nucleolar RNA host gene 5 Other	other		No implications in coexilncRNA intergenp_IncRNA_intergen			-0.32		0.41 -0.								0.99 0.2		27	32		10 18	25		72 73	68	71	90 82	75	75
ENSG00000226423 ENSG00000237310	AC093642.4 GS1-124KS.4	CEL LIVER				1 eQTL linked co-expresincRNA intergenothers			0.45	0.61	0.12 0.0		0.84		0.15			99 0.55 99 1.00	0.2			76		50 73 50 64		-	19 30 16 38	24	34	50 27 50 36		17
ENSG00000237310 ENSG00000237940	GS1-124KS.4 AC093642.3		uncharacterized LOC100289098 Other			2 eQTL linked co-expresincRNA antisensothers		0.33	0.45			13 74 0.54		0.27	0.71 (0.6		76	76	68	90 93		50 2	16 38	24	32	30 36	42	33
ENS600000237940	ACD93842.3	UNCD1238	long intergenic non-protein coding RNA 12380 ther	other		4 eQTL linked co-expresincRNA sense intothers	0.20	0.48	0.44	0.29	0.20 0.	/4 0.54	0.11	002	0.00 (0.05	30 0.	99 003	U.BD 0.9	12	76	68	61	8U 8Z	35	50 2	a 24	32	39	zu 18	42	50

IL32 coregulated genes

CD4+		CD8+		CD4-CD8-		PBMC	
iene	Median Euclid		Median Euc		Median Euclid		Median Euclidi
.32	0.00	IL32	0.00	IL32	0.00	IL32	0.00
D52	1.18						
TMEM14C	1.20					TMEM14C	2.13
BTN3A2	1.36	BTN3 A2	1.91	BTN3A2	1.32	BTN3A2	1.60
RBV4-1	1.56	1400	2.00			TRBV4.1	1.86
ARS	1.74	LARS	2.06			LARS	1.85
TA-445C915 GS14	1.83 1.85					+	
JROS	1.89		- 	UROS	1.03		
H3BP1	1.92		- 	OKOS	1.03		-
RP11-747H7.3	2.13						
AMICA1	2.15			AMICA1	2.22	AMICA1	2.02
NSG00000269996	2.18						
17orf62	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		1.00
				BTN3A3	1.87	BTN3A3	1.95
	 	+		CCDC167	1.95	CCDC167	2.08
	 	+	-	CDC167	2.16 1.55	CCDC10/	2.08
		+	- 	CD27	1.32		+
	 	+		CD3D	1.49		+
		1	1	ENSG00000211953	2.14		
		1		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 IGHV4.31	2.45 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 PRKCQ-AS1	2.23		
		+	_	PSMD5-AS1	2.02		_
				RP11-111M22.3	2.04		
			<u> </u>	RP11-222K16.2	2.16		
	1	1		SH3YL1	2.22		
		1		STX8	2.14		
				SUCLG2	2.18		
				SUSD3	2.41		
				SYNGAP1	2.05		
				TCOM			
				TC2N	1.90		
				TESPA1	2.31		
				TESPA1 TMIGD2	2.31 1.95		
				TESPA1 TMIGD2 TRABD2A	2.31 1.95 2.02		
				TESPA1 TMIGD2 TRABD2A TRBV2	2.31 1.95 2.02 1.83		
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV20.1	2.31 1.95 2.02 1.83 1.76		
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11		
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV20.1	2.31 1.95 2.02 1.83 1.76	ANYAE	1.27
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXAS ANXAS	2.37
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6	1.57
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6 V0E2	1.57 1.83
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6	1.57
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD8B	1.57 1.83 2.03
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6 V0E2 CD8B CPNE1	1.57 1.83 2.03 1.59
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6 VOE2 CD8B CPNE1 CST7	1.57 1.83 2.03 1.59 2.01
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6 V0E2 CD8B CPNE1 CST7 DGKQ	1.57 1.83 2.03 1.59 2.01 2.08
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD8B CPNE1 CST7 DGKQ FLI1	1.57 1.83 2.03 1.59 2.01 2.08 2.33
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD8B CPNE1 CST7 DGKQ FLI1 GLG1	1.57 1.83 2.03 1.59 2.01 2.08 2.33 2.41
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD8B CPNE1 CST7 DGKQ FLI1 GLG1 GLIPR2	1.57 1.83 2.03 1.59 2.01 2.08 2.33 2.41 2.34
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXAG ATP6V0E2 CD88 CPNE1 CST7 DGKQ FLI1 GLG1 GLIPR2 HLA.F IPCEF1 LILRA1	1.57 1.83 2.03 1.59 2.01 2.08 2.33 2.41 2.34 1.42 2.29 2.10
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD88 CPNE1 CST7 DGKQ FLI1 GLG1 GLIPR2 HLA.F IPCEF1 LILRA1 NAGA	1.57 1.83 2.03 1.59 2.01 2.08 2.33 2.41 2.34 1.42 2.29 2.10 2.18
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD8B CPNE1 CST7 DGKQ FLI1 GLG1 GLIPR2 HLA.F IPCEF1 LILRA1 NAGA NCAPD2	1.57 1.83 2.03 1.59 2.01 2.08 2.33 2.41 2.34 1.42 2.29 2.10 2.18 1.67
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD8B CPNE1 CST7 DGKQ FLI1 GLG1 GLIPR2 HLA.F IPCEF1 LILRA1 NAGA NCAPD2 NMRAL1	1.57 1.83 2.03 1.59 2.01 2.08 2.33 2.41 2.34 1.42 2.29 2.10 2.18 1.67 1.46
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD8B CPNE1 CST7 DGKQ FLI1 GLG1 GLIPR2 HLA.F IPCEF1 LILRA1 NAGA NCAPD2 NMRAL1 OGDH	1.57 1.83 2.03 1.59 2.01 2.08 2.33 2.41 2.34 1.42 2.29 2.10 2.18 1.67 1.46 2.02
				TESPA1 TMIGD2 TRABD2A TRBV2 TRBV2 TRBV20.1 TXK	2.31 1.95 2.02 1.83 1.76 2.11	ANXA6 ATP6V0E2 CD8B CPNE1 CST7 DGKQ FLI1 GLG1 GLIPR2 HLA.F IPCEF1 LILRA1 NAGA NCAPD2 NMRAL1	1.57 1.83 2.03 1.59 2.01 2.08 2.33 2.41 2.34 1.42 2.29 2.10 2.18 1.67 1.46

			DARVE	1.00
			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 codustered genes for overpresented transcription factor binding sites with FDR < 0.05

Final: https://eachforoverpresentedTFbindingsites), background=randomly sected gene set, default parameters, using bet supported promoter (-10 000 to +1000 region of the gene 'promoter'). Paul set threshold 1.1 Paul set the rended with Benjamini Holchberg method (FRR), FPR-010 were consident digit fixed and are shown below.

C	D4+IL32 co	duter*	Profile (group	of matrices)	: Taxon: Verteb	orate_non_red	du ndant_minFP		
١,	fatrix	Accession	Factorname	Yes	No	Yes/No	p value	FDR/BH corne Gene swi	thmatricescount
			KLF6	42.9	27.3	1.6	0.00		5H3BP1, UROS, IL32, CD52, RGS14, TMEM14C, LARS, BTN3A2, WASH7P (LOC100288778), RP11-747H7.3 (BNSG00000260711), C17orf62
v	\$IK_Q5_01	M07260	Ikaros	13.3	7.4	1.8	0.00	0.00 AMICA1,	SH38P1, UROS, IL32, CD52, RGS14, TMEM14C, LARS, BTN3A2, WASH7P (LOC100288778), RP11-747 H7.3 (BNSG00000260711), C17orf62
v	\$ING4_01	M01743	ING4	15.3	9.5	1.6	0.00		SH3BP1, UROS, IL32, CD52, RGS14, TMBM14C, LARS, BTN3A2, WASH7P (LOC100288778), RP11-747H7.3 (BNSG00000260711), C17orf62
v	\$GKLF_Q4	M0 1835	KLF4 group	10.1	5.8	1.8	0.00	0.00 AMICA1,	SH3BP1, UROS, IL32, CD52, RGS14, TMBM14C, LARS, BTN3A2, WASH7P (LOC100288778), RP11-747H7.3 (BNSG00000260711), C17orf62
v	\$RREB1_01	M00257	RREB-1	2.0	0.4	4.8	0.00	0.00 AMICA1,	SH38P1, UROS, IL32, CD52, RGS14, TMBM14C, LARS, WASH7P (LOC100288778)
v	\$ERALPHA_	0 MO 1801	ER group	1.3	0.2	8.0	0.00	0.01 AMICA1,	5H3BP1, UROS, IL32, CD52, RGS14, TMBM14C, LARS
	NSG00000026	9996, TREVI-1 a	d CR-44509.15 e	cluded due to	un available promo	ters and mess day			

CD8+IL32 codu#er	Profile (group of matrices): Taxon: Vertebrate	•	
Matrix Accession No findings with FDR < 0.0	Factorname Yes	No Ye	s/No pvalue	FDR (BH corne Genes with matrices count
CD4.CD8.II32 codusts d	Profile (group of matrices	h Tawner Vertebrate	non redundant min	,

Yes/No p value FDR(BH corre Gene:

Matrix Accession Factor name Yes No Yes/No public FDR (
No findings with FDR < 0.05
**MG000000 21 1933, IN 5000000 293 64, PMCQAS1, P3MOS AS1, and HARIA excluded due to unwalled a promoter requesce

PBMC IL32	PBMC IL32 cocluster*		Profile (group of matrices): Taxon: Vertebrate_non_redundant_minFP						
Matrix	Accessio	ion Fa	actorname Yo	s	No	Yes/No	p value	FDR(BH core Genes with matrices count	
V\$IK_Q5_0	M07260	O Ika	karos	12.9	9.0	1.4	0.00	0.00 AMICAL, ANXAS, ANX	
V\$CPBP_Q	MO 1822	2 KL	ILF6	38.2	33.0	1.2	0.00	0.00 AMICA1, ANXAS, ANX	
V\$ING4_01	MD 1743	3 IN	NG4	14.5	11.4	1.3	0.00	0.00 AMICA1, ANXAS, ANX	
*GLG1,TRBV	NO.CO., TRIVIS and TRIVI I excluded due to unwandate promoter separace								

Description of column names

Matrix

The ET matrix that was enriched

Accession

Factor name

Name of the factor corresponding to the matrix

The factor name Name of the factor corresponding to the matrix

No

The factor corresponding to the matrix

The factor corresponding to the matrix

The factor corresponding to the matrix

The factor of the factor corresponding to the matrix

The factor of the factor

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

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

18396

1	Number of individual cells	
Naive T cells	8438	45.87%
RGCC+Tcells	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+Tcells	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