Supplementary Data for:

Single-cell multiomics reveal the scale of multi-layered adaptations enabling CLL relapse during venetoclax therapy

Supplementary Methods

Human Research Ethics Committee approvals

Melbourne Health 2011.044, 2012.092, 2013.016, 2005.008, 2012.274; Peter MacCallum Cancer Centre 03/90, 11/18, 12/45, 13/163, 17/133; Walter and Eliza Hall Institute 05/04, 13/01.

Drug sensitivity of CLL samples

Freshly isolated mononuclear cells were seeded into 96-well plates at 100,000 cells/well. 6-point 1:8 serial dilutions of venetoclax (Active Biochem #A-1231) or MCL1 inhibitor (S63845; Active Biochem #A-6044) starting from 4 µM were used for the cell viability assays. After 24 hrs, cells were stained with CD5-APC (clone BL1a, Beckman Coulter, cat #A60790,) and CD19-BV510 (clone SJ25CI, Becton Dickinson (BD) Biosciences, cat #562947) and cell viability was assessed by propidium iodide (PI, Sigma, cat #P4864) exclusion using a FACSCytoflex (BD). FACS data were analyzed using FlowJo software, and GraphPad Prism software was used to calculate drug concentrations causing 50% cell killing (LC50).

Whole Exome Sequencing

DNA was extracted from fresh or thawed cryopreserved patient samples using the QIAamp DNA Mini Kit (Qiagen, cat #51304) according to the manufacturer's instructions. For cryopreserved patient samples, PBMCs were thawed and stained with CD19-BV510 antibody (BD Biosciences) at 4°C for 30 min. PBMCs were washed and stained with propidium iodide (PI, Sigma). Viable cells (PI negative) were flow-sorted into tumor (CD19^{+ve}) and normal (CD19^{-}) samples using the FACSAria (BD). For the CLL2 relapsed sample, cells were stained with CD5-APC and CD19-BV510 for 30 min on ice. Cells were fixed with 1.6% paraformaldehyde (Electron Microscope Science) and permeabilized with 1xPerm buffer (Affymetrix eBiosciences). Cells were stained with BCLxL-PE (1:100, clone E18, Abcam, cat #ab208747). Viable CD5^{+ve}CD19^{+ve} BCLxL^{lo} cells and viable CD5^{+ve}CD19^{+ve} BCLxL^{hi} cells were sorted using the FACSAria (BD). Library preparation and sequencing were performed at the Australian Genome Research Facility (AGRF), using the TruSeq Nano kit (Illumina), SureSelectXT2 Target Enrichment System and Human All Exon v6 Capture Library (Agilent Technologies) and 150bp paired-end sequencing protocol.

The exome sequencing data were aligned to hg38 with BWA MEM (v0.7.17)[1], and analyzed for somatic SNVs and CNAs with superFreq (v1.4.2)[2]. All samples were marked as cancer samples for the analysis to lessen the influence of any residual leukemia cells that remained in the normal fraction after sorting. Clonal tracking was used to designate candidate somatic variants, and variants present in the germline clone were removed from the analysis.

ATAC sequencing

PBMCs were thawed and stained with CD19-BV510 antibody (BD Biosciences) at 4°C for 30 min. PBMCs were washed and stained with propidium iodide (PI, Sigma). 50,000 viable (PI^{-ve}) CD19^{+ve} cells were flow-sorted using the FACSAria (BD). ATAC-seq was performed exactly as described in the protocol[3]. ATAC-seq libraries were subjected to 80bp paired-end sequencing on the Illumina NextSeq platform.

Prior to alignment, adaptor sequences were trimmed from all reads using trim galore (v0.4.4). All fastq files were then aligned to the human genome, build hg38, using Rsubread's (v2.4.2) align function with the 'type' option set to 'dna'[4]. In all cases, at least 85% of fragments were successfully mapped. The resulting bams files were then sorted and indexed, and PCR duplicate reads marked using Sambamba (v0.6.6). The deepTools software (v3.5.1) was then used to generate coverage profiles around genes. All PCR duplicate reads were excluded from coverage calculations. Coverage plots were generated using the R statistical software (v4.0.2).

ChIP sequencing

ChIP for H3K27ac (2ug/sample, Abcam, cat #ab4729) and transcription factor binding (c-Rel; 1:100, clone D5G1A, CST, cat #12659, NF-kB2; 1:50, clone D7A9K, CST, cat #12659) was performed as per the 'ChIP for Histone Proteins' method[5], with minor modifications. PBMCs were thawed and stained with CD19-BV510 antibody (BD Biosciences) at 4°C for 30 min. Cells were crosslinked with 1.6% paraformaldehyde (Electron Microscope Science) for 10 min at 37°C. PBMCs were washed and stained with propidium iodide (PI, Sigma). Viable (PI negative) CD19^{+ve} cells were flow-sorted using the FACSAria (BD). For CLL2 relapsed sample, after crosslinking, cells were permeabilized with 1xPerm buffer (Affymetrix eBiosciences). Cells were stained with BCLxL-PE (1:100, clone E18, Abcam). Viable CD5^{+ve}CD19^{+ve} BCLxL^{lo} cells and viable CD5^{+ve}CD19^{+ve} BCLxL^{hi} cells were sorted using the FACSAria (BD). Nuclei were extracted by washing three times in nuclear isolation buffer (20 mM Tris, pH 8.0, 10 mM NaCl, 2 mM EDTA, pH 8.0, 0.5% Igepal CA-630 and 1× Complete Protease Inhibitor (Roche)). Nuclei were resuspended in sonication buffer (20 mM Tris, pH 7.5, 150 mM NaCl, 2 mM EDTA, 1% Igepal CA-630, 0.3% sodium dodecyl sulphate and 1× Complete Protease Inhibitor (Roche)) and sonicated with a Covaris S220 sonicator (peak power, 105W; duty factor, 20%; cycle/burst, 200; duration, 600 sec). Immunoprecipitation with 2 μg anti-Histone H3 (acetyl K27) antibody (Abcam); 10 μl NF-κB2 p100/p52 antibody (Cell Signaling Technology); 5 μl c-REL antibody (Cell Signaling Technology) was performed for a minimum of 16 hrs at 4°C. Immunoprecipitated samples were captured by incubation with 20 μl Dynabeads Protein G (Life Technologies). Reverse crosslinking of DNA was followed by DNA purification with the ChIP DNA Clean and Concentrator Kit (Zymo Research). An input of 100ng of genomic DNA per sample was prepared and indexed for Illumina sequencing using the TruSeq DNA sample Prep Kit (Illumina) as per the manufacturer's instructions. The indexed libraries were then pooled and prepared for paired end sequencing on a NextSeq500 instrument using the 150 cycle kit v2 chemistry (Illumina) as per the manufacturer's instructions. The base calling and quality scoring were determined using Real-Time Analysis on board software (v2.4.6), while the FASTQ file generation and de-multiplexing utilized bcl2fastq conversion software (v2.15.0.4).

All samples were aligned to the hg38 build of the human genome using Rsubread's align function with the 'type' argument set to 'dna'. This process also sorted and indexed the samples. In all cases at least 78% of fragments were successfully aligned. Following alignment, PCR duplicate reads were marked using Sambamba. Similarly, to the ATACseq data, the deepTools software was used to generate coverage profiles around genes, which were then visualized using the R statistical software.

TotalSeq C antibodies

CD3 (clone UCHT1, cat #300479, lot #B282150), CD4 (clone RPA-T4, cat #300567, lot #B282146), CD8 (clone SK1, cat #344753 lot #B280232), CD16 (clone 3G8, cat #302065, lot #B273582), CD11c (S-HCL-3, cat #371521, lot #B281421), CD14 (clone 63D3, cat #367137, lot #B283728), CD45RA (clone HI100, cat #304163, lot #B282142), CD5 (clone UCHT2, cat #300637, lot #B281430), CD56 (clone 5.1H11, cat #362559, lot #B283279), CXCR4 (clone 12G5, cat #306533, lot #B28022), CD20 (clone 2H7, cat #302363, lot #B274537), CD25 (clone BC96, cat #302649, lot #B282145), CD38 (clone HIT2, cat #30354, lot #B280225), CCR7 (clone G043H7, cat #353251, lot #B280225), HLA-DR (clone L243, cat #307663, lot #B282155), IgM (clone MHM-88, cat #314547, lot #B283295).

Mass Cytometry

Freshly thawed patient samples were incubated with cisplatin to allow detection of non-viable cells, fixed with 1.6% paraformaldehyde (PFA: Electron Microscopy Sciences), washed and stored at -80°C. Samples for batch analysis were barcoded using the 20-plex palladium barcoding kit according to the manufacturer's instructions (Fluidigm, South San Francisco, CA, USA). Following barcoding, cells were washed then stained with specific antibody-metal conjugates (CD19-142 Nd, CD5-143 Nd) for 1 hr at room temperature. Cells were permeabilized with methanol at 4°C for 10 min and washed. Cells were then stained antibodies against intracellular markers (cCaspase3-173 Yb, Cyclin D1-139 La, Cyclin B1-151 Eu, pRb [S807/811] - 166 Er, pPLCg2 [pY759]- 144 Nd, pERK 1/2 [T202/Y204]-167 Er, pS6 [S235/S236]-175 Lu, pCREB [S133] 87G3-176 Yb, MCL1-160 Gd, BCLxL-153 Eu), washed and stained with 125nM ^{191}Ir/^{193}Ir DNA intercalator (Fluidigm) overnight. After washing, cells were resuspended with EQ normalization beads immediately before analysis using a Helios mass cytometer (Fluidigm). Data concatenation, normalization and debarcoding are done with the Premessa R package (https://github.com/ParkerICI/premessa). Single cells were gated using the FlowJo based on event length and ^{191}Ir/^{193}Ir DNA contents to avoid debris and doublets. CD5^{+ve}CD19^{+ve} live non-apoptotic cisplatin^{lo} cells were analyzed for levels of the various metal conjugates.

Proliferation assay

Cryopreserved patient samples were thawed and labelled with 1 μM Cell Trace Violet (ThermoFisher) as described previously[6]. Cells were cultured on mouse embryonic fibroblast cells stably expressing the human CD40 ligand in the presence of rhIL-21 (25 ng/ml, R&D systems). After 7 days, cells were stained with CD5-APC (clone BL1a, Beckman Coulter) and CD19-BV510 (clone SJ25CI, BD Biosciences), and analyzed by FACSCytoflex (BD) before assessing proliferation using FlowJo software.

CLL cell culture

Peripheral blood mononuclear cells (PBMCs) from CLL patients were cultured with 1 μM NFκB inhibitor (IKK-16, Selleckchem), 1 μM JAK inhibitor (Tofacitinib, Selleckchem) or 100 nM PI3K inhibitor (buparlisib, Selleckchem) or DMSO control for 3 days. Afterwards, viability was measured by propidium iodide (PI, Sigma) exclusion using a FACSCytoflex (BD).

qRT-PCR

RNA was extracted using the standard phenol-chloroform extraction protocol using TRIzol™ (Ambion Inc). Isolated RNA was reverse transcribed using oligo-dT primers and the Super Script III First Strand cDNA Synthesis Kit (Invitrogen) according to the manufacturer's instructions. Quantitative RT-PCR reactions were performed in triplicate using the TaqMan™ Fast Advanced Master Mix (Applied Biosystems, Thermo Fisher) for *BCL2* (Cat #Hs00608023_m1), *MCL1* (Cat #Hs03043899_m1), *BCLxL* (Cat #Hs00236329_m1), *BCL2A1* (Cat #Hs00187845_m1), *PMAIP1* (Cat #Hs00560402_m1), *REL* (Cat #Hs00968440_m1) and *NFKB2* (Cat #Hs00174517_m1). Data were collected using the Viia7 PCR System (Thermo Fischer Scientific) using the Viia7™

software package (Thermo Fischer Scientific). Probing for GAPDH (Cat# Hs02786624_g1) served as a housekeeping control gene. Data were calculated using the $2^{-\Delta\Delta ct}$ method.

Generation of cell lines expressing *PMAIP1*/*NOXA*

HA-tagged $\mathrm{PMAIP1}^{\mathrm{WT}}$ or $\mathrm{PMAIP1}^{\Delta 22\mathrm{bp}}$ were synthesized as gene fragments by Integrated DNA Technologies (IDT) and subcloned into retroviral vector pMSCV-IRES-BFP. The constructs were sequenced (AGRF) and transduced into $PMAIP1^{\Delta/\Delta}$ RS4;11 cells as previously described [7]. Cells successfully integrated with the retroviruses (BFP^{+ve}) were sorted by flow cytometry.

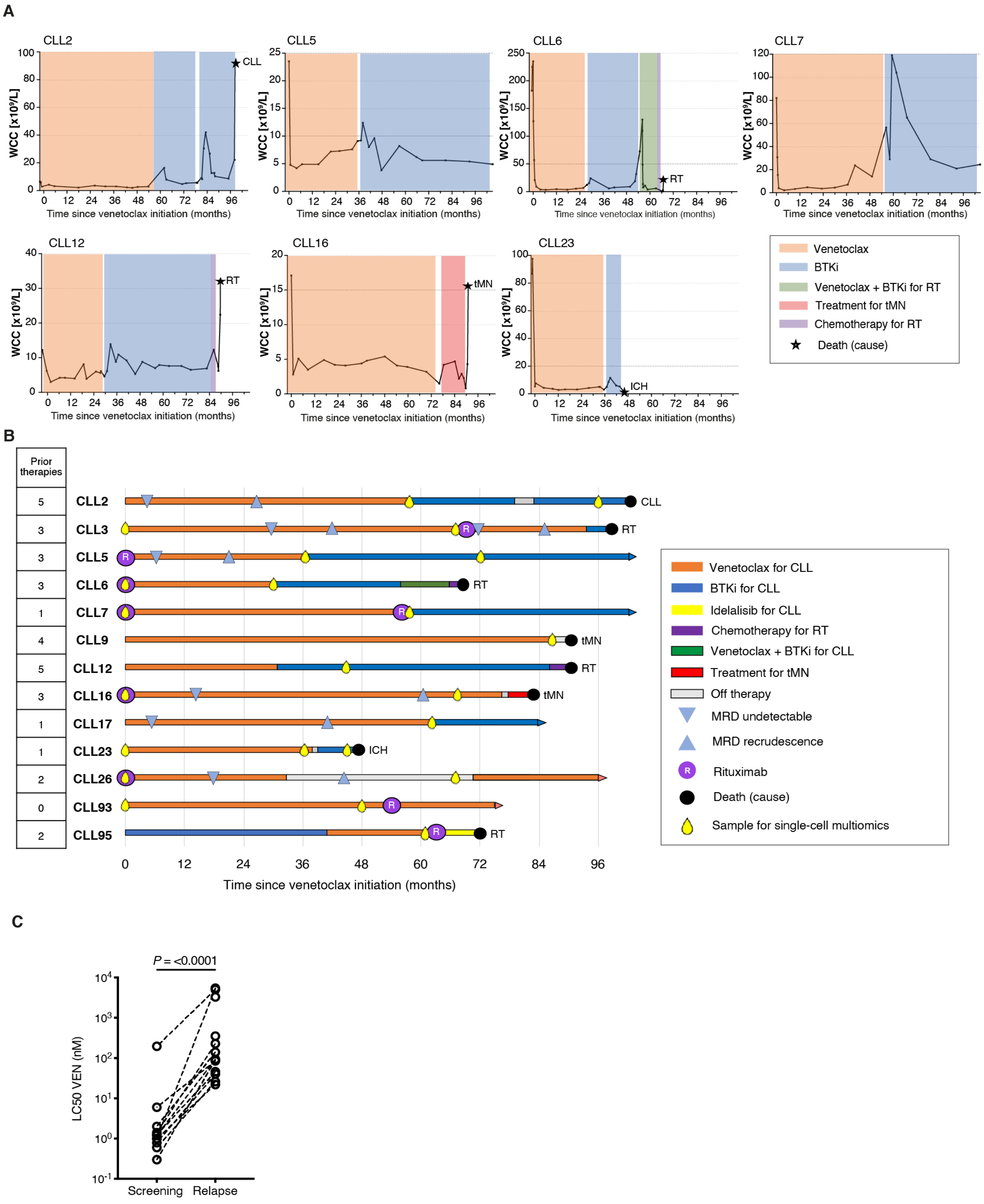
Immunoblotting

Immunoblotting was carried out as described previously[7]. Briefly, total protein from cells was isolated using lysis buffer (20 mM Tris-HCl pH 7.4, 135 mM NaCl, 1.5 mM $MgCl_2$, 1 mM EDTA, 10% glycerol) supplemented with complete protease inhibitors (Roche). Membranes were probed with antibodies against MCL1 (clone 19C4, WEHI Antibody Services), HA (3F10; Roche Applied Science) or HSP70 (clone N6, gift of Drs R Anderson and W Welch) as the protein loading control. Detection was performed by ChemiDoc Imaging System (Bio-Rad).

Targeted DNA sequencing

The 22bp *PMAIP1*/*NOXA* deletion in CLL2 was confirmed by sequencing PCR amplicons encompassing the genomic loci of *PMAIP1*/*NOXA* using the following primers: Fwd: 5'-AGTCAGGTTCCTGAGCAGAA-3', 5'-GGATATCAGATCAGTTTGTCTC-3', 5'-CAGAAGTTTCTGCCGGAAGT-3'and Rvs: 5'-GCTTTCGGTGAGTCACAATG-'3. BAX splice side mutation (chr19: 49458803 A→C) in the samples from CLL6 were confirmed by sequencing the amplicons generated using the primers 5'- TAGCGTTCCCCTAGCCTCTT-3' and 5'-ATGGAGTGAGGGTGCAGAAT-3'.

Supplementary Figure 1



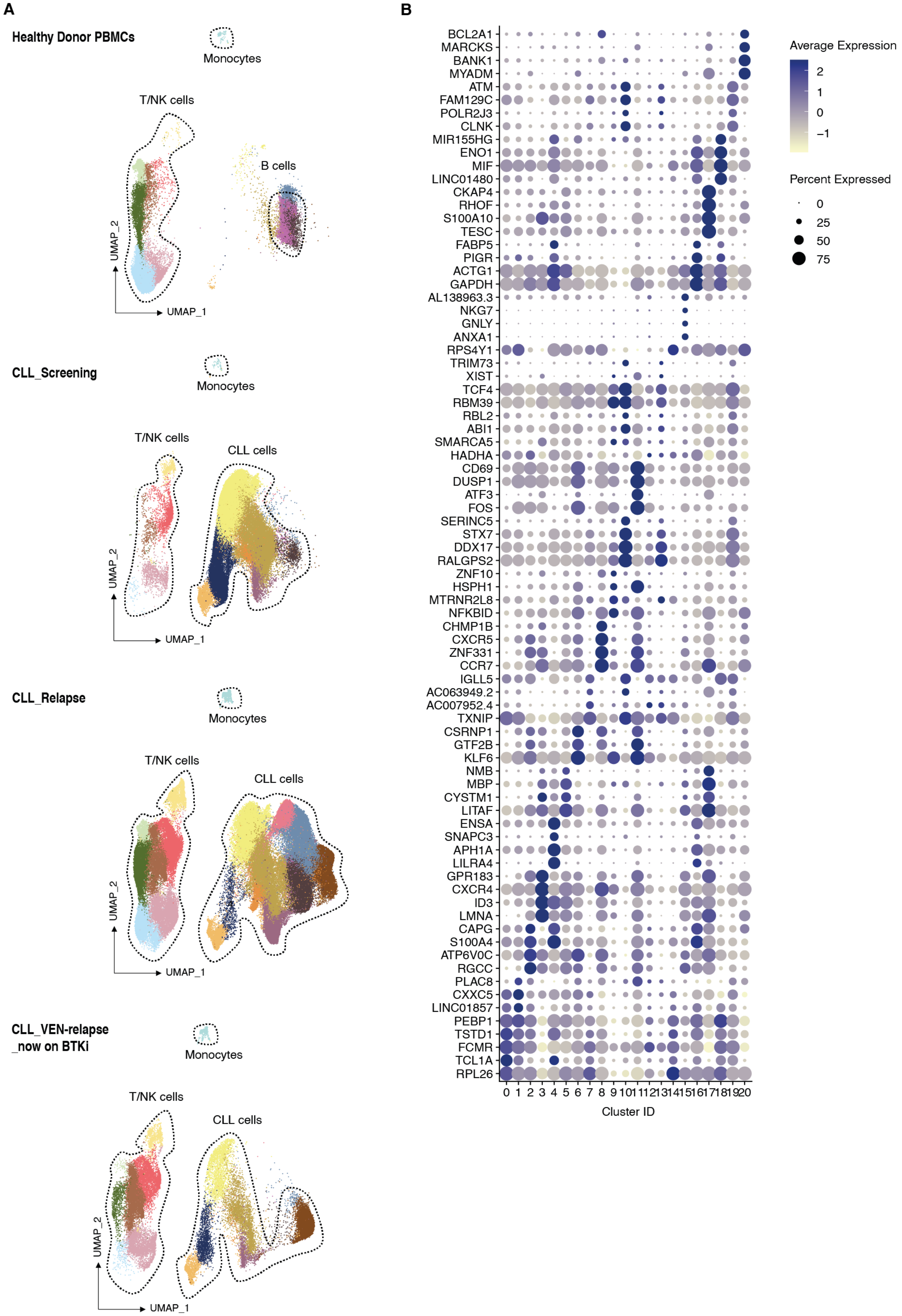
Supplementary Figure 1 CLL cells from patients with disease progressing after prolonged venetoclax treatment are less sensitive to venetoclax *in vitro*.

(A) Peripheral blood white cell counts (WCC x10^9/L) during VEN treatment and subsequent therapies. BTKi: Bruton Tyrosine Kinase inhibitor; tMN: therapy-related myeloid neoplasm; ICH: intracranial hemorrhage; RT: Richter transformation**.**

(B) Individual timelines for each patient showing treatments, outcomes and points at which samples were collected for single-cell multiomics. MRD (measurable residual disease) undetectable: first confirmation of peripheral blood undetectable MRD (CLL cells <0.01% of leukocytes), MRD recrudescence: first confirmation of re-emergence of positivity for MRD in peripheral blood (CLL cells $\geq$ 0.01% of leukocytes).

(C) *In vitro* sensitivity to VEN (0-4 μM for 24 hours) of peripheral blood CLL cells (CD5^{+ve}CD19^{+ve}) from patients prior to commencing VEN (n=11) or at leukaemic relapse (n=13). LC50 values are indicated. Dashed lines indicate paired samples. *P* value is from a two-sided paired t-test.

Supplementary Figure 2

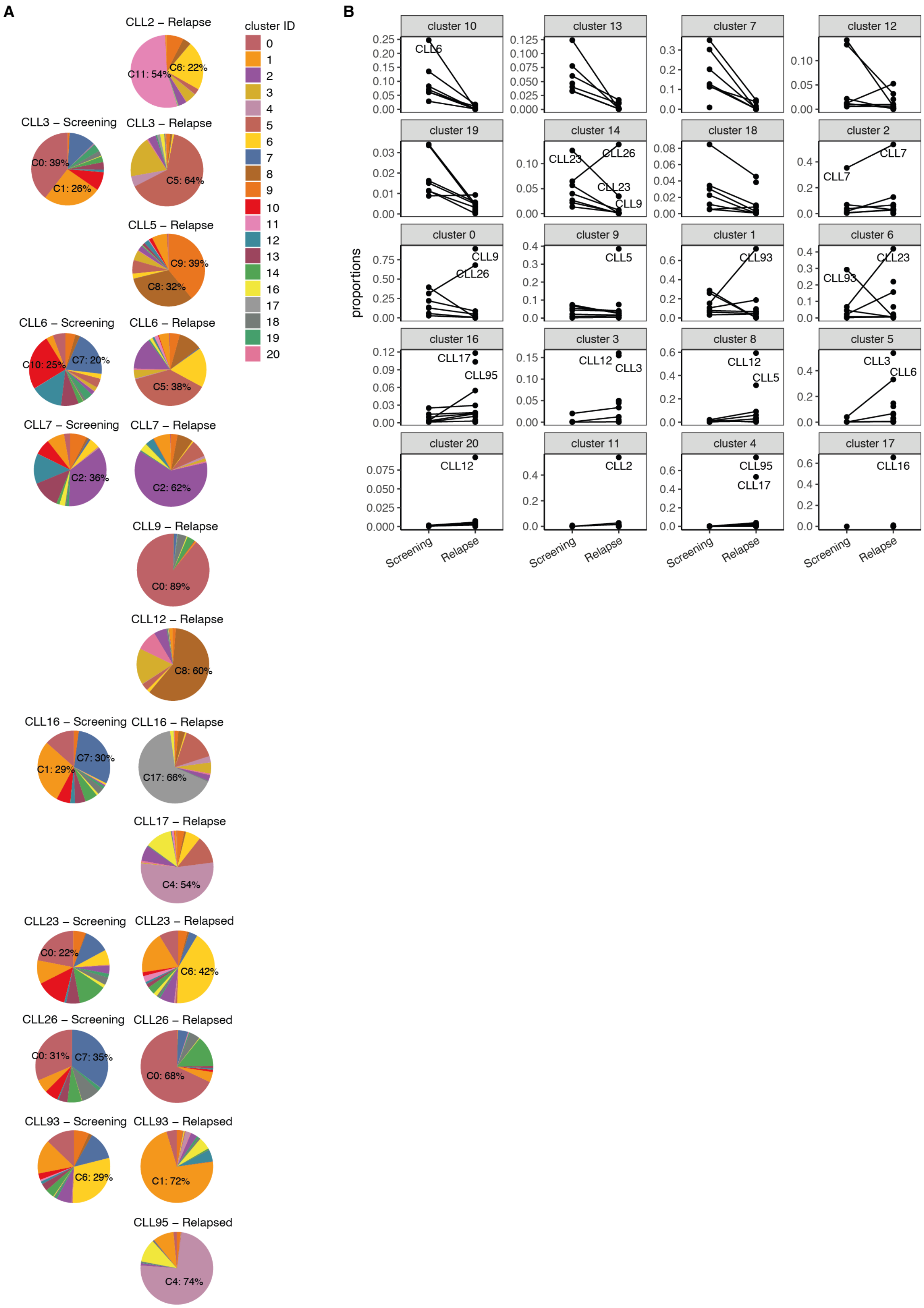


Supplementary Figure 2 CLL cells have a unique transcriptional profile.

(A) Uniform Manifold Approximation and Projection (UMAP) of PBMCs (peripheral blood mononuclear cells) from healthy donors (top panel), or CLL cells from patients at screening (2nd panel), from CLL patients at disease relapse on VEN (3rd panel), or from patients with relapsed disease subsequently treated with a Bruton Tyrosine Kinase inhibitor (BTKi; bottom panel).

(B) Dot plots showing the top 4 marker genes that distinguish each of the 20 clusters in Figure 1c. Color intensity indicates relative level of gene expression, and the size of dot indicates fraction of cells expressing that gene in the cluster.

Supplementary Figure 3

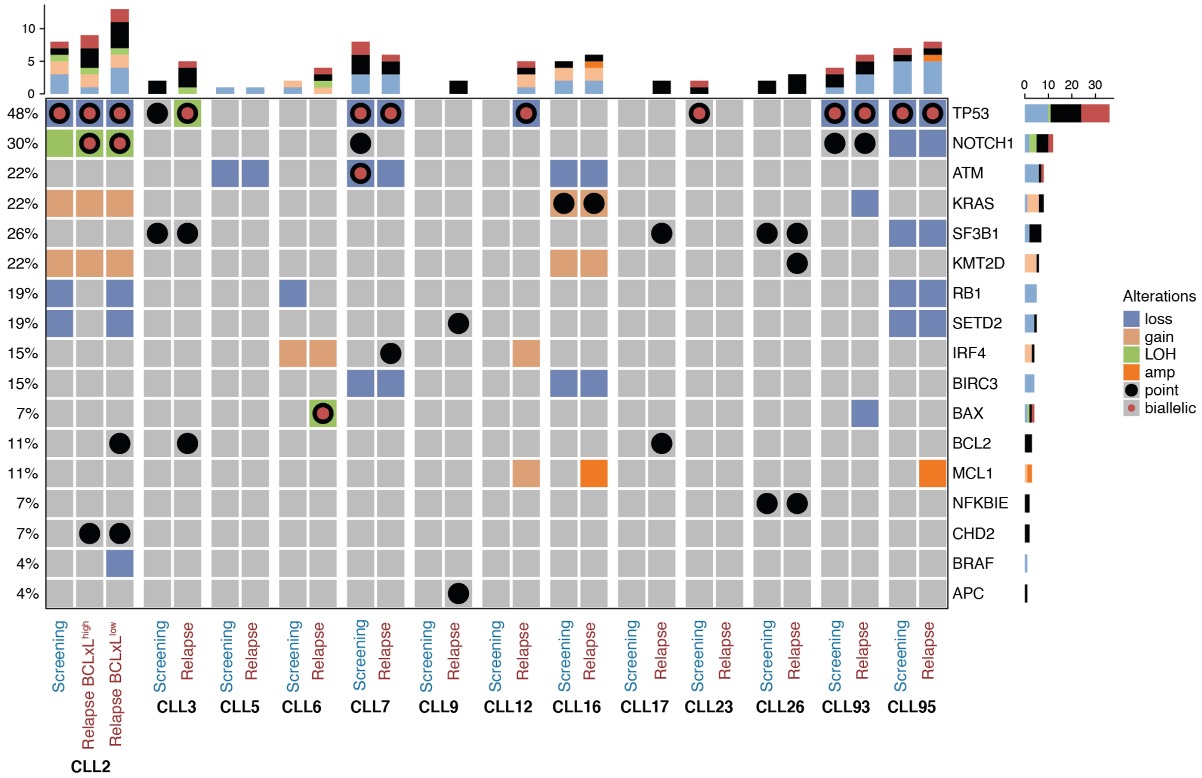


Supplementary Figure 3 High degree of intra-patient and inter-patient heterogeneity in cluster distribution.

(A) Pie charts showing the proportion of CLL cells in each cluster for the indicated individual patient sample. Dominant clusters (C) are noted for each sample.

(B) Box plots showing the change in representation of each cluster at VEN-relapse (except for CLL26 where CLL recurred occurred after many months off VEN therapy). Outlying samples are indicated by the sample number e.g., decreased representation of cells in cluster 10 for CLL6 at relapse (top left panel); where samples are available, the lines join the paired samples. Note that the scales of the Y-axes are varied.

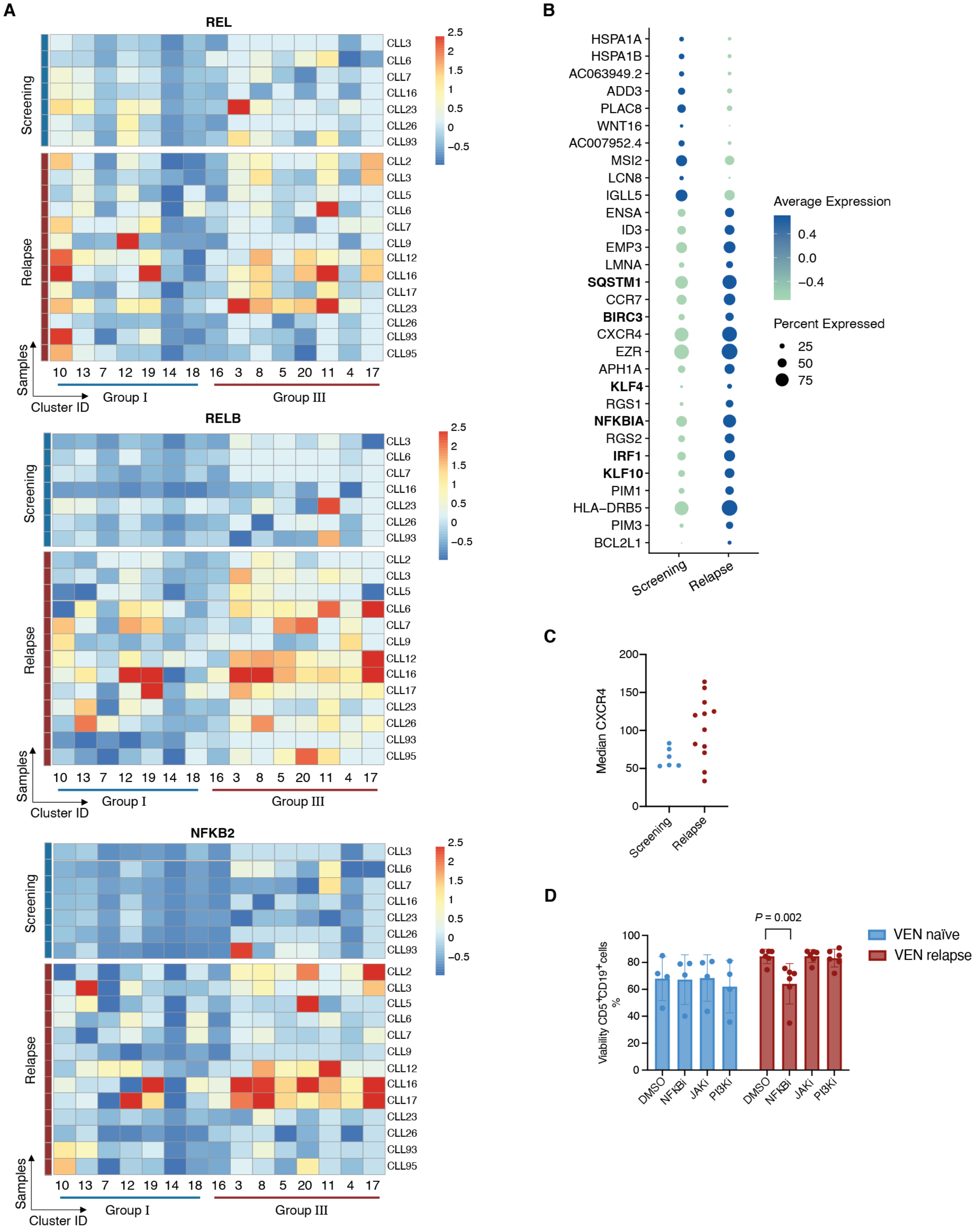
Supplementary Figure 4



Supplementary Figure 4 Landscape of genetic changes upon venetoclax relapse.

Somatic mutations or copy number alterations detected in key CLL and apoptosis pathway genes by bulk whole exome sequencing (WES) of 13 patients with VEN-relapse in this study. VAF alterations detected at >15% are shown. LOH: loss of heterozygosity, amp: amplification. Loss of SETD2 and RB1 in relapsed CLL2 BCLxL^{hi} population and loss of RB1 in relapsed CLL6 were not called by SuperFreq, but visual inspection of the gene-level data suggests these events were present at relapse as well at screening prior to starting VEN.

Supplementary Figure 5



Supplementary Figure 5 Venetoclax resistant cells display show increased NF-κB signalling.

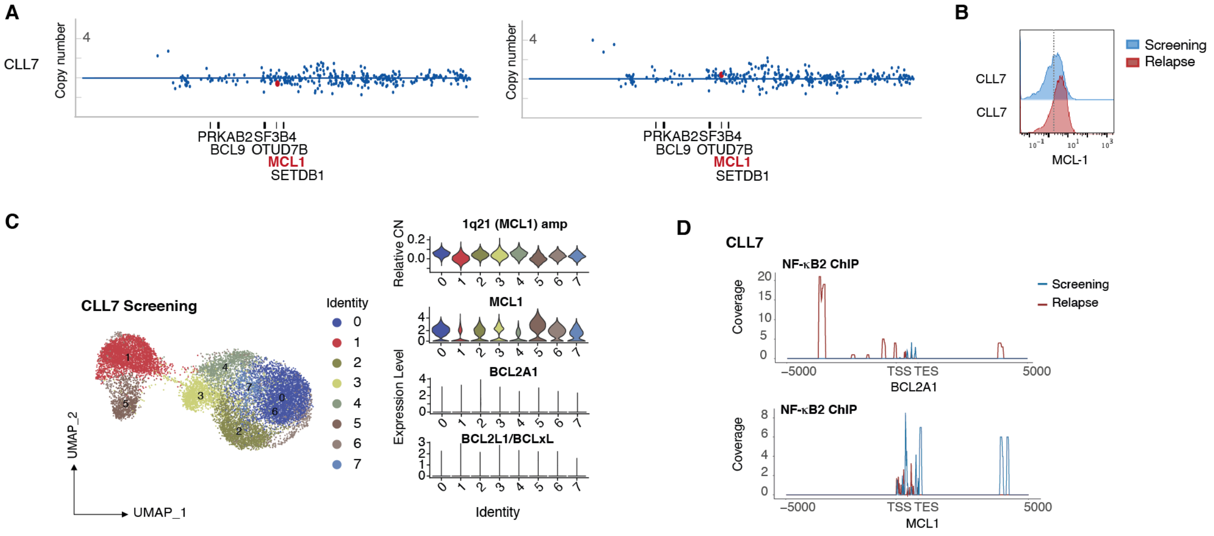
(A) Heatmaps showing expression of *REL* (top), *RELB* (middle) or *NFKB2* (bottom) in each cluster (columns) across the patient samples (rows).

(B) Dot plots showing marker genes that distinguish VEN-relapse cells from the pre-VEN cells present in the 5 clusters shared by the screening and relapsed samples (Group II in Figure 1d). Genes related to the NF-κB pathway are indicated in bold.

(C) Mass cytometric analysis of CXCR4 protein expression in viable (cisplatin^{lo}) CD5^{+ve}CD19^{+ve} CLL cells from screening (blue, n=6) or relapsed samples (red, n=11). Median expression for each sample was calculated by FlowJo. A two-sided paired T-test was used to determine statistical significance: no significant difference was detected.

(D) PBMCs from VEN-naïve (n=4) or relapsed (n=6) patient samples were cultured with 1 μM IKK16 (NF-κBi), 1 μM tofacitinib (JAKi), 100 nM buparlisib (PI3Ki) or DMSO control for 3 days. Data represent means ± SD of CLL cell (CD5^{+ve}CD19^{+ve} viability (PI^{-ve}) calculated for each patient sample, assayed in triplicate, for each condition in a single experiment. A one-way ANOVA was used followed by Dunnett's multiple comparison test to determine statistical significance.

Supplementary Figure 6



Supplementary Figure 6 Increased *MCL1* expression driven by NF-κB at venetoclax relapse.

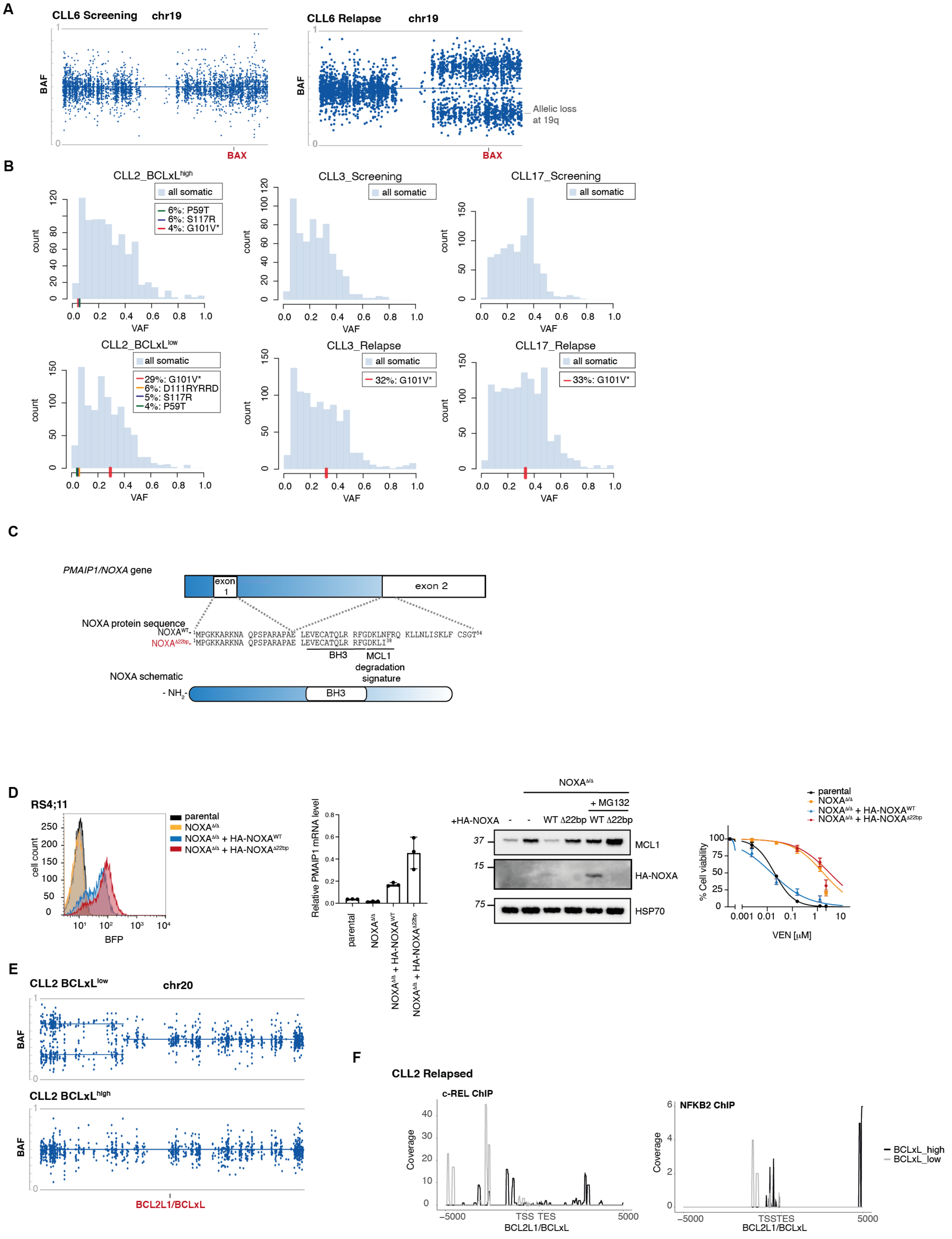
(A) Representation of the gained genomic regions in the 1q locus across the screening and relapsed samples from CLL7 analyzed by WES. *MCL1* is highlighted in red. Grey dotted lines indicates copy number of 2. Blue lines indicate copy number inferred from WES data.

(B) Histograms showing mass cytometric analysis of MCL1 protein expression in viable (cisplatin^{lo}) CD5^{+ve}CD19^{+ve} peripheral blood mononuclear cells (PBMCs) from screening and relapsed sample from CLL7.

(C) UMAP projections of CLL cells (left) from relapse samples from the screening sample from patient CLL7. Violin plots (right) show inferred copy number (CN) variation of 1q21 [*MCL1*] (top) and expression of *MCL1*, *BCL2A1* or *BCLxL* (*BCL2L1*) across the different clusters.

(D) NF-κB2 ChIP at the *BCL2A1* and *MCL1* loci 5,000 kb upstream of the transcriptional start site (TSS) or 5,000 kb downstream of the transcriptional end site (TES) in CLL cells at screening or relapse of CLL7.

Supplementary Figure 7



Supplementary Figure 7 In addition to *BCL2* G101V, multiple independent changes confer resistance to venetoclax.

(A) BAF analysis of chromosome 19 for CLL6 at screening (left) and relapsed (right) based on WES data. The location of the *BAX* locus is indicated.

(B) Bar plots showing the variant allele frequency (VAF) of all somatic mutations measured by WES on flow-sorted CD19^{+ve}CD5^{+ve} cells from screening and relapsed samples of CLL3 and CLL17, or relapsed CLL2 (BCLxL^{lo} or BCLxL^{hi}). The VAFs for the indicated *BCL2* mutations are represented with coloured ticks at the bottom. **BCL2* mutations previously reported in these samples. Number of somatic nucleotide variations with the germline clone and dbSNP variants removed for CLL3 was 163 (screening) vs 251 (relapse), and 228 (screening) vs 376 (relapse) for CLL17.

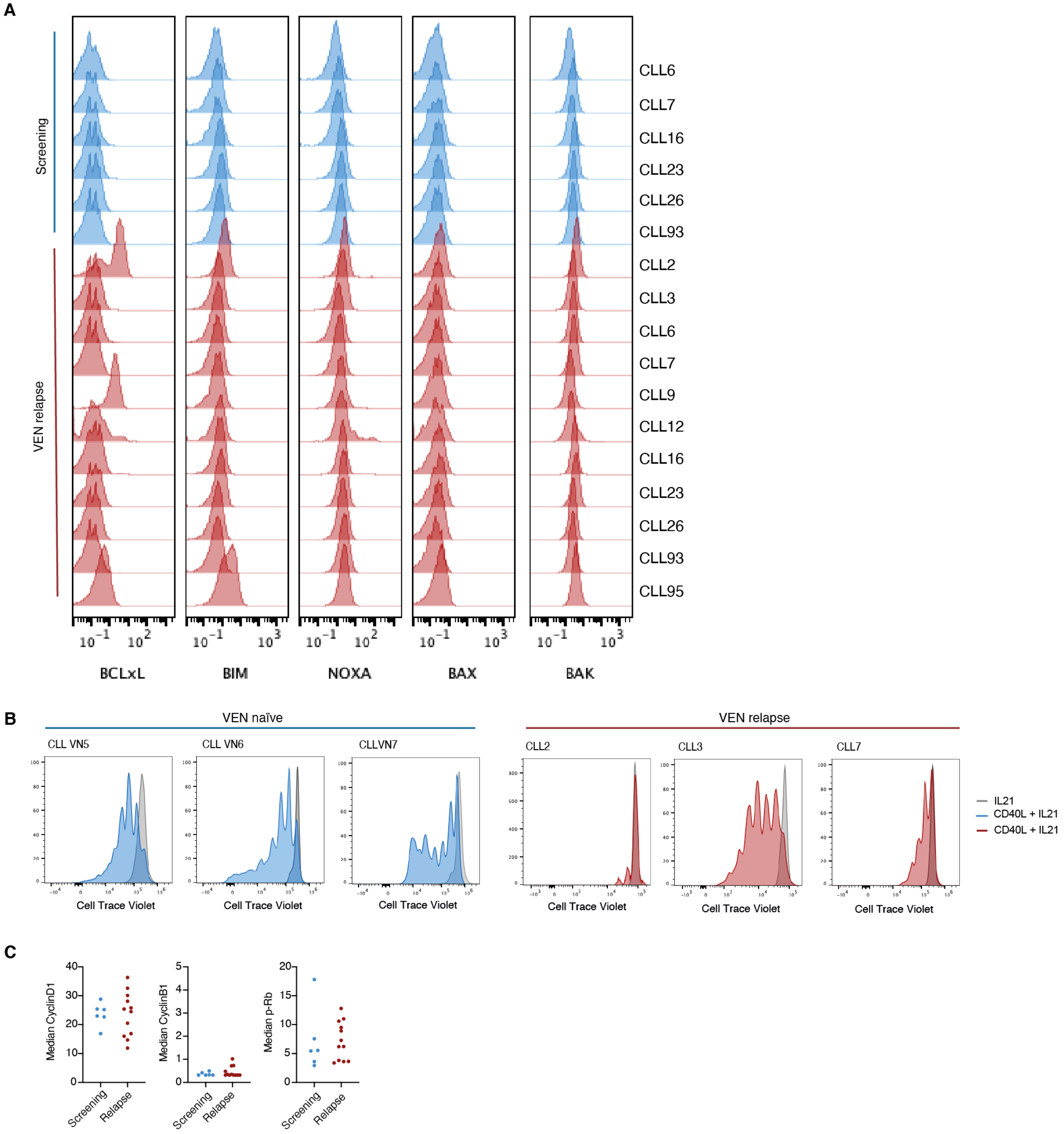
(C) Schematic of *NOXA* (*PMAIP1*) gene, protein sequence and BH3 domain, detailing both *NOXA-WT* and the *NOXA* with 22 bp deletion (*NOXA*$^{\Delta 22bp}$) found in CLL2.

(D) Expression of *HA-NOXA*^{WT} and *HA-NOXA*$^{\Delta 22bp}$ assessed by BFP levels (pMSCV-IRES-BFP) measured by flow cytometry (left), mRNA levels measured by qPCR (middle), or NOXA and MCL1 protein levels measured by western blot in parental or engineered RS4;11 B-ALL cells (treated with the proteasome inhibitor MG132 to block degradation of NOXA and MCL1) (right); HSP70 blotting served as the loading control. Experiments were repeated on three separate occasions. Viability was determined by CellTiter-Glo assay on cells treated with 0-10 μM of VEN for 24 hrs (far right). Data shown are means ± SD of ≥3 independent experiments.

(E) BAF analysis of chromosome 20 for BCLxL^{lo} (top) and BCLxL^{hi} (bottom) cells from CLL2 at relapse inferred from WES. The location of *BCLxL* (*BCL2L1*) on the locus is indicated.

(F) c-REL or NF-κB2 ChIP at the *BCLxL* (*BCL2L1*) locus 5,000 kb upstream of the TSS and 5,000 kb downstream of the TES in flow-sorted CD19^{+ve}CD5^{+ve} BCLxL^{hi} (black) or BCLxL^{lo} (grey) cells from CLL2.

Supplementary Figure 8



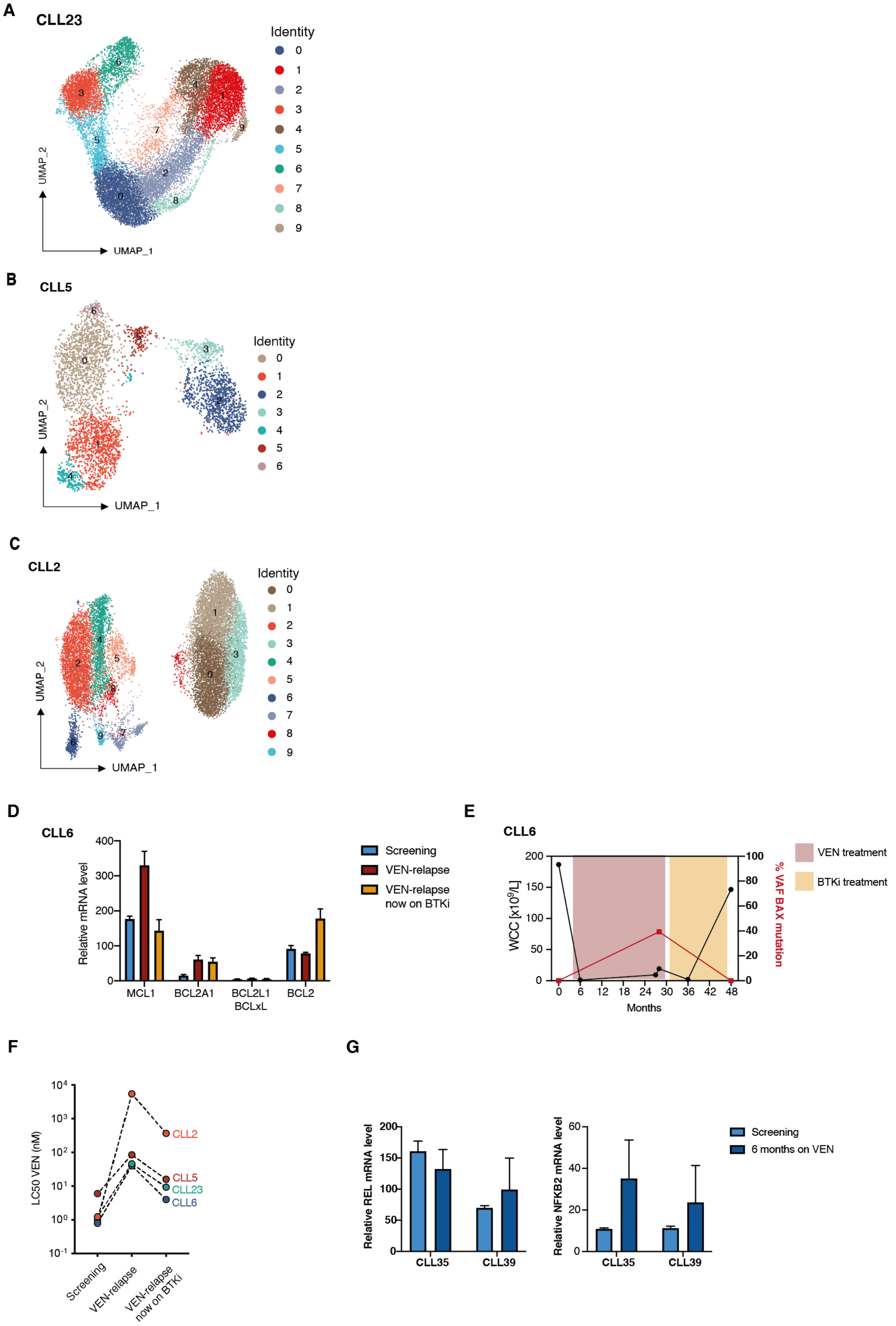
Supplementary Figure 8 Proliferation was unaffected at venetoclax relapse.

(A) Mass cytometric analysis of BCLxL, BIM, NOXA, BAX and BAK protein expression in viable (cisplatin^{lo}) CD5^{+ve}CD19^{+ve} PBMCs from screening samples (blue, n=6) and relapsed samples (red, n=11). MCL-1 protein expression data is in Figure 2C.

(B) PBMCs from VEN-naïve (VN; n=3) or VEN-relapse patients were labelled with cell trace violet and cultured with 25 ng/ml IL21 only (grey lines) or CD40L + IL21 (blue lines: VEN-naïve samples, red lines: VEN-relapsed samples). After 7 days, cells were stained with CD5 and CD19 antibodies, and cell trace violet was measured in CLL cells by flow cytometry. Plots representative of triplicate experiments.

(C) Mass cytometric analysis of Cyclin D1, Cyclin B1 protein or phosphorylated-Rb expression in viable (cisplatin^{lo}) CD5^{+ve}CD19^{+ve} PBMCs from screening samples (blue, n=6) and relapsed samples (red, n=11). Median expression for indicated protein was calculated using FlowJo. A two-sided paired t-test was used to determine statistical significance: no significant difference was detected.

Supplementary Figure 9



Supplementary Figure 9 Transcriptional changes maintained by venetoclax therapy.

(A-C) UMAP projections with cluster assignment for all CLL cells from CLL23 (**A**), CLL5 (**B**) and CLL2 (**C**).

(D) Expression, determined by qPCR, of *MCL1*, *BCL2A1*, *BCLxL* (*BCL2L1*) and *BCL2* in CLL6 samples collected at screening, VEN-relapse or after switching to a BTKi. Data represent means ± SD of triplicate measurements from a single experiment.

(E) White cell counts (left) and *BAX* mutation VAF were measured by targeted DNA sequencing while on or off VEN.

(F) *In vitro* VEN sensitivity of CLL cells (LC50s) from the indicated patients prior to VEN, at VEN-relapse or after VEN discontinuation (and on a BTKi >1year).

(G) Thawed samples from screening and after 6 months of ongoing VEN treatment from CLL35 and CLL39 were flow sorted for CD19^{+ve} cells. *REL* and *NFKB2* expression were measured by qPCR. Data represent means ± SD of triplicate measurements in a single experiment.

Supplementary References

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Supplementary Table 1. Marker genes for the 20 CLL clusters. List of differently expressing genes for the clusters in Fig. 1c.

p_val	avg_logFC	pct.1	pct.2	p_val_adj	cluster	gene
6.14E-191	0.641222666	0.992	0.858	1.14E-186	0	RPL26
3.24E-165	0.938522612	0.829	0.437	6.05E-161	0	TCL1A
7.38E-139	0.568763068	0.976	0.766	1.38E-134	0	TXNIP
9.82E-119	0.482732881	0.926	0.704	1.83E-114	0	NCF1
1.33E-118	0.53642068	0.978	0.822	2.47E-114	0	FCMR
1.31E-115	0.529348196	0.852	0.586	2.44E-111	0	TSTD1
3.90E-113	0.454395631	0.967	0.818	7.27E-109	0	PFN1
1.00E-111	0.465305453	0.849	0.51	1.87E-107	0	CD79B
1.16E-97	0.504282104	0.656	0.348	2.17E-93	0	HCST
2.81E-96	0.487941612	0.912	0.681	5.23E-92	0	RAC2
2.73E-93	0.426829571	0.988	0.869	5.08E-89	0	CD79A
2.13E-89	0.4765378	0.817	0.562	3.97E-85	0	SMARCB1
1.03E-86	0.437450441	0.909	0.708	1.92E-82	0	ERP29
2.36E-85	0.435410126	0.781	0.51	4.41E-81	0	GMFG
3.02E-84	0.399092705	0.81	0.53	5.63E-80	0	FCRLA
1.76E-82	0.425844542	0.504	0.228	3.28E-78	0	GYPC
2.31E-82	0.433339009	0.536	0.218	4.31E-78	0	AC243960.1
1.62E-81	0.302378242	0.672	0.363	3.01E-77	0	TRAF3IP3
3.03E-80	0.329568419	0.925	0.726	5.65E-76	0	TMA7
1.52E-79	0.385635991	0.992	0.886	2.84E-75	0	RPS20
6.80E-75	0.428835202	0.534	0.254	1.27E-70	0	ALOX5AP
4.57E-74	0.391642664	0.753	0.498	8.52E-70	0	ANAPC16
1.17E-71	0.472426229	0.637	0.372	2.18E-67	0	GLO1
2.71E-70	0.367093791	0.907	0.71	5.06E-66	0	SRSF5
5.12E-70	0.38945183	0.586	0.334	9.55E-66	0	FAM96A
6.06E-70	0.35883098	0.94	0.769	1.13E-65	0	PEBP1
4.53E-69	0.443435916	0.945	0.794	8.45E-65	0	HLA-DMA
5.74E-69	0.383680785	0.831	0.62	1.07E-64	0	GABARAP
9.06E-69	0.348463372	0.981	0.869	1.69E-64	0	ATP5F1E
3.18E-65	0.328537901	0.288	0.073	5.93E-61	0	LINC02422
1.67E-64	0.366986817	0.681	0.415	3.11E-60	0	POU2AF1
2.05E-64	0.407255504	0.445	0.2	3.83E-60	0	FMOD
1.57E-63	0.31706392	0.967	0.846	2.92E-59	0	COX7C
7.29E-63	0.395250535	0.638	0.401	1.36E-58	0	BRK1
1.12E-62	0.308068896	0.873	0.694	2.08E-58	0	RPL36A
2.32E-62	0.336781579	0.626	0.397	4.33E-58	0	POLD4
3.07E-56	0.308335999	0.879	0.652	5.72E-52	0	FCER2
1.58E-54	0.346856764	0.791	0.574	2.94E-50	0	GPSM3
2.03E-54	0.355820034	0.948	0.781	3.78E-50	0	ATP5MC2
4.37E-54	0.334460533	0.568	0.341	8.15E-50	0	TRAPPC1
1.27E-53	0.400820012	0.824	0.622	2.37E-49	0	LTB
3.11E-53	0.353573589	0.554	0.328	5.79E-49	0	LSM2

4.06E-53	0.526010046	0.429	0.21	7.57E-49	0	IFITM1
7.32E-53	0.304593713	0.621	0.402	1.37E-48	0	LINC01857
7.30E-52	0.336623163	0.911	0.744	1.36E-47	0	CYBA
3.21E-51	0.339329368	0.784	0.557	5.99E-47	0	CD27
3.80E-51	0.336143098	0.461	0.253	7.08E-47	0	PNOC
7.51E-51	0.295469176	0.535	0.323	1.40E-46	0	SHISA5
1.45E-50	0.27586241	0.945	0.796	2.71E-46	0	ARHGDIB
4.47E-50	0.357338871	0.507	0.292	8.33E-46	0	PTRHD1
5.01E-49	0.288911055	0.769	0.588	9.33E-45	0	RNASET2
2.06E-48	0.308031995	0.972	0.834	3.84E-44	0	TOMM7
6.28E-48	0.280603518	0.657	0.442	1.17E-43	0	CSK
1.19E-47	0.250030912	0.758	0.525	2.22E-43	0	EVL
1.54E-47	0.254822682	0.307	0.131	2.87E-43	0	ITGAE
1.87E-47	0.273714533	0.711	0.508	3.49E-43	0	CUTA
5.26E-47	0.260228113	0.938	0.815	9.81E-43	0	PCBP2
6.42E-47	0.261273379	0.469	0.273	1.20E-42	0	REX1BD
1.97E-46	0.295531755	0.639	0.413	3.67E-42	0	LAMTOR4
2.29E-46	0.353906828	0.665	0.436	4.26E-42	0	IFITM2
2.36E-46	0.325716658	0.691	0.476	4.40E-42	0	AES
1.02E-45	0.299081528	0.826	0.643	1.89E-41	0	CD48
3.99E-45	0.303686398	0.647	0.439	7.44E-41	0	CCND3
4.04E-45	0.271213038	0.771	0.57	7.53E-41	0	CYB561A3
6.25E-44	0.291548226	0.451	0.225	1.17E-39	0	TNFRSF13B
7.07E-44	0.570328529	0.206	0.05	1.32E-39	0	APOD
1.09E-43	0.256877243	0.54	0.357	2.03E-39	0	ABHD14B
2.20E-43	0.264844093	0.662	0.473	4.11E-39	0	PSMB9
2.20E-43	0.39614653	0.446	0.235	4.11E-39	0	C16orf74
7.53E-43	0.257510923	0.943	0.809	1.40E-38	0	ARPC3
7.57E-43	0.266588913	0.724	0.536	1.41E-38	0	DRAP1
1.48E-42	0.253780351	0.575	0.335	2.76E-38	0	KIAA0040
1.56E-42	0.27978188	0.402	0.214	2.91E-38	0	C1orf162
1.58E-42	0.254830004	0.577	0.357	2.95E-38	0	CCDC191
2.02E-42	0.261515926	0.537	0.346	3.76E-38	0	PTPRCAP
2.05E-42	0.265998301	0.713	0.5	3.83E-38	0	ATP5IF1
3.03E-40	0.514289508	0.242	0.085	5.65E-36	0	BCL2L1
4.13E-40	0.25758195	0.94	0.817	7.70E-36	0	LIMD2
5.33E-39	0.314157747	0.489	0.291	9.93E-35	0	NAPSA
6.91E-39	0.285601687	0.362	0.163	1.29E-34	0	LCK
1.18E-37	0.264187171	0.545	0.355	2.20E-33	0	FLOT2
1.01E-36	0.277199561	0.951	0.811	1.88E-32	0	NOP53
7.14E-36	0.30660501	0.344	0.182	1.33E-31	0	SERPINF1
1.83E-35	0.257636437	0.503	0.306	3.40E-31	0	NEDD8
1.02E-34	0.272140427	0.742	0.566	1.90E-30	0	EIF3G
2.85E-34	0.271460824	0.549	0.353	5.32E-30	0	YPEL3
4.17E-34	0.293746159	0.398	0.213	7.77E-30	0	VPREB3
4.68E-33	0.28917967	0.324	0.168	8.73E-29	0	FAM30A

7.40E-33	0.256260324	0.77	0.608	1.38E-28	0	EIF3E
1.41E-24	0.324317943	0.619	0.474	2.62E-20	0	IGLL5
1.79E-90	0.546168924	0.825	0.547	3.34E-86	1	RPS4Y1
2.48E-88	0.469204782	0.914	0.774	4.62E-84	1	PEBP1
6.00E-83	0.969173603	0.618	0.404	1.12E-78	1	LINC01857
4.66E-77	0.313912816	0.927	0.723	8.69E-73	1	JUN
3.57E-72	0.462754275	0.349	0.132	6.66E-68	1	PTPN18
2.17E-69	0.371002569	0.763	0.538	4.04E-65	1	FCRLA
2.68E-65	0.36355215	0.891	0.711	4.99E-61	1	NCF1
1.71E-63	0.40942192	0.833	0.623	3.18E-59	1	LTB
1.31E-58	0.42382674	0.352	0.149	2.45E-54	1	AL928742.1
4.43E-58	0.48168141	0.726	0.533	8.26E-54	1	CXXC5
6.05E-58	0.381055692	0.759	0.572	1.13E-53	1	SMARCB1
3.99E-57	0.355516148	0.842	0.659	7.44E-53	1	FCER2
8.54E-54	0.40550504	0.65	0.422	1.59E-49	1	POU2AF1
1.43E-53	0.367935285	0.464	0.23	2.67E-49	1	AC243960.1
4.04E-53	0.398488194	0.318	0.129	7.54E-49	1	CLLU1OS
6.47E-52	0.325793515	0.926	0.809	1.21E-47	1	PNRC1
1.32E-49	0.292546441	0.95	0.827	2.46E-45	1	FCMR
4.44E-49	0.595113473	0.487	0.28	8.28E-45	1	PLAC8
1.17E-47	0.403275207	0.561	0.362	2.18E-43	1	HCST
1.54E-47	0.270970847	0.864	0.716	2.87E-43	1	ERP29
2.04E-47	0.287820277	0.737	0.53	3.80E-43	1	EVL
1.63E-45	0.293252402	0.875	0.735	3.04E-41	1	Sep-09
1.50E-44	0.260059904	0.774	0.598	2.80E-40	1	TSTD1
8.87E-44	0.368529931	0.757	0.563	1.65E-39	1	CD27
1.40E-43	0.410256825	0.422	0.26	2.61E-39	1	PIGR
2.68E-43	0.275052681	0.963	0.836	4.99E-39	1	TOMM7
2.50E-42	0.314546549	0.618	0.444	4.67E-38	1	CCND3
1.04E-41	0.274077113	0.712	0.521	1.93E-37	1	GMFG
1.43E-41	0.319116303	0.75	0.581	2.67E-37	1	GPSM3
1.53E-41	0.324738987	0.764	0.63	2.85E-37	1	NOSIP
4.85E-41	0.37056573	0.451	0.266	9.05E-37	1	RGS1
9.53E-41	0.321362676	0.328	0.155	1.78E-36	1	EAF2
1.02E-40	0.34147104	0.369	0.2	1.89E-36	1	CPNE5
9.04E-40	0.289255887	0.746	0.575	1.69E-35	1	CYB561A3
2.01E-39	0.31119985	0.424	0.241	3.75E-35	1	GYPC
2.36E-39	0.336642402	0.927	0.774	4.40E-35	1	TXNIP
2.83E-37	0.324177653	0.46	0.293	5.28E-33	1	VAMP5
5.47E-33	0.373763093	0.61	0.478	1.02E-28	1	SELL
2.13E-32	0.252721407	0.671	0.459	3.97E-28	1	TCL1A
1.06E-31	0.909687483	0.187	0.07	1.98E-27	1	CHI3L2
2.63E-31	0.323692337	0.367	0.214	4.89E-27	1	ATP2B1-AS1
3.95E-31	0.250539654	0.679	0.521	7.36E-27	1	SMDT1
7.91E-31	0.410086118	0.436	0.292	1.47E-26	1	H1FX
1.14E-29	0.287029224	0.579	0.397	2.13E-25	1	KLF2

6.49E-25	0.252469447	0.426	0.276	1.21E-20	1	PLEKHJ1
2.15E-24	0.304997278	0.755	0.617	4.00E-20	1	DBI
1.08E-22	0.253740822	0.601	0.43	2.01E-18	1	CD19
7.50E-20	0.252871618	0.756	0.633	1.40E-15	1	HLA-DMB
4.02E-181	1.223183251	0.834	0.482	7.50E-177	2	RGCC
4.33E-140	0.543796933	0.87	0.491	8.07E-136	2	NR4A2
2.21E-139	0.617425653	0.934	0.715	4.12E-135	2	YPEL5
1.12E-136	0.783425319	0.784	0.394	2.08E-132	2	ZNF331
7.05E-121	0.611682906	0.961	0.837	1.31E-116	2	SH3BGRL3
3.07E-120	0.525669935	0.792	0.447	5.72E-116	2	GPR183
2.90E-115	0.267996734	0.932	0.656	5.41E-111	2	CD83
6.68E-115	0.658248612	0.875	0.669	1.25E-110	2	ATP6V0C
1.69E-111	0.861726134	0.84	0.621	3.15E-107	2	S100A4
5.00E-108	0.490571138	0.964	0.817	9.32E-104	2	JUNB
5.15E-108	0.671716903	0.95	0.845	9.60E-104	2	KLF6
1.36E-105	0.319868715	0.831	0.519	2.54E-101	2	DUSP2
5.24E-102	0.306977778	0.879	0.658	9.77E-98	2	CD69
1.13E-88	0.568274886	0.564	0.286	2.11E-84	2	AC020916.1
4.67E-88	0.522042343	0.918	0.774	8.71E-84	2	HSPA8
6.94E-88	0.586138351	0.734	0.474	1.29E-83	2	SELENOK
1.16E-80	0.544611838	0.651	0.394	2.16E-76	2	GTF2B
2.05E-75	0.499208745	0.798	0.612	3.82E-71	2	HIGD2A
2.40E-74	0.524946738	0.693	0.449	4.48E-70	2	CXCR5
1.21E-70	0.573946023	0.664	0.45	2.26E-66	2	CAPG
3.86E-70	0.497598114	0.855	0.702	7.20E-66	2	COTL1
3.69E-68	0.429252031	0.958	0.84	6.88E-64	2	GAPDH
9.00E-68	0.371498354	0.48	0.205	1.68E-63	2	EGR1
7.09E-67	0.415600427	0.928	0.789	1.32E-62	2	ATP5MC2
7.24E-67	0.469291908	0.368	0.142	1.35E-62	2	DUSP4
4.30E-66	0.439652544	0.712	0.507	8.02E-62	2	CRIP1
7.31E-65	0.449177697	0.861	0.705	1.36E-60	2	CLIC1
2.26E-64	0.404044646	0.863	0.693	4.21E-60	2	RAC2
1.10E-61	0.491414247	0.734	0.551	2.05E-57	2	G3BP2
1.87E-61	0.369220846	0.88	0.748	3.48E-57	2	SNRPD2
4.35E-61	0.434516552	0.914	0.779	8.10E-57	2	PPDPF
1.02E-60	0.414781912	0.6	0.393	1.91E-56	2	CSRNP1
2.72E-59	0.716715031	0.473	0.252	5.07E-55	2	SLC2A3
1.46E-52	0.45043592	0.733	0.536	2.72E-48	2	HSPA5
1.99E-52	0.339792197	0.886	0.774	3.70E-48	2	EIF3F
5.02E-51	0.539768289	0.228	0.062	9.36E-47	2	ARL4D
6.08E-51	0.369703231	0.312	0.128	1.13E-46	2	MYADM
8.35E-49	0.367008735	0.904	0.778	1.56E-44	2	FXYD5
2.09E-48	0.355666386	0.942	0.835	3.89E-44	2	RPL36AL
6.47E-48	0.398162317	0.913	0.794	1.21E-43	2	S100A6
3.06E-46	0.302237813	0.923	0.811	5.71E-42	2	HINT1
3.01E-45	0.253821599	0.941	0.826	5.60E-41	2	BTG2

2.06E-44	0.360694975	0.635	0.429	3.85E-40	2	KLF10
2.38E-43	0.384642049	0.759	0.598	4.44E-39	2	C12orf57
7.45E-43	0.293883936	0.868	0.738	1.39E-38	2	TMA7
1.03E-41	0.328154017	0.932	0.832	1.92E-37	2	SLC25A6
1.34E-40	0.38136529	0.678	0.525	2.50E-36	2	SMDT1
1.71E-40	0.362123772	0.847	0.715	3.18E-36	2	EIF3K
2.80E-40	0.381469142	0.297	0.14	5.22E-36	2	DUSP5
8.88E-40	0.38051767	0.795	0.652	1.65E-35	2	CD48
9.45E-40	0.343629635	0.853	0.72	1.76E-35	2	ERP29
4.57E-39	0.340011564	0.48	0.291	8.51E-35	2	PTMS
1.58E-38	0.326196479	0.766	0.632	2.94E-34	2	SSR2
3.68E-38	0.323367359	0.422	0.262	6.86E-34	2	IGFLR1
1.66E-37	0.296361302	0.432	0.271	3.09E-33	2	ARL4A
2.38E-37	0.360113709	0.585	0.401	4.43E-33	2	KLF2
3.78E-37	0.352430426	0.695	0.518	7.05E-33	2	LGALS1
1.52E-36	0.307216997	0.898	0.788	2.83E-32	2	YBX1
1.72E-36	0.317445208	0.705	0.549	3.21E-32	2	FCRLA
1.61E-35	0.354081107	0.573	0.384	3.00E-31	2	TENT5C
2.36E-35	0.25907444	0.708	0.54	4.41E-31	2	RAB11FIP1
3.39E-35	0.250177066	0.51	0.303	6.31E-31	2	RASGEF1B
6.70E-35	0.351609475	0.769	0.615	1.25E-30	2	CNN2
2.12E-34	0.323416141	0.865	0.737	3.95E-30	2	COMMD6
3.78E-34	0.361755709	0.654	0.503	7.06E-30	2	CHCHD10
1.86E-33	0.302119857	0.793	0.685	3.47E-29	2	PPIB
2.46E-33	0.47408779	0.486	0.297	4.59E-29	2	ATF5
2.55E-33	0.318872037	0.658	0.497	4.76E-29	2	SBDS
9.78E-33	0.279764538	0.747	0.633	1.82E-28	2	ANXA11
1.64E-32	0.351368863	0.68	0.531	3.06E-28	2	NDUFB11
8.21E-32	0.335749993	0.757	0.613	1.53E-27	2	SLC25A5
8.65E-30	0.286179108	0.41	0.246	1.61E-25	2	FAM53C
2.50E-29	0.314246594	0.47	0.302	4.67E-25	2	OSER1
2.59E-29	0.276886573	0.346	0.208	4.83E-25	2	GM2A
6.37E-29	0.250502581	0.657	0.513	1.19E-24	2	CYCS
8.75E-29	0.260231038	0.73	0.617	1.63E-24	2	EIF3E
3.80E-28	0.322278478	0.62	0.472	7.07E-24	2	C9orf16
7.70E-28	0.304438524	0.392	0.24	1.44E-23	2	TP53I11
2.48E-27	0.262457157	0.662	0.548	4.63E-23	2	DRAP1
7.56E-27	0.295412494	0.574	0.429	1.41E-22	2	LY6E
1.73E-26	0.253186346	0.721	0.581	3.23E-22	2	CYTIP
1.73E-25	0.298250495	0.547	0.405	3.23E-21	2	TSPO
2.73E-25	0.300028433	0.461	0.296	5.09E-21	2	SERTAD1
6.17E-25	0.260881804	0.647	0.52	1.15E-20	2	CUTA
1.04E-24	0.268071569	0.506	0.373	1.94E-20	2	SHMT2
2.09E-24	0.296311236	0.613	0.485	3.90E-20	2	RNH1
4.24E-23	0.264184528	0.614	0.501	7.91E-19	2	UQCR11
2.24E-22	0.283904929	0.461	0.329	4.18E-18	2	ALKBH7

2.55E-21	0.257894988	0.794	0.678	4.76E-17	2	SERP1
5.55E-20	0.261420219	0.472	0.354	1.03E-15	2	FCGRT
0	1.871198443	0.957	0.433	0	3	LMNA
0	1.816139334	0.98	0.578	0	3	ID3
0	1.788764059	0.999	0.796	0	3	CXCR4
0	1.495993767	0.97	0.73	0	3	HIST1H4C
0	1.409016188	0.999	0.869	0	3	EZR
0	1.295587767	0.991	0.659	0	3	CD55
0	1.279444132	0.673	0.095	0	3	GABARAPL1
0	1.215562037	0.928	0.416	0	3	CDKN1A
0	1.102625678	0.996	0.786	0	3	TAGLN2
0	1.030640292	0.989	0.788	0	3	SARAF
3.86E-300	1.407700473	0.916	0.529	7.20E-296	3	ODC1
5.27E-298	1.76279423	0.873	0.44	9.83E-294	3	GPR183
1.80E-289	1.043263537	0.756	0.269	3.36E-285	3	RARA
3.71E-276	1.003811935	0.94	0.596	6.92E-272	3	LRRFIP1
4.04E-272	1.315707273	0.897	0.494	7.53E-268	3	S100A10
1.45E-271	1.332971251	0.671	0.15	2.70E-267	3	KLF3
2.15E-270	1.15051713	0.662	0.172	4.00E-266	3	TUBB6
2.12E-258	1.128084739	0.824	0.361	3.96E-254	3	SYAP1
2.83E-258	1.035347778	0.86	0.435	5.28E-254	3	TPM4
4.67E-256	1.066297831	0.962	0.707	8.70E-252	3	SAT1
4.69E-250	0.977457974	0.895	0.458	8.75E-246	3	TUBB4B
3.39E-247	0.947890554	0.937	0.613	6.32E-243	3	PDE4B
9.08E-245	0.988088843	0.716	0.234	1.69E-240	3	SKIL
6.70E-240	1.264396212	0.734	0.277	1.25E-235	3	CREM
1.14E-239	1.042468922	0.676	0.204	2.12E-235	3	SLC7A5
3.32E-237	0.770814261	0.974	0.765	6.19E-233	3	SQSTM1
7.73E-237	0.866156656	0.994	0.834	1.44E-232	3	ZFP36
6.14E-230	1.086971923	0.778	0.321	1.15E-225	3	GNB5
1.94E-225	0.790980599	0.972	0.712	3.61E-221	3	YPEL5
9.31E-224	0.925553911	0.935	0.658	1.73E-219	3	TUBA1B
2.04E-219	0.932976597	0.986	0.822	3.80E-215	3	BTG2
1.40E-215	0.925926547	0.622	0.19	2.60E-211	3	SLC16A3
1.68E-215	1.155349988	0.887	0.58	3.13E-211	3	ARID5B
1.94E-214	0.747480122	0.838	0.358	3.62E-210	3	NR4A1
4.11E-208	0.946576323	0.983	0.856	7.67E-204	3	UCP2
6.53E-208	0.902695265	0.594	0.146	1.22E-203	3	ELL2
1.70E-206	0.826662436	0.713	0.312	3.17E-202	3	FYTTD1
2.48E-203	1.327322337	0.408	0.025	4.63E-199	3	ANGPT2
4.96E-198	0.91502401	0.833	0.474	9.24E-194	3	RAP1B
8.44E-190	0.638045994	0.98	0.832	1.57E-185	3	CALM1
2.08E-189	0.86428717	0.835	0.479	3.88E-185	3	BIRC3
6.10E-184	1.225511189	0.461	0.068	1.14E-179	3	ID1
6.45E-182	0.826325082	0.576	0.184	1.20E-177	3	NDRG1
1.79E-181	0.856944203	0.942	0.662	3.33E-177	3	EMP3

2.46E-181	0.78577364	0.637	0.221	4.58E-177	3	TYROBP
3.66E-177	0.889992297	0.755	0.37	6.83E-173	3	TMEM123
8.77E-177	0.77704967	0.948	0.643	1.64E-172	3	CCR7
1.14E-176	0.826381873	0.941	0.694	2.13E-172	3	SRGN
1.42E-174	0.897560619	0.527	0.155	2.64E-170	3	S1PR1
2.79E-174	0.825164373	0.698	0.301	5.20E-170	3	PAK1
1.54E-173	0.847585045	0.835	0.416	2.88E-169	3	RGS2
1.65E-173	0.84549237	0.988	0.815	3.07E-169	3	JUNB
1.78E-172	0.935024479	0.796	0.46	3.31E-168	3	TUBA4A
1.61E-171	0.932670176	0.777	0.415	3.00E-167	3	IDI1
1.14E-170	0.665322946	0.95	0.697	2.13E-166	3	CALM2
3.22E-170	0.753147874	0.623	0.25	6.01E-166	3	CYSTM1
2.09E-169	0.838821486	0.719	0.379	3.90E-165	3	COL9A3
3.90E-168	0.752025116	0.66	0.252	7.28E-164	3	GLUL
1.19E-163	0.983769004	0.677	0.297	2.22E-159	3	LDLRAD4
1.35E-163	0.782665556	0.697	0.306	2.52E-159	3	S100A11
2.89E-163	0.738346268	0.478	0.123	5.39E-159	3	OAT
1.05E-162	0.798439921	0.783	0.452	1.97E-158	3	RNF41
6.66E-158	0.841926861	0.745	0.404	1.24E-153	3	CD63
1.27E-155	0.678854452	0.506	0.144	2.37E-151	3	SNED1
1.08E-154	1.043337631	0.654	0.286	2.02E-150	3	MAP2K3
2.78E-152	0.692827837	0.71	0.389	5.19E-148	3	LDHA
7.06E-151	0.777781254	0.726	0.392	1.32E-146	3	SLC3A2
2.26E-150	0.798566602	0.773	0.461	4.22E-146	3	H2AFZ
8.72E-148	0.862289299	0.777	0.414	1.63E-143	3	ADGRE5
6.61E-147	0.708739701	0.852	0.545	1.23E-142	3	DYNLL1
5.91E-145	0.716077268	0.899	0.637	1.10E-140	3	TUBA1A
4.77E-143	0.687781311	0.447	0.104	8.89E-139	3	PARD6A
1.04E-140	0.705386093	0.67	0.32	1.93E-136	3	ISCA1
3.84E-140	0.56893628	0.908	0.609	7.16E-136	3	HERPUD1
1.94E-138	0.864917118	0.296	0.017	3.61E-134	3	BDKRB2
2.81E-134	0.831971085	0.816	0.561	5.23E-130	3	ISG20
4.48E-133	0.662757932	0.42	0.121	8.35E-129	3	C15orf39
2.17E-132	0.79528594	0.482	0.146	4.05E-128	3	CRIP2
4.37E-132	0.627570599	0.68	0.344	8.14E-128	3	NFE2L2
5.89E-132	0.588269769	0.735	0.438	1.10E-127	3	STRAP
4.17E-131	0.508283047	0.874	0.64	7.77E-127	3	CHD2
1.28E-130	0.656419464	0.602	0.27	2.39E-126	3	ARID5A
2.24E-129	0.596925323	0.67	0.353	4.18E-125	3	CSNK1D
3.27E-129	0.627214656	0.63	0.282	6.10E-125	3	SERTAD1
1.64E-128	0.610631121	0.636	0.322	3.05E-124	3	SLBP
6.72E-128	0.564629513	0.603	0.306	1.25E-123	3	STX5
9.93E-125	0.686676318	0.585	0.251	1.85E-120	3	USP36
1.79E-122	0.694517876	0.772	0.468	3.34E-118	3	KRAS
3.91E-122	0.572470047	0.838	0.558	7.28E-118	3	UBE2B
2.25E-119	0.654921302	0.552	0.221	4.19E-115	3	BCL2L11

1.58E-118	0.649370426	0.59	0.267	2.94E-114	3	TIPARP
3.88E-118	0.590178295	0.434	0.111	7.24E-114	3	SIK2
6.33E-118	0.635191441	0.739	0.44	1.18E-113	3	EIF1AX
1.85E-117	0.498926193	0.802	0.531	3.45E-113	3	SSH2
2.86E-117	0.578271182	0.311	0.054	5.34E-113	3	VPS37B
3.18E-117	0.673861021	0.693	0.367	5.92E-113	3	RIPOR1
9.46E-116	0.753111645	0.593	0.287	1.76E-111	3	ATP1B3
2.35E-115	0.507981111	0.955	0.769	4.38E-111	3	NCL
3.38E-115	0.527362057	0.677	0.405	6.31E-111	3	NR1H2
4.58E-114	0.57472487	0.629	0.34	8.55E-110	3	ATP6V0D1
6.25E-114	0.590749352	0.342	0.073	1.17E-109	3	LGMN
4.57E-113	0.707372388	0.769	0.481	8.52E-109	3	TNFRSF1B
2.00E-112	0.715396123	0.696	0.399	3.73E-108	3	TGFB1
1.08E-111	0.513180171	0.855	0.614	2.01E-107	3	ATP5F1B
4.08E-111	0.619057129	0.575	0.263	7.61E-107	3	IVNS1ABP
4.26E-109	0.846943931	0.916	0.722	7.94E-105	3	ZFP36L2
4.65E-109	0.659408905	0.782	0.526	8.67E-105	3	AGPAT5
8.03E-109	0.65703944	0.612	0.328	1.50E-104	3	RASSF5
1.69E-108	0.697220326	0.491	0.18	3.15E-104	3	SC5D
6.07E-106	0.62958711	0.347	0.089	1.13E-101	3	ATP1B1
1.36E-105	0.558929058	0.576	0.292	2.54E-101	3	PLK3
9.41E-105	0.676206262	0.625	0.319	1.75E-100	3	SERPINB9
1.79E-104	0.544514055	0.736	0.445	3.33E-100	3	AMD1
6.46E-104	0.689935466	0.591	0.285	1.20E-99	3	MAD1L1
7.75E-104	0.511635571	0.665	0.338	1.44E-99	3	KDM6B
1.94E-103	0.505247565	0.272	0.047	3.61E-99	3	PNMA2
3.83E-103	0.535339065	0.832	0.587	7.13E-99	3	SPOCK2
4.91E-102	0.460600626	0.763	0.497	9.15E-98	3	GPBP1
1.50E-101	0.588548847	0.509	0.215	2.80E-97	3	SGTA
3.12E-101	0.482800425	0.642	0.362	5.81E-97	3	CHD1
9.72E-101	0.548231658	0.429	0.152	1.81E-96	3	GPR132
2.24E-100	0.573023479	0.649	0.36	4.17E-96	3	USP11
3.90E-100	0.48132179	0.905	0.709	7.27E-96	3	TMBIM6
2.74E-99	0.536166752	0.353	0.095	5.11E-95	3	PLEKHG2
4.40E-99	0.405510615	0.863	0.612	8.20E-95	3	PMAIP1
4.61E-98	0.594528078	0.824	0.585	8.60E-94	3	SYNE2
4.86E-98	0.549236398	0.626	0.345	9.05E-94	3	SINHCAF
1.43E-97	0.648762001	0.741	0.398	2.66E-93	3	ZNF331
2.03E-97	0.548076413	0.632	0.347	3.79E-93	3	ELF2
6.27E-97	0.542727649	0.48	0.198	1.17E-92	3	ABCG1
2.71E-96	0.462494762	0.538	0.243	5.05E-92	3	AHI1
5.53E-96	0.480401514	0.575	0.294	1.03E-91	3	ITPR2
5.86E-95	0.515673459	0.685	0.371	1.09E-90	3	PIM3
1.20E-94	0.430453894	0.665	0.39	2.25E-90	3	SLC38A2
2.51E-94	0.487008775	0.654	0.373	4.68E-90	3	ADK
2.98E-94	0.641157236	0.245	0.028	5.55E-90	3	LRRC32

4.62E-94	0.527647412	0.647	0.365	8.62E-90	3	FAM177A1
9.11E-94	0.583633973	0.511	0.221	1.70E-89	3	MIDN
4.65E-93	0.641732684	0.582	0.272	8.68E-89	3	BHLHE40
5.38E-92	0.457478742	0.881	0.657	1.00E-87	3	ARF1
1.21E-91	0.49520828	0.823	0.52	2.26E-87	3	IDS
3.29E-91	0.507167386	0.681	0.435	6.13E-87	3	SELENOT
4.84E-91	0.525594495	0.63	0.356	9.01E-87	3	SEC14L1
5.16E-91	0.516925383	0.558	0.298	9.61E-87	3	PAF1
3.10E-90	0.453852075	0.733	0.485	5.78E-86	3	EHMT1
1.16E-89	0.417379704	0.779	0.533	2.16E-85	3	HSPA5
1.17E-89	0.523081218	0.638	0.365	2.19E-85	3	TGIF1
2.65E-89	0.478262539	0.873	0.672	4.94E-85	3	YBX3
4.04E-89	0.539387764	0.77	0.508	7.53E-85	3	ATP2B1
4.99E-89	0.457108981	0.839	0.601	9.31E-85	3	SRSF2
6.08E-89	0.488278009	0.556	0.295	1.13E-84	3	TSPYL1
1.12E-88	0.544450485	0.735	0.524	2.10E-84	3	ATP6V0B
5.15E-88	0.459855777	0.213	0.019	9.60E-84	3	SCD
5.45E-88	0.507685034	0.427	0.178	1.02E-83	3	MED29
2.01E-87	0.611302647	0.435	0.164	3.75E-83	3	TUBB2A
4.50E-87	0.457759105	0.513	0.253	8.39E-83	3	SELENOS
1.26E-86	0.597556282	0.211	0.014	2.36E-82	3	EMP1
1.40E-86	0.413850023	0.772	0.538	2.61E-82	3	PSMA7
3.08E-86	0.481724593	0.332	0.098	5.74E-82	3	PDE4A
1.67E-85	0.375696306	0.905	0.71	3.11E-81	3	SLC25A3
3.03E-85	0.494382041	0.725	0.462	5.66E-81	3	EMD
4.96E-85	0.751000571	0.505	0.267	9.24E-81	3	WARS
1.87E-84	0.489818167	0.742	0.493	3.48E-80	3	MAPK1IP1L
2.29E-84	0.478962111	0.435	0.189	4.27E-80	3	KCTD20
1.13E-83	0.459308595	0.834	0.597	2.11E-79	3	SRSF3
1.21E-83	0.521520801	0.683	0.429	2.25E-79	3	ZEB2
2.35E-83	0.467348539	0.404	0.163	4.39E-79	3	RBBP8
8.11E-83	0.454618029	0.46	0.22	1.51E-78	3	MANBA
1.47E-82	0.479726368	0.537	0.276	2.74E-78	3	GNA13
1.99E-82	0.523332255	0.622	0.358	3.70E-78	3	FBXO21
3.14E-82	0.322940547	0.735	0.449	5.85E-78	3	BACH2
3.31E-82	0.418372147	0.637	0.395	6.18E-78	3	RPN1
3.40E-82	0.438766339	0.279	0.066	6.34E-78	3	SLC25A4
1.46E-81	0.41926564	0.775	0.535	2.71E-77	3	RAB11FIP1
9.08E-81	0.472803845	0.287	0.061	1.69E-76	3	CYBB
1.05E-80	0.458644866	0.445	0.168	1.95E-76	3	KLF4
4.03E-80	0.511208432	0.394	0.136	7.52E-76	3	SLCO4A1
6.08E-80	0.446997262	0.629	0.378	1.13E-75	3	CDKN1B
1.68E-79	0.480233199	0.413	0.159	3.13E-75	3	JOSD1
2.03E-79	0.459863624	0.511	0.276	3.79E-75	3	JPT1
2.43E-79	0.364210387	0.897	0.726	4.53E-75	3	MORF4L1
1.03E-78	0.541332991	0.629	0.39	1.91E-74	3	PBXIP1

2.12E-78	0.479939486	0.588	0.331	3.95E-74	3	STMN1
2.12E-77	0.444465039	0.555	0.311	3.95E-73	3	UBE2A
2.85E-77	0.389636051	0.491	0.254	5.32E-73	3	NEU1
1.64E-76	0.426492426	0.759	0.504	3.06E-72	3	CYCS
2.38E-76	0.402158566	0.51	0.266	4.43E-72	3	FGFR1OP2
2.52E-76	0.466361657	0.622	0.373	4.70E-72	3	WBP11
4.92E-76	0.351142176	0.84	0.62	9.16E-72	3	DDX3X
5.08E-76	0.413035692	0.775	0.556	9.48E-72	3	GNG2
1.09E-75	0.509668761	0.591	0.329	2.02E-71	3	RANBP2
4.78E-75	0.472633318	0.73	0.518	8.92E-71	3	CIB1
6.06E-75	0.559808521	0.498	0.247	1.13E-70	3	NXT1
7.06E-75	0.398800593	0.703	0.485	1.32E-70	3	VDAC2
1.03E-74	0.516864031	0.44	0.209	1.92E-70	3	PRNP
1.81E-74	0.415942828	0.516	0.263	3.38E-70	3	WDR74
2.06E-74	0.544282623	0.577	0.342	3.85E-70	3	CDK2AP2
4.19E-74	0.456941146	0.352	0.121	7.81E-70	3	FAM49A
6.75E-74	0.528119658	0.283	0.077	1.26E-69	3	FOSL2
7.60E-74	0.300219193	0.53	0.243	1.42E-69	3	NR4A3
1.07E-73	0.458908165	0.665	0.425	2.00E-69	3	UBE2N
2.30E-73	0.439636254	0.718	0.476	4.28E-69	3	PRKAR1A
5.59E-73	0.50010343	0.472	0.225	1.04E-68	3	EHD4
6.47E-73	0.367423639	0.903	0.73	1.21E-68	3	CNBP
6.63E-73	0.350921979	0.926	0.782	1.24E-68	3	DAZAP2
2.27E-72	0.428320984	0.46	0.223	4.23E-68	3	PNP
2.99E-72	0.405422939	0.733	0.517	5.57E-68	3	SNRPG
6.81E-72	0.431905088	0.589	0.33	1.27E-67	3	MAPRE2
7.94E-72	0.409799389	0.743	0.521	1.48E-67	3	HNRNPF
8.61E-72	0.431355845	0.344	0.107	1.60E-67	3	BAIAP3
1.66E-71	0.407455616	0.501	0.282	3.09E-67	3	NIPA2
2.21E-71	0.417865879	0.75	0.543	4.13E-67	3	SNU13
2.27E-71	0.647988615	0.333	0.129	4.23E-67	3	EPS8L2
2.59E-71	0.386426341	0.609	0.376	4.82E-67	3	G3BP1
5.33E-71	0.443212092	0.438	0.202	9.93E-67	3	ZHX2
9.78E-71	0.502181868	0.556	0.273	1.82E-66	3	PER1
1.04E-70	0.388988279	0.213	0.03	1.94E-66	3	HCK
1.18E-70	0.577029176	0.574	0.334	2.19E-66	3	ACSM3
2.57E-70	0.425625274	0.303	0.083	4.79E-66	3	AL136454.1
3.42E-70	0.422733614	0.819	0.601	6.37E-66	3	XRCC6
1.37E-69	0.452586878	0.766	0.549	2.55E-65	3	DDX21
8.50E-69	0.451652288	0.63	0.379	1.58E-64	3	TENT5C
6.03E-68	0.398046834	0.341	0.133	1.12E-63	3	NANS
1.02E-67	0.426500862	0.237	0.051	1.91E-63	3	SLC25A29
1.66E-67	0.4320865	0.499	0.26	3.09E-63	3	GNL1
3.24E-67	0.446244661	0.384	0.148	6.03E-63	3	SLC9A3R1
4.41E-67	0.40486079	0.426	0.202	8.21E-63	3	SAR1A
4.58E-67	0.468981877	0.513	0.262	8.54E-63	3	RUBCN

6.55E-67	0.390170077	0.352	0.144	1.22E-62	3	CHST15
1.19E-66	0.455166189	0.728	0.514	2.22E-62	3	RELB
1.64E-66	0.367230108	0.608	0.39	3.06E-62	3	SRPRA
2.84E-66	0.382169553	0.461	0.24	5.29E-62	3	RNF168
6.52E-66	0.385986372	0.268	0.076	1.22E-61	3	GNB4
6.65E-66	0.373626792	0.221	0.042	1.24E-61	3	CTU2
1.26E-65	0.41549881	0.38	0.16	2.35E-61	3	PPFIBP2
2.13E-65	0.318931845	0.542	0.353	3.96E-61	3	PFDN2
2.22E-65	0.358177113	0.686	0.462	4.13E-61	3	HSPA9
2.99E-65	0.495777802	0.415	0.184	5.58E-61	3	TOB1
1.12E-64	0.407585484	0.68	0.42	2.10E-60	3	HSPD1
1.38E-64	0.310042772	0.903	0.734	2.58E-60	3	SUMO2
1.60E-64	0.407537028	0.537	0.302	2.99E-60	3	STAU1
1.94E-64	0.358679882	0.609	0.391	3.62E-60	3	MAT2A
3.38E-64	0.402867432	0.347	0.134	6.31E-60	3	TIGAR
6.70E-64	0.341889219	0.755	0.562	1.25E-59	3	VCP
9.66E-64	0.42248074	0.461	0.234	1.80E-59	3	KIAA1191
2.55E-63	0.409426174	0.647	0.432	4.75E-59	3	MBP
5.91E-63	0.356711803	0.369	0.176	1.10E-58	3	ARFGAP3
1.02E-62	0.393853031	0.394	0.204	1.91E-58	3	KPNA2
1.39E-62	0.415314379	0.535	0.333	2.58E-58	3	TMX4
3.40E-62	0.355852921	0.408	0.2	6.34E-58	3	H2AFX
4.72E-62	0.469365764	0.734	0.515	8.79E-58	3	ANXA2
5.25E-62	0.399091906	0.453	0.226	9.79E-58	3	PLEKHB2
6.09E-62	0.400099113	0.261	0.083	1.14E-57	3	KIF21A
8.85E-62	0.405580831	0.612	0.395	1.65E-57	3	SF3A1
1.64E-61	0.371671198	0.782	0.579	3.06E-57	3	RBM8A
1.67E-61	0.299053777	0.274	0.096	3.11E-57	3	XIST
1.72E-61	0.406888585	0.447	0.228	3.20E-57	3	TOB2
2.71E-61	0.327806959	0.867	0.675	5.06E-57	3	RAN
3.13E-61	0.319276337	0.372	0.18	5.84E-57	3	MED21
3.57E-61	0.372104143	0.584	0.362	6.65E-57	3	HIVEP1
4.26E-61	0.362355892	0.789	0.6	7.94E-57	3	ORAI2
5.00E-61	0.328381803	0.189	0.026	9.33E-57	3	ALDH2
9.91E-61	0.43769793	0.306	0.097	1.85E-56	3	SPAG1
2.74E-60	0.393976737	0.572	0.349	5.10E-56	3	DNAJA2
3.12E-60	0.291196289	0.141	0.008	5.82E-56	3	GPRC5C
4.53E-60	0.511271117	0.85	0.684	8.44E-56	3	LITAF
4.66E-60	0.365613877	0.299	0.121	8.69E-56	3	HMCES
6.69E-60	0.377766416	0.705	0.509	1.25E-55	3	MAP1LC3B
1.08E-59	0.381772361	0.323	0.124	2.01E-55	3	FBXO34
1.75E-59	0.334389342	0.256	0.073	3.26E-55	3	RORA
2.38E-59	0.443175344	0.421	0.212	4.43E-55	3	MTHFD2
2.88E-59	0.410078217	0.604	0.383	5.36E-55	3	AKIRIN1
3.06E-59	0.354337732	0.835	0.623	5.71E-55	3	CD44
3.40E-59	0.310439092	0.419	0.238	6.33E-55	3	CCDC47

5.71E-59	0.330994653	0.323	0.151	1.06E-54	3	CDK16
8.78E-59	0.330839806	0.376	0.2	1.64E-54	3	WIPF2
2.10E-58	0.325738309	0.581	0.389	3.92E-54	3	TMED10
2.11E-58	0.329256926	0.746	0.49	3.93E-54	3	RGCC
2.59E-58	0.453149507	0.637	0.395	4.82E-54	3	PLEKHA2
3.91E-58	0.352430153	0.573	0.382	7.29E-54	3	TMED2
4.43E-58	0.379649324	0.376	0.169	8.25E-54	3	HGSNAT
5.38E-58	0.34169227	0.214	0.049	1.00E-53	3	SYNJ2
5.64E-58	0.404660608	0.479	0.262	1.05E-53	3	HIF1A
5.70E-58	0.38233693	0.774	0.593	1.06E-53	3	GPX4
6.05E-58	0.343654205	0.19	0.036	1.13E-53	3	COL18A1
7.77E-58	0.330315485	0.326	0.148	1.45E-53	3	RAB35
2.81E-57	0.4819225	0.515	0.289	5.24E-53	3	PPP1CB
2.91E-57	0.359700512	0.242	0.069	5.42E-53	3	DUSP3
3.10E-57	0.390811297	0.485	0.267	5.79E-53	3	ADIPOR1
3.81E-57	0.33754988	0.983	0.867	7.10E-53	3	MYL6
6.09E-57	0.311969261	0.335	0.158	1.14E-52	3	POR
9.81E-57	0.392985628	0.387	0.189	1.83E-52	3	DNAJB2
1.40E-56	0.389190584	0.771	0.571	2.62E-52	3	YWHAQ
1.45E-56	0.44706648	0.282	0.098	2.71E-52	3	KLK1
5.77E-56	0.440818316	0.471	0.26	1.07E-51	3	NRROS
9.66E-56	0.369771958	0.699	0.507	1.80E-51	3	EIF3A
1.00E-55	0.372404223	0.532	0.311	1.87E-51	3	RNF138
2.08E-55	0.450223814	0.463	0.246	3.89E-51	3	SOD2-ENSG00000112096
3.37E-55	0.322657173	0.586	0.393	6.29E-51	3	C1orf43
4.97E-55	0.310719431	0.564	0.384	9.26E-51	3	ADRM1
5.21E-55	0.398876576	0.518	0.311	9.70E-51	3	RELA
9.22E-55	0.314628866	0.5	0.305	1.72E-50	3	RNF114
1.51E-54	0.351014324	0.585	0.375	2.81E-50	3	ARPP19
3.06E-54	0.431520605	0.365	0.171	5.70E-50	3	ARRDC2
7.86E-54	0.458103972	0.361	0.157	1.47E-49	3	STX11
8.13E-54	0.408492278	0.37	0.168	1.52E-49	3	CORO1C
9.84E-54	0.344655211	0.247	0.083	1.83E-49	3	FUZ
1.02E-53	0.395488505	0.556	0.337	1.90E-49	3	SDCBP
1.24E-53	0.315442268	0.228	0.074	2.31E-49	3	TM2D2
1.79E-53	0.314041332	0.643	0.426	3.34E-49	3	BACH1
2.22E-53	0.563703288	0.387	0.205	4.13E-49	3	ISG15
2.54E-53	0.299317132	0.53	0.298	4.73E-49	3	RALGAPA1
3.32E-53	0.368267496	0.458	0.277	6.18E-49	3	PITHD1
1.34E-52	0.332814062	0.526	0.337	2.49E-48	3	MAPRE1
1.55E-52	0.486064326	0.41	0.219	2.89E-48	3	MRPS6
2.11E-52	0.281843286	0.225	0.072	3.94E-48	3	WDR47
2.22E-52	0.353902871	0.432	0.221	4.13E-48	3	CCPG1
2.85E-52	0.396475001	0.365	0.159	5.30E-48	3	APBB2
2.85E-52	0.415116286	0.537	0.319	5.31E-48	3	RNF149
3.87E-52	0.330551102	0.38	0.204	7.22E-48	3	PDE4DIP

4.53E-52	0.344922407	0.601	0.393	8.45E-48	3	PHF1
7.52E-52	0.268717404	0.518	0.32	1.40E-47	3	EIF4A3
1.24E-51	0.284559799	0.588	0.408	2.31E-47	3	CLTA
1.95E-51	0.332480935	0.336	0.164	3.64E-47	3	ARID3A
1.98E-51	0.301843844	0.223	0.074	3.70E-47	3	DUSP14
2.12E-51	0.314365001	0.356	0.195	3.95E-47	3	C14orf119
2.16E-51	0.355189594	0.392	0.185	4.02E-47	3	ACSL3
2.30E-51	0.409789937	0.448	0.262	4.28E-47	3	SRRT
2.39E-51	0.317540635	0.846	0.665	4.46E-47	3	GSTP1
2.97E-51	0.293030238	0.353	0.195	5.54E-47	3	UBE2D1
3.33E-51	0.287604956	0.272	0.122	6.20E-47	3	CNIH4
3.98E-51	0.381641489	0.505	0.303	7.41E-47	3	TACC1
4.50E-51	0.274528229	0.152	0.02	8.39E-47	3	SMAD7
5.57E-51	0.318733868	0.32	0.152	1.04E-46	3	ACD
4.42E-50	0.331621373	0.356	0.187	8.23E-46	3	IL21R
5.45E-50	0.39400787	0.28	0.096	1.02E-45	3	N4BP3
7.24E-50	0.323483831	0.376	0.183	1.35E-45	3	GTPBP1
8.80E-50	0.282698935	0.68	0.507	1.64E-45	3	TOP1
9.72E-50	0.338320446	0.448	0.242	1.81E-45	3	PPIL4
1.43E-49	0.359826158	0.269	0.1	2.66E-45	3	SLC5A3
1.81E-49	0.353054256	0.15	0.023	3.37E-45	3	CHAC1
5.82E-49	0.349830396	0.275	0.111	1.08E-44	3	SOCS3
1.42E-48	0.28343794	0.694	0.425	2.66E-44	3	KLF10
1.81E-48	0.338533644	0.398	0.212	3.37E-44	3	AFG3L2
1.93E-48	0.329537467	0.85	0.681	3.59E-44	3	HNRNPA0
3.17E-48	0.447884886	0.441	0.233	5.91E-44	3	TMBIM1
4.31E-48	0.389563792	0.252	0.074	8.04E-44	3	SLC1A4
4.78E-48	0.29342668	0.373	0.213	8.91E-44	3	SURF4
5.98E-48	0.272096096	0.383	0.21	1.11E-43	3	TMEM50B
6.55E-48	0.358996178	0.829	0.675	1.22E-43	3	SERP1
1.35E-47	0.373160441	0.355	0.164	2.52E-43	3	NBEAL1
1.36E-47	0.343177117	0.623	0.437	2.53E-43	3	PPP2R1A
2.05E-47	0.259710236	0.424	0.265	3.82E-43	3	TNPO1
2.18E-47	0.307913331	0.668	0.467	4.07E-43	3	B4GALT1
2.37E-47	0.519465866	0.552	0.35	4.41E-43	3	IGFBP4
5.75E-47	0.356274508	0.626	0.459	1.07E-42	3	HNRNPUL1
5.94E-47	0.36623308	0.153	0.025	1.11E-42	3	RGS12
7.11E-47	0.41281466	0.253	0.09	1.33E-42	3	CD9
8.29E-47	0.397964718	0.256	0.09	1.55E-42	3	GZF1
9.61E-47	0.372253247	0.504	0.28	1.79E-42	3	NUP98
1.35E-46	0.254941869	0.142	0.017	2.51E-42	3	TBC1D8
1.39E-46	0.460466495	0.492	0.301	2.60E-42	3	CHMP1B
1.42E-46	0.286293946	0.375	0.198	2.66E-42	3	TWF1
1.86E-46	0.32597585	0.522	0.343	3.46E-42	3	VPS35
2.04E-46	0.3070327	0.435	0.252	3.81E-42	3	USP9X
2.49E-46	0.329385687	0.326	0.154	4.65E-42	3	LRRC41

3.03E-46	0.279771871	0.484	0.301	5.65E-42	3	VMP1
3.71E-46	0.326482861	0.415	0.231	6.91E-42	3	RRP12
7.84E-46	0.269794807	0.302	0.16	1.46E-41	3	MGAT2
9.05E-46	0.396512857	0.547	0.362	1.69E-41	3	HMGA1
1.08E-45	0.259149802	0.806	0.659	2.01E-41	3	DDX24
1.10E-45	0.487314909	0.68	0.514	2.04E-41	3	ST6GAL1
1.10E-45	0.339304838	0.461	0.272	2.06E-41	3	EIF4G1
2.41E-45	0.364523876	0.245	0.087	4.50E-41	3	RNF166
2.71E-45	0.405106127	0.263	0.106	5.05E-41	3	NINJ1
3.93E-45	0.345599237	0.633	0.456	7.33E-41	3	GNG5
8.53E-45	0.312835404	0.75	0.568	1.59E-40	3	PRDX1
9.99E-45	0.353357826	0.558	0.382	1.86E-40	3	NDUFA6
1.85E-44	0.353683118	0.394	0.208	3.45E-40	3	CEBPG
3.64E-44	0.280663546	0.615	0.434	6.78E-40	3	GCC2
6.80E-44	0.330455045	0.395	0.232	1.27E-39	3	THEMIS2
7.71E-44	0.356224638	0.335	0.153	1.44E-39	3	DYNLT3
8.92E-44	0.374999186	0.335	0.164	1.66E-39	3	DSTN
8.93E-44	0.299302836	0.346	0.177	1.66E-39	3	PSEN1
1.10E-43	0.319527417	0.351	0.168	2.06E-39	3	CXCL16
1.22E-43	0.363230776	0.439	0.251	2.27E-39	3	RUNX3
2.06E-43	0.265638368	0.581	0.411	3.84E-39	3	AZIN1
5.23E-43	0.293432041	0.287	0.13	9.75E-39	3	RCE1
1.04E-42	0.316679212	0.571	0.401	1.94E-38	3	MLF2
2.10E-42	0.279765876	0.712	0.527	3.91E-38	3	BZW1
2.23E-42	0.330256574	0.28	0.129	4.16E-38	3	WNT10A
3.81E-42	0.281322343	0.538	0.352	7.10E-38	3	GOLGB1
4.96E-42	0.27789118	0.221	0.081	9.24E-38	3	TP53INP2
5.69E-42	0.271428359	0.227	0.081	1.06E-37	3	CFAP36
6.75E-42	0.280187037	0.182	0.047	1.26E-37	3	DEAF1
7.82E-42	0.293808265	0.672	0.491	1.46E-37	3	CD164
1.52E-41	0.267833223	0.228	0.09	2.84E-37	3	TM9SF1
1.68E-41	0.328468249	0.507	0.33	3.14E-37	3	NRBP1
1.74E-41	0.278167484	0.592	0.42	3.24E-37	3	ATP1A1
1.94E-41	0.296832539	0.425	0.253	3.62E-37	3	GARS
2.99E-41	0.281125979	0.393	0.241	5.58E-37	3	TSPAN3
5.74E-41	0.290333998	0.469	0.276	1.07E-36	3	SIPA1L1
6.36E-41	0.308288339	0.346	0.196	1.19E-36	3	CCDC97
6.87E-41	0.338973518	0.369	0.197	1.28E-36	3	GFOD1
8.30E-41	0.416656408	0.53	0.35	1.55E-36	3	SPIB
8.59E-41	0.397188506	0.455	0.272	1.60E-36	3	MARCKSL1
9.90E-41	0.290903516	0.282	0.143	1.85E-36	3	NTMT1
1.79E-40	0.326872964	0.439	0.253	3.33E-36	3	MORF4L2
1.89E-40	0.277159673	0.364	0.204	3.53E-36	3	FAM120AOS
4.72E-40	0.320444707	0.419	0.252	8.81E-36	3	RHEB
6.14E-40	0.3130927	0.395	0.225	1.14E-35	3	TSG101
9.14E-40	0.271868311	0.601	0.44	1.70E-35	3	RAB7A

1.22E-39	0.277265811	0.417	0.256	2.27E-35	3	PSMD11
1.26E-39	0.470841582	0.336	0.165	2.35E-35	3	NMB
2.06E-39	0.28418291	0.436	0.291	3.83E-35	3	NOP56
2.62E-39	0.298246001	0.764	0.594	4.88E-35	3	ARHGDIA
2.84E-39	0.404079595	0.331	0.167	5.30E-35	3	MID1IP1
3.01E-39	0.282836144	0.307	0.155	5.61E-35	3	TXNDC15
3.42E-39	0.255564383	0.576	0.387	6.38E-35	3	SMARCA5
3.51E-39	0.281492492	0.397	0.25	6.55E-35	3	CNIH1
3.80E-39	0.250913456	0.256	0.123	7.09E-35	3	FAM210A
3.89E-39	0.274104181	0.628	0.462	7.25E-35	3	SNX9
4.48E-39	0.274494945	0.477	0.317	8.36E-35	3	VDAC1
7.64E-39	0.302687401	0.296	0.148	1.42E-34	3	TLE1
8.24E-39	0.31106539	0.364	0.207	1.54E-34	3	CISD2
8.88E-39	0.302665937	0.443	0.297	1.66E-34	3	COX17
9.44E-39	0.280002639	0.259	0.107	1.76E-34	3	ADIPOR2
1.02E-38	0.325136688	0.509	0.332	1.91E-34	3	PTP4A1
2.55E-38	0.356840015	0.245	0.095	4.75E-34	3	PLIN2
2.62E-38	0.255709413	0.702	0.543	4.88E-34	3	C11orf58
2.66E-38	0.274271029	0.356	0.181	4.96E-34	3	DNM1L
2.86E-38	0.343431627	0.225	0.09	5.34E-34	3	LGALS3
6.12E-38	0.333141909	0.542	0.343	1.14E-33	3	NASP
6.32E-38	0.305908593	0.514	0.35	1.18E-33	3	MAGOH
6.54E-38	0.311576985	0.298	0.132	1.22E-33	3	VAMP3
7.24E-38	0.280196111	0.818	0.659	1.35E-33	3	CALR
7.50E-38	0.293973645	0.542	0.37	1.40E-33	3	CHD4
9.80E-38	0.311692904	0.664	0.491	1.83E-33	3	LAMTOR5
1.01E-37	0.254062368	0.235	0.102	1.88E-33	3	PWWP2A
2.46E-37	0.390668982	0.604	0.413	4.59E-33	3	PIM1
2.88E-37	0.25495143	0.418	0.264	5.36E-33	3	POGZ
4.71E-37	0.252552112	0.729	0.558	8.79E-33	3	KIAA1551
6.36E-37	0.295570998	0.257	0.106	1.19E-32	3	HRK
7.34E-37	0.309232802	0.314	0.148	1.37E-32	3	UAP1
7.38E-37	0.253456571	0.57	0.419	1.38E-32	3	GHITM
7.52E-37	0.255480622	0.357	0.217	1.40E-32	3	ZPR1
1.01E-36	0.330419585	0.402	0.25	1.88E-32	3	HNRNPAB
1.09E-36	0.392655597	0.483	0.317	2.03E-32	3	PEA15
1.19E-36	0.334464925	0.503	0.324	2.21E-32	3	MRPL20
1.38E-36	0.306136927	0.209	0.074	2.57E-32	3	IFI44L
1.73E-36	0.318502168	0.334	0.175	3.22E-32	3	BTG3
2.03E-36	0.349056746	0.376	0.218	3.78E-32	3	MX2
2.41E-36	0.298695339	0.35	0.195	4.48E-32	3	CYP51A1
2.46E-36	0.265840594	0.354	0.217	4.59E-32	3	MRPS18C
2.72E-36	0.438889466	0.312	0.151	5.06E-32	3	MXD1
3.73E-36	0.278762494	0.439	0.292	6.95E-32	3	GTF2F1
4.00E-36	0.275593573	0.754	0.612	7.45E-32	3	PTGES3
4.42E-36	0.320298233	0.407	0.259	8.24E-32	3	TOM1

5.11E-36	0.314843226	0.429	0.267	9.53E-32	3	SLIRP
5.25E-36	0.258592482	0.195	0.078	9.78E-32	3	CASP9
5.26E-36	0.476586648	0.139	0.03	9.81E-32	3	RASD1
5.35E-36	0.386441768	0.329	0.159	9.98E-32	3	PRR7
8.82E-36	0.257168783	0.552	0.411	1.64E-31	3	TMED9
1.59E-35	0.29558666	0.531	0.368	2.97E-31	3	SSB
2.14E-35	0.274183306	0.436	0.252	4.00E-31	3	SIMC1
2.56E-35	0.297160326	0.277	0.13	4.78E-31	3	PLBD1
4.14E-35	0.250644052	0.405	0.275	7.72E-31	3	USP1
5.49E-35	0.250204563	0.35	0.209	1.02E-30	3	EIF2S1
5.85E-35	0.284943122	0.31	0.158	1.09E-30	3	WDR45B
6.81E-35	0.434436523	0.436	0.269	1.27E-30	3	IRF7
7.32E-35	0.312236791	0.286	0.124	1.36E-30	3	AGO2
8.28E-35	0.26729965	0.672	0.518	1.54E-30	3	EIF4H
9.60E-35	0.394454979	0.436	0.29	1.79E-30	3	TXN
1.68E-34	0.276327406	0.476	0.3	3.13E-30	3	SMU1
1.86E-34	0.290418856	0.34	0.198	3.47E-30	3	ORMDL2
2.45E-34	0.289998172	0.215	0.076	4.56E-30	3	RPGR
3.43E-34	0.312862234	0.275	0.152	6.39E-30	3	VSIR
5.30E-34	0.289592464	0.443	0.28	9.89E-30	3	ABCF1
9.43E-34	0.269314729	0.425	0.258	1.76E-29	3	PHF20L1
2.45E-33	0.30215297	0.209	0.063	4.56E-29	3	NBPF26
2.46E-33	0.276752317	0.384	0.223	4.59E-29	3	ZBTB43
4.22E-33	0.332402984	0.26	0.129	7.88E-29	3	PDCD1
6.61E-33	0.261756181	0.281	0.149	1.23E-28	3	RAB9A
1.85E-32	0.267038357	0.517	0.353	3.45E-28	3	NUDC
2.92E-32	0.286554033	0.421	0.265	5.44E-28	3	CHPT1
3.66E-32	0.33630379	0.838	0.707	6.82E-28	3	WASF2
1.23E-31	0.307821585	0.252	0.109	2.28E-27	3	FAM45A
1.77E-31	0.26238174	0.529	0.375	3.29E-27	3	YWHAE
5.85E-31	0.346128338	0.684	0.526	1.09E-26	3	NR3C1
8.40E-31	0.260773706	0.299	0.151	1.56E-26	3	RTN3
1.70E-30	0.322729265	0.274	0.128	3.16E-26	3	PNMA1
1.97E-30	0.271167278	0.358	0.216	3.67E-26	3	DEGS1
2.34E-30	0.250453041	0.43	0.276	4.36E-26	3	RAB1A
2.63E-30	0.290385922	0.259	0.132	4.90E-26	3	GYG1
3.19E-30	0.264681618	0.236	0.107	5.95E-26	3	CAMKK2
4.91E-30	0.280500288	0.301	0.168	9.16E-26	3	ITPKB
6.18E-30	0.257782493	0.287	0.165	1.15E-25	3	SLC25A19
6.44E-30	0.25306158	0.459	0.327	1.20E-25	3	ELOC
6.62E-30	0.252135418	0.907	0.794	1.23E-25	3	S100A6
1.19E-29	0.278814336	0.951	0.842	2.22E-25	3	HLA-DRB5
1.96E-29	0.283643692	0.431	0.288	3.65E-25	3	XBP1
2.92E-29	0.297882239	0.399	0.231	5.43E-25	3	ECE1
3.10E-29	0.273736074	0.335	0.195	5.77E-25	3	SQLE
3.11E-29	0.289702935	0.383	0.213	5.79E-25	3	NOLC1

4.90E-29	0.321043165	0.351	0.214	9.14E-25	3	BCL3
5.93E-29	0.269445044	0.337	0.192	1.10E-24	3	CHCHD7
7.35E-29	0.279683364	0.386	0.226	1.37E-24	3	HIVEP2
1.14E-28	0.266741695	0.267	0.14	2.12E-24	3	TARS
1.17E-28	0.28046031	0.366	0.213	2.18E-24	3	BIRC2
2.28E-28	0.27202349	0.447	0.309	4.25E-24	3	IRF2BP2
2.64E-28	0.264005884	0.384	0.233	4.92E-24	3	COPB2
4.40E-28	0.267211509	0.512	0.362	8.20E-24	3	KDM4B
4.48E-28	0.261076946	0.401	0.253	8.35E-24	3	CTR9
1.02E-27	0.274980137	0.34	0.2	1.91E-23	3	GNG7
1.22E-27	0.270365665	0.341	0.196	2.27E-23	3	MESD
1.65E-27	0.307399582	0.372	0.228	3.08E-23	3	GLIPR1
5.99E-27	0.321599845	0.391	0.246	1.12E-22	3	AAED1
7.08E-27	0.260443073	0.423	0.271	1.32E-22	3	ZFAND6
9.32E-27	0.256082229	0.371	0.23	1.74E-22	3	HSBP1
1.40E-26	0.267113367	0.329	0.197	2.61E-22	3	TUBA1C
1.47E-26	0.255144977	0.214	0.09	2.75E-22	3	SLC9B2
2.43E-26	0.261497781	0.355	0.209	4.53E-22	3	GNL2
2.57E-26	0.277814964	0.427	0.288	4.79E-22	3	HMOX1
4.64E-26	0.256331291	0.265	0.156	8.65E-22	3	PPIF
5.61E-26	0.298211351	0.612	0.459	1.05E-21	3	CNPPD1
6.88E-26	0.252471725	0.349	0.225	1.28E-21	3	HDLBP
1.12E-25	0.251342824	0.296	0.174	2.08E-21	3	FDX1
1.35E-25	0.250907751	0.55	0.432	2.52E-21	3	BNIP3L
6.65E-25	0.260760922	0.564	0.407	1.24E-20	3	POLR2A
2.09E-24	0.260112457	0.338	0.203	3.90E-20	3	LEPROTL1
3.57E-24	0.254884375	0.238	0.124	6.65E-20	3	CARHSP1
6.16E-24	0.271710335	0.338	0.21	1.15E-19	3	LAP3
1.64E-23	0.32702292	0.617	0.466	3.06E-19	3	CD24
3.08E-23	0.250089409	0.497	0.369	5.75E-19	3	RHOG
4.05E-23	0.263106221	0.324	0.194	7.55E-19	3	EEA1
5.73E-23	0.26885732	0.509	0.37	1.07E-18	3	WBP2
1.68E-21	0.275787044	0.394	0.261	3.14E-17	3	SNX8
2.09E-21	0.546872163	0.656	0.508	3.89E-17	3	HIST1H1E
8.56E-21	0.284262844	0.504	0.369	1.60E-16	3	NFATC1
1.19E-20	0.256555365	0.419	0.283	2.22E-16	3	SFT2D1
2.47E-18	0.252563057	0.28	0.166	4.61E-14	3	SLC10A3
4.70E-18	0.263007493	0.438	0.314	8.76E-14	3	YWHAH
0	1.761977458	0.836	0.082	0	4	LILRA4
0	1.563024195	0.944	0.498	0	4	LGALS1
0	1.329757375	0.674	0.052	0	4	MS4A6A
0	1.326484931	0.768	0.115	0	4	LILRB4
0	1.317868753	0.976	0.603	0	4	DBI
0	1.166687266	0.82	0.187	0	4	LAG3
1.51E-300	1.033578937	0.841	0.262	2.81E-296	4	PTMS
1.58E-298	0.86867511	0.989	0.695	2.95E-294	4	CLIC1

3.19E-294	1.046609951	0.865	0.279	5.94E-290	4	YWHAH
8.51E-293	0.983779776	0.958	0.497	1.59E-288	4	ANXA2
1.74E-279	0.955517945	0.971	0.605	3.24E-275	4	PLP2
2.26E-275	1.1971482	0.917	0.488	4.20E-271	4	GRN
4.17E-273	2.57227093	0.896	0.459	7.78E-269	4	APH1A
2.80E-271	0.885996565	0.921	0.428	5.22E-267	4	APOBEC3G
1.90E-265	0.792026468	0.997	0.834	3.54E-261	4	SH3BGRL3
5.30E-259	0.927234243	0.997	0.843	9.87E-255	4	ACTG1
1.51E-256	0.708701334	0.995	0.807	2.81E-252	4	RHOA
8.12E-256	1.106310966	0.98	0.659	1.51E-251	4	EMP3
6.46E-252	0.927316137	0.998	0.876	1.20E-247	4	VIM
2.54E-243	0.874831367	0.997	0.837	4.73E-239	4	GAPDH
1.26E-235	0.828812796	0.973	0.58	2.35E-231	4	ID3
1.54E-227	0.820453572	0.932	0.51	2.87E-223	4	PTPN6
1.75E-227	1.771159027	0.578	0.119	3.27E-223	4	SNAPC3
6.02E-226	0.903533972	0.607	0.091	1.12E-221	4	CST7
2.01E-224	0.785503571	0.962	0.576	3.76E-220	4	CD99
2.92E-223	0.781388156	0.973	0.713	5.44E-219	4	CORO1A
2.33E-222	0.696215683	0.974	0.641	4.34E-218	4	MYL12B
1.58E-220	0.887265201	0.992	0.788	2.95E-216	4	S100A6
1.59E-220	1.406572254	0.606	0.15	2.96E-216	4	TOR1AIP2
1.46E-219	2.63629693	0.86	0.456	2.71E-215	4	ENSA
3.78E-219	0.700455976	0.899	0.461	7.04E-215	4	RNH1
1.67E-213	1.602255575	0.721	0.264	3.11E-209	4	CEP350
2.38E-213	0.727242007	0.994	0.838	4.44E-209	4	HLA-DRB5
1.69E-211	0.749574918	0.435	0.022	3.15E-207	4	CDK6
4.15E-209	1.235145013	0.559	0.111	7.74E-205	4	FABP5
1.34E-203	0.736118464	0.59	0.127	2.49E-199	4	COCH
1.16E-200	0.696769296	0.974	0.655	2.16E-196	4	MYL12A
6.14E-200	1.598699754	0.663	0.236	1.14E-195	4	RPRD2
1.08E-199	0.779621275	0.906	0.488	2.01E-195	4	NDUFV2
6.03E-195	2.486022835	0.711	0.348	1.12E-190	4	PSIP1
1.81E-193	0.67473015	0.983	0.684	3.37E-189	4	RAC2
1.63E-190	0.720274974	0.997	0.865	3.03E-186	4	CFL1
1.35E-188	0.701712069	0.968	0.693	2.51E-184	4	COTL1
3.64E-188	0.573953873	0.611	0.133	6.79E-184	4	RHOC
1.67E-186	1.032145048	0.845	0.393	3.11E-182	4	RHOB
5.59E-186	0.577261314	0.585	0.123	1.04E-181	4	DGKG
8.73E-186	0.722005641	0.985	0.767	1.63E-181	4	LSP1
1.32E-185	1.028679528	0.939	0.613	2.45E-181	4	S100A4
5.37E-185	0.471473754	0.484	0.052	1.00E-180	4	MS4A4E
6.80E-185	0.580855087	0.869	0.406	1.27E-180	4	GNB2
1.28E-184	0.791730938	0.992	0.829	2.39E-180	4	AHNAK
3.23E-181	0.598692834	0.794	0.307	6.02E-177	4	AP2S1
4.47E-181	0.592036402	0.674	0.218	8.34E-177	4	RGS19
8.85E-181	0.694735656	0.88	0.441	1.65E-176	4	TUBB

9.49E-181	0.606061856	0.618	0.155	1.77E-176	4	CNP
2.99E-176	0.842586359	0.911	0.535	5.57E-172	4	LBH
8.47E-176	0.58021775	0.833	0.363	1.58E-171	4	NOP10
3.39E-174	0.468378426	0.862	0.433	6.31E-170	4	CSK
1.28E-172	0.418914409	0.407	0.037	2.38E-168	4	C3orf14
1.10E-169	0.621492562	0.997	0.866	2.06E-165	4	MYL6
3.01E-166	0.539614122	0.731	0.263	5.60E-162	4	HMOX1
3.50E-163	0.539206478	0.456	0.08	6.52E-159	4	DRAIC
8.89E-163	0.597982289	0.981	0.665	1.66E-158	4	PCBP1
6.52E-160	0.640645326	0.704	0.252	1.22E-155	4	TYMP
1.11E-159	0.611932061	0.985	0.772	2.07E-155	4	FXYD5
1.25E-159	0.53583387	0.729	0.274	2.32E-155	4	FAM107B
1.68E-159	0.51294676	0.998	0.855	3.14E-155	4	UCP2
2.62E-158	0.453183363	0.596	0.176	4.89E-154	4	PRKCD
3.30E-158	0.639316459	0.331	0.007	6.14E-154	4	CA14
6.41E-158	0.482318507	0.736	0.275	1.19E-153	4	TWF2
7.73E-158	0.612712887	0.528	0.108	1.44E-153	4	PDCD1
1.65E-157	0.602395427	0.767	0.327	3.07E-153	4	APOBEC3C
2.32E-157	0.608939684	0.427	0.071	4.32E-153	4	TARS2
2.68E-157	0.572582957	0.676	0.217	5.00E-153	4	TP53I11
3.74E-157	0.586002964	0.991	0.806	6.97E-153	4	HINT1
2.43E-154	0.580202732	0.664	0.224	4.53E-150	4	SIT1
2.65E-154	0.644683917	0.642	0.218	4.95E-150	4	PLEK
2.83E-154	0.573213758	0.782	0.365	5.28E-150	4	CTSZ
6.85E-151	0.675105249	0.783	0.319	1.28E-146	4	PLEC
2.31E-149	0.444924282	0.617	0.202	4.30E-145	4	IRF5
3.01E-149	0.477850631	0.826	0.389	5.60E-145	4	RBX1
8.59E-149	0.480073699	0.794	0.376	1.60E-144	4	CSTB
9.40E-148	1.908374469	0.946	0.667	1.75E-143	4	MCL1
4.96E-147	0.638444023	0.531	0.155	9.24E-143	4	RNF38
8.60E-147	0.86693564	0.968	0.755	1.60E-142	4	ZFP36L1
8.88E-146	0.562215697	0.793	0.345	1.65E-141	4	NFATC1
6.98E-145	1.04314915	0.624	0.222	1.30E-140	4	TOR1AIP1
1.48E-144	0.392061497	0.624	0.206	2.75E-140	4	FAM50A
2.04E-139	0.498624624	0.308	0.011	3.81E-135	4	GNG11
1.37E-138	0.474767009	0.722	0.318	2.56E-134	4	SEM1
3.70E-138	0.676697295	0.902	0.562	6.91E-134	4	PKM
5.15E-138	0.464052224	0.799	0.381	9.59E-134	4	TBCB
2.62E-134	0.380514711	0.607	0.209	4.88E-130	4	ILK
1.16E-133	0.414460146	0.792	0.379	2.17E-129	4	ARPC1B
4.58E-133	0.43106151	0.682	0.265	8.53E-129	4	DDAH2
1.17E-131	0.519728673	0.913	0.569	2.18E-127	4	GDI2
5.07E-129	0.42666754	0.849	0.439	9.45E-125	4	GNG5
3.59E-128	0.48326494	0.819	0.398	6.69E-124	4	ARF6
3.89E-128	0.399287281	0.451	0.109	7.24E-124	4	SH3BP2
4.60E-128	0.413730041	0.855	0.467	8.57E-124	4	INPP5F

2.29E-126	0.508546813	0.843	0.449	4.26E-122	4	PGAM1
1.67E-125	0.390078844	0.557	0.177	3.10E-121	4	TRAF7
2.38E-125	0.448837782	0.887	0.496	4.44E-121	4	CAP1
2.67E-125	0.446955987	0.33	0.038	4.98E-121	4	IL2RB
1.42E-124	0.51107527	0.765	0.348	2.64E-120	4	VASP
2.11E-124	0.485008388	0.471	0.129	3.93E-120	4	CXCR3
2.50E-124	0.550524659	0.723	0.311	4.66E-120	4	BANF1
4.09E-124	0.460545692	0.909	0.571	7.62E-120	4	POU2F2
1.89E-123	0.388163318	0.628	0.222	3.52E-119	4	PPP1R18
2.56E-123	0.789905429	0.832	0.473	4.77E-119	4	MRPS21
3.83E-123	0.539127108	0.318	0.035	7.14E-119	4	MGLL
4.35E-123	0.406919635	0.488	0.124	8.10E-119	4	SPN
1.02E-122	0.341377627	0.316	0.03	1.90E-118	4	PDPN
3.98E-122	0.40083139	0.927	0.586	7.43E-118	4	CAST
9.97E-122	0.42643612	0.883	0.526	1.86E-117	4	PPP1CA
1.01E-121	0.328749282	0.572	0.187	1.88E-117	4	IDH3G
5.87E-121	0.353809152	0.824	0.426	1.09E-116	4	ARL6IP5
6.57E-121	0.308027042	0.446	0.11	1.22E-116	4	FUOM
1.59E-120	0.419707575	0.418	0.099	2.96E-116	4	MYL9
5.53E-120	0.396019304	0.346	0.046	1.03E-115	4	JUP
8.25E-120	0.442005276	0.789	0.373	1.54E-115	4	ARHGAP30
8.95E-120	0.579771836	0.861	0.491	1.67E-115	4	RAC1
9.19E-120	0.635958722	0.719	0.334	1.71E-115	4	SPIB
2.88E-119	0.502981966	0.979	0.743	5.36E-115	4	SYNGR2
6.52E-119	1.162684911	0.319	0.04	1.21E-114	4	CCL3
3.07E-118	0.372934163	0.664	0.267	5.72E-114	4	MRPL51
4.12E-118	0.450620634	0.77	0.377	7.68E-114	4	RAB11A
8.18E-118	0.33748444	0.346	0.051	1.52E-113	4	SULF2
1.56E-117	0.337130318	0.468	0.117	2.92E-113	4	SSBP2
5.91E-117	0.46767137	0.99	0.821	1.10E-112	4	PFN1
1.64E-116	0.444699081	0.813	0.411	3.05E-112	4	R3HDM4
1.65E-116	0.457587257	0.811	0.429	3.07E-112	4	DAD1
3.67E-116	0.319881827	0.626	0.248	6.83E-112	4	MGAT1
6.64E-116	0.421463302	0.686	0.286	1.24E-111	4	SPI1
2.72E-115	0.361438403	0.762	0.391	5.07E-111	4	ARPC5
3.31E-115	0.40472218	0.838	0.474	6.18E-111	4	COX5A
4.19E-115	0.374023759	0.739	0.346	7.81E-111	4	FLOT2
5.85E-115	0.386128806	0.772	0.378	1.09E-110	4	DDOST
7.27E-115	0.377634646	0.587	0.211	1.35E-110	4	ELOVL1
8.19E-115	0.383448129	0.461	0.107	1.53E-110	4	HIVEP3
1.33E-114	0.314409539	0.682	0.277	2.48E-110	4	FGD2
8.87E-113	0.486236537	0.894	0.529	1.65E-108	4	PSMA7
8.59E-112	0.397665365	0.277	0.026	1.60E-107	4	CCDC171
1.32E-111	0.353948444	0.446	0.116	2.45E-107	4	PLBD1
3.89E-111	0.318603594	0.399	0.092	7.26E-107	4	IL6R
5.53E-111	0.417141238	0.616	0.248	1.03E-106	4	PIGR

1.34E-110	0.296140685	0.931	0.602	2.49E-106	4	NEAT1
1.35E-110	0.471300457	0.869	0.501	2.52E-106	4	PDLIM1
6.86E-109	0.320215206	0.581	0.238	1.28E-104	4	MYO1G
4.02E-108	0.33935456	0.655	0.285	7.48E-104	4	DCTN2
6.32E-108	0.318385446	0.646	0.256	1.18E-103	4	PCMT1
1.03E-107	0.377822853	0.763	0.37	1.92E-103	4	PRDX5
3.16E-107	0.32886191	0.653	0.273	5.89E-103	4	TPP1
3.56E-107	0.406146441	0.647	0.268	6.64E-103	4	PIK3AP1
4.39E-107	0.549595585	0.883	0.537	8.19E-103	4	TPI1
4.25E-106	0.408959088	0.642	0.252	7.93E-102	4	GBP2
1.15E-105	0.363798715	0.687	0.282	2.15E-101	4	MVP
1.23E-105	0.441201765	0.968	0.696	2.30E-101	4	CALM2
2.16E-105	0.319982922	0.465	0.134	4.03E-101	4	WSB2
1.39E-104	0.413527339	0.79	0.383	2.60E-100	4	ANXA5
4.73E-104	0.388076547	0.83	0.463	8.81E-100	4	ALDOA
1.65E-103	0.301449483	0.516	0.196	3.08E-99	4	ITPA
5.80E-103	0.305657337	0.359	0.064	1.08E-98	4	BCAR3
2.47E-102	0.319885358	0.545	0.181	4.60E-98	4	ORMDL2
2.92E-102	0.342648559	0.69	0.296	5.44E-98	4	ESYT1
2.94E-102	0.326193906	0.614	0.226	5.49E-98	4	HMOX2
2.95E-102	0.377567225	0.942	0.614	5.50E-98	4	CD44
4.33E-102	0.560217426	0.908	0.567	8.08E-98	4	CYB561A3
6.35E-102	0.293374127	0.479	0.142	1.18E-97	4	DCTPP1
7.64E-101	0.339453947	0.541	0.191	1.42E-96	4	LYSMD2
1.17E-100	0.385180942	0.75	0.379	2.17E-96	4	RGS10
1.97E-100	0.41955601	0.638	0.254	3.67E-96	4	PFKP
2.84E-100	0.308486935	0.617	0.244	5.29E-96	4	MYO1E
2.89E-100	0.574831461	0.965	0.775	5.39E-96	4	PPDPF
3.56E-100	0.797792747	0.829	0.553	6.64E-96	4	FLNA
1.98E-99	0.313577454	0.575	0.214	3.68E-95	4	HSBP1
2.11E-99	0.347732129	0.661	0.284	3.93E-95	4	NAPSA
2.85E-99	0.460614151	0.275	0.028	5.31E-95	4	AL353708.3
6.19E-99	0.297478298	0.639	0.281	1.15E-94	4	MAP4
2.90E-98	0.302743813	0.657	0.286	5.41E-94	4	LINC01480
3.11E-98	0.45202847	0.987	0.787	5.80E-94	4	TAGLN2
5.47E-98	0.371202711	0.524	0.187	1.02E-93	4	ADAM8
1.39E-97	0.422013457	0.792	0.415	2.59E-93	4	AP2M1
1.66E-97	0.373305916	0.923	0.619	3.10E-93	4	COX6C
2.83E-96	0.422987604	0.814	0.439	5.28E-92	4	CAPG
3.75E-96	0.386272283	0.908	0.604	6.99E-92	4	CNN2
1.02E-95	0.37860993	0.655	0.311	1.90E-91	4	FKBP1A
2.09E-95	0.314065555	0.774	0.393	3.89E-91	4	CLTA
2.37E-95	0.357147588	0.557	0.197	4.42E-91	4	FERMT3
5.96E-95	0.346144771	0.561	0.205	1.11E-90	4	PYCARD
1.08E-94	0.728271407	0.551	0.27	2.01E-90	4	HLA-DQA2
4.04E-94	0.44568192	0.893	0.557	7.52E-90	4	CD27

5.33E-94	0.257264708	0.512	0.196	9.93E-90	4	DECR1
7.67E-94	0.304061815	0.872	0.519	1.43E-89	4	LRMP
1.98E-93	0.426571948	0.577	0.24	3.69E-89	4	RUNX3
3.65E-93	0.380365964	0.641	0.263	6.79E-89	4	LSM10
5.08E-93	0.306062733	0.445	0.126	9.47E-89	4	BMP2K
1.28E-92	0.398567208	0.751	0.381	2.39E-88	4	DYNLRB1
1.76E-92	0.308321928	0.744	0.37	3.28E-88	4	ADRM1
3.72E-92	0.288486885	0.538	0.203	6.94E-88	4	CCDC107
4.69E-92	0.264709178	0.354	0.083	8.74E-88	4	SYT17
6.93E-92	0.4395625	0.651	0.303	1.29E-87	4	CD40
8.93E-92	0.289988955	0.519	0.196	1.67E-87	4	ITGB1BP1
1.02E-91	0.513770594	0.519	0.187	1.91E-87	4	PTGER4
1.15E-91	0.295960243	0.619	0.259	2.14E-87	4	NDUFAB1
2.35E-91	0.305307808	0.757	0.385	4.39E-87	4	BCAP31
5.12E-91	0.272867706	0.705	0.341	9.54E-87	4	REEP5
7.47E-91	0.728824185	0.648	0.314	1.39E-86	4	MIR155HG
1.92E-90	0.36288907	0.827	0.457	3.58E-86	4	ARF5
2.24E-90	0.4943958	0.444	0.14	4.17E-86	4	SEMA7A
2.73E-90	0.307702933	0.445	0.153	5.10E-86	4	SLC10A3
4.63E-90	0.575254801	0.237	0.028	8.62E-86	4	IL4I1
1.00E-89	0.285841461	0.528	0.208	1.87E-85	4	IAH1
1.07E-89	0.383666294	0.797	0.425	1.99E-85	4	PSMB3
1.11E-89	0.414881273	0.887	0.575	2.06E-85	4	GPSM3
4.60E-89	0.273207947	0.305	0.054	8.58E-85	4	DOK2
1.27E-88	0.271904842	0.322	0.064	2.37E-84	4	GYS1
1.97E-88	0.337688714	0.239	0.024	3.66E-84	4	RGS7
2.12E-88	0.592993839	0.488	0.194	3.95E-84	4	CD72
4.17E-88	0.296243421	0.399	0.126	7.77E-84	4	ACAT2
1.50E-87	0.344368075	0.758	0.42	2.79E-83	4	SMIM14
1.99E-87	0.253806146	0.48	0.176	3.72E-83	4	TNIP2
8.67E-87	0.347001774	0.882	0.574	1.62E-82	4	SSR4
4.37E-86	0.29674859	0.457	0.153	8.15E-82	4	SLC35B2
4.65E-86	0.380139224	0.787	0.429	8.67E-82	4	NDUFB2
5.46E-86	0.382708053	0.26	0.025	1.02E-81	4	PLD4
1.34E-85	0.320006724	0.568	0.214	2.50E-81	4	SREBF2
1.88E-85	0.297018637	0.573	0.224	3.51E-81	4	C11orf24
2.46E-85	0.430415464	0.578	0.223	4.59E-81	4	TMBIM1
4.71E-85	0.426812713	0.742	0.379	8.77E-81	4	LIMS1
4.83E-85	0.706432359	0.567	0.318	8.99E-81	4	S100A11
5.70E-85	0.309970233	0.459	0.132	1.06E-80	4	PRDX3
1.35E-84	0.253683947	0.519	0.2	2.52E-80	4	CLIC4
2.46E-84	0.344625203	0.713	0.367	4.58E-80	4	TAP1
2.46E-84	0.27262537	0.638	0.279	4.59E-80	4	CDC42EP3
5.37E-84	0.647624207	0.801	0.451	1.00E-79	4	CD24
6.28E-84	0.2646624	0.21	0.01	1.17E-79	4	RSPO1
1.85E-83	0.309094223	0.734	0.381	3.45E-79	4	CCT3

1.95E-83	0.275351371	0.61	0.281	3.63E-79	4	BAX
2.08E-83	0.395914319	0.887	0.543	3.89E-79	4	DYNLL1
2.10E-83	0.297206416	0.411	0.119	3.92E-79	4	PARVB
2.43E-83	0.331210454	0.666	0.324	4.53E-79	4	TALDO1
3.11E-83	0.291594554	0.611	0.273	5.80E-79	4	SIDT2
7.10E-83	0.263129972	0.58	0.26	1.32E-78	4	PDCD5
1.30E-82	0.267692015	0.752	0.406	2.43E-78	4	GNAI2
1.35E-82	0.324751897	0.696	0.346	2.52E-78	4	CORO1B
1.67E-82	0.346983919	0.671	0.335	3.12E-78	4	CDK2AP2
2.84E-82	0.37155337	0.913	0.555	5.29E-78	4	PRDX1
3.95E-82	0.263032418	0.509	0.203	7.36E-78	4	CAPNS1
7.32E-82	0.264287545	0.3	0.06	1.37E-77	4	WNT3
7.51E-82	0.251484323	0.484	0.166	1.40E-77	4	CD58
1.01E-81	0.285091118	0.627	0.288	1.89E-77	4	PSMA4
1.12E-81	0.325344562	0.762	0.386	2.08E-77	4	LDHA
1.65E-81	0.382381172	0.198	0.01	3.07E-77	4	UCHL1
2.41E-81	0.673904752	0.307	0.06	4.49E-77	4	CCL4
2.54E-81	0.256539974	0.485	0.166	4.74E-77	4	RGS14
2.74E-81	0.358960512	0.976	0.745	5.10E-77	4	CYBA
3.15E-81	0.356152064	0.8	0.424	5.87E-77	4	ATP5MD
1.45E-80	0.364802524	0.888	0.559	2.71E-76	4	SNX3
1.58E-80	0.303138715	0.676	0.301	2.95E-76	4	VDAC1
2.19E-80	0.281432247	0.221	0.018	4.08E-76	4	FAM129A
2.54E-80	0.3622603	0.829	0.478	4.74E-76	4	ENO1
3.25E-80	0.316962524	0.491	0.167	6.05E-76	4	ICAM2
1.23E-79	0.266069874	0.511	0.191	2.29E-75	4	C4orf48
1.40E-79	0.277217843	0.877	0.536	2.62E-75	4	ACTR3
1.67E-79	0.274562744	0.624	0.28	3.11E-75	4	NDUFA12
2.93E-79	0.37186083	0.674	0.333	5.47E-75	4	FDFT1
3.66E-79	0.281181906	0.832	0.464	6.82E-75	4	KRAS
4.45E-79	0.339131387	0.753	0.41	8.29E-75	4	ATOX1
5.40E-79	0.278982699	0.614	0.273	1.01E-74	4	PSMB2
7.91E-79	0.306467092	0.893	0.546	1.47E-74	4	ATP6V0E1
2.29E-78	0.294153126	0.751	0.391	4.27E-74	4	NPC2
9.76E-78	0.2698542	0.696	0.347	1.82E-73	4	ATP5PD
1.79E-77	0.32335078	0.988	0.811	3.34E-73	4	ARPC3
5.10E-77	0.279993764	0.568	0.25	9.51E-73	4	FLOT1
7.23E-77	0.298226465	0.866	0.511	1.35E-72	4	HNRNPF
7.35E-77	0.359319174	0.378	0.138	1.37E-72	4	CD68
9.46E-77	0.30571865	0.375	0.111	1.76E-72	4	MSMO1
2.36E-76	0.362134864	0.403	0.136	4.40E-72	4	BBC3
2.81E-76	0.6238953	0.272	0.053	5.23E-72	4	AQP3
3.99E-76	0.324161364	0.612	0.278	7.44E-72	4	RHOF
5.11E-76	0.278111277	0.675	0.33	9.53E-72	4	FMNL1
8.00E-76	0.309858782	0.985	0.818	1.49E-71	4	LIMD2
1.12E-75	0.322989077	0.6	0.257	2.08E-71	4	SCIMP

1.19E-75	0.310618056	0.149	0.003	2.23E-71	4	POSTN
1.64E-75	0.259535554	0.797	0.457	3.05E-71	4	CAPZB
2.05E-75	0.299804214	0.606	0.279	3.82E-71	4	EIF6
1.50E-74	0.251795134	0.783	0.441	2.80E-70	4	COPE
3.46E-74	0.497139408	0.549	0.256	6.44E-70	4	GRHPR
9.66E-74	0.37204383	0.7	0.361	1.80E-69	4	CD5
1.11E-72	0.287493125	0.943	0.652	2.06E-68	4	TRIR
4.77E-72	0.361023797	0.498	0.182	8.88E-68	4	SQLE
7.00E-72	0.306698995	0.617	0.297	1.31E-67	4	MIEN1
7.37E-72	0.260472211	0.497	0.194	1.37E-67	4	KRCC1
9.19E-72	0.261543133	0.804	0.47	1.71E-67	4	PRELID1
1.28E-71	0.467263447	0.68	0.394	2.38E-67	4	TSPO
1.38E-71	0.268441243	0.717	0.356	2.57E-67	4	SHMT2
2.81E-71	0.254678319	0.897	0.593	5.23E-67	4	TSTD1
3.08E-71	0.320470508	0.599	0.282	5.73E-67	4	H1FX
1.18E-70	0.252353819	0.67	0.302	2.21E-66	4	UBE2A
1.75E-70	0.306353368	0.74	0.407	3.27E-66	4	POMP
3.10E-70	0.288532304	0.713	0.356	5.79E-66	4	CCT6A
2.72E-69	0.325755493	0.906	0.583	5.07E-65	4	ARHGDIA
5.89E-69	0.281615486	0.581	0.267	1.10E-64	4	NFATC2
7.28E-69	0.28307683	0.86	0.512	1.36E-64	4	GABARAPL2
1.68E-68	0.25928447	0.526	0.217	3.13E-64	4	TKT
4.45E-68	0.273393397	0.803	0.477	8.30E-64	4	HLA-F
1.45E-67	0.289838232	0.406	0.141	2.71E-63	4	VSIR
1.46E-67	0.303973289	0.924	0.645	2.73E-63	4	UQCRH
1.74E-67	0.35168402	0.781	0.458	3.25E-63	4	EMD
2.78E-67	0.28157819	0.231	0.05	5.17E-63	4	RASSF6
2.90E-67	0.290786775	0.161	0.004	5.40E-63	4	CAVIN1
2.90E-67	0.253779013	0.865	0.558	5.40E-63	4	PSAP
5.37E-67	0.261907538	0.47	0.194	1.00E-62	4	GRK6
7.06E-67	0.329639105	0.315	0.076	1.32E-62	4	BID
1.38E-66	0.251928003	0.702	0.366	2.57E-62	4	ITGB7
2.89E-66	0.292419707	0.847	0.517	5.39E-62	4	TRMT112
4.41E-66	0.274985398	0.896	0.607	8.21E-62	4	UBL5
4.46E-66	0.259968885	0.851	0.527	8.31E-62	4	PSMB1
6.85E-65	0.379674712	0.607	0.295	1.28E-60	4	ZBTB32
1.46E-64	0.261391404	0.633	0.311	2.73E-60	4	PDIA6
7.14E-64	0.279966218	0.554	0.26	1.33E-59	4	BST2
9.10E-64	0.318335623	0.668	0.367	1.70E-59	4	PSME2
2.59E-63	0.262856671	0.688	0.351	4.82E-59	4	NDUFB10
3.53E-63	0.290433555	0.842	0.505	6.58E-59	4	RELB
6.98E-63	0.345585894	0.909	0.622	1.30E-58	4	NOSIP
1.66E-62	0.270041609	0.329	0.1	3.10E-58	4	RNASE6
3.97E-62	0.292842965	0.626	0.318	7.39E-58	4	NCF4
6.89E-62	0.297444069	0.903	0.601	1.28E-57	4	SLC25A5
1.86E-61	0.258092354	0.17	0.015	3.48E-57	4	ACY3

2.84E-61	0.274419753	0.746	0.383	5.29E-57	4	MAT2B
7.85E-59	0.273306319	0.762	0.443	1.46E-54	4	ATP5MF
4.82E-58	0.30155295	0.577	0.29	8.99E-54	4	ACP5
8.97E-58	0.254072468	0.662	0.354	1.67E-53	4	TRAF4
1.28E-57	0.484190665	0.539	0.277	2.39E-53	4	BHLHE40
2.52E-57	0.251919835	0.41	0.17	4.70E-53	4	SLC7A7
1.95E-56	0.297276105	0.454	0.183	3.63E-52	4	IRF4
2.69E-56	0.274184303	0.828	0.524	5.02E-52	4	PARK7
1.65E-55	0.266590082	0.559	0.264	3.08E-51	4	MARCKSL1
4.11E-55	0.291760387	0.237	0.057	7.65E-51	4	BIK
4.30E-55	0.272105611	0.563	0.291	8.01E-51	4	ATF5
2.03E-54	0.296934483	0.948	0.707	3.79E-50	4	MIF
2.28E-54	0.254922047	0.931	0.687	4.25E-50	4	UBE2D2
2.52E-53	0.254667593	0.977	0.782	4.69E-49	4	YBX1
5.64E-53	0.366000003	0.743	0.484	1.05E-48	4	MS4A1
9.66E-51	0.268439982	0.76	0.472	1.80E-46	4	PSMB9
3.63E-49	0.283655677	0.989	0.874	6.76E-45	4	HLA-DQA1
3.63E-48	0.843427214	0.636	0.468	6.76E-44	4	TCL1A
4.34E-46	0.273595142	0.726	0.409	8.09E-42	4	ATP5PF
1.08E-44	0.302484059	0.786	0.543	2.02E-40	4	FCRLA
1.99E-44	0.269688255	0.92	0.66	3.71E-40	4	TUBA1B
6.68E-42	0.292954485	0.554	0.312	1.24E-37	4	RAB29
1.69E-40	0.300021805	0.271	0.089	3.15E-36	4	CD9
2.54E-39	0.299933813	0.149	0.024	4.74E-35	4	CD1C
1.50E-36	0.620202892	0.667	0.514	2.80E-32	4	S100A10
2.00E-36	0.436365883	0.752	0.527	3.73E-32	4	IDS
8.20E-238	0.890681433	0.999	0.87	1.53E-233	5	EZR
1.94E-182	0.62250741	0.994	0.788	3.61E-178	5	TAGLN2
5.94E-151	0.563205349	0.713	0.263	1.11E-146	5	ARID5A
1.07E-146	0.771103526	0.937	0.679	1.99E-142	5	LITAF
5.83E-140	0.908954586	0.913	0.666	1.09E-135	5	EMP3
5.13E-138	0.594885851	0.66	0.249	9.56E-134	5	CYSTM1
9.91E-135	0.604371859	0.786	0.423	1.85E-130	5	MBP
7.97E-134	0.631580733	0.807	0.443	1.48E-129	5	TPM4
1.45E-130	0.526965766	0.964	0.698	2.71E-126	5	CALM2
1.09E-127	0.506168875	0.719	0.324	2.04E-123	5	ACSM3
6.33E-127	0.699432535	0.936	0.696	1.18E-122	5	SRGN
8.55E-126	0.468648231	0.987	0.832	1.59E-121	5	CALM1
8.31E-125	0.66635415	0.886	0.603	1.55E-120	5	LRRFIP1
1.30E-124	0.459517918	0.926	0.585	2.41E-120	5	ID3
1.37E-123	0.451192811	0.921	0.617	2.55E-119	5	CD44
1.37E-122	0.47588453	0.643	0.244	2.55E-118	5	SKIL
2.15E-120	0.320130403	0.993	0.798	4.00E-116	5	CXCR4
8.93E-118	0.42149297	0.72	0.361	1.66E-113	5	TGIF1
3.01E-117	0.491793767	0.843	0.514	5.62E-113	5	NR3C1
8.64E-117	0.344628134	0.858	0.444	1.61E-112	5	LMNA

8.25E-113	0.516328075	0.684	0.321	1.54E-108	5	SLBP
1.02E-111	0.808711518	0.472	0.156	1.89E-107	5	NMB
1.40E-109	0.504871261	0.906	0.583	2.61E-105	5	SPOCK2
2.93E-109	0.474741003	0.871	0.519	5.46E-105	5	IDS
2.71E-106	0.644867188	0.645	0.288	5.04E-102	5	CREM
9.04E-106	0.448194108	0.737	0.371	1.69E-101	5	SYAP1
2.79E-104	0.480453149	0.76	0.402	5.20E-100	5	PIM1
9.89E-102	0.43722684	0.691	0.317	1.84E-97	5	FYTTD1
1.62E-100	0.597532761	0.766	0.485	3.03E-96	5	TESC
1.77E-100	0.458656176	0.482	0.159	3.30E-96	5	CXCL16
2.33E-100	0.308329909	0.685	0.331	4.34E-96	5	GNB5
1.37E-98	0.276894625	0.695	0.339	2.56E-94	5	KDM6B
2.00E-98	0.320130147	0.968	0.663	3.74E-94	5	CD55
8.53E-98	0.37506118	0.426	0.119	1.59E-93	5	GABARAPL1
4.04E-96	0.457583326	0.807	0.481	7.53E-92	5	EHMT1
1.65E-95	0.439634451	0.879	0.57	3.08E-91	5	CYTIP
8.73E-92	0.427777965	0.521	0.199	1.63E-87	5	LSR
2.34E-91	0.349642336	0.621	0.258	4.36E-87	5	GLUL
4.60E-91	0.3946014	0.844	0.552	8.57E-87	5	GNG2
1.60E-89	0.534639454	0.706	0.376	2.99E-85	5	TMEM123
1.85E-88	0.554748403	0.797	0.512	3.46E-84	5	ANXA2
4.34E-87	0.272769373	0.432	0.158	8.09E-83	5	RFTN1
2.84E-84	0.548570131	0.77	0.483	5.29E-80	5	TNFRSF1B
1.38E-83	0.317922105	0.729	0.418	2.57E-79	5	LAPTM4A
4.33E-83	0.402003016	0.452	0.157	8.06E-79	5	PPFIBP2
6.83E-83	0.323690928	0.923	0.646	1.27E-78	5	MYL12B
1.11E-82	0.293201816	0.791	0.503	2.08E-78	5	PAIP2
9.15E-82	0.335637556	0.834	0.515	1.71E-77	5	HNRNPF
1.05E-81	0.412226183	0.989	0.856	1.95E-77	5	UCP2
1.33E-81	0.366636252	0.798	0.5	2.48E-77	5	EIF3A
6.92E-81	0.303638485	0.446	0.153	1.29E-76	5	GPR132
1.60E-79	0.384656022	0.734	0.419	2.97E-75	5	R3HDM4
3.58E-79	0.338742547	0.651	0.338	6.67E-75	5	TRABD
4.99E-79	0.365100301	0.477	0.193	9.31E-75	5	ST14
5.03E-79	0.542540054	0.919	0.713	9.37E-75	5	SAT1
3.15E-78	0.294008387	0.519	0.226	5.86E-74	5	CRLF3
2.64E-77	0.339783422	0.493	0.204	4.92E-73	5	SLC16A3
6.39E-77	0.33817377	0.865	0.558	1.19E-72	5	UBE2B
7.88E-77	0.562506585	0.539	0.244	1.47E-72	5	SESN3
1.05E-76	0.434069748	0.807	0.501	1.96E-72	5	CRIP1
2.04E-76	0.420042839	0.673	0.371	3.80E-72	5	RIPOR1
2.32E-76	0.495304119	0.803	0.515	4.33E-72	5	GGA2
3.13E-76	0.257310719	0.626	0.339	5.84E-72	5	CKAP4
2.24E-74	0.382866254	0.71	0.382	4.18E-70	5	COL9A3
1.11E-73	0.718743676	0.572	0.318	2.08E-69	5	S100A11
1.82E-73	0.355124924	0.829	0.485	3.39E-69	5	RGCC

3.56E-73	0.354258022	0.405	0.123	6.63E-69	5	SAMSN1
4.22E-73	0.404280804	0.673	0.365	7.87E-69	5	CD5
1.01E-72	0.322651832	0.784	0.472	1.87E-68	5	PRKAR1A
3.56E-72	0.397457965	0.977	0.81	6.63E-68	5	RHOA
5.61E-72	0.407302245	0.44	0.157	1.05E-67	5	ARID3A
2.28E-71	0.393360762	0.668	0.403	4.25E-67	5	TGFB1
1.66E-69	0.262217365	0.551	0.29	3.10E-65	5	MAD1L1
2.72E-69	0.273073581	0.567	0.27	5.06E-65	5	SIPA1L1
4.54E-69	0.389818826	0.925	0.723	8.47E-65	5	ZFP36L2
2.54E-68	0.329377639	0.802	0.49	4.73E-64	5	MAPK1IP1L
3.68E-68	0.330166327	0.481	0.208	6.87E-64	5	PRNP
3.78E-67	0.293802286	0.874	0.6	7.05E-63	5	SRSF2
2.24E-66	0.266222951	0.388	0.139	4.17E-62	5	SLCO4A1
4.76E-66	0.252686763	0.659	0.376	8.87E-62	5	PAFAH1B1
1.01E-65	0.320195602	0.687	0.385	1.88E-61	5	ANKRD11
1.23E-65	0.301988594	0.995	0.89	2.29E-61	5	RPS20
1.57E-65	0.310624778	0.643	0.359	2.92E-61	5	RHOG
1.89E-65	0.293107502	0.94	0.708	3.53E-61	5	SLC25A3
2.03E-65	0.273603882	0.342	0.118	3.79E-61	5	INSIG2
7.55E-65	0.377349385	0.297	0.086	1.41E-60	5	LGALS3
3.21E-64	0.270404523	0.563	0.276	5.99E-60	5	GNA13
5.62E-64	0.315070297	0.447	0.19	1.05E-59	5	PRKAR2A
3.07E-63	0.368271595	0.574	0.304	5.72E-59	5	YWHAH
4.43E-63	0.316551342	0.97	0.791	8.26E-59	5	SARAF
1.39E-62	0.43265552	0.45	0.192	2.60E-58	5	SH3TC1
1.50E-62	0.266346853	0.637	0.346	2.80E-58	5	DNAJA2
1.84E-62	0.287599438	0.733	0.42	3.42E-58	5	ADGRE5
3.53E-62	0.311902895	0.563	0.289	6.58E-58	5	RAB31
3.91E-62	0.326673454	0.637	0.327	7.28E-58	5	TMX4
2.39E-61	0.274079511	0.878	0.614	4.46E-57	5	ATP5F1B
2.94E-61	0.256792547	0.63	0.342	5.48E-57	5	SBNO1
7.00E-61	0.642820877	0.971	0.846	1.31E-56	5	ACTG1
1.90E-60	0.294298695	0.454	0.197	3.54E-56	5	NDRG1
1.93E-60	0.370973205	0.393	0.142	3.59E-56	5	DUSP4
2.45E-60	0.254291029	0.568	0.276	4.57E-56	5	BHLHE40
2.80E-60	0.271153978	0.782	0.481	5.21E-56	5	RAP1B
9.74E-60	0.431426042	0.705	0.449	1.82E-55	5	IL16
1.23E-59	0.309415987	0.832	0.545	2.30E-55	5	DDX21
1.42E-59	0.278525864	0.485	0.231	2.64E-55	5	TMBIM1
4.67E-59	0.267235855	0.648	0.357	8.71E-55	5	SEC14L1
8.24E-58	0.301566678	0.611	0.349	1.54E-53	5	TMEM154
1.13E-57	0.277872767	0.662	0.348	2.10E-53	5	NFE2L2
2.38E-57	0.31324401	0.776	0.51	4.43E-53	5	PDLIM1
4.87E-57	0.284303012	0.684	0.411	9.08E-53	5	LY9
7.55E-57	0.298710883	0.484	0.219	1.41E-52	5	SGTA
9.44E-57	0.279504719	0.756	0.462	1.76E-52	5	EMD

4.23E-56	0.271303889	0.995	0.877	7.88E-52	5	COX4I1
4.34E-56	0.342013317	0.536	0.285	8.08E-52	5	RHOF
4.91E-56	0.286030921	0.634	0.353	9.16E-52	5	KDM4B
1.14E-55	0.400494608	0.538	0.281	2.12E-51	5	HMOX1
1.79E-54	0.264572116	0.602	0.345	3.34E-50	5	SPIB
2.38E-53	0.292359119	0.565	0.295	4.44E-49	5	MAP2K3
3.39E-52	0.265565773	0.643	0.368	6.32E-48	5	YWHAE
5.25E-52	0.2588815	0.358	0.139	9.79E-48	5	TES
9.14E-52	0.278159796	0.731	0.458	1.70E-47	5	RNF41
3.70E-51	0.258330211	0.354	0.148	6.90E-47	5	SEMA7A
2.78E-50	0.499738722	0.742	0.509	5.17E-46	5	S100A10
3.48E-50	0.259695997	0.825	0.55	6.48E-46	5	DYNLL1
9.14E-50	0.338258352	0.596	0.348	1.70E-45	5	IGFBP4
3.69E-49	0.291704045	0.782	0.515	6.87E-45	5	CIB1
1.57E-46	0.25349397	0.695	0.421	2.93E-42	5	GNB2
2.44E-45	0.271613423	0.552	0.339	4.55E-41	5	PLEC
3.52E-44	0.25304066	0.478	0.243	6.57E-40	5	BACE2
1.02E-43	0.276163812	0.642	0.39	1.90E-39	5	PBXIP1
1.45E-41	0.272748509	0.394	0.168	2.70E-37	5	S1PR1
3.73E-41	0.300113527	0.582	0.364	6.95E-37	5	VASP
1.31E-35	0.360751832	0.498	0.297	2.44E-31	5	ACP5
1.42E-20	0.298879501	0.297	0.182	2.64E-16	5	SFTPB
0	1.888920563	0.987	0.526	0	6	FOS
0	1.715075873	0.848	0.27	0	6	DNAJB1
0	1.635067878	0.837	0.186	0	6	EGR1
0	1.62096201	0.989	0.655	0	6	CD69
0	1.530949204	0.987	0.706	0	6	DUSP1
0	1.46752898	0.996	0.662	0	6	PPP1R15A
0	1.420406355	0.992	0.836	0	6	HSP90AA1
0	1.368760352	0.989	0.512	0	6	FOSB
0	1.346080375	0.989	0.727	0	6	JUN
0	1.336894912	0.996	0.844	0	6	KLF6
0	1.12384313	0.852	0.323	0	6	DDIT3
0	1.106547831	0.951	0.536	0	6	DNAJA1
1.28E-293	1.273199563	0.894	0.363	2.38E-289	6	NR4A1
5.76E-293	1.109852995	0.988	0.658	1.07E-288	6	CD83
7.26E-264	1.150768614	0.997	0.836	1.35E-259	6	ZFP36
4.98E-231	1.067330081	0.929	0.494	9.28E-227	6	NR4A2
2.33E-220	0.85484112	0.888	0.52	4.34E-216	6	RSRC2
1.33E-219	0.793348765	0.964	0.749	2.48E-215	6	SRSF7
5.61E-218	0.824585939	0.935	0.634	1.04E-213	6	TRA2B
2.57E-216	1.038751433	0.927	0.581	4.79E-212	6	IER2
3.05E-214	0.939855197	0.964	0.773	5.69E-210	6	HSPA8
6.54E-198	0.759088089	0.942	0.668	1.22E-193	6	BRD2
8.59E-195	0.769618712	0.991	0.867	1.60E-190	6	HSP90AB1
6.51E-190	0.669419144	0.945	0.64	1.21E-185	6	CCNL1

5.85E-186	1.022241957	0.941	0.654	1.09E-181	6	NFKBIA
1.24E-181	0.686056246	0.949	0.704	2.31E-177	6	EIF5
4.93E-180	0.666911957	0.796	0.39	9.19E-176	6	GTF2B
2.18E-178	0.791721742	0.993	0.817	4.06E-174	6	JUNB
5.91E-176	0.766317765	0.902	0.597	1.10E-171	6	SRSF3
4.68E-171	0.775943916	0.807	0.383	8.72E-167	6	CSRNP1
1.65E-166	0.977197069	0.656	0.248	3.07E-162	6	NEU1
3.43E-164	0.647286247	0.709	0.283	6.40E-160	6	SERTAD1
1.33E-163	0.70840701	0.973	0.716	2.48E-159	6	YPEL5
2.21E-159	1.190787492	0.847	0.524	4.13E-155	6	DUSP2
3.38E-152	0.647787781	0.419	0.074	6.30E-148	6	EGR2
1.96E-151	0.848990892	0.92	0.598	3.66E-147	6	TAGAP
1.33E-148	0.587597938	0.598	0.22	2.47E-144	6	DEDD2
1.33E-146	0.621490178	0.876	0.529	2.49E-142	6	NFKBID
2.62E-146	0.91858968	0.874	0.552	4.88E-142	6	IRF1
2.02E-145	0.600106252	0.947	0.734	3.76E-141	6	ZFAS1
1.44E-140	0.597818972	0.671	0.306	2.69E-136	6	HSPH1
2.91E-140	1.723417858	0.547	0.186	5.42E-136	6	HSPA1B
4.63E-132	0.906971877	0.74	0.394	8.64E-128	6	KLF2
4.32E-131	0.527825561	0.834	0.488	8.06E-127	6	SBDS
1.47E-130	0.721261113	0.517	0.189	2.75E-126	6	GLA
5.30E-128	0.568114383	0.834	0.511	9.88E-124	6	RPL22L1
2.73E-127	0.493145272	0.714	0.339	5.08E-123	6	HBP1
2.20E-125	0.602129028	0.508	0.169	4.11E-121	6	CKS2
2.98E-123	0.87294196	0.886	0.615	5.55E-119	6	PMAIP1
3.06E-123	0.801316185	0.515	0.168	5.71E-119	6	KLF4
1.81E-122	0.659156461	0.672	0.296	3.37E-118	6	RASGEF1B
1.51E-121	0.431933749	0.781	0.414	2.81E-117	6	CLK1
2.25E-120	0.581470764	0.932	0.717	4.19E-116	6	EIF4A2
5.13E-120	0.872106377	0.648	0.285	9.56E-116	6	NFKBIZ
1.42E-119	0.538713003	0.825	0.504	2.66E-115	6	CYCS
8.16E-118	0.44642907	0.632	0.294	1.52E-113	6	OSER1
1.71E-113	0.439080424	0.648	0.322	3.19E-109	6	ZFAND5
1.94E-113	0.880089632	0.776	0.424	3.61E-109	6	KLF10
3.10E-110	0.543115872	0.595	0.263	5.78E-106	6	ARL4A
1.21E-108	0.474764856	0.44	0.118	2.25E-104	6	DNAJB4
4.50E-108	0.622932325	0.876	0.59	8.39E-104	6	PIM2
5.44E-108	0.52322314	0.842	0.534	1.01E-103	6	PELI1
1.04E-106	0.62570869	0.489	0.17	1.94E-102	6	DUSP10
1.38E-106	0.429714852	0.644	0.286	2.58E-102	6	AC020916.1
3.28E-106	1.758321702	0.444	0.154	6.11E-102	6	HSPA1A
1.21E-105	0.549546129	0.566	0.232	2.26E-101	6	ZC3H12A
6.55E-103	0.49723097	0.979	0.873	1.22E-98	6	TSC22D3
8.70E-103	0.823541189	0.764	0.428	1.62E-98	6	RGS2
9.56E-103	0.444487089	0.466	0.157	1.78E-98	6	UBE2S
2.85E-100	0.553458758	0.912	0.671	5.31E-96	6	ATP6V0C

2.73E-99	0.345542349	0.88	0.622	5.10E-95	6	DDX3X
3.39E-99	0.468573642	0.902	0.641	6.31E-95	6	TUBA1A
4.57E-99	0.354983648	0.486	0.17	8.52E-95	6	ZBTB10
4.18E-98	0.434267132	0.6	0.273	7.80E-94	6	TIPARP
3.04E-97	0.387308919	0.563	0.239	5.67E-93	6	FAM53C
5.46E-95	0.427993634	0.565	0.243	1.02E-90	6	DNAJB9
8.16E-95	0.377717407	0.838	0.578	1.52E-90	6	ELF1
4.45E-94	0.491519636	0.954	0.76	8.30E-90	6	UBB
1.50E-89	0.397529723	0.669	0.377	2.79E-85	6	BUD31
1.26E-86	0.962771842	0.651	0.345	2.34E-82	6	GADD45B
1.40E-85	0.739556903	0.383	0.13	2.60E-81	6	TNF
4.72E-85	0.452921809	0.548	0.247	8.81E-81	6	NR4A3
2.78E-84	0.901994014	0.383	0.127	5.19E-80	6	MYADM
9.05E-84	0.359932627	0.963	0.812	1.69E-79	6	PNRC1
1.01E-83	0.289570659	0.555	0.259	1.87E-79	6	ZNF394
2.16E-83	0.5264364	0.633	0.336	4.03E-79	6	SDCBP
1.20E-82	1.053683919	0.568	0.266	2.23E-78	6	RGS1
1.73E-78	0.400013461	0.373	0.136	3.23E-74	6	NFKBIE
1.59E-77	0.468259122	0.488	0.18	2.96E-73	6	ZFAND2A
5.14E-77	0.477730352	0.723	0.462	9.58E-73	6	RILPL2
3.98E-75	0.335375758	0.493	0.207	7.42E-71	6	PPP1R15B
4.27E-75	0.315956581	0.417	0.169	7.97E-71	6	NRBF2
2.31E-74	0.359755937	0.295	0.068	4.31E-70	6	BAG3
4.69E-74	0.378716453	0.818	0.542	8.74E-70	6	SFPQ
3.95E-73	0.308649141	0.626	0.355	7.36E-69	6	WTAP
6.99E-73	0.420256105	0.429	0.174	1.30E-68	6	IER5
4.63E-72	0.344665741	0.559	0.286	8.62E-68	6	NAMPT
6.88E-70	0.309321614	0.907	0.71	1.28E-65	6	REL
1.37E-68	0.296912409	0.574	0.279	2.55E-64	6	COQ10B
4.05E-68	0.312339274	0.469	0.21	7.55E-64	6	SDE2
1.04E-67	0.455390214	0.969	0.826	1.94E-63	6	BTG2
1.44E-67	0.262483818	0.378	0.145	2.68E-63	6	SLC25A33
5.06E-67	0.268929748	0.576	0.297	9.44E-63	6	CREBRF
1.10E-66	0.273472579	0.628	0.332	2.06E-62	6	IFRD1
1.85E-66	0.360518659	0.673	0.408	3.45E-62	6	AZIN1
2.26E-66	0.339721273	0.483	0.23	4.21E-62	6	AHSA1
2.77E-64	0.343274202	0.726	0.479	5.17E-60	6	SELENOK
1.12E-63	0.362441735	0.729	0.45	2.09E-59	6	AMD1
1.63E-63	0.301507323	0.5	0.246	3.03E-59	6	SNHG15
1.79E-63	0.381002871	0.771	0.508	3.34E-59	6	SNHG8
6.01E-63	0.429418786	0.958	0.814	1.12E-58	6	RHOH
1.41E-62	0.326945664	0.576	0.319	2.63E-58	6	EIF4A3
1.44E-62	0.280084662	0.19	0.028	2.69E-58	6	EGR3
2.38E-62	0.321593501	0.531	0.25	4.44E-58	6	CWC25
3.70E-62	0.331279787	0.594	0.337	6.90E-58	6	PHACTR1
8.09E-61	0.351055442	0.664	0.441	1.51E-56	6	MTRNR2L8

1.04E-60	0.261939611	0.713	0.471	1.94E-56	6	HNRNPH3
2.23E-60	0.267711929	0.352	0.127	4.16E-56	6	ARL5B
7.46E-60	0.377934655	0.745	0.476	1.39E-55	6	TUBB4B
7.71E-60	0.329034096	0.426	0.202	1.44E-55	6	H2AFX
1.62E-58	0.284240421	0.838	0.605	3.02E-54	6	SRSF2
3.81E-58	0.349707334	0.88	0.653	7.10E-54	6	CCR7
4.59E-58	0.283134903	0.653	0.384	8.56E-54	6	DDX39A
6.86E-58	0.458696102	0.711	0.46	1.28E-53	6	HSPE1
1.60E-57	0.306009301	0.654	0.384	2.98E-53	6	TANK
1.29E-56	0.280662042	0.424	0.189	2.40E-52	6	ATG101
1.42E-56	0.253154607	0.809	0.581	2.65E-52	6	RBM8A
1.86E-56	0.889073207	0.338	0.139	3.46E-52	6	ATF3
3.55E-56	0.258863207	0.545	0.295	6.62E-52	6	PPP2CA
7.14E-56	0.364341521	0.376	0.176	1.33E-51	6	MRPL18
3.44E-55	0.342922669	0.682	0.426	6.41E-51	6	ATF4
8.81E-55	0.278382748	0.586	0.343	1.64E-50	6	BCAS2
1.80E-53	0.34319595	0.151	0.024	3.35E-49	6	EGR4
2.19E-52	0.296274615	0.75	0.509	4.09E-48	6	MAP1LC3B
1.54E-51	0.384265198	0.7	0.453	2.87E-47	6	CXCR5
2.07E-51	0.383269706	0.46	0.227	3.86E-47	6	PNP
3.23E-51	0.347576482	0.386	0.159	6.03E-47	6	CITED2
7.15E-50	0.282696444	0.48	0.268	1.33E-45	6	DDX3Y
1.09E-49	0.275799337	0.362	0.16	2.04E-45	6	SERTAD3
5.54E-49	0.399385819	0.536	0.326	1.03E-44	6	MIR155HG
6.11E-49	0.303726704	0.739	0.509	1.14E-44	6	NOP58
6.42E-49	0.327945564	0.53	0.28	1.20E-44	6	PER1
9.47E-49	0.288242941	0.788	0.551	1.77E-44	6	G3BP2
1.45E-48	0.289441042	0.848	0.618	2.70E-44	6	HERPUD1
8.19E-48	0.294062958	0.48	0.24	1.53E-43	6	TNFAIP3
3.61E-47	0.314074446	0.792	0.538	6.72E-43	6	RAB11FIP1
1.21E-46	0.374492015	0.652	0.41	2.26E-42	6	ZNF331
1.48E-45	0.31133629	0.692	0.468	2.76E-41	6	JUND
2.21E-45	0.255838591	0.661	0.426	4.12E-41	6	HSPD1
2.95E-44	0.303847221	0.458	0.238	5.50E-40	6	DNAAF2
3.40E-44	0.250388341	0.191	0.052	6.33E-40	6	RND1
1.94E-43	0.345365248	0.293	0.114	3.61E-39	6	FILIP1L
9.10E-42	0.280451709	0.289	0.111	1.70E-37	6	ANKRD37
1.61E-41	0.559595025	0.403	0.221	3.01E-37	6	CTLA4
3.27E-41	0.336216223	0.659	0.412	6.10E-37	6	RHOB
1.35E-39	0.280827945	0.872	0.675	2.52E-35	6	YBX3
2.90E-38	0.409662419	0.259	0.114	5.40E-34	6	CLEC2B
4.59E-37	0.35418727	0.54	0.3	8.55E-33	6	MAP3K8
1.75E-36	0.276093801	0.505	0.302	3.26E-32	6	PLK3
2.37E-36	0.505699063	0.247	0.104	4.43E-32	6	MYC
3.21E-36	0.285610533	0.601	0.419	5.99E-32	6	LY9
2.69E-34	0.533902511	0.65	0.501	5.01E-30	6	RGCC

3.63E-31	0.268535087	0.364	0.194	6.76E-27	6	GPR18
6.31E-28	0.565175845	0.602	0.417	1.18E-23	6	PIM1
9.15E-28	0.27985505	0.251	0.109	1.71E-23	6	ICAM1
1.61E-26	0.271182353	0.465	0.284	3.00E-22	6	TOR3A
1.86E-13	0.26407233	0.492	0.344	3.46E-09	6	HSPB1
1.17E-92	0.664606351	0.905	0.782	2.18E-88	7	TXNIP
1.85E-78	1.047308646	0.496	0.234	3.45E-74	7	AC007952.4
1.12E-58	0.88992381	0.395	0.205	2.08E-54	7	AC063949.2
6.53E-49	0.617073141	0.516	0.391	1.22E-44	7	TRAF3IP3
1.14E-36	0.699511551	0.593	0.484	2.13E-32	7	IGLL5
9.11E-33	0.636002507	0.209	0.09	1.70E-28	7	LCN8
2.37E-19	0.498386019	0.343	0.24	4.41E-15	7	PCDH9
0	1.366568915	0.968	0.649	0	8	CCR7
0	1.365694829	0.91	0.397	0	8	ZNF331
0	1.206317295	0.978	0.494	0	8	NR4A2
0	1.010423341	0.999	0.801	0	8	CXCR4
1.95E-298	0.961508516	0.993	0.66	3.63E-294	8	CD83
7.52E-289	1.049254407	0.997	0.818	1.40E-284	8	JUNB
2.95E-288	0.983786728	0.987	0.717	5.50E-284	8	YPEL5
1.39E-284	1.117799858	0.891	0.444	2.58E-280	8	CXCR5
9.18E-265	0.782741426	0.983	0.515	1.71E-260	8	FOSB
3.25E-256	0.918863138	0.959	0.655	6.06E-252	8	NFKBIA
3.63E-245	0.903885465	0.763	0.268	6.78E-241	8	PER1
1.48E-230	0.998976342	0.874	0.421	2.75E-226	8	KLF10
1.50E-228	0.925448267	0.897	0.423	2.80E-224	8	RGS2
1.29E-222	0.862051321	0.882	0.431	2.41E-218	8	CDKN1A
9.21E-218	0.983068343	0.936	0.614	1.72E-213	8	HERPUD1
9.64E-216	1.325185665	0.729	0.292	1.80E-211	8	CHMP1B
3.49E-206	0.699605132	0.932	0.551	6.51E-202	8	IRF1
1.62E-204	0.975097875	0.911	0.61	3.02E-200	8	HSP90B1
3.71E-201	0.681706944	0.974	0.668	6.92E-197	8	CD55
9.65E-201	0.814170649	0.931	0.589	1.80E-196	8	PIM2
3.22E-196	0.724864348	0.854	0.473	6.00E-192	8	SELENOK
8.50E-191	0.867840096	0.755	0.355	1.58E-186	8	TRAF4
1.77E-189	0.756353904	0.948	0.598	3.30E-185	8	TAGAP
7.52E-185	0.778558395	0.859	0.486	1.40E-180	8	BIRC3
2.50E-180	0.752170544	0.738	0.347	4.67E-176	8	NUAK2
2.03E-178	0.849089534	0.729	0.238	3.78E-174	8	NR4A3
2.22E-175	0.875338719	0.785	0.373	4.14E-171	8	PIM3
1.10E-174	0.835532816	0.721	0.291	2.05E-170	8	MAP3K8
9.90E-167	0.367576581	0.774	0.34	1.85E-162	8	GADD45B
1.72E-166	0.654638788	0.941	0.71	3.20E-162	8	REL
7.23E-162	0.710232171	0.642	0.232	1.35E-157	8	TNFAIP3
2.46E-158	0.832030254	0.805	0.408	4.58E-154	8	LY9
2.63E-157	0.736441786	0.614	0.212	4.90E-153	8	VPREB3
1.38E-147	0.702343232	0.8	0.375	2.57E-143	8	TENT5C

2.67E-146	0.816412664	0.526	0.141	4.98E-142	8	BCL2A1
9.53E-146	0.735293325	0.652	0.247	1.78E-141	8	SLC2A3
2.41E-144	0.740114751	0.487	0.096	4.49E-140	8	ICAM1
5.43E-144	0.685667939	0.741	0.366	1.01E-139	8	TGIF1
2.80E-137	0.791928377	0.829	0.574	5.22E-133	8	ITM2B
2.29E-136	0.481464683	0.689	0.297	4.27E-132	8	RASGEF1B
1.39E-130	0.531875791	0.872	0.535	2.59E-126	8	RAB11FIP1
4.83E-129	0.602665695	0.696	0.369	9.00E-125	8	FAM177A1
4.46E-128	0.582724396	0.825	0.517	8.31E-124	8	ADTRP
7.65E-125	0.554037947	0.534	0.185	1.43E-120	8	SC5D
1.85E-124	0.570961335	0.638	0.273	3.44E-120	8	TIPARP
3.10E-122	0.569143097	0.692	0.334	5.78E-118	8	NFKB2
5.71E-122	0.59540443	0.735	0.342	1.06E-117	8	KDM6B
1.00E-121	0.421666298	0.859	0.532	1.87E-117	8	NFKBID
6.56E-121	0.447507506	0.991	0.826	1.22E-116	8	BTG2
2.35E-116	0.502228026	0.738	0.39	4.38E-112	8	CSRNP1
4.67E-113	0.509272214	0.599	0.259	8.71E-109	8	USP36
7.78E-111	0.517061758	0.696	0.351	1.45E-106	8	NFE2L2
3.66E-110	0.492744316	0.982	0.813	6.81E-106	8	RHOH
3.81E-110	0.417980207	0.565	0.246	7.11E-106	8	MBNL2
1.64E-104	0.472192169	0.925	0.622	3.05E-100	8	PDE4B
2.51E-104	0.510921109	0.571	0.249	4.67E-100	8	NXT1
1.58E-103	0.483527425	0.409	0.105	2.95E-99	8	ANKRD37
1.64E-100	0.429636833	0.653	0.293	3.05E-96	8	CREM
3.38E-96	0.660138843	0.5	0.18	6.29E-92	8	DDIT4
6.84E-96	0.445172843	0.645	0.33	1.27E-91	8	ISCA1
4.39E-95	0.563574937	0.512	0.188	8.17E-91	8	TWISTNB
4.61E-95	0.464071703	0.8	0.508	8.59E-91	8	CYCS
8.06E-94	0.496403422	0.601	0.304	1.50E-89	8	IRF2BP2
5.29E-92	0.579149022	0.361	0.099	9.86E-88	8	GEM
6.18E-92	0.615922437	0.724	0.411	1.15E-87	8	PIM1
3.29E-91	0.466967957	0.642	0.344	6.13E-87	8	MOB3A
4.87E-91	0.463804086	0.58	0.267	9.07E-87	8	ARL4A
7.67E-90	0.328828479	0.964	0.794	1.43E-85	8	SARAF
1.45E-89	0.461786208	0.323	0.068	2.71E-85	8	GRASP
4.61E-89	0.450952957	0.515	0.222	8.59E-85	8	MANBA
1.32E-87	0.475985171	0.623	0.322	2.46E-83	8	ALG13
2.08E-87	0.442185883	0.527	0.231	3.87E-83	8	BCL2L11
6.64E-87	0.307277855	0.816	0.528	1.24E-82	8	IDS
9.65E-86	0.430755856	0.841	0.579	1.80E-81	8	ELF1
1.29E-85	0.497613692	0.481	0.188	2.40E-81	8	IL2RA
5.31E-85	0.352482795	0.444	0.166	9.90E-81	8	ELL2
5.21E-84	0.363900833	0.713	0.397	9.72E-80	8	GTF2B
1.85E-83	0.336122621	0.529	0.225	3.45E-79	8	ZNF10
3.72E-82	0.387364865	0.818	0.569	6.93E-78	8	SNX2
4.63E-81	0.56447753	0.874	0.667	8.63E-77	8	GSTP1

9.89E-81	0.419981167	0.598	0.305	1.84E-76	8	RRBP1
1.03E-79	0.32235815	0.478	0.21	1.92E-75	8	PPP1R15B
1.92E-79	0.312701655	0.958	0.78	3.58E-75	8	PPDPF
1.70E-78	0.360318234	0.613	0.328	3.16E-74	8	FYTTD1
6.88E-78	0.473120853	0.321	0.086	1.28E-73	8	ID1
2.85E-77	0.384074293	0.503	0.217	5.32E-73	8	NUP58
4.26E-77	0.310736256	0.558	0.265	7.93E-73	8	DDX3Y
3.85E-76	0.456730046	0.362	0.114	7.17E-72	8	ENC1
7.81E-75	0.475830416	0.707	0.454	1.46E-70	8	IL16
3.29E-74	0.454276315	0.757	0.47	6.13E-70	8	TUBA4A
1.39E-73	0.361558099	0.249	0.056	2.59E-69	8	MYBL2
2.77E-72	0.431119207	0.563	0.281	5.17E-68	8	BHLHE40
1.07E-71	0.367593127	0.678	0.427	1.99E-67	8	LAPTM4A
1.19E-71	0.253902528	0.518	0.24	2.22E-67	8	LYST
3.98E-71	0.386381619	0.732	0.458	7.41E-67	8	ITGB1
3.70E-70	0.404373494	0.726	0.464	6.90E-66	8	RILPL2
2.52E-69	0.363433099	0.418	0.167	4.69E-65	8	NEK1
9.98E-69	0.253138923	0.472	0.206	1.86E-64	8	ABCG1
4.45E-68	0.342631554	0.28	0.063	8.29E-64	8	VPS37B
4.65E-68	0.405308863	0.83	0.578	8.67E-64	8	CYTIP
2.10E-67	0.351836771	0.431	0.17	3.91E-63	8	S1PR1
3.69E-67	0.315129932	0.544	0.289	6.88E-63	8	NAMPT
1.47E-66	0.330614019	0.571	0.314	2.74E-62	8	RNF138
1.99E-66	0.393460275	0.983	0.874	3.71E-62	8	TSC22D3
6.00E-66	0.32186571	0.629	0.397	1.12E-61	8	SPINT2
3.30E-65	0.401840759	0.481	0.23	6.15E-61	8	MIDN
1.24E-64	0.316075001	0.685	0.429	2.31E-60	8	BACH1
2.21E-64	0.322735299	0.843	0.626	4.11E-60	8	RUBCNL
7.37E-63	0.363794278	0.723	0.473	1.37E-58	8	STK17B
1.13E-62	0.359892473	0.638	0.366	2.11E-58	8	P2RY10
1.80E-62	0.388737573	0.429	0.176	3.36E-58	8	DUSP10
7.63E-62	0.327560777	0.402	0.188	1.42E-57	8	DYNLT1
9.50E-62	0.344361569	0.904	0.733	1.77E-57	8	PRRC2C
1.86E-61	0.34626776	0.614	0.343	3.46E-57	8	BCAS2
4.31E-61	0.348254842	0.752	0.503	8.04E-57	8	PTPN1
5.74E-61	0.319257944	0.691	0.429	1.07E-56	8	IDI1
1.86E-60	0.323559673	0.979	0.877	3.46E-56	8	HLA-DQA1
1.65E-59	0.2624682	0.302	0.108	3.07E-55	8	EEF2K
2.85E-59	0.331614797	0.939	0.762	5.31E-55	8	UBB
5.86E-59	0.331018752	0.382	0.16	1.09E-54	8	SNN
1.88E-58	0.336602705	0.755	0.498	3.50E-54	8	MAPK1IP1L
3.24E-58	0.284363267	0.609	0.335	6.04E-54	8	IFRD1
3.87E-58	0.269570446	0.761	0.525	7.22E-54	8	NR3C1
7.13E-58	0.276846683	0.503	0.27	1.33E-53	8	ZFAND6
1.02E-57	0.320248594	0.632	0.384	1.90E-53	8	CDKN1B
5.08E-57	0.376322628	0.876	0.659	9.46E-53	8	CALR

6.83E-57	0.314459361	0.368	0.161	1.27E-52	8	PRR7
8.16E-57	0.365335262	0.575	0.33	1.52E-52	8	SERPINB9
8.18E-56	0.326812876	0.284	0.092	1.53E-51	8	CD9
1.55E-55	0.317327647	0.594	0.35	2.89E-51	8	CMTM6
1.39E-54	0.281267623	0.625	0.37	2.59E-50	8	CHD1
2.09E-54	0.356851642	0.899	0.673	3.89E-50	8	ATP6V0C
4.05E-54	0.266820984	0.547	0.293	7.54E-50	8	RARA
4.74E-54	0.357820218	0.642	0.395	8.84E-50	8	PBXIP1
7.82E-54	0.304206519	0.525	0.287	1.46E-49	8	ARL4C
2.58E-53	0.278852468	0.436	0.197	4.81E-49	8	BANK1
2.28E-52	0.308700046	0.794	0.538	4.25E-48	8	HSPA5
3.89E-52	0.332769799	0.37	0.15	7.25E-48	8	CFAP20
3.42E-51	0.336003043	0.298	0.102	6.37E-47	8	BCL9L
6.45E-51	0.269648386	0.746	0.496	1.20E-46	8	SBDS
3.73E-50	0.268585258	0.63	0.385	6.96E-46	8	RNMT
8.80E-50	0.287645711	0.77	0.554	1.64E-45	8	G3BP2
1.67E-49	0.312359419	0.276	0.096	3.12E-45	8	PLIN2
1.72E-49	0.314061401	0.56	0.301	3.21E-45	8	OSER1
1.88E-49	0.280451535	0.61	0.38	3.50E-45	8	WBP11
4.35E-49	0.274058131	0.764	0.517	8.10E-45	8	RELB
1.08E-47	0.367847011	0.375	0.152	2.01E-43	8	PPIF
1.25E-47	0.27606085	0.311	0.116	2.32E-43	8	IFIH1
2.78E-47	0.250751448	0.638	0.408	5.18E-43	8	DENND4A
1.61E-46	0.260421667	0.985	0.88	3.00E-42	8	COX4I1
2.78E-46	0.308747979	0.463	0.256	5.18E-42	8	MX1
3.33E-45	0.282666843	0.522	0.283	6.20E-41	8	ARID5A
2.06E-44	0.256933478	0.542	0.323	3.84E-40	8	EIF4A3
1.55E-43	0.26927503	0.61	0.401	2.90E-39	8	SF3A1
4.60E-43	0.250885789	0.665	0.456	8.58E-39	8	AMD1
1.19E-42	0.285369967	0.344	0.135	2.21E-38	8	ALG2
3.28E-42	0.272252608	0.772	0.554	6.11E-38	8	DDX21
1.65E-41	0.40895314	0.723	0.498	3.07E-37	8	RGCC
1.68E-41	0.260255904	0.359	0.175	3.14E-37	8	TUBB2A
5.19E-40	0.261967889	0.403	0.201	9.67E-36	8	MOB4
9.81E-40	0.251877605	0.87	0.684	1.83E-35	8	HNRNPA0
1.04E-39	0.258058672	0.967	0.836	1.94E-35	8	CALM1
1.40E-39	0.304250612	0.842	0.662	2.60E-35	8	CTSS
2.08E-39	0.269527663	0.51	0.294	3.87E-35	8	APLP2
4.93E-38	0.270011554	0.507	0.322	9.18E-34	8	ELMSAN1
1.09E-37	0.278871042	0.3	0.116	2.03E-33	8	PRMT9
1.34E-37	0.309481222	0.215	0.07	2.49E-33	8	FAM111B
1.77E-37	0.256418504	0.513	0.31	3.30E-33	8	MKNK2
2.57E-35	0.463285673	0.278	0.114	4.78E-31	8	CLEC2B
8.09E-35	0.257704525	0.868	0.687	1.51E-30	8	LITAF
1.46E-30	0.272390758	0.368	0.195	2.72E-26	8	GPR18
4.69E-27	0.265646585	0.344	0.194	8.75E-23	8	CXorf21

1.37E-26	0.275552168	0.502	0.34	2.55E-22	8	HIST1H1C
2.49E-20	0.44661103	0.645	0.483	4.63E-16	8	SELL
1.78E-86	1.436489298	0.656	0.545	3.31E-82	9	NFKBID
1.27E-81	0.600498681	0.761	0.546	2.37E-77	9	FOS
2.80E-77	0.735715668	0.801	0.673	5.21E-73	9	CD83
2.96E-67	0.867377976	0.721	0.533	5.51E-63	9	FOSB
1.39E-60	0.55487874	0.78	0.67	2.60E-56	9	CD69
4.53E-48	1.463595307	0.561	0.45	8.44E-44	9	MTRNR2L8
9.84E-47	1.803337953	0.449	0.323	1.83E-42	9	HSPH1
5.80E-46	0.820565515	0.662	0.515	1.08E-41	9	NR4A2
4.94E-42	0.328769473	0.126	0.363	9.21E-38	9	HSPB1
1.79E-35	1.14301331	0.356	0.237	3.33E-31	9	ZNF10
8.43E-29	1.710793851	0.327	0.203	1.57E-24	9	HSPA1B
2.86E-22	0.253427645	0.167	0.328	5.33E-18	9	BUD23
3.04E-22	0.250705969	0.268	0.497	5.67E-18	9	PPIG
9.64E-22	0.260920137	0.199	0.359	1.80E-17	9	ZNF24
6.44E-20	0.259023603	0.291	0.521	1.20E-15	9	HNRNPR
1.56E-19	0.789747647	0.222	0.12	2.90E-15	9	ZBED6
1.91E-19	0.28137923	0.193	0.366	3.56E-15	9	PPM1G
5.79E-19	0.886659674	0.344	0.221	1.08E-14	9	EGR1
3.48E-18	0.278792056	0.236	0.443	6.49E-14	9	CCDC12
3.68E-18	0.643569313	0.736	0.843	6.86E-14	9	TCF4
2.28E-17	0.274824856	0.191	0.35	4.25E-13	9	FXR1
2.43E-17	0.585694811	0.745	0.873	4.53E-13	9	FOXP1
2.46E-17	0.254510351	0.284	0.487	4.59E-13	9	RNF41
4.63E-17	0.266284928	0.224	0.381	8.64E-13	9	TAOK3
6.92E-17	0.283296669	0.167	0.31	1.29E-12	9	EMC10
1.19E-16	0.289013379	0.198	0.326	2.21E-12	9	MZB1
1.81E-16	0.261184719	0.155	0.283	3.37E-12	9	DERL1
2.42E-16	0.261821088	0.206	0.379	4.52E-12	9	WTAP
5.06E-16	0.262900603	0.222	0.397	9.43E-12	9	NDUFV1
6.44E-16	0.265829746	0.226	0.394	1.20E-11	9	CLASRP
6.62E-16	0.319224122	0.303	0.493	1.23E-11	9	BCL11A
2.25E-15	0.254380411	0.127	0.228	4.20E-11	9	PIH1D1
3.12E-15	0.276114717	0.254	0.404	5.82E-11	9	SYAP1
3.53E-15	0.791471562	0.595	0.7	6.58E-11	9	HNRNPU
4.28E-15	0.252096586	0.148	0.267	7.98E-11	9	SNHG15
1.33E-14	0.270634942	0.185	0.305	2.47E-10	9	DNMBP
1.42E-14	0.288129924	0.198	0.35	2.65E-10	9	CCDC50
1.53E-14	0.297640269	0.329	0.587	2.85E-10	9	GNAS
1.58E-14	0.318462595	0.276	0.48	2.95E-10	9	RAD21
2.12E-14	0.322385883	0.229	0.417	3.96E-10	9	RBBP6
2.13E-14	0.300090751	0.209	0.362	3.97E-10	9	ZFR
2.41E-14	0.252963566	0.183	0.361	4.50E-10	9	METAP2
3.04E-14	0.292262582	0.236	0.439	5.66E-10	9	TAF7
3.51E-14	0.258059905	0.206	0.345	6.54E-10	9	ALG13

6.47E-14	0.369136841	0.296	0.49	1.21E-09	9	NONO
8.96E-14	0.262603097	0.185	0.321	1.67E-09	9	IFNAR1
1.49E-13	0.333377237	0.235	0.388	2.78E-09	9	P2RY10
1.51E-13	0.621840299	0.601	0.741	2.81E-09	9	ANKRD12
1.53E-13	0.665104937	0.567	0.69	2.85E-09	9	EPC1
1.77E-13	0.252756743	0.414	0.683	3.30E-09	9	CALR
2.13E-13	0.257527223	0.151	0.259	3.98E-09	9	CASP3
2.15E-13	0.253237667	0.188	0.339	4.00E-09	9	NAP1L4
2.30E-13	0.266585436	0.151	0.263	4.29E-09	9	CGGBP1
2.70E-13	0.262373037	0.186	0.335	5.04E-09	9	PMPCB
2.83E-13	0.355757068	0.353	0.598	5.28E-09	9	YWHAQ
3.04E-13	0.251039698	0.344	0.608	5.67E-09	9	SF3B2
3.95E-13	0.331141902	0.2	0.347	7.36E-09	9	SHOC2
4.09E-13	0.285566475	0.206	0.373	7.63E-09	9	DDX18
5.95E-13	0.254012101	0.165	0.292	1.11E-08	9	EIF4G1
7.09E-13	0.259046754	0.187	0.334	1.32E-08	9	ANP32E
7.29E-13	0.2754481	0.26	0.449	1.36E-08	9	MBD4
9.75E-13	0.322967104	0.199	0.359	1.82E-08	9	DNTTIP2
1.14E-12	0.355238189	0.276	0.465	2.13E-08	9	NDFIP1
1.14E-12	0.311460347	0.207	0.363	2.13E-08	9	TLN1
1.18E-12	0.252013458	0.181	0.31	2.20E-08	9	SEL1L3
1.19E-12	0.251185167	0.158	0.289	2.22E-08	9	TRIM44
1.39E-12	0.301855792	0.206	0.353	2.59E-08	9	PHF20
1.77E-12	0.320873991	0.186	0.303	3.29E-08	9	COQ10B
1.82E-12	0.271268931	0.216	0.378	3.39E-08	9	FAM49B
1.93E-12	0.27867784	0.212	0.384	3.60E-08	9	LSM8
2.23E-12	0.251150815	0.171	0.309	4.15E-08	9	AKT2
2.32E-12	0.304924966	0.212	0.384	4.33E-08	9	ARHGAP9
2.92E-12	0.275006442	0.16	0.271	5.44E-08	9	GARS
2.95E-12	0.352260806	0.238	0.402	5.49E-08	9	DDX46
3.16E-12	0.281319174	0.18	0.302	5.90E-08	9	PIK3IP1
3.46E-12	0.252934147	0.169	0.315	6.45E-08	9	MAP4
3.55E-12	0.274419245	0.164	0.301	6.62E-08	9	TOR3A
4.35E-12	0.260105972	0.152	0.256	8.12E-08	9	PPP1R16B
5.10E-12	0.333101795	0.218	0.354	9.50E-08	9	BBX
5.18E-12	0.266301395	0.211	0.376	9.65E-08	9	MTCH1
5.85E-12	0.263476073	0.238	0.423	1.09E-07	9	RBBP4
6.40E-12	0.341620916	0.296	0.472	1.19E-07	9	FNBP1
8.77E-12	0.25455444	0.222	0.389	1.63E-07	9	ANAPC5
1.09E-11	0.360719954	0.22	0.353	2.03E-07	9	RSBN1L
1.14E-11	0.271125972	0.337	0.516	2.12E-07	9	FAM129C
1.48E-11	0.325168884	0.175	0.295	2.75E-07	9	NGDN
1.50E-11	0.301212395	0.217	0.375	2.79E-07	9	HDAC7
1.92E-11	0.333425241	0.283	0.447	3.59E-07	9	CFLAR
1.94E-11	0.30504836	0.182	0.315	3.62E-07	9	GNAI3
2.10E-11	0.297935699	0.147	0.248	3.91E-07	9	KIF2A

2.55E-11	0.268326376	0.168	0.291	4.75E-07	9	TIAL1
2.56E-11	0.291305932	0.208	0.348	4.77E-07	9	ZFAND5
3.13E-11	0.298928382	0.163	0.268	5.84E-07	9	DNAJB9
3.33E-11	0.251106095	0.357	0.591	6.20E-07	9	UBE2B
5.16E-11	0.263437941	0.208	0.373	9.63E-07	9	CDC40
5.18E-11	0.378664732	0.222	0.362	9.66E-07	9	PTPN7
5.37E-11	0.30077219	0.241	0.405	1.00E-06	9	CDKN1B
5.58E-11	0.313315404	0.265	0.469	1.04E-06	9	PCGF5
5.96E-11	0.25763394	0.154	0.271	1.11E-06	9	SMAP1
5.98E-11	0.334445887	0.204	0.369	1.11E-06	9	NAPA
8.93E-11	0.322539604	0.182	0.298	1.67E-06	9	NDE1
9.00E-11	0.326123403	0.248	0.415	1.68E-06	9	HSPA4
1.21E-10	0.369052064	0.199	0.342	2.25E-06	9	EIF4A3
1.37E-10	0.337326988	0.24	0.371	2.55E-06	9	TBC1D22A
1.44E-10	0.282088199	0.281	0.504	2.69E-06	9	TERF2IP
1.44E-10	0.319606725	0.255	0.4	2.69E-06	9	CLINT1
2.11E-10	0.263780492	0.149	0.25	3.93E-06	9	SNX1
2.14E-10	0.27815392	0.145	0.246	3.99E-06	9	SNRNP40
2.45E-10	0.615685273	0.535	0.677	4.57E-06	9	DDX24
2.48E-10	0.28588388	0.207	0.381	4.62E-06	9	TMC6
2.89E-10	0.391852314	0.271	0.43	5.39E-06	9	UBE2J1
3.22E-10	0.345594303	0.206	0.355	5.99E-06	9	DDX27
3.31E-10	0.35904114	0.237	0.374	6.18E-06	9	SUPT5H
3.60E-10	0.305994805	0.176	0.289	6.71E-06	9	ARL4A
3.61E-10	0.315760089	0.185	0.305	6.73E-06	9	ATG12
4.08E-10	0.322380043	0.286	0.469	7.61E-06	9	STRAP
4.41E-10	0.281744692	0.174	0.296	8.23E-06	9	ERICH1
4.48E-10	0.366165432	0.182	0.291	8.36E-06	9	NBPF14
5.22E-10	0.260573324	0.153	0.259	9.73E-06	9	EFCAB14
5.53E-10	0.322715341	0.236	0.417	1.03E-05	9	CCT2
7.13E-10	0.28625784	0.207	0.342	1.33E-05	9	CCDC32
7.18E-10	0.324447818	0.199	0.31	1.34E-05	9	SFMBT1
9.15E-10	0.522092821	0.584	0.767	1.71E-05	9	EIF4G2
9.36E-10	0.312361611	0.171	0.273	1.75E-05	9	C6orf62
1.24E-09	0.259835375	0.214	0.384	2.32E-05	9	OS9
1.53E-09	0.305281033	0.281	0.458	2.86E-05	9	PTPN2
1.62E-09	0.273669321	0.182	0.305	3.01E-05	9	SRPK2
1.63E-09	0.324694212	0.191	0.314	3.04E-05	9	SND1
1.73E-09	0.273981753	0.235	0.379	3.22E-05	9	PAX5
1.79E-09	0.285451962	0.42	0.666	3.34E-05	9	PRKCB
2.43E-09	0.357639211	0.188	0.308	4.53E-05	9	ATXN2L
2.56E-09	0.277207216	0.354	0.584	4.77E-05	9	FLNA
2.67E-09	0.27216874	0.295	0.504	4.98E-05	9	PRKAR1A
2.69E-09	0.265418677	0.177	0.306	5.02E-05	9	GIT2
2.83E-09	0.271971518	0.246	0.407	5.27E-05	9	TMEM123
2.90E-09	0.655759494	0.523	0.636	5.40E-05	9	AKAP13

3.34E-09	0.349013618	0.209	0.333	6.23E-05	9	MIS18BP1
3.38E-09	0.273223718	0.305	0.526	6.29E-05	9	HNRNPM
3.39E-09	0.311226575	0.162	0.278	6.31E-05	9	EIF3J
3.45E-09	0.353008499	0.22	0.359	6.43E-05	9	PRRC2A
3.66E-09	0.26904143	0.154	0.267	6.83E-05	9	SUPT16H
3.80E-09	0.303169727	0.192	0.304	7.09E-05	9	TMOD3
4.82E-09	0.322846729	0.253	0.416	8.98E-05	9	ATP2A3
5.51E-09	0.27622903	0.182	0.321	0.00010268	9	DCAF7
5.79E-09	0.28907361	0.179	0.29	0.000107954	9	SYNRG
5.94E-09	0.252874381	0.144	0.253	0.000110766	9	PSME3
5.95E-09	0.258002857	0.247	0.361	0.000110848	9	DDIT3
6.08E-09	0.362883753	0.188	0.297	0.00011335	9	ABCF1
6.13E-09	0.282527217	0.176	0.299	0.000114227	9	FAM3C
6.65E-09	0.308868667	0.373	0.594	0.000123931	9	THRAP3
7.02E-09	0.254396783	0.15	0.269	0.000130885	9	DDB1
7.50E-09	0.30822339	0.236	0.386	0.000139764	9	ACAP1
8.70E-09	0.286050535	0.24	0.376	0.000162246	9	NFE2L2
9.18E-09	0.368508045	0.25	0.378	0.000171145	9	WDR33
1.17E-08	0.319202819	0.263	0.405	0.000218168	9	TENT5C
1.25E-08	0.470598288	0.236	0.386	0.00023233	9	ENY2
1.46E-08	0.360764714	0.201	0.316	0.000272959	9	ATP1B3
1.82E-08	0.267346752	0.254	0.448	0.000339824	9	STAT6
2.00E-08	0.313436961	0.205	0.341	0.000373689	9	SNX18
2.11E-08	0.293442909	0.174	0.284	0.000394249	9	RNF115
2.12E-08	0.513892007	0.211	0.316	0.000395401	9	ATF5
2.19E-08	0.733981946	0.553	0.657	0.000407801	9	TRA2B
2.21E-08	0.319719494	0.201	0.303	0.00041143	9	CEP350
2.26E-08	0.28539853	0.383	0.656	0.000421955	9	CDC37
2.40E-08	0.344911934	0.194	0.311	0.000447035	9	SYNCRIP
2.41E-08	0.378319296	0.316	0.514	0.000448986	9	PAPOLA
2.65E-08	0.266960586	0.167	0.276	0.000494448	9	ANKRD10
2.77E-08	0.294769443	0.256	0.423	0.000515847	9	KLF2
2.78E-08	0.352909988	0.204	0.315	0.000517632	9	SLC25A36
3.08E-08	0.356417932	0.184	0.287	0.000574321	9	RSBN1
3.16E-08	0.345868442	0.344	0.538	0.00058931	9	CD47
3.35E-08	0.281979932	0.175	0.303	0.000625145	9	RAB10
3.63E-08	0.338968881	0.242	0.384	0.000675745	9	SEC14L1
3.80E-08	0.378185913	0.253	0.408	0.000707794	9	BPTF
4.32E-08	0.267362352	0.233	0.379	0.000806171	9	GTF2I
4.45E-08	0.269899278	0.284	0.481	0.000829032	9	EPB41
4.48E-08	0.26359384	0.171	0.302	0.000834972	9	PDCD10
4.48E-08	0.251037963	0.162	0.275	0.000835141	9	ARHGEF3
4.66E-08	0.323817167	0.283	0.483	0.000867777	9	PNRC2
4.99E-08	0.364680279	0.29	0.466	0.000930748	9	TTC3
5.18E-08	0.286552536	0.227	0.38	0.000966491	9	KDM4B
6.06E-08	0.580436945	0.532	0.67	0.00112996	9	ARGLU1

6.23E-08	0.326455703	0.198	0.317	0.001161093	9	WAPL
8.19E-08	0.406895066	0.218	0.327	0.001527356	9	BOD1L1
9.12E-08	0.265755511	0.27	0.439	0.001699887	9	EBLN3P
1.17E-07	0.316995594	0.185	0.302	0.002177866	9	IST1
1.36E-07	0.377184126	0.16	0.266	0.002528392	9	STAP1
1.38E-07	0.324546717	0.206	0.328	0.002564653	9	MIER1
1.52E-07	0.676793937	0.571	0.69	0.002825961	9	BRD2
1.55E-07	0.501955733	0.292	0.49	0.002892582	9	JUND
1.68E-07	0.285734541	0.149	0.273	0.00312567	9	SNAP23
1.77E-07	0.344807584	0.349	0.571	0.003296502	9	ACTR2
1.94E-07	0.301520878	0.231	0.385	0.00361709	9	CSNK1D
2.14E-07	0.334413676	0.306	0.493	0.003991017	9	WIPF1
2.68E-07	0.360646379	0.224	0.354	0.004993558	9	ADPGK
2.90E-07	0.32824517	0.225	0.367	0.005409162	9	UFM1
3.02E-07	0.374866796	0.219	0.333	0.005622404	9	UHMK1
3.27E-07	0.262416335	0.151	0.254	0.006093131	9	TMC8
3.43E-07	0.340441057	0.171	0.277	0.006392405	9	ZBTB24
3.68E-07	0.362765906	0.201	0.319	0.006860223	9	SMU1
3.88E-07	0.452337531	0.295	0.456	0.007223857	9	MBP
4.25E-07	0.36162083	0.208	0.316	0.007920513	9	SAP30BP
4.29E-07	0.293967706	0.275	0.443	0.008005483	9	PPM1K
4.70E-07	0.612670448	0.599	0.749	0.008760439	9	PRRC2C
5.01E-07	0.445396391	0.317	0.488	0.009339003	9	EIF5B
5.32E-07	0.338800843	0.269	0.421	0.009918017	9	PLEKHA2
6.26E-07	0.350765821	0.202	0.31	0.011672902	9	EP400
6.30E-07	0.308992618	0.211	0.333	0.011748091	9	DGKA
6.32E-07	0.394158656	0.256	0.399	0.011778814	9	ARHGAP4
6.33E-07	0.426865669	0.273	0.422	0.011799488	9	U2SURP
7.11E-07	0.652492332	0.46	0.564	0.013255604	9	SFPQ
7.86E-07	0.299573213	0.215	0.355	0.014657746	9	STK10
9.21E-07	0.25407864	0.147	0.254	0.017163711	9	IRF3
9.28E-07	0.346483489	0.192	0.308	0.017296941	9	VPS4B
1.05E-06	0.411260139	0.264	0.414	0.019587842	9	SRPRA
1.05E-06	0.483695559	0.267	0.378	0.019658905	9	GNPTAB
1.09E-06	0.331608088	0.398	0.574	0.020292795	9	IKZF3
1.12E-06	0.400574629	0.267	0.415	0.020934066	9	PBXIP1
1.37E-06	0.354584928	0.217	0.365	0.025568898	9	LAMP1
1.45E-06	0.340036564	0.29	0.481	0.026961285	9	ARHGEF1
1.46E-06	0.271810802	0.151	0.257	0.027134762	9	RBM22
1.85E-06	0.335212934	0.197	0.313	0.034507547	9	ZNFX1
2.04E-06	0.304069512	0.216	0.323	0.037967559	9	AP3B1
2.13E-06	0.352068718	0.206	0.309	0.039670384	9	SFT2D2
2.26E-06	0.382374939	0.192	0.297	0.042046517	9	COPB1
2.29E-06	0.433931939	0.667	0.81	0.042720798	9	SARAF
2.30E-06	0.385835726	0.162	0.267	0.04291671	9	KDM2B
2.76E-06	0.260485231	0.224	0.39	0.051358202	9	IKZF1

2.85E-06	0.352372381	0.362	0.599	0.0531598	9	CD53
3.46E-06	0.265232747	0.302	0.501	0.064478068	9	KRAS
3.85E-06	0.36461425	0.216	0.328	0.07184991	9	TMED4
3.87E-06	0.327028404	0.244	0.384	0.072215172	9	CDK5RAP3
4.02E-06	0.354805903	0.31	0.494	0.074843839	9	HNRNPH3
5.44E-06	0.363045007	0.305	0.474	0.101356145	9	NCOR1
5.57E-06	0.34623735	0.301	0.475	0.103901104	9	AMD1
6.21E-06	0.64953457	0.462	0.582	0.115794506	9	VCP
6.40E-06	0.383417982	0.339	0.537	0.119350201	9	CDC42SE2
7.23E-06	0.31170303	0.179	0.294	0.134841498	9	RAB1A
9.92E-06	0.351209198	0.353	0.544	0.18499772	9	GGA2
1.09E-05	0.364221965	0.263	0.39	0.203000549	9	RIC3
1.12E-05	0.307436016	0.205	0.349	0.208658751	9	DNAJC7
1.33E-05	0.384564446	0.38	0.571	0.247361131	9	ARHGAP25
1.36E-05	0.459269781	0.226	0.355	0.253162273	9	TMX4
1.43E-05	0.372066176	0.209	0.311	0.266483943	9	PPP4R3A
1.51E-05	0.364182537	0.22	0.329	0.281245661	9	PNPLA8
1.52E-05	0.445654808	0.233	0.337	0.282429846	9	TOX4
1.80E-05	0.459581196	0.242	0.355	0.33607034	9	THUMPD3-AS1
1.85E-05	0.425142232	0.233	0.343	0.345660815	9	WAC
2.09E-05	0.378409246	0.22	0.336	0.390194623	9	ETF1
2.31E-05	0.434217734	0.243	0.374	0.43096489	9	NUAK2
2.44E-05	0.349581892	0.4	0.615	0.454120047	9	SPOCK2
2.68E-05	0.391762606	0.272	0.391	0.499398601	9	ZNF107
2.86E-05	0.412612321	0.312	0.488	0.53370977	9	TAX1BP1
2.87E-05	0.300726131	0.213	0.359	0.535329506	9	NUMA1
3.08E-05	0.295999564	0.18	0.284	0.574886319	9	VPS36
3.10E-05	0.436965085	0.227	0.329	0.578075399	9	OSBPL8
3.28E-05	0.371012057	0.37	0.571	0.610531009	9	KPNB1
3.49E-05	0.368814234	0.321	0.501	0.650196949	9	ELOVL5
3.67E-05	0.408811032	0.28	0.442	0.684985871	9	RTN4
3.84E-05	0.64430114	0.237	0.344	0.71500818	9	MIR155HG
4.03E-05	0.421316443	0.432	0.645	0.75039896	9	SRRM2
4.99E-05	0.443397218	0.283	0.401	0.929659299	9	ACIN1
5.12E-05	0.391094027	0.218	0.339	0.953592587	9	STAT1
5.50E-05	0.295957208	0.164	0.268	1	9	MICAL1
6.59E-05	0.844902309	0.445	0.557	1	9	HSPA5
7.03E-05	0.370654053	0.362	0.571	1	9	ACTR3
7.61E-05	0.526929035	0.572	0.726	1	9	EIF5
8.49E-05	0.332327379	0.333	0.525	1	9	PTPN1
9.14E-05	0.40383978	0.291	0.438	1	9	MTSS1
0.000104808	0.381149238	0.26	0.404	1	9	INSIG1
0.000126942	0.46245398	0.347	0.528	1	9	KTN1
0.00014209	0.391442334	0.2	0.307	1	9	TROVE2
0.000152248	0.423340807	0.296	0.461	1	9	RSF1
0.00018666	0.442516937	0.309	0.454	1	9	ADAR

0.000188498	0.558003742	0.403	0.526	1	9	ROCK1
0.000197837	0.623788327	0.487	0.617	1	9	SCAF11
0.000212674	0.424186011	0.419	0.631	1	9	PAK2
0.000310046	0.397522797	0.245	0.362	1	9	CNOT1
0.000340148	0.540232883	0.49	0.61	1	9	NCOA3
0.000359462	0.475846263	0.248	0.379	1	9	TCP1
0.000378193	0.398969807	0.329	0.513	1	9	CD164
0.000379275	0.34527394	0.249	0.367	1	9	CREB3L2
0.000428567	0.367000537	0.468	0.697	1	9	YBX3
0.00053535	0.601659126	0.475	0.599	1	9	ELF1
0.000603642	0.289555374	0.376	0.542	1	9	STX7
0.000608292	0.462663248	0.29	0.396	1	9	DOCK8
0.000643108	0.345448198	0.274	0.393	1	9	Mar-01
0.00065398	0.366502084	0.249	0.383	1	9	CELF1
0.000719766	0.386203496	0.215	0.324	1	9	TACC1
0.000773748	0.342834217	0.177	0.284	1	9	HIF1A
0.000880066	0.339060305	0.193	0.309	1	9	RAB6A
0.000901146	0.412618782	0.269	0.389	1	9	LENG8
0.000966695	0.465793222	0.288	0.411	1	9	WDFY4
0.001126214	0.513903126	0.285	0.412	1	9	ANKRD11
0.001174885	0.449701131	0.326	0.468	1	9	CAPZA1
0.001216778	0.430093374	0.235	0.36	1	9	PLEC
0.001330302	0.412437055	0.269	0.388	1	9	USP11
0.001357885	0.627196041	0.443	0.55	1	9	CELF2
0.00148872	0.402955376	0.28	0.408	1	9	CHD9
0.001538111	0.381436103	0.236	0.368	1	9	SBNO1
0.001667761	0.395932908	0.257	0.401	1	9	G3BP1
0.001686434	0.416808759	0.252	0.362	1	9	MORC3
0.001698921	0.504150845	0.26	0.363	1	9	NASP
0.001810344	0.504591239	0.285	0.414	1	9	PPP2R5C
0.001870886	0.391753555	0.779	0.905	1	9	HLA-DQB1
0.002169268	0.39557567	0.267	0.381	1	9	WDR11
0.002177974	0.684029014	0.447	0.558	1	9	IL10RA
0.002181032	0.641547061	0.429	0.532	1	9	ITSN2
0.00236188	0.421484391	0.371	0.534	1	9	ST6GAL1
0.002972133	0.403493637	0.421	0.633	1	9	SH3BP5
0.003015843	0.564735497	0.427	0.535	1	9	LUC7L3
0.003501234	0.422435218	0.291	0.415	1	9	NCKAP1L
0.004808719	0.386351995	0.584	0.798	1	9	GRB2
0.005601439	0.556209514	0.297	0.405	1	9	TANK
0.005913638	0.37374546	0.232	0.341	1	9	RNF149
0.005931781	0.432126677	0.232	0.333	1	9	RNF138
0.006764783	0.546480885	0.51	0.667	1	9	HNRNPA3
0.006807683	0.471895877	0.263	0.367	1	9	SPTAN1
0.007349054	0.4189427	0.412	0.607	1	9	JAK1
0.007703962	0.415342894	0.312	0.432	1	9	SP140

0.007901561	0.423564705	0.366	0.541	1	9	RBMX
0.007919293	0.627655314	0.457	0.576	1	9	TAF1D
0.008660843	0.502876227	0.576	0.739	1	9	SRSF5
0.00965119	0.473617454	0.277	0.413	1	9	ARF4
0	1.971244018	0.978	0.751	0	10	RALGPS2
0	1.911519998	0.966	0.676	0	10	DDX17
0	1.88466106	0.879	0.519	0	10	STX7
0	1.827397808	0.826	0.392	0	10	PARP15
0	1.679580064	0.871	0.53	0	10	MSI2
0	1.635837478	0.871	0.56	0	10	CDK14
0	1.633214299	0.868	0.575	0	10	ABCA6
0	1.522793613	0.906	0.646	0	10	AFF3
5.88E-308	1.265248918	0.935	0.832	1.10E-303	10	SF1
4.78E-295	1.361548497	0.892	0.715	8.91E-291	10	ARHGAP24
1.09E-292	1.432944594	0.902	0.704	2.03E-288	10	SMCHD1
3.64E-237	1.229011782	0.868	0.657	6.79E-233	10	RSRP1
2.66E-232	1.409551773	0.791	0.505	4.96E-228	10	OGT
4.17E-231	1.517035658	0.717	0.347	7.77E-227	10	CAMK2D
1.90E-225	1.436807841	0.78	0.52	3.55E-221	10	BCL2
2.53E-225	1.394353155	0.711	0.365	4.71E-221	10	NKTR
1.26E-214	1.386333041	0.765	0.481	2.35E-210	10	ANKRD44
2.11E-211	1.37256992	0.743	0.457	3.93E-207	10	TUT4
1.27E-207	1.327158168	0.819	0.631	2.37E-203	10	CCDC88A
7.80E-203	1.387321854	0.815	0.625	1.45E-198	10	RIPOR2
2.53E-198	1.912775246	0.594	0.19	4.71E-194	10	SERINC5
1.09E-192	1.080519406	0.902	0.785	2.02E-188	10	FUS
2.11E-192	1.103727392	0.811	0.668	3.94E-188	10	SF3B1
2.09E-189	1.406108319	0.796	0.562	3.89E-185	10	TTN
1.41E-188	1.268920886	0.77	0.543	2.63E-184	10	SSH2
2.89E-187	1.197799816	0.744	0.527	5.38E-183	10	N4BP2L2
7.27E-186	1.277115607	0.736	0.459	1.36E-181	10	SNRNP70
1.42E-182	1.241930861	0.714	0.463	2.65E-178	10	OGA
5.63E-182	1.482098284	0.651	0.339	1.05E-177	10	GABPB1-AS1
1.20E-178	1.422112121	0.597	0.234	2.25E-174	10	CCDC141
4.44E-177	1.089203303	0.812	0.647	8.28E-173	10	SRSF11
7.27E-177	1.585164996	0.67	0.338	1.36E-172	10	CLNK
6.91E-176	1.225502784	0.685	0.42	1.29E-171	10	TMEM131L
3.66E-175	1.327673991	0.652	0.329	6.82E-171	10	MCTP2
6.36E-172	1.12438225	0.761	0.559	1.18E-167	10	PNN
6.68E-169	1.133197458	0.771	0.597	1.24E-164	10	NCOA3
3.19E-168	1.349812665	0.673	0.392	5.94E-164	10	ATM
2.57E-167	1.3199843	0.628	0.28	4.79E-163	10	RNPC3
2.14E-164	1.131007452	0.729	0.522	3.98E-160	10	LUC7L3
1.15E-162	1.455093702	0.76	0.537	2.14E-158	10	LRMP
1.59E-162	0.976807396	0.835	0.732	2.96E-158	10	PNISR
2.66E-161	1.328497016	0.578	0.249	4.96E-157	10	UTY

3.77E-161	1.408562208	0.558	0.207	7.03E-157	10	GAB1
6.36E-161	1.233243674	0.697	0.453	1.18E-156	10	VPS13C
7.50E-151	1.260613863	0.597	0.304	1.40E-146	10	PHC3
7.31E-149	1.12720013	0.721	0.537	1.36E-144	10	CELF2
1.21E-147	1.072940403	0.729	0.556	2.26E-143	10	USP15
1.39E-147	1.177258327	0.693	0.488	2.58E-143	10	INPP5F
1.01E-146	1.124565409	0.669	0.439	1.89E-142	10	ARHGAP15
3.70E-146	1.132287395	0.735	0.559	6.89E-142	10	IKZF3
9.04E-146	0.988754277	0.767	0.632	1.69E-141	10	RUBCNL
2.27E-144	1.290626634	0.711	0.499	4.23E-140	10	FAM129C
7.36E-144	1.195446616	0.609	0.315	1.37E-139	10	DOCK10
3.39E-142	1.247351814	0.623	0.359	6.31E-138	10	ARID1B
7.74E-142	1.077592556	0.633	0.415	1.44E-137	10	SNX29
6.24E-140	0.981320887	0.751	0.619	1.16E-135	10	JMJD1C
1.06E-136	1.040188252	0.685	0.504	1.98E-132	10	UVRAG
6.75E-134	1.030129013	0.722	0.546	1.26E-129	10	PELI1
2.25E-133	1.08521619	0.397	0.093	4.20E-129	10	TRIM73
2.56E-132	0.879949512	0.894	0.785	4.77E-128	10	TXNIP
1.91E-131	1.09496203	0.646	0.416	3.55E-127	10	ZNF292
4.45E-131	1.077532877	0.674	0.457	8.29E-127	10	ZCCHC7
6.79E-131	1.143097023	0.5	0.198	1.27E-126	10	KHDRBS2
1.42E-129	1.13350453	0.514	0.252	2.64E-125	10	BTLA
2.37E-127	1.18661595	0.482	0.189	4.42E-123	10	HIBCH
2.59E-125	1.181465123	0.504	0.198	4.83E-121	10	ADAMTS6
1.67E-124	1.070318297	0.633	0.406	3.11E-120	10	ZRANB2
2.53E-124	1.174090337	0.442	0.142	4.71E-120	10	FTX
8.14E-124	1.051532272	0.736	0.622	1.52E-119	10	SLC38A1
5.73E-121	1.185614764	0.504	0.225	1.07E-116	10	ADAM19
1.92E-119	1.314213871	0.668	0.476	3.59E-115	10	BCL11A
2.13E-119	1.249284587	0.63	0.377	3.96E-115	10	Mar-01
3.04E-118	1.16359272	0.533	0.264	5.66E-114	10	IMMP2L
2.75E-117	1.170734404	0.712	0.536	5.13E-113	10	LINC00926
6.00E-116	1.075550509	0.487	0.228	1.12E-111	10	GOLGA8B
1.43E-112	1.158084726	0.601	0.351	2.67E-108	10	CREB3L2
1.87E-112	1.143093174	0.616	0.355	3.49E-108	10	MDM4
2.30E-112	1.074762178	0.62	0.423	4.28E-108	10	EBLN3P
2.24E-111	0.980405319	0.655	0.514	4.18E-107	10	ABI1
1.62E-110	1.050848973	0.49	0.236	3.01E-106	10	SLC23A2
7.31E-110	1.034806978	0.503	0.281	1.36E-105	10	FCHSD2
2.11E-109	1.003038308	0.583	0.383	3.94E-105	10	PPP4R3B
6.99E-107	1.115208054	0.531	0.289	1.30E-102	10	TTC14
1.13E-106	1.011163402	0.648	0.502	2.10E-102	10	RABGAP1L
1.51E-106	1.032144846	0.527	0.286	2.81E-102	10	PHTF2
1.91E-106	1.198806336	0.547	0.286	3.55E-102	10	NSF
4.20E-106	1.294110484	0.472	0.204	7.82E-102	10	AC063949.2
1.08E-105	1.193187286	0.409	0.129	2.01E-101	10	HDAC9

4.40E-105	1.04589687	0.496	0.246	8.21E-101	10	DDHD1
5.00E-105	1.107179335	0.528	0.264	9.31E-101	10	MCOLN2
9.49E-105	1.011739408	0.607	0.425	1.77E-100	10	EML4
1.28E-102	1.018621829	0.55	0.343	2.38E-98	10	NFAT5
8.78E-102	1.066210994	0.56	0.343	1.64E-97	10	UTRN
2.58E-100	1.077629466	0.551	0.302	4.81E-96	10	CD46
8.02E-100	0.982881674	0.575	0.384	1.50E-95	10	ASH1L
2.21E-99	1.010544333	0.433	0.188	4.12E-95	10	STAMBPL1
3.65E-99	1.080767101	0.484	0.237	6.81E-95	10	CBLB
4.13E-99	1.100352782	0.482	0.248	7.70E-95	10	DNAJC10
1.32E-98	0.916192248	0.702	0.598	2.45E-94	10	SWAP70
3.40E-98	0.81747218	0.756	0.655	6.34E-94	10	CCNL1
4.98E-98	1.498141671	0.533	0.28	9.28E-94	10	ZNF266
8.23E-98	1.008643182	0.461	0.212	1.53E-93	10	CREBZF
1.28E-96	0.933931716	0.526	0.366	2.39E-92	10	GTF2I
1.53E-96	1.168379966	0.577	0.364	2.86E-92	10	CIITA
2.02E-96	0.994008209	0.55	0.341	3.76E-92	10	RNF19A
2.15E-96	1.025923879	0.66	0.524	4.00E-92	10	CD47
4.88E-96	0.93563092	0.577	0.436	9.10E-92	10	SMG1
1.23E-95	1.02739781	0.55	0.368	2.28E-91	10	WDR11
3.38E-95	0.994785422	0.517	0.307	6.31E-91	10	SLC9A7
2.34E-94	1.068504861	0.456	0.19	4.35E-90	10	MAML2
9.77E-94	0.918537085	0.714	0.48	1.82E-89	10	IGLL5
7.80E-93	0.927226176	0.445	0.221	1.45E-88	10	EXOC4
9.30E-93	0.939841789	0.513	0.313	1.73E-88	10	TTC17
1.42E-92	1.100260819	0.555	0.315	2.65E-88	10	TLE4
1.73E-92	0.921881848	0.609	0.47	3.23E-88	10	PCM1
3.76E-91	0.978740849	0.643	0.523	7.02E-87	10	TNRC6B
3.71E-90	1.031910939	0.436	0.195	6.92E-86	10	RASA1
4.79E-90	0.964275678	0.525	0.338	8.93E-86	10	BIRC6
6.66E-90	1.123991382	0.535	0.32	1.24E-85	10	DMD
8.95E-89	1.065114151	0.582	0.376	1.67E-84	10	ZBTB20
1.17E-88	1.069699654	0.489	0.236	2.18E-84	10	JAK2
3.74E-88	1.033941358	0.564	0.378	6.97E-84	10	ZNF107
8.39E-88	1.041968957	0.573	0.343	1.56E-83	10	ACSM3
9.50E-88	0.951836385	0.5	0.297	1.77E-83	10	FRYL
2.06E-87	0.933962803	0.441	0.212	3.84E-83	10	CCNT2
5.58E-86	0.961835926	0.631	0.475	1.04E-81	10	TLK1
1.88E-85	0.937738251	0.511	0.32	3.50E-81	10	MATR3-ENSG00000015479
1.52E-84	0.921571302	0.627	0.517	2.83E-80	10	ZNF207
2.93E-84	0.928577403	0.405	0.178	5.46E-80	10	FBXL20
3.17E-84	0.968467826	0.489	0.279	5.92E-80	10	MAN2A1
1.17E-83	1.004728624	0.459	0.255	2.19E-79	10	PARP14
2.56E-83	1.012367924	0.316	0.087	4.77E-79	10	AL445673.1
2.93E-83	0.994072835	0.6	0.443	5.45E-79	10	HNRNPH1
1.47E-81	0.85779827	0.599	0.487	2.74E-77	10	LMBRD1

1.60E-81	0.981154684	0.38	0.148	2.97E-77	10	POLR2J3-ENSG00000285437
1.61E-81	0.937662318	0.483	0.296	3.00E-77	10	PCMTD1
7.59E-81	1.082245393	0.491	0.27	1.42E-76	10	SLC12A6
1.25E-80	0.990405076	0.387	0.156	2.33E-76	10	LRRK2
2.48E-79	1.021187116	0.581	0.443	4.62E-75	10	ATF7IP
3.39E-79	0.860545085	0.375	0.16	6.32E-75	10	DIP2B
3.75E-79	0.920580162	0.581	0.391	6.99E-75	10	SKAP1
7.85E-79	1.033138091	0.579	0.39	1.46E-74	10	TRAF3IP3
1.22E-78	0.954302223	0.559	0.403	2.28E-74	10	NCKAP1L
3.91E-78	0.939087958	0.435	0.211	7.29E-74	10	CEP95
1.30E-77	1.23896758	0.628	0.499	2.43E-73	10	IL4R
2.58E-77	0.860681472	0.351	0.131	4.82E-73	10	ZNF708
6.52E-77	1.248176059	0.456	0.237	1.21E-72	10	PCDH9
1.28E-76	0.911755926	0.447	0.242	2.38E-72	10	MON2
1.02E-75	1.015462418	0.609	0.465	1.90E-71	10	PLEKHG1
1.06E-74	0.874393137	0.459	0.278	1.98E-70	10	RIC1
1.23E-74	1.00455906	0.467	0.278	2.30E-70	10	WDFY1
1.56E-74	0.845987588	0.536	0.412	2.91E-70	10	PHF3
2.47E-74	0.840215731	0.357	0.159	4.60E-70	10	AVL9
8.01E-74	0.984655168	0.433	0.213	1.49E-69	10	AC119396.1
1.49E-73	0.936735149	0.546	0.396	2.78E-69	10	CHD9
4.42E-73	0.911202025	0.428	0.224	8.23E-69	10	DMTF1
5.74E-73	0.932394672	0.589	0.464	1.07E-68	10	ADAM28
1.33E-72	0.960126142	0.509	0.322	2.49E-68	10	AL158850.1
1.34E-72	0.83893051	0.55	0.445	2.50E-68	10	MYCBP2
3.79E-72	0.86952599	0.395	0.2	7.06E-68	10	VPS13B
5.90E-72	0.868444798	0.257	0.056	1.10E-67	10	RGPD2
2.55E-71	0.857264527	0.585	0.458	4.76E-67	10	NIPBL
5.24E-71	0.95544969	0.52	0.349	9.77E-67	10	SREK1
2.68E-70	0.822935276	0.328	0.13	4.99E-66	10	CCDC14
7.80E-70	0.840948789	0.367	0.182	1.45E-65	10	STX16
9.28E-70	0.944587757	0.443	0.259	1.73E-65	10	TRAF5
2.14E-69	0.872282783	0.416	0.236	3.99E-65	10	XRN1
2.83E-69	0.885920146	0.556	0.416	5.28E-65	10	NEMF
3.40E-69	1.006057405	0.438	0.237	6.35E-65	10	CD84
8.86E-69	0.934374497	0.477	0.279	1.65E-64	10	TBC1D5
4.72E-68	0.928558655	0.491	0.32	8.80E-64	10	LPP
5.73E-68	0.884487074	0.436	0.269	1.07E-63	10	KANSL1
1.18E-67	0.95081611	0.489	0.322	2.19E-63	10	USP34
2.08E-67	0.996126444	0.475	0.257	3.89E-63	10	GSAP
2.67E-67	0.884353892	0.375	0.188	4.97E-63	10	NUP88
2.70E-67	0.8969857	0.344	0.135	5.03E-63	10	ZDHHC21
2.83E-67	0.91427283	0.427	0.277	5.27E-63	10	CLEC17A
5.35E-67	1.108568583	0.457	0.25	9.97E-63	10	ARHGAP44
2.84E-65	0.87680517	0.552	0.421	5.30E-61	10	SP140
5.68E-65	0.826917897	0.348	0.147	1.06E-60	10	RUNX1

6.40E-65	0.853325507	0.459	0.294	1.19E-60	10	SENP6
1.58E-64	0.949837449	0.41	0.223	2.95E-60	10	MRNIP
2.02E-64	0.894451383	0.418	0.24	3.77E-60	10	BICD1
2.10E-64	0.836797564	0.362	0.18	3.91E-60	10	ANKRD36B
1.12E-63	0.86678154	0.314	0.114	2.09E-59	10	ZNF439
9.93E-63	0.887597806	0.479	0.325	1.85E-58	10	SECISBP2
1.23E-62	0.882767359	0.527	0.383	2.29E-58	10	LUC7L2
2.44E-62	0.837019927	0.51	0.379	4.54E-58	10	HECTD1
1.08E-61	0.878357154	0.351	0.152	2.02E-57	10	ANKRD36C
2.71E-61	1.123329585	0.408	0.233	5.05E-57	10	LINC02397
2.96E-61	0.790755478	0.322	0.152	5.53E-57	10	NPIPB5
2.23E-60	0.880853315	0.441	0.265	4.16E-56	10	DMXL1
2.65E-60	0.884555657	0.543	0.431	4.95E-56	10	PPM1K
5.16E-60	0.964680199	0.396	0.191	9.63E-56	10	AC012368.1
6.85E-60	0.892855461	0.543	0.435	1.28E-55	10	CFLAR
1.53E-59	0.883534145	0.357	0.151	2.85E-55	10	MBD5
1.79E-59	0.884954856	0.347	0.157	3.34E-55	10	PMS1
2.52E-59	0.779262184	0.391	0.203	4.71E-55	10	KDM6A
2.62E-59	0.991072435	0.41	0.236	4.88E-55	10	CLEC2D
3.68E-59	0.877764794	0.344	0.152	6.86E-55	10	SUGP2
3.97E-59	0.901931083	0.493	0.351	7.41E-55	10	MORC3
4.13E-59	0.875595994	0.449	0.286	7.70E-55	10	ZMYM2
6.25E-59	0.802655025	0.353	0.169	1.17E-54	10	FNDC3A
8.74E-59	0.78439324	0.399	0.227	1.63E-54	10	VTI1A
1.12E-58	0.826854672	0.369	0.205	2.08E-54	10	KHDC4
5.98E-58	0.867912003	0.481	0.341	1.11E-53	10	ZNF644
6.40E-58	0.848832434	0.42	0.259	1.19E-53	10	RBM5
1.56E-57	0.797411578	0.469	0.337	2.90E-53	10	SCAF4
7.14E-56	0.763926469	0.283	0.109	1.33E-51	10	GMDS-DT
8.41E-56	0.886476012	0.543	0.42	1.57E-51	10	TNFAIP8
9.06E-56	0.998979666	0.425	0.248	1.69E-51	10	LYST
1.20E-55	0.824195238	0.42	0.252	2.25E-51	10	LRBA
2.22E-55	0.871480579	0.499	0.371	4.14E-51	10	SETX
4.85E-55	0.865127649	0.47	0.322	9.04E-51	10	LNPEP
7.14E-55	0.826819597	0.419	0.257	1.33E-50	10	PKN2
1.98E-54	0.794268851	0.327	0.161	3.69E-50	10	IL6ST
2.85E-54	0.852442514	0.485	0.349	5.32E-50	10	ELMO1
4.41E-54	0.625765778	0.2	0.052	8.23E-50	10	RBMS3
4.66E-54	0.886051724	0.38	0.214	8.68E-50	10	ARRDC3
4.72E-54	0.910306704	0.337	0.16	8.80E-50	10	KSR2
7.95E-54	0.861277179	0.442	0.285	1.48E-49	10	BRWD1
1.93E-53	0.769239923	0.399	0.253	3.60E-49	10	TRPM7
1.61E-52	0.88503277	0.431	0.253	2.99E-48	10	PHKB
1.97E-52	0.85256969	0.366	0.235	3.68E-48	10	RASGRP3
1.99E-52	0.811666356	0.343	0.16	3.71E-48	10	ANKRD36
2.14E-52	0.736984283	0.276	0.128	3.99E-48	10	SLC16A1-AS1

3.24E-52	0.841963632	0.392	0.222	6.04E-48	10	DGKD
3.34E-52	0.765582561	0.438	0.306	6.22E-48	10	CNST
4.46E-52	0.766547812	0.256	0.095	8.31E-48	10	UBR5-AS1
6.14E-52	0.73130139	0.544	0.444	1.14E-47	10	ZEB2
7.10E-52	0.826015964	0.437	0.3	1.32E-47	10	NSD1
1.07E-51	0.817418934	0.306	0.133	2.00E-47	10	KDM5D
1.52E-51	0.616263749	0.156	0.023	2.83E-47	10	C1orf220
2.51E-51	0.74440394	0.291	0.127	4.67E-47	10	ATP8A1
3.31E-51	0.773548692	0.469	0.361	6.17E-47	10	TBC1D22A
3.74E-51	0.783004555	0.307	0.149	6.98E-47	10	C11orf80
4.01E-51	0.76751783	0.307	0.143	7.47E-47	10	HERC4
5.20E-51	0.77335208	0.356	0.196	9.69E-47	10	YTHDC2
6.15E-51	0.809988201	0.356	0.186	1.15E-46	10	DCLK2
6.57E-51	0.750347165	0.324	0.171	1.22E-46	10	PPIP5K2
6.73E-51	0.778023721	0.42	0.3	1.26E-46	10	SFMBT1
7.09E-51	0.803454174	0.463	0.334	1.32E-46	10	Mar-06
8.51E-51	0.785720352	0.46	0.348	1.59E-46	10	USP3
1.52E-50	0.804437935	0.489	0.387	2.83E-46	10	DOCK8
1.56E-50	0.798391175	0.438	0.311	2.92E-46	10	MARF1
3.86E-50	0.814314558	0.383	0.234	7.20E-46	10	ZNF506
6.32E-50	0.767882591	0.405	0.268	1.18E-45	10	AP1G1
8.26E-50	0.810238751	0.412	0.257	1.54E-45	10	PRKCE
9.08E-50	0.750386373	0.402	0.275	1.69E-45	10	RERE
1.25E-49	0.713583848	0.263	0.105	2.33E-45	10	USP45
2.29E-49	0.799797125	0.455	0.316	4.28E-45	10	BTAF1
5.56E-49	0.702062679	0.276	0.111	1.04E-44	10	CCDC84
1.07E-48	0.700504053	0.287	0.117	2.00E-44	10	ZBED6
1.71E-48	0.781555955	0.355	0.193	3.18E-44	10	TCF12
1.72E-48	0.69726179	0.236	0.078	3.21E-44	10	ARL15
7.27E-48	0.801888739	0.427	0.295	1.35E-43	10	LUC7L
1.84E-47	0.824535937	0.452	0.318	3.42E-43	10	ZNF638
6.29E-47	0.889940669	0.418	0.25	1.17E-42	10	RABEP2
6.90E-47	0.759274727	0.33	0.174	1.29E-42	10	NHLRC3
1.45E-46	0.857615376	0.459	0.322	2.71E-42	10	DGKA
2.29E-46	0.761672114	0.336	0.178	4.27E-42	10	EZH1
2.93E-46	0.695756315	0.305	0.166	5.47E-42	10	ATP9B
3.25E-46	0.876705693	0.504	0.388	6.06E-42	10	CLINT1
4.01E-46	0.676839655	0.264	0.121	7.47E-42	10	LIMD1
5.98E-46	0.822668385	0.413	0.264	1.12E-41	10	SFSWAP
8.73E-46	0.815809101	0.312	0.156	1.63E-41	10	SESTD1
1.50E-45	0.75743686	0.247	0.094	2.79E-41	10	LINC02363
1.51E-45	0.73086779	0.335	0.187	2.82E-41	10	ADAM10
2.18E-45	0.678815203	0.323	0.193	4.07E-41	10	GSK3B
6.19E-45	0.748129695	0.342	0.191	1.15E-40	10	ATAD2B
8.52E-45	0.75879591	0.4	0.274	1.59E-40	10	VPS36
8.91E-45	0.782900349	0.416	0.27	1.66E-40	10	MEF2A

9.63E-45	0.835816745	0.383	0.223	1.80E-40	10	SMC6
2.09E-44	0.752336223	0.329	0.181	3.89E-40	10	SP4
2.47E-44	0.778797814	0.363	0.214	4.60E-40	10	UBR2
3.25E-44	0.687433526	0.3	0.162	6.06E-40	10	ZDHHC20
3.42E-44	0.78148508	0.445	0.338	6.38E-40	10	CCDC50
3.56E-44	0.706585271	0.29	0.134	6.64E-40	10	ZNF736
6.69E-44	0.774904249	0.461	0.345	1.25E-39	10	LEF1
1.94E-43	0.729867091	0.383	0.264	3.61E-39	10	HERC1
4.04E-43	0.617703148	0.235	0.097	7.53E-39	10	ANAPC4
8.55E-43	0.765748591	0.437	0.328	1.59E-38	10	PTBP3
4.62E-42	0.72447015	0.247	0.099	8.61E-38	10	L3MBTL3
5.56E-42	0.547336499	0.193	0.074	1.04E-37	10	AUH
5.80E-42	0.826057516	0.443	0.315	1.08E-37	10	MZB1
1.20E-41	0.760522342	0.365	0.234	2.24E-37	10	LONP2
1.31E-41	0.743985618	0.445	0.344	2.45E-37	10	PCF11
2.04E-41	0.743162992	0.367	0.223	3.80E-37	10	TENT2
2.78E-41	0.544851245	0.187	0.068	5.18E-37	10	EFCAB13
3.46E-41	0.831052978	0.377	0.241	6.45E-37	10	YIPF4
4.11E-41	0.661450734	0.259	0.117	7.67E-37	10	DLEU2
4.32E-41	0.67128232	0.266	0.127	8.06E-37	10	PBX3
9.35E-41	0.735494858	0.343	0.202	1.74E-36	10	SPG11
1.63E-40	0.668587017	0.279	0.129	3.04E-36	10	MED23
2.76E-40	0.773803436	0.364	0.234	5.15E-36	10	XPO1
7.74E-40	0.667965289	0.289	0.157	1.44E-35	10	SYNE1
2.47E-39	0.757131368	0.333	0.201	4.60E-35	10	DICER1
3.92E-39	0.494194749	0.148	0.034	7.31E-35	10	LINC00278
5.76E-39	0.677013669	0.3	0.18	1.07E-34	10	KIAA1109
6.26E-39	0.651724565	0.233	0.107	1.17E-34	10	NLRC3
6.34E-39	0.788207773	0.386	0.238	1.18E-34	10	GMDS
1.25E-38	0.695800592	0.365	0.237	2.33E-34	10	CEMIP2
1.58E-38	0.718459023	0.384	0.262	2.95E-34	10	ITCH
1.77E-38	0.727785521	0.387	0.286	3.31E-34	10	ERICH1
2.37E-38	0.76122851	0.422	0.307	4.42E-34	10	GPCPD1
4.28E-38	0.704092632	0.262	0.116	7.97E-34	10	PPP1R3E
4.80E-38	0.560246386	0.192	0.074	8.95E-34	10	ZNF507
6.16E-38	0.808503755	0.439	0.332	1.15E-33	10	TRIM38
6.85E-38	0.676807224	0.21	0.083	1.28E-33	10	SGSM1
8.47E-38	0.806782429	0.427	0.316	1.58E-33	10	WASHC4
1.06E-37	0.736179855	0.371	0.238	1.97E-33	10	KDM4C
1.31E-37	0.707764295	0.343	0.223	2.44E-33	10	ERBIN
1.83E-37	0.704570648	0.317	0.189	3.42E-33	10	CD200
2.38E-37	0.733506052	0.319	0.192	4.44E-33	10	ARHGAP5
3.36E-37	0.702411703	0.258	0.117	6.26E-33	10	SESN1
7.37E-37	0.649171009	0.303	0.196	1.37E-32	10	CEP85L
9.30E-37	0.735297704	0.418	0.314	1.73E-32	10	AP3B1
1.10E-36	0.669131923	0.258	0.115	2.05E-32	10	ANKAR

1.31E-36	0.503605288	0.169	0.064	2.45E-32	10	TMEM161B-AS1
1.82E-36	0.724296757	0.386	0.279	3.39E-32	10	CAPRIN1
1.94E-36	0.553444556	0.178	0.063	3.61E-32	10	AL669831.5
1.99E-36	0.624090798	0.269	0.156	3.72E-32	10	NCOA2
2.34E-36	0.659961133	0.267	0.137	4.36E-32	10	RHBDD1
2.48E-36	0.727730854	0.408	0.293	4.63E-32	10	ZFC3H1
2.63E-36	0.765409546	0.252	0.135	4.91E-32	10	KLF8
2.65E-36	0.531513516	0.193	0.08	4.94E-32	10	TTC21B
2.69E-36	0.717917342	0.333	0.199	5.01E-32	10	UHRF2
4.70E-36	0.672085133	0.296	0.158	8.77E-32	10	FAM172A
7.56E-36	0.704389686	0.367	0.262	1.41E-31	10	UBR5
8.96E-36	0.691713978	0.31	0.192	1.67E-31	10	JPX
1.18E-35	0.543737453	0.187	0.074	2.20E-31	10	DPH6
1.75E-35	0.70206034	0.352	0.245	3.26E-31	10	CUL5
1.93E-35	0.465946746	0.136	0.032	3.59E-31	10	GRAMD1B
1.99E-35	0.675123901	0.281	0.145	3.70E-31	10	NBPF11
2.32E-35	0.640016463	0.324	0.219	4.33E-31	10	WDR43
3.36E-35	0.825167372	0.409	0.278	6.26E-31	10	SPG7
3.84E-35	0.725985979	0.287	0.148	7.16E-31	10	SHPRH
3.95E-35	0.707458663	0.329	0.209	7.37E-31	10	MKLN1
4.04E-35	0.629658697	0.238	0.096	7.53E-31	10	NIPAL2
4.94E-35	0.596923335	0.202	0.079	9.21E-31	10	NEK3
5.16E-35	0.621049795	0.147	0.03	9.62E-31	10	PXDNL
6.90E-35	0.722424097	0.345	0.229	1.29E-30	10	VRK2
9.45E-35	0.575445401	0.212	0.089	1.76E-30	10	TRMT11
1.06E-34	0.658574228	0.273	0.144	1.98E-30	10	MYSM1
1.13E-34	0.695684517	0.288	0.163	2.11E-30	10	HEATR5B
1.97E-34	0.721001664	0.297	0.167	3.68E-30	10	AC007569.1
2.08E-34	0.501368897	0.161	0.055	3.88E-30	10	PIGL
2.23E-34	0.814188012	0.362	0.228	4.16E-30	10	ITPR1
2.78E-34	0.751210904	0.429	0.323	5.19E-30	10	MIS18BP1
2.80E-34	0.742632402	0.386	0.264	5.22E-30	10	USP48
2.87E-34	0.674155599	0.308	0.198	5.35E-30	10	NCOA7
3.75E-34	0.57104996	0.21	0.098	7.00E-30	10	NHLRC2
3.89E-34	0.535474479	0.19	0.083	7.26E-30	10	FAM98B
4.10E-34	0.697019855	0.35	0.249	7.64E-30	10	ATXN1
4.88E-34	0.61156862	0.203	0.081	9.11E-30	10	AC093010.2
6.22E-34	0.57431617	0.22	0.105	1.16E-29	10	HS2ST1
6.66E-34	0.639958015	0.287	0.18	1.24E-29	10	AGTPBP1
3.69E-33	0.653859902	0.263	0.135	6.89E-29	10	PTAR1
3.91E-33	0.687681241	0.275	0.154	7.28E-29	10	TMEM63A
4.10E-33	0.606129934	0.234	0.105	7.64E-29	10	UNKL
4.57E-33	0.481057174	0.151	0.047	8.53E-29	10	GCNT2
4.82E-33	0.804456053	0.272	0.132	8.99E-29	10	KLHL14
5.64E-33	0.707966803	0.371	0.244	1.05E-28	10	ETNK1
8.96E-33	1.00665973	0.238	0.102	1.67E-28	10	FCRL2

1.24E-32	0.746763356	0.363	0.237	2.32E-28	10	PUM2
1.58E-32	0.628780288	0.188	0.076	2.95E-28	10	PDGFD
1.62E-32	0.724796565	0.415	0.304	3.03E-28	10	FBXW11
1.67E-32	0.724549247	0.337	0.204	3.12E-28	10	FRY
2.00E-32	0.689470215	0.317	0.208	3.72E-28	10	RICTOR
2.34E-32	0.682809904	0.269	0.135	4.37E-28	10	TBCK
2.49E-32	0.680975986	0.319	0.19	4.65E-28	10	ADAM17
2.65E-32	0.606358467	0.211	0.091	4.94E-28	10	AL662796.1
3.63E-32	0.737381972	0.391	0.281	6.77E-28	10	DNAJB14
3.67E-32	0.657906901	0.262	0.143	6.84E-28	10	ZNF83
4.70E-32	0.616416151	0.208	0.092	8.77E-28	10	ZFP14
5.76E-32	0.675262244	0.331	0.213	1.07E-27	10	ITFG1
6.09E-32	0.720101038	0.377	0.267	1.14E-27	10	ANKRD10
6.71E-32	0.625631907	0.259	0.14	1.25E-27	10	MFN1
9.19E-32	0.670164535	0.305	0.204	1.71E-27	10	INO80D
1.63E-31	0.692459733	0.432	0.331	3.05E-27	10	SPTBN1
2.66E-31	0.583275445	0.251	0.136	4.97E-27	10	ATG14
3.81E-31	0.536243989	0.188	0.079	7.09E-27	10	TMEM117
4.20E-31	0.672228877	0.276	0.144	7.83E-27	10	DDX39B
5.11E-31	0.647688425	0.294	0.179	9.53E-27	10	VPS13D
8.37E-31	0.721556395	0.386	0.279	1.56E-26	10	FAM208A
9.98E-31	0.677678492	0.26	0.139	1.86E-26	10	POU2F1
1.25E-30	0.602627755	0.244	0.124	2.34E-26	10	TMEM41B
1.33E-30	0.718123152	0.359	0.238	2.49E-26	10	MAP4K5
1.54E-30	0.609496892	0.265	0.153	2.86E-26	10	ASCC3
2.50E-30	0.51486537	0.169	0.064	4.66E-26	10	CARF
2.51E-30	0.690742122	0.275	0.15	4.69E-26	10	PHF21A
3.78E-30	0.62201245	0.234	0.119	7.04E-26	10	S100PBP
8.82E-30	0.635395668	0.285	0.172	1.64E-25	10	CLASP2
8.89E-30	0.64448401	0.249	0.119	1.66E-25	10	CARMIL1
1.12E-29	0.635999568	0.248	0.12	2.09E-25	10	SENP7
1.25E-29	0.53052115	0.195	0.076	2.33E-25	10	ASB3
1.65E-29	0.685615314	0.29	0.165	3.08E-25	10	RCOR3
1.87E-29	0.626109549	0.281	0.181	3.49E-25	10	SNX14
2.37E-29	0.670449532	0.306	0.205	4.43E-25	10	CCDC6
4.04E-29	0.575264966	0.21	0.107	7.54E-25	10	VPS8
4.28E-29	0.747211608	0.361	0.258	7.98E-25	10	GLS
8.46E-29	0.527237718	0.184	0.077	1.58E-24	10	ZNF718
9.32E-29	0.587757032	0.266	0.154	1.74E-24	10	CTDSPL2
1.32E-28	0.61436335	0.277	0.176	2.45E-24	10	ARHGEF7
1.52E-28	1.040975646	0.327	0.184	2.84E-24	10	SFTPB
2.14E-28	0.639391921	0.304	0.188	3.99E-24	10	CAPN7
2.41E-28	0.56461779	0.182	0.071	4.49E-24	10	PEX1
3.59E-28	0.64673237	0.271	0.152	6.70E-24	10	ANKZF1
4.69E-28	0.665045914	0.333	0.227	8.74E-24	10	PSMA3-AS1
5.60E-28	0.627334899	0.273	0.149	1.04E-23	10	ARHGAP12

5.85E-28	0.797444935	0.383	0.265	1.09E-23	10	ARHGEF3
6.23E-28	0.611922845	0.234	0.126	1.16E-23	10	PIAS2
8.81E-28	0.70335926	0.257	0.12	1.64E-23	10	ZMAT1
1.08E-27	0.619062856	0.247	0.136	2.01E-23	10	ALDH5A1
1.17E-27	0.561283712	0.204	0.086	2.18E-23	10	MTMR4
1.29E-27	0.5542139	0.212	0.101	2.41E-23	10	SLC25A16
1.30E-27	0.594034742	0.258	0.144	2.42E-23	10	TNKS
1.59E-27	0.523065649	0.178	0.071	2.96E-23	10	ZNF407
1.87E-27	0.662952274	0.291	0.167	3.49E-23	10	ZNF493
2.44E-27	0.700651396	0.376	0.275	4.55E-23	10	CASP8
4.05E-27	0.695570485	0.34	0.222	7.55E-23	10	NLRP1
4.48E-27	0.549788736	0.209	0.101	8.36E-23	10	TPK1
5.57E-27	0.736065319	0.397	0.293	1.04E-22	10	ADD3
5.90E-27	0.728460958	0.301	0.189	1.10E-22	10	ATG16L2
6.68E-27	0.575016108	0.235	0.126	1.25E-22	10	FAM91A1
9.62E-27	0.729227846	0.34	0.229	1.79E-22	10	CRYBG1
1.47E-26	0.475790043	0.164	0.061	2.74E-22	10	WNT16
1.50E-26	0.628061499	0.31	0.207	2.80E-22	10	DYM
1.60E-26	0.527407047	0.202	0.098	2.98E-22	10	VPS13A
1.64E-26	0.644327455	0.312	0.197	3.07E-22	10	TGFBR3
1.92E-26	0.610735286	0.242	0.115	3.58E-22	10	SNX13
1.95E-26	0.649795378	0.278	0.155	3.64E-22	10	MTR
4.24E-26	0.559197709	0.226	0.12	7.90E-22	10	NBAS
4.95E-26	0.635313386	0.297	0.192	9.22E-22	10	KRIT1
5.36E-26	0.666244692	0.295	0.186	1.00E-21	10	ENTPD4
5.78E-26	0.500150448	0.174	0.067	1.08E-21	10	FANCL
6.28E-26	0.631517398	0.246	0.128	1.17E-21	10	RFX3
7.70E-26	0.591467469	0.171	0.069	1.43E-21	10	ZNF860
7.90E-26	0.541867584	0.196	0.09	1.47E-21	10	AP001636.3
1.01E-25	0.719346418	0.22	0.109	1.89E-21	10	TSHZ2
1.41E-25	0.66146763	0.303	0.181	2.62E-21	10	ZMYND8
1.56E-25	0.7523158	0.278	0.167	2.91E-21	10	FCRL1
1.57E-25	0.692380658	0.293	0.17	2.92E-21	10	GPM6A
1.68E-25	0.609326705	0.293	0.188	3.14E-21	10	TPP2
2.51E-25	0.760743913	0.319	0.198	4.69E-21	10	ENTPD1
2.61E-25	0.576414887	0.25	0.145	4.86E-21	10	NAA16
3.76E-25	0.788517961	0.383	0.269	7.01E-21	10	RNASEH2B
5.86E-25	0.663541038	0.248	0.127	1.09E-20	10	SLC39A10
7.76E-25	0.645108909	0.308	0.194	1.45E-20	10	MTG1
1.02E-24	0.49132542	0.162	0.059	1.91E-20	10	PRH1
1.80E-24	0.544740135	0.196	0.087	3.36E-20	10	SLC16A7
2.52E-24	0.65227883	0.309	0.208	4.69E-20	10	RAB3GAP2
2.78E-24	0.555583912	0.196	0.085	5.17E-20	10	POLG2
3.08E-24	0.565312119	0.228	0.117	5.74E-20	10	THADA
3.12E-24	0.528958037	0.208	0.101	5.82E-20	10	MAP3K4
7.97E-24	0.674501957	0.29	0.164	1.49E-19	10	DIP2A

6.29E-23	0.628993158	0.256	0.152	1.17E-18	10	IKBKB
9.64E-23	0.686443564	0.323	0.217	1.80E-18	10	POLK
9.88E-23	0.601699102	0.246	0.138	1.84E-18	10	CTC1
3.15E-21	0.538471261	0.203	0.103	5.87E-17	10	TUBGCP3
5.13E-21	0.59356263	0.258	0.157	9.55E-17	10	KIAA1468
7.30E-21	0.553472135	0.214	0.105	1.36E-16	10	TEP1
1.96E-19	0.62751572	0.304	0.201	3.65E-15	10	NUP107
4.98E-19	0.551582532	0.194	0.084	9.28E-15	10	TMEM168
7.89E-19	0.478714298	0.356	0.244	1.47E-14	10	AC007952.4
1.80E-11	0.392357362	0.649	0.764	3.35E-07	10	EIF4G2
4.25E-11	0.33170189	0.636	0.744	7.92E-07	10	MORF4L1
1.71E-06	0.262596333	0.264	0.38	0.031890442	10	DBNL
0.000257716	0.327081809	0.555	0.686	1	10	SEC62
0.000568369	0.373803789	0.554	0.671	1	10	Sep-06
0.003902834	0.264388073	0.284	0.417	1	10	FBXO7
0.009179654	0.266371842	0.324	0.445	1	10	STAT6
0	3.050406937	0.998	0.54	0	11	FOS
0	2.996633528	0.803	0.13	0	11	ATF3
0	2.71371127	1	0.714	0	11	DUSP1
0	2.683368188	0.998	0.665	0	11	CD69
0	2.600467588	0.986	0.283	0	11	DNAJB1
0	2.595925063	0.988	0.529	0	11	DUSP2
0	2.45139147	0.939	0.345	0	11	GADD45B
0	2.42153934	0.984	0.201	0	11	EGR1
0	2.41446588	0.994	0.376	0	11	NR4A1
0	2.356079729	0.755	0.04	0	11	HES1
0	2.334127074	0.99	0.62	0	11	PMAIP1
0	2.307580188	1	0.526	0	11	FOSB
0	2.285964096	0.999	0.668	0	11	CD83
0	2.260755144	0.919	0.165	0	11	KLF4
0	2.254638205	0.993	0.661	0	11	NFKBIA
0	2.231867029	0.998	0.841	0	11	HSP90AA1
0	2.052613316	0.994	0.547	0	11	DNAJA1
0	2.022719899	0.994	0.505	0	11	NR4A2
0	2.020977072	0.983	0.559	0	11	IRF1
0	1.985924094	0.993	0.589	0	11	IER2
0	1.9442259	0.958	0.336	0	11	DDIT3
0	1.851511078	0.997	0.672	0	11	PPP1R15A
0	1.846855078	0.828	0.188	0	11	HSPA1B
0	1.825851534	0.996	0.778	0	11	HSPA8
0	1.733740332	0.999	0.735	0	11	JUN
0	1.662280048	0.944	0.432	0	11	RGS2
0	1.605714158	0.989	0.675	0	11	BRD2
0	1.568760701	0.999	0.87	0	11	HSP90AB1
0	1.546073138	0.992	0.775	0	11	SQSTM1
0	1.542508765	0.972	0.528	0	11	RSRC2

0	1.513120122	0.953	0.477	0	11	TUBB4B
0	1.490122271	1	0.841	0	11	ZFP36
0	1.456670079	0.91	0.309	0	11	HSPH1
0	1.369231699	0.981	0.722	0	11	EIF4A2
0	1.352205533	0.838	0.254	0	11	NEU1
0	1.349126242	0.985	0.648	0	11	CCNL1
0	1.322822344	0.8	0.156	0	11	UBE2S
0	1.310517046	0.971	0.604	0	11	SRSF3
0	1.27630276	0.864	0.245	0	11	NR4A3
0	1.270912071	0.99	0.754	0	11	SRSF7
0	1.259373091	0.876	0.301	0	11	RASGEF1B
0	1.2470554	0.841	0.234	0	11	TYROBP
0	1.230391308	0.998	0.849	0	11	KLF6
0	1.219079972	0.967	0.627	0	11	DDX3X
0	1.203547206	0.824	0.234	0	11	ZC3H12A
0	1.136143965	0.965	0.642	0	11	TRA2B
0	1.132732792	0.602	0.043	0	11	RND1
0	1.014013598	0.881	0.332	0	11	IFRD1
0	0.957443716	0.965	0.711	0	11	EIF5
5.50E-294	1.079259152	0.973	0.657	1.03E-289	11	CCR7
2.53E-291	1.227085622	0.923	0.441	4.72E-287	11	CDKN1A
1.29E-287	1.900294679	0.772	0.268	2.41E-283	11	RGS1
6.07E-282	1.747360071	0.69	0.155	1.13E-277	11	HSPA1A
2.19E-281	1.010793722	0.961	0.667	4.09E-277	11	PRDM2
2.75E-276	0.926389401	0.872	0.4	5.13E-272	11	GTF2B
2.18E-275	0.978092931	0.96	0.621	4.06E-271	11	HERPUD1
4.36E-275	1.170534126	0.742	0.225	8.14E-271	11	PNP
7.41E-268	0.992204024	0.81	0.319	1.38E-263	11	EIF4A3
4.82E-263	1.401745523	0.616	0.101	8.98E-259	11	ICAM1
1.54E-262	0.846378091	0.813	0.326	2.86E-258	11	ZFAND5
5.04E-260	0.881204543	0.96	0.741	9.40E-256	11	ZFAS1
1.37E-258	0.974473566	0.84	0.326	2.55E-254	11	PPP1R10
2.74E-258	0.884125906	0.853	0.346	5.11E-254	11	HBP1
3.45E-257	1.010328458	0.876	0.426	6.43E-253	11	HSPD1
6.67E-252	0.967306386	0.887	0.511	1.24E-247	11	NOP58
8.75E-252	1.04102303	0.591	0.079	1.63E-247	11	EGR2
2.49E-248	0.894546094	0.844	0.386	4.63E-244	11	TANK
1.32E-247	0.99828377	0.998	0.823	2.47E-243	11	JUNB
1.77E-247	0.894387455	0.783	0.277	3.29E-243	11	TIPARP
2.83E-241	1.013932247	0.889	0.41	5.27E-237	11	ZNF331
2.24E-238	0.832216708	0.623	0.122	4.18E-234	11	DNAJB4
3.55E-237	0.920023367	0.952	0.648	6.61E-233	11	TUBA1A
1.93E-236	0.819509605	0.747	0.227	3.61E-232	11	DEDD2
1.78E-232	1.138798621	0.692	0.193	3.32E-228	11	GLA
9.62E-230	0.945661274	0.878	0.52	1.79E-225	11	RPL22L1
6.60E-227	1.445223996	0.608	0.13	1.23E-222	11	TNF

1.39E-225	0.944715866	0.918	0.547	2.60E-221	11	ODC1
4.23E-219	0.935129051	0.771	0.294	7.88E-215	11	SERTAD1
7.63E-219	0.803929121	0.762	0.288	1.42E-214	11	NAMPT
5.73E-216	0.74141314	0.827	0.384	1.07E-211	11	DNAJB6
4.28E-214	0.902527252	0.511	0.068	7.99E-210	11	BAG3
4.45E-213	0.871863744	0.959	0.67	8.29E-209	11	TUBA1B
7.28E-211	0.998494818	0.854	0.401	1.36E-206	11	KLF2
1.38E-209	0.790257496	0.932	0.609	2.58E-205	11	SRSF2
8.04E-207	0.754174267	0.926	0.597	1.50E-202	11	PIM2
9.13E-206	0.815165051	0.513	0.063	1.70E-201	11	PLK2
3.04E-203	0.940135239	0.658	0.182	5.66E-199	11	DDIT4
1.24E-201	0.897508173	0.723	0.248	2.31E-197	11	SNHG12
3.17E-201	0.932803896	0.637	0.158	5.91E-197	11	CITED2
1.18E-200	0.712653954	0.84	0.397	2.20E-196	11	SLC38A2
8.11E-200	0.633378135	0.417	0.024	1.51E-195	11	DNAJA4
4.93E-197	0.563292551	0.582	0.145	9.19E-193	11	SLC25A33
1.50E-196	0.924924577	0.923	0.635	2.81E-192	11	NOSIP
1.26E-194	0.608642376	0.515	0.073	2.34E-190	11	RORA
2.46E-194	0.710075481	0.626	0.174	4.58E-190	11	ZNF296
4.90E-193	0.674468507	0.917	0.538	9.14E-189	11	NFKBID
9.26E-192	0.791446638	0.753	0.3	1.73E-187	11	MAP3K8
6.78E-191	0.732535952	0.647	0.193	1.26E-186	11	TUBA1C
2.69E-188	0.937570001	0.457	0.045	5.02E-184	11	IER3
7.42E-186	0.738541538	0.925	0.593	1.38E-181	11	ARID5B
9.38E-183	0.892822866	0.881	0.572	1.75E-178	11	PRDX1
5.44E-181	0.74626464	0.622	0.176	1.01E-176	11	CKS2
1.26E-178	0.625212404	0.943	0.662	2.35E-174	11	DDX24
2.27E-176	0.726754834	0.742	0.269	4.23E-172	11	GLUL
2.68E-176	0.753764815	0.649	0.202	4.99E-172	11	H2AFX
2.43E-174	0.685131016	0.914	0.583	4.53E-170	11	ELF1
9.75E-170	0.839151855	0.928	0.607	1.82E-165	11	TAGAP
2.84E-169	0.567760285	0.963	0.72	5.30E-165	11	SAT1
8.77E-169	0.721357098	0.619	0.185	1.64E-164	11	ZFAND2A
9.91E-169	0.454629204	0.521	0.096	1.85E-164	11	XIST
5.10E-168	0.731896476	0.519	0.108	9.52E-164	11	ANKRD37
8.14E-165	0.522768688	0.69	0.254	1.52E-160	11	CWC25
1.44E-163	0.722397811	0.479	0.112	2.68E-159	11	SOCS3
2.75E-159	0.51216425	0.892	0.573	5.13E-155	11	ARID4B
5.81E-158	0.67219097	0.395	0.035	1.08E-153	11	CHRNA1
5.37E-155	0.611520615	0.884	0.495	1.00E-150	11	BIRC3
1.01E-154	0.697893268	0.854	0.462	1.89E-150	11	GPR183
6.38E-153	0.580257255	0.46	0.082	1.19E-148	11	FCRL3
1.83E-152	0.436864419	0.384	0.04	3.41E-148	11	AC007364.1
3.01E-152	0.529657101	0.953	0.715	5.61E-148	11	REL
1.21E-151	0.613057356	0.697	0.274	2.26E-147	11	IVNS1ABP
1.76E-150	0.542507141	0.749	0.346	3.28E-146	11	NASP

3.31E-150	0.519873186	0.827	0.424	6.17E-146	11	CLK1
8.54E-150	0.578471976	0.971	0.724	1.59E-145	11	YPEL5
4.93E-149	0.59712441	0.684	0.245	9.19E-145	11	FAM53C
1.38E-148	0.591157079	0.538	0.14	2.57E-144	11	DUSP5
4.58E-148	0.621828226	0.633	0.204	8.54E-144	11	PDE4DIP
1.99E-144	0.554460241	0.743	0.34	3.72E-140	11	TSPYL2
4.40E-143	0.566566404	0.582	0.177	8.20E-139	11	C12orf65
9.37E-143	0.634926019	0.792	0.432	1.75E-138	11	IDI1
2.27E-141	0.491149011	0.512	0.137	4.24E-137	11	JMJD6
8.99E-140	0.563670473	0.736	0.355	1.68E-135	11	SINHCAF
9.20E-140	0.533138385	0.862	0.498	1.71E-135	11	SBDS
3.82E-139	0.629859125	0.461	0.091	7.12E-135	11	BCL2L1
4.97E-139	0.518079365	0.98	0.839	9.27E-135	11	CALM1
3.59E-138	0.707370039	0.711	0.294	6.70E-134	11	NFKBIZ
3.89E-135	0.598977391	0.851	0.513	7.24E-131	11	CYCS
4.29E-135	0.516057744	0.656	0.25	8.00E-131	11	DNAJB9
1.17E-134	0.564722583	0.329	0.042	2.19E-130	11	SGK1
6.93E-133	0.417539676	0.32	0.029	1.29E-128	11	EGR3
2.03E-132	0.563396466	0.734	0.338	3.79E-128	11	STMN1
1.14E-129	0.457390012	0.603	0.195	2.12E-125	11	KANSL2
4.18E-129	0.335755231	0.46	0.096	7.80E-125	11	FCRL2
1.65E-128	0.4646374	0.843	0.501	3.08E-124	11	UVRAG
5.19E-128	0.541803793	0.663	0.253	9.68E-124	11	TFRC
6.40E-128	0.49033115	0.723	0.295	1.19E-123	11	AC020916.1
4.82E-127	0.384687525	0.956	0.785	8.98E-123	11	FUS
1.47E-126	0.474274585	0.675	0.288	2.75E-122	11	PLAC8
3.43E-125	0.572655541	0.834	0.475	6.40E-121	11	TUBA4A
5.70E-125	0.477531894	0.687	0.303	1.06E-120	11	OSER1
3.41E-124	0.45059362	0.972	0.818	6.35E-120	11	RHOH
4.23E-124	0.555523147	0.722	0.351	7.89E-120	11	ATP6V0D1
3.40E-123	0.407613151	0.909	0.65	6.33E-119	11	CHD2
1.13E-122	0.547110638	0.479	0.129	2.11E-118	11	ARL5B
1.31E-122	0.567711086	0.808	0.464	2.43E-118	11	HSPE1
9.25E-122	0.918613514	0.952	0.743	1.72E-117	11	HIST1H4C
3.23E-121	0.599484129	0.903	0.618	6.02E-117	11	NEAT1
4.10E-121	0.473815223	0.768	0.413	7.65E-117	11	AZIN1
1.44E-120	0.459057676	0.278	0.016	2.68E-116	11	HSPA2
2.70E-120	0.474499594	0.594	0.234	5.03E-116	11	AHSA1
3.35E-120	0.878716478	0.889	0.637	6.25E-116	11	LTB
3.92E-120	0.603712983	0.842	0.513	7.31E-116	11	MAP1LC3B
5.66E-120	0.534430012	0.706	0.342	1.05E-115	11	SDCBP
1.72E-119	0.539894015	0.786	0.428	3.21E-115	11	YME1L1
4.52E-119	0.564446308	0.876	0.559	8.43E-115	11	DYNLL1
1.73E-118	0.520706465	0.767	0.397	3.23E-114	11	CSRNP1
7.75E-117	0.466715638	0.813	0.456	1.45E-112	11	AMD1
3.59E-116	0.480062936	0.303	0.025	6.69E-112	11	ID2

1.62E-115	0.494745816	0.627	0.25	3.01E-111	11	HNRNPAB
1.72E-115	0.681153828	0.631	0.284	3.21E-111	11	TOR3A
6.85E-115	0.506661164	0.845	0.51	1.28E-110	11	TOP1
6.87E-115	0.478274784	0.766	0.382	1.28E-110	11	OFD1
2.82E-113	0.397207777	0.428	0.095	5.26E-109	11	SIRT1
4.39E-113	0.434974808	0.867	0.561	8.19E-109	11	TAF1D
2.60E-112	0.472489174	0.853	0.518	4.85E-108	11	ATP2B1
6.75E-112	0.420799321	0.562	0.213	1.26E-107	11	PPP1R15B
7.97E-112	0.505205869	0.831	0.462	1.49E-107	11	LMNA
1.79E-111	0.322496964	0.354	0.07	3.34E-107	11	PPP1R9A
2.04E-111	0.417383009	0.934	0.717	3.80E-107	11	LYN
4.28E-111	0.544665906	0.951	0.766	7.98E-107	11	UBB
8.48E-111	0.633445305	0.791	0.434	1.58E-106	11	KLF10
1.37E-110	0.384978157	0.608	0.256	2.56E-106	11	RRAS2
6.55E-110	0.439562915	0.442	0.107	1.22E-105	11	HRK
1.21E-109	0.417550758	0.615	0.246	2.26E-105	11	CARS2
1.38E-108	0.622368128	0.619	0.243	2.57E-104	11	TNFAIP3
1.63E-108	0.57926747	0.494	0.18	3.04E-104	11	DUSP10
3.11E-108	0.373933315	0.236	0.008	5.80E-104	11	GADD45G
3.17E-108	0.438946528	0.84	0.508	5.91E-104	11	WSB1
4.26E-108	0.438735961	0.583	0.225	7.95E-104	11	TSC22D2
1.14E-106	0.362290804	0.987	0.806	2.12E-102	11	CXCR4
1.54E-105	0.412839862	0.728	0.384	2.86E-101	11	BUD31
3.23E-105	0.460970993	0.909	0.664	6.02E-101	11	CALR
3.80E-105	0.366650497	0.368	0.085	7.09E-101	11	LGMN
3.22E-103	0.504117435	0.659	0.274	6.00E-99	11	MARCKSL1
3.81E-103	0.411536392	0.474	0.15	7.10E-99	11	SLC1A5
4.97E-103	0.400595196	0.53	0.193	9.26E-99	11	ATG101
5.93E-103	0.530191152	0.864	0.603	1.11E-98	11	SAP18
8.73E-103	0.273307305	0.254	0.03	1.63E-98	11	CA8
2.85E-102	0.447924482	0.564	0.188	5.32E-98	11	SERPINF1
3.94E-102	0.403789491	0.848	0.549	7.35E-98	11	SFPQ
3.58E-101	0.42305555	0.487	0.162	6.67E-97	11	PRR7
8.40E-101	0.276244767	0.357	0.087	1.57E-96	11	RABGEF1
2.36E-100	0.360368285	0.699	0.368	4.40E-96	11	CSNK1D
2.97E-100	0.33666406	0.512	0.18	5.54E-96	11	SAMD8
7.84E-100	0.53251092	0.793	0.458	1.46E-95	11	CXCR5
1.17E-98	0.470337648	0.834	0.564	2.18E-94	11	ATP6V0E1
5.85E-98	0.770591979	0.262	0.024	1.09E-93	11	EGR4
7.90E-98	0.533149423	0.521	0.195	1.47E-93	11	TWISTNB
1.59E-97	0.365871144	0.537	0.207	2.97E-93	11	NUDT4
2.95E-97	0.396407944	0.758	0.433	5.50E-93	11	BACH1
3.37E-97	0.367169404	0.544	0.21	6.29E-93	11	MYLIP
3.93E-97	0.340562935	0.369	0.069	7.32E-93	11	CYBB
7.72E-97	0.315724884	0.291	0.04	1.44E-92	11	NET1
1.41E-96	0.28594176	0.292	0.036	2.62E-92	11	HCK

6.73E-96	0.331727368	0.626	0.266	1.25E-91	11	ZNF394
9.25E-96	0.405380226	0.522	0.192	1.72E-91	11	TOB1
1.16E-95	0.403303995	0.916	0.69	2.15E-91	11	LITAF
2.86E-95	0.423671863	0.606	0.273	5.33E-91	11	ARL4A
4.48E-94	0.388792887	0.712	0.372	8.36E-90	11	CHD4
1.86E-93	0.428658173	0.657	0.343	3.46E-89	11	PHACTR1
3.50E-93	0.542011938	0.98	0.83	6.53E-89	11	BTG2
5.39E-93	0.525443469	0.845	0.554	1.00E-88	11	TPI1
5.60E-93	0.336749159	0.634	0.304	1.04E-88	11	CREBRF
1.16E-92	0.473782303	0.307	0.056	2.16E-88	11	RGS16
3.48E-92	0.384581767	0.475	0.18	6.49E-88	11	IER5
5.85E-92	0.362980196	0.769	0.481	1.09E-87	11	ZC3H15
5.96E-92	0.7776032	0.23	0.02	1.11E-87	11	RRAD
1.86E-91	0.325144878	0.523	0.204	3.46E-87	11	YAF2
8.34E-89	0.307216869	0.306	0.046	1.55E-84	11	GTSF1
1.42E-88	0.336752746	0.562	0.234	2.65E-84	11	TOB2
1.94E-88	0.396369837	0.691	0.362	3.61E-84	11	KDM2A
6.89E-88	0.35039458	0.77	0.465	1.28E-83	11	SNX9
1.85E-87	0.402958108	0.788	0.476	3.45E-83	11	HNRNPH3
3.94E-87	0.368794885	0.803	0.492	7.35E-83	11	RAP1B
2.03E-86	0.308315305	0.475	0.166	3.79E-82	11	APBB2
4.00E-86	0.330099933	0.511	0.179	7.46E-82	11	ZBTB10
4.42E-86	0.311314577	0.35	0.101	8.23E-82	11	ATP1B1
2.30E-85	0.327743992	0.658	0.316	4.29E-81	11	CIR1
3.46E-85	0.357141423	0.417	0.142	6.45E-81	11	NFKBIE
1.18E-84	0.399128873	0.963	0.783	2.19E-80	11	TXNIP
4.03E-83	0.27042814	0.348	0.091	7.51E-79	11	CHKA
4.75E-83	0.3237296	0.594	0.284	8.85E-79	11	BCL7B
6.61E-83	0.258456073	0.358	0.105	1.23E-78	11	MEPCE
9.28E-83	0.381251526	0.851	0.542	1.73E-78	11	HSPA5
1.30E-82	0.477370833	0.46	0.174	2.43E-78	11	TRAF1
1.40E-82	0.357608836	0.664	0.319	2.61E-78	11	ETF1
2.85E-82	0.685191419	0.369	0.105	5.32E-78	11	GEM
3.77E-82	0.37536714	0.331	0.074	7.03E-78	11	GRASP
4.16E-82	0.305920531	0.451	0.158	7.76E-78	11	NBPF10
9.82E-82	0.385173129	0.366	0.098	1.83E-77	11	MARCKS
1.24E-81	0.324985168	0.575	0.261	2.30E-77	11	ARIH1
1.83E-81	0.297583741	0.196	0.011	3.40E-77	11	BAMBI
2.58E-81	0.36651414	0.827	0.532	4.80E-77	11	BZW1
4.81E-80	0.281984578	0.526	0.223	8.96E-76	11	NFKBIB
6.98E-80	0.364947065	0.716	0.39	1.30E-75	11	DDX39A
7.49E-80	0.425667761	0.384	0.117	1.40E-75	11	SOCS1
8.25E-80	0.259525847	0.209	0.016	1.54E-75	11	SNAI1
9.82E-80	0.300435753	0.61	0.287	1.83E-75	11	COQ10B
1.07E-79	0.251931252	0.362	0.112	2.00E-75	11	SLC16A1
1.17E-79	0.293098136	0.485	0.194	2.18E-75	11	EEA1

3.22E-79	0.396497689	0.747	0.417	6.01E-75	11	FGR
4.55E-79	0.42226925	0.866	0.629	8.48E-75	11	SOD1
7.02E-79	0.425320657	0.983	0.876	1.31E-74	11	TSC22D3
8.34E-79	0.359985241	0.627	0.308	1.55E-74	11	PAF1
8.43E-79	0.287215522	0.411	0.132	1.57E-74	11	ATF1
9.34E-79	0.282167626	0.384	0.125	1.74E-74	11	NABP1
2.90E-78	0.419339909	0.245	0.037	5.41E-74	11	PHLDA1
4.44E-78	0.323333799	0.429	0.159	8.27E-74	11	MAP1LC3A
1.48E-77	0.337097387	0.234	0.046	2.76E-73	11	ARG2
2.80E-77	0.35405773	0.573	0.255	5.21E-73	11	RHEB
4.64E-75	0.285053889	0.611	0.285	8.65E-71	11	PER1
4.12E-74	0.284483429	0.284	0.073	7.68E-70	11	RNF144B
4.51E-74	0.355294041	0.496	0.204	8.40E-70	11	ZNF106
6.25E-74	0.304180462	0.393	0.126	1.16E-69	11	JMY
1.11E-73	0.374408017	0.613	0.275	2.06E-69	11	NBPF14
5.55E-73	0.328468798	0.712	0.411	1.03E-68	11	DENND4A
1.18E-72	0.284507131	0.495	0.201	2.21E-68	11	CHORDC1
1.42E-72	0.390923893	0.734	0.432	2.65E-68	11	ATF4
1.64E-72	0.424941846	0.645	0.333	3.07E-68	11	SERPINB9
5.80E-72	0.316169647	0.682	0.36	1.08E-67	11	NFE2L2
1.88E-71	0.395318994	0.425	0.156	3.50E-67	11	PPIF
7.25E-71	0.266632487	0.663	0.357	1.35E-66	11	GOLGB1
3.48E-70	0.289421196	0.722	0.421	6.49E-66	11	STK17A
4.05E-70	0.270779205	0.516	0.218	7.55E-66	11	SEMA4B
3.62E-69	0.304824093	0.584	0.272	6.75E-65	11	RSBN1
4.89E-68	0.301343497	0.151	0.007	9.12E-64	11	C6orf222
5.57E-68	0.272711328	0.805	0.509	1.04E-63	11	GPBP1
1.23E-67	0.356502687	0.332	0.091	2.29E-63	11	ID1
5.90E-67	0.293040988	0.607	0.302	1.10E-62	11	ATF5
7.72E-67	0.252951053	0.51	0.249	1.44E-62	11	RAB8B
1.50E-66	0.500312366	0.771	0.501	2.79E-62	11	RGCC
1.95E-66	0.328624777	0.664	0.362	3.64E-62	11	WTAP
2.78E-66	0.309122578	0.41	0.151	5.18E-62	11	TLE1
5.78E-66	0.27010276	0.49	0.202	1.08E-61	11	SLC20A1
7.67E-66	0.278681517	0.71	0.389	1.43E-61	11	TRA2A
1.58E-65	0.658498821	0.617	0.344	2.94E-61	11	HSPB1
7.96E-65	0.274396635	0.526	0.238	1.48E-60	11	BCL2L11
9.53E-65	1.411107533	0.168	0.015	1.78E-60	11	HSPA6
1.34E-64	0.397115209	0.964	0.852	2.49E-60	11	NPM1
1.72E-64	0.28140044	0.342	0.11	3.20E-60	11	AL121944.1
5.57E-64	0.294332887	0.542	0.26	1.04E-59	11	WHAMM
7.44E-64	0.299788955	0.831	0.539	1.39E-59	11	CD79B
1.80E-63	0.287838368	0.699	0.371	3.36E-59	11	CCDC191
2.60E-63	0.338017003	0.926	0.731	4.85E-59	11	ZFP36L2
7.30E-63	0.432696924	0.539	0.253	1.36E-58	11	KDM2B
8.21E-63	0.487145595	0.649	0.388	1.53E-58	11	PIM3

1.41E-62	0.304986188	0.838	0.585	2.63E-58	11	BCLAF1
1.78E-62	0.250505942	0.164	0.012	3.32E-58	11	IFI27
1.81E-62	0.261523462	0.336	0.1	3.38E-58	11	SLC37A1
4.43E-62	0.262624981	0.322	0.108	8.25E-58	11	ZBTB2
6.82E-62	0.26066866	0.507	0.23	1.27E-57	11	GLIPR1
1.63E-61	0.289114098	0.807	0.567	3.04E-57	11	AC016831.7
1.92E-61	0.287492236	0.577	0.293	3.58E-57	11	NOP56
5.33E-61	0.390502024	0.674	0.388	9.94E-57	11	INSIG1
9.89E-61	0.412720512	0.754	0.469	1.84E-56	11	RILPL2
4.31E-60	0.296444962	0.667	0.389	8.04E-56	11	SYAP1
4.42E-59	0.324486606	0.774	0.527	8.24E-55	11	CIB1
8.82E-59	0.302089816	0.478	0.216	1.64E-54	11	BCL3
6.20E-58	0.318156427	0.912	0.718	1.16E-53	11	TMBIM6
9.50E-58	0.485595974	0.733	0.478	1.77E-53	11	H2AFZ
3.57E-57	0.352861056	0.458	0.217	6.65E-53	11	METTL21A
6.35E-57	0.274225958	0.562	0.308	1.18E-52	11	EHD1
6.44E-57	0.295883319	0.875	0.681	1.20E-52	11	YBX3
9.90E-57	0.257838731	0.472	0.226	1.85E-52	11	MRPS6
5.87E-56	0.301160648	0.576	0.292	1.09E-51	11	SNHG7
7.56E-56	0.308241633	0.861	0.636	1.41E-51	11	IRF8
1.41E-55	0.270741026	0.39	0.166	2.63E-51	11	STX11
1.17E-53	0.269439831	0.824	0.557	2.17E-49	11	DDX21
2.68E-53	0.257707915	0.336	0.127	4.99E-49	11	FAM210A
2.86E-53	0.382626234	0.421	0.18	5.34E-49	11	MRPL18
7.24E-53	0.255644549	0.866	0.681	1.35E-48	11	SERP1
7.56E-51	0.284901329	0.761	0.493	1.41E-46	11	VDAC2
2.37E-50	0.308769476	0.759	0.516	4.41E-46	11	SNHG8
9.02E-50	0.309237903	0.507	0.242	1.68E-45	11	PLEK
1.09E-49	0.259085363	0.227	0.07	2.04E-45	11	AREG
6.77E-48	0.25462896	0.165	0.035	1.26E-43	11	RASD1
1.61E-47	0.316469234	0.781	0.546	3.00E-43	11	PELI1
3.63E-46	0.341499549	0.577	0.298	6.76E-42	11	H1FX
1.23E-44	0.256917259	0.553	0.323	2.29E-40	11	PEA15
1.35E-44	0.253953278	0.517	0.287	2.51E-40	11	JPT1
1.38E-43	0.355330209	0.439	0.205	2.58E-39	11	PTGER4
6.76E-43	0.273959178	0.979	0.872	1.26E-38	11	CFL1
6.03E-34	0.336427425	0.199	0.069	1.12E-29	11	CCL5
8.31E-25	0.40121643	0.149	0.044	1.55E-20	11	IFIT2
1.24E-24	0.271208536	0.846	0.68	2.32E-20	11	ATP6V0C
8.80E-24	0.851816063	0.199	0.075	1.64E-19	11	CCL4
2.49E-21	0.356901104	0.693	0.514	4.64E-17	11	HIST1H1E
7.51E-49	0.265033843	0.217	0.515	1.40E-44	12	PAPOLA
3.71E-48	0.261918851	0.177	0.45	6.92E-44	12	NT5C
6.02E-47	0.251357789	0.173	0.445	1.12E-42	12	SCAND1
7.10E-46	0.251685859	0.168	0.414	1.32E-41	12	SEC31A
3.97E-44	0.314852014	0.235	0.542	7.41E-40	12	HADHA

4.17E-43	0.25435129	0.163	0.409	7.78E-39	12	GLO1
4.95E-43	0.278403447	0.272	0.599	9.23E-39	12	CD53
2.24E-42	0.259361643	0.252	0.596	4.18E-38	12	THRAP3
4.90E-42	0.262961087	0.252	0.569	9.14E-38	12	CNPY3
5.65E-40	0.293008878	0.177	0.409	1.05E-35	12	SMARCA5
7.06E-40	0.308073325	0.24	0.529	1.32E-35	12	ABI1
9.08E-40	0.262158961	0.212	0.515	1.69E-35	12	SPCS1
1.69E-39	0.254378681	0.138	0.334	3.15E-35	12	DGKA
7.18E-39	0.254279654	0.131	0.329	1.34E-34	12	CDK12
7.69E-39	0.265616336	0.161	0.404	1.43E-34	12	ACIN1
8.80E-39	0.258223224	0.176	0.427	1.64E-34	12	HMGB2
4.08E-38	0.284985308	0.19	0.451	7.60E-34	12	SERPINB1
5.27E-38	0.270696201	0.217	0.503	9.83E-34	12	EIF1B
1.15E-37	0.270240062	0.157	0.382	2.14E-33	12	TAOK3
1.48E-37	0.29097137	0.255	0.551	2.76E-33	12	GTF3A
2.04E-37	0.257018836	0.206	0.473	3.80E-33	12	SECISBP2L
2.29E-37	0.268468958	0.157	0.389	4.26E-33	12	ANAPC5
5.66E-37	0.273711952	0.192	0.444	1.06E-32	12	ATOX1
6.27E-37	0.259715147	0.186	0.424	1.17E-32	12	PRPF4B
6.79E-37	0.261080779	0.148	0.384	1.27E-32	12	OS9
1.42E-36	0.267583786	0.19	0.466	2.65E-32	12	NDFIP1
1.89E-36	0.254599077	0.119	0.294	3.53E-32	12	SUN1
2.28E-36	0.267698415	0.225	0.518	4.25E-32	12	Sep-02
2.90E-36	0.291045266	0.134	0.313	5.40E-32	12	RBL2
3.52E-36	0.28269528	0.163	0.396	6.56E-32	12	DNAJC15
6.35E-36	0.281192383	0.174	0.423	1.18E-31	12	RBBP4
7.75E-36	0.271135093	0.202	0.483	1.44E-31	12	PNRC2
9.76E-36	0.305450788	0.171	0.42	1.82E-31	12	IK
1.07E-35	0.304160419	0.186	0.399	2.00E-31	12	ASH1L
2.46E-35	0.252407021	0.105	0.262	4.58E-31	12	BIN2
3.62E-35	0.25367135	0.174	0.424	6.75E-31	12	U2SURP
4.23E-35	0.267884057	0.112	0.286	7.88E-31	12	Mar-07
4.78E-35	0.25111176	0.203	0.472	8.91E-31	12	NIPBL
5.39E-35	0.254168187	0.256	0.571	1.00E-30	12	ACTR2
6.71E-35	0.260879243	0.137	0.338	1.25E-30	12	HSD17B11
7.35E-35	0.283226373	0.254	0.537	1.37E-30	12	TNRC6B
1.28E-34	0.272386397	0.176	0.406	2.38E-30	12	RNMT
2.16E-34	0.259718004	0.188	0.431	4.03E-30	12	UBE2J1
2.96E-34	0.277576877	0.168	0.39	5.52E-30	12	UPF3A
1.14E-33	0.250758435	0.156	0.363	2.13E-29	12	SREK1
1.29E-33	0.278798471	0.203	0.47	2.41E-29	12	ACAP2
1.78E-33	0.279286915	0.125	0.285	3.31E-29	12	CASP8
3.89E-33	0.271458382	0.207	0.447	7.25E-29	12	CFLAR
9.43E-33	0.272796665	0.222	0.492	1.76E-28	12	B4GALT1
9.59E-33	0.330814697	0.178	0.406	1.79E-28	12	CANX
1.04E-32	0.307219565	0.281	0.591	1.94E-28	12	PSAP

1.24E-32	0.309510264	0.258	0.566	2.31E-28	12	ILF3
1.62E-32	0.28674815	0.246	0.546	3.02E-28	12	SMDT1
1.63E-32	0.288608204	0.2	0.472	3.04E-28	12	LTA4H
1.72E-32	0.260130345	0.098	0.253	3.21E-28	12	IRF2
8.89E-32	0.297359928	0.157	0.353	1.66E-27	12	ZNF644
1.22E-31	0.25988301	0.279	0.622	2.27E-27	12	PPP1CC
2.13E-31	0.298733779	0.174	0.404	3.96E-27	12	BTK
2.19E-31	0.291658779	0.199	0.445	4.08E-27	12	CCDC69
2.21E-31	0.26914815	0.167	0.38	4.13E-27	12	PAX5
4.03E-31	0.276066685	0.182	0.409	7.52E-27	12	CHD9
4.77E-31	0.253709083	0.186	0.411	8.89E-27	12	ATM
4.85E-31	0.284848647	0.129	0.312	9.05E-27	12	TBC1D1
5.35E-31	0.28380665	0.272	0.561	9.98E-27	12	EVL
7.06E-31	0.257059755	0.116	0.304	1.32E-26	12	SSR1
7.68E-31	0.341529452	0.202	0.44	1.43E-26	12	SPCS2
1.02E-30	0.252696424	0.162	0.387	1.91E-26	12	GLG1
1.05E-30	0.251465953	0.311	0.65	1.96E-26	12	MTDH
1.31E-30	0.250207484	0.131	0.312	2.45E-26	12	FRYL
1.49E-30	0.285212345	0.111	0.272	2.77E-26	12	PARVG
2.18E-30	0.314113027	0.21	0.465	4.07E-26	12	ARL6IP5
9.35E-30	0.323748038	0.233	0.512	1.74E-25	12	EIF2S3
9.95E-30	0.317390827	0.219	0.455	1.85E-25	12	CD19
1.79E-29	0.327713843	0.169	0.383	3.33E-25	12	SETX
8.85E-29	0.268280253	0.16	0.372	1.65E-24	12	TBC1D22A
1.10E-28	0.302916283	0.274	0.596	2.05E-24	12	MSN
1.52E-28	0.300122432	0.169	0.364	2.84E-24	12	UGCG
2.17E-28	0.275434611	0.225	0.453	4.05E-24	12	SMIM14
5.05E-28	0.277014069	0.107	0.268	9.41E-24	12	NDUFB5
5.59E-28	0.325223992	0.143	0.334	1.04E-23	12	ANP32E
6.95E-28	0.274778801	0.157	0.349	1.30E-23	12	SCAF4
1.01E-27	0.302991806	0.202	0.439	1.88E-23	12	EBLN3P
1.19E-27	0.257742274	0.108	0.285	2.23E-23	12	CACYBP
1.26E-27	0.268472944	0.18	0.413	2.34E-23	12	WDFY4
3.67E-27	0.267231931	0.206	0.45	6.84E-23	12	PTPN22
5.27E-27	0.261338319	0.1	0.239	9.83E-23	12	NT5DC1
5.87E-27	0.278996227	0.255	0.541	1.09E-22	12	ATRX
6.69E-27	0.292345097	0.129	0.29	1.25E-22	12	ETS1
7.21E-27	0.339043753	0.213	0.448	1.34E-22	12	MBD4
7.23E-27	0.271642184	0.121	0.284	1.35E-22	12	VPS36
8.21E-27	0.253139613	0.33	0.677	1.53E-22	12	Sep-06
8.99E-27	1.170667913	0.359	0.245	1.68E-22	12	AC007952.4
9.76E-27	0.270162566	0.108	0.261	1.82E-22	12	FUBP1
1.08E-26	0.359462697	0.24	0.474	2.01E-22	12	ZCCHC7
1.13E-26	0.25883077	0.201	0.48	2.11E-22	12	RAD21
1.44E-26	0.317206914	0.275	0.583	2.69E-22	12	SET
1.59E-26	0.259493572	0.16	0.358	2.96E-22	12	NFAT5

1.75E-26	0.280887471	0.23	0.484	3.26E-22	12	BLNK
1.91E-26	0.262371979	0.359	0.732	3.56E-22	12	SKP1
2.15E-26	0.272562772	0.34	0.671	4.01E-22	12	HNRNPA3
2.29E-26	0.331346608	0.236	0.479	4.27E-22	12	ZC3HAV1
2.50E-26	0.279877467	0.153	0.341	4.67E-22	12	SYTL1
2.98E-26	0.257462588	0.233	0.526	5.56E-22	12	PTPN1
3.85E-26	0.28909315	0.147	0.327	7.18E-22	12	TTC17
4.23E-26	0.271650088	0.106	0.245	7.89E-22	12	ZNF506
4.81E-26	0.259841967	0.302	0.621	8.97E-22	12	C12orf57
7.11E-26	0.284550388	0.125	0.275	1.32E-21	12	ARHGEF3
7.36E-26	0.355499641	0.189	0.382	1.37E-21	12	WDR11
1.07E-25	0.575557889	0.659	0.764	2.00E-21	12	RALGPS2
1.27E-25	0.278946174	0.25	0.554	2.37E-21	12	IQGAP1
1.46E-25	0.287791497	0.131	0.291	2.73E-21	12	WDFY1
1.84E-25	0.271613236	0.196	0.394	3.42E-21	12	Mar-01
1.85E-25	0.259831408	0.165	0.372	3.45E-21	12	GOLGA4
1.99E-25	0.26915389	0.1	0.248	3.71E-21	12	STAT2
2.23E-25	0.299405549	0.135	0.293	4.15E-21	12	TBC1D5
2.94E-25	0.321617031	0.248	0.517	5.48E-21	12	RABGAP1L
3.32E-25	0.353363488	0.175	0.368	6.20E-21	12	KIAA0040
3.61E-25	0.270417043	0.089	0.199	6.73E-21	12	ZBED5
4.34E-25	0.261646231	0.15	0.338	8.10E-21	12	SECISBP2
4.45E-25	0.265732834	0.22	0.479	8.30E-21	12	PLEKHG1
4.55E-25	0.303144586	0.152	0.327	8.48E-21	12	RRBP1
4.97E-25	0.254217276	0.085	0.207	9.27E-21	12	LMAN1
6.30E-25	0.312958813	0.304	0.584	1.18E-20	12	SYK
7.44E-25	0.276360363	0.24	0.531	1.39E-20	12	ZNF207
9.77E-25	0.31553649	0.17	0.366	1.82E-20	12	FCGR2B
2.00E-24	0.267832165	0.107	0.251	3.73E-20	12	ZC3H7A
3.06E-24	0.274651719	0.225	0.475	5.70E-20	12	CAPG
3.19E-24	0.321787831	0.256	0.492	5.95E-20	12	BCL11A
6.62E-24	0.367507707	0.177	0.342	1.23E-19	12	USP22
7.40E-24	0.271246525	0.12	0.269	1.38E-19	12	STIM2
8.07E-24	0.260957908	0.095	0.228	1.50E-19	12	CALCOCO1
9.56E-24	0.270255841	0.271	0.554	1.78E-19	12	CELF2
9.69E-24	0.275034249	0.153	0.334	1.81E-19	12	LNPEP
1.07E-23	0.264498148	0.093	0.201	2.00E-19	12	SAMD9L
1.31E-23	0.28373756	0.203	0.404	2.45E-19	12	TRAF3IP3
1.54E-23	0.270999087	0.11	0.265	2.88E-19	12	SPCS3
1.58E-23	0.259370142	0.101	0.249	2.95E-19	12	GMDS
1.59E-23	0.299223975	0.122	0.274	2.97E-19	12	USP48
2.02E-23	0.298629042	0.176	0.37	3.76E-19	12	TGFBR2
2.51E-23	0.314674682	0.163	0.321	4.67E-19	12	SLC9A7
2.74E-23	0.266778891	0.155	0.343	5.10E-19	12	CNTRL
3.37E-23	0.278281369	0.151	0.35	6.27E-19	12	PDCD6IP
4.30E-23	0.312563529	0.135	0.271	8.02E-19	12	GSAP

5.26E-23	0.327489874	0.3	0.591	9.80E-19	12	TMEM243
6.28E-23	0.257206112	0.105	0.248	1.17E-18	12	JAZF1
7.49E-23	0.275256552	0.125	0.286	1.40E-18	12	RERE
8.08E-23	0.306021448	0.157	0.344	1.51E-18	12	PJA2
1.08E-22	0.368080207	0.249	0.489	2.02E-18	12	TLK1
1.22E-22	0.357883154	0.158	0.35	2.27E-18	12	TM9SF2
1.87E-22	0.296704679	0.366	0.712	3.48E-18	12	CDC42
1.93E-22	0.273105362	0.112	0.269	3.60E-18	12	SLC25A32
2.24E-22	0.26518042	0.106	0.245	4.17E-18	12	CAPN2
2.32E-22	0.283489288	0.137	0.318	4.32E-18	12	CNST
2.64E-22	0.341179718	0.138	0.284	4.93E-18	12	SLC12A6
2.99E-22	0.37493886	0.144	0.288	5.58E-18	12	FAM208A
3.42E-22	0.281044534	0.184	0.391	6.37E-18	12	LENG8
3.55E-22	0.28404967	0.11	0.25	6.62E-18	12	CTSC
4.85E-22	0.255010811	0.108	0.249	9.04E-18	12	XRN1
5.16E-22	0.322277504	0.125	0.274	9.61E-18	12	TUT7
5.45E-22	0.423003426	0.261	0.496	1.02E-17	12	LCP1
5.76E-22	0.260294996	0.351	0.671	1.07E-17	12	MBNL1
6.04E-22	0.373446356	0.2	0.392	1.13E-17	12	ZNF107
7.05E-22	0.430570131	0.163	0.314	1.31E-17	12	TMPO
9.88E-22	0.251387748	0.109	0.244	1.84E-17	12	LINC02397
1.27E-21	0.300015594	0.152	0.328	2.37E-17	12	BTAF1
1.59E-21	0.422367717	0.227	0.458	2.96E-17	12	PTPN2
1.70E-21	0.29073638	0.113	0.244	3.17E-17	12	LONP2
1.97E-21	0.251076997	0.12	0.289	3.68E-17	12	CAPRIN1
2.48E-21	0.371732537	0.162	0.334	4.63E-17	12	MATR3-ENSG00000015479
2.61E-21	0.266162481	0.119	0.279	4.86E-17	12	AP1G1
2.99E-21	0.311110136	0.249	0.513	5.58E-17	12	IL4R
3.37E-21	0.322848721	0.29	0.572	6.27E-17	12	USP15
3.83E-21	0.296037171	0.348	0.696	7.14E-17	12	EPC1
4.08E-21	0.321917832	0.175	0.356	7.60E-17	12	RNF19A
5.66E-21	0.277237387	0.147	0.305	1.05E-16	12	TTC14
5.75E-21	0.309033695	0.18	0.355	1.07E-16	12	HIST1H1C
6.53E-21	0.2775043	0.308	0.573	1.22E-16	12	LBH
9.96E-21	0.286166611	0.211	0.456	1.86E-16	12	ARHGAP15
1.03E-20	0.313790568	0.161	0.341	1.91E-16	12	SETD2
1.38E-20	0.323175632	0.143	0.28	2.58E-16	12	IMMP2L
1.83E-20	0.296712349	0.15	0.326	3.41E-16	12	CCNH
1.97E-20	0.28570851	0.15	0.322	3.67E-16	12	PHC3
2.18E-20	0.352413101	0.194	0.379	4.07E-16	12	CIITA
2.29E-20	0.264470803	0.115	0.236	4.27E-16	12	AC025164.1
3.12E-20	0.326770739	0.176	0.385	5.81E-16	12	CDK5RAP3
3.23E-20	0.349596866	0.252	0.49	6.03E-16	12	SP110
3.35E-20	0.28569976	0.116	0.272	6.25E-16	12	MAP4K1
5.46E-20	0.272222028	0.157	0.333	1.02E-15	12	LPP
5.71E-20	0.346852285	0.197	0.41	1.07E-15	12	ARHGAP17

6.24E-20	0.292225807	0.338	0.634	1.16E-15	12	JMJD1C
6.43E-20	0.312615218	0.159	0.343	1.20E-15	12	CDC25B
9.13E-20	0.352583684	0.315	0.603	1.70E-15	12	BCLAF1
9.16E-20	0.253874973	0.193	0.386	1.71E-15	12	NKTR
9.32E-20	0.261440825	0.121	0.272	1.74E-15	12	SIMC1
1.07E-19	0.303123072	0.143	0.309	1.99E-15	12	PCMTD1
1.08E-19	0.255679904	0.121	0.272	2.01E-15	12	TRAF5
1.11E-19	0.330702644	0.123	0.263	2.07E-15	12	CGGBP1
1.85E-19	0.391283921	0.144	0.288	3.44E-15	12	SCIMP
2.35E-19	0.384435971	0.282	0.544	4.38E-15	12	N4BP2L2
2.48E-19	0.266747308	0.111	0.243	4.63E-15	12	GOLGA8B
2.97E-19	0.338643858	0.18	0.358	5.54E-15	12	UTRN
4.00E-19	0.275335674	0.142	0.302	7.45E-15	12	ADD3
4.02E-19	0.316901188	0.134	0.262	7.50E-15	12	DNAJC10
4.89E-19	0.31077936	0.361	0.685	9.12E-15	12	SF3B1
5.46E-19	0.270821055	0.11	0.234	1.02E-14	12	DGKD
5.62E-19	0.345682927	0.154	0.325	1.05E-14	12	RBM33
6.35E-19	0.422773727	0.226	0.432	1.18E-14	12	TNFAIP8
6.52E-19	0.319331981	0.135	0.28	1.21E-14	12	MCOLN2
7.63E-19	0.439195883	0.2	0.4	1.42E-14	12	CLINT1
9.63E-19	0.380100789	0.222	0.433	1.80E-14	12	ZNF292
1.01E-18	0.277062612	0.187	0.358	1.88E-14	12	TSPYL2
1.14E-18	0.286737306	0.342	0.683	2.12E-14	12	CTSS
1.23E-18	0.329480432	0.313	0.617	2.29E-14	12	PDIA3
1.32E-18	0.253484398	0.321	0.614	2.45E-14	12	NCOA3
1.40E-18	0.365324183	0.225	0.422	2.62E-14	12	ZRANB2
2.37E-18	0.326356139	0.273	0.549	4.42E-14	12	HMGN3
2.57E-18	0.282088259	0.122	0.271	4.80E-14	12	RBM5
3.73E-18	0.317095255	0.31	0.577	6.96E-14	12	PNN
4.18E-18	0.260096748	0.088	0.19	7.78E-14	12	ZMYND8
4.65E-18	0.284871427	0.312	0.569	8.66E-14	12	FCRLA
5.54E-18	0.322969832	0.156	0.327	1.03E-13	12	NORAD
5.68E-18	0.31013706	0.332	0.64	1.06E-13	12	SRSF10
6.11E-18	0.389203817	0.225	0.45	1.14E-13	12	TGOLN2
8.25E-18	0.342253682	0.151	0.313	1.54E-13	12	MAP4
1.01E-17	0.374550392	0.164	0.334	1.89E-13	12	DMD
1.37E-17	0.329186371	0.095	0.21	2.55E-13	12	SLAMF6
1.49E-17	0.363325209	0.234	0.438	2.77E-13	12	TMEM131L
1.52E-17	0.280929453	0.256	0.478	2.84E-13	12	BACH2
1.72E-17	0.250844306	0.085	0.197	3.20E-13	12	ADAM10
2.18E-17	0.344397499	0.161	0.339	4.07E-13	12	PTBP3
2.31E-17	0.276296238	0.085	0.194	4.30E-13	12	ZNF217
2.47E-17	0.286807632	0.107	0.241	4.61E-13	12	ANKRD49
2.84E-17	0.417207284	0.279	0.538	5.29E-13	12	CD47
3.22E-17	0.26058131	0.139	0.291	5.99E-13	12	RIC1
4.63E-17	0.436287601	0.203	0.367	8.63E-13	12	CREB3L2

5.34E-17	0.266842441	0.123	0.265	9.96E-13	12	PHKB
5.59E-17	0.260193134	0.091	0.2	1.04E-12	12	NUP88
5.62E-17	0.27581111	0.095	0.202	1.05E-12	12	STAMBPL1
6.32E-17	0.274402533	0.097	0.212	1.18E-12	12	ZAP70
6.50E-17	0.290021836	0.089	0.202	1.21E-12	12	PECAM1
6.84E-17	0.274841055	0.094	0.207	1.28E-12	12	NCOA7
7.36E-17	0.262882768	0.371	0.689	1.37E-12	12	BLK
7.81E-17	0.388119272	0.31	0.539	1.46E-12	12	BCL2
8.60E-17	0.396880261	0.2	0.358	1.60E-12	12	CLNK
1.83E-16	0.39812143	0.3	0.581	3.41E-12	12	DDX6
2.01E-16	0.300869609	0.34	0.637	3.74E-12	12	SLC38A1
2.07E-16	0.335442799	0.391	0.704	3.85E-12	12	PPIB
2.51E-16	0.364401107	0.177	0.33	4.67E-12	12	TLE4
2.68E-16	0.287213946	0.094	0.196	4.99E-12	12	DCLK2
3.18E-16	0.368016752	0.146	0.288	5.92E-12	12	CLEC17A
3.55E-16	0.46345605	0.231	0.433	6.61E-12	12	SP140
6.24E-16	0.305116914	0.267	0.539	1.16E-11	12	LUC7L3
6.87E-16	0.262128109	0.153	0.305	1.28E-11	12	ARL4C
1.13E-15	0.387508112	0.174	0.299	2.11E-11	12	RNPC3
2.30E-15	0.416588066	0.253	0.484	4.29E-11	12	PCM1
3.31E-15	0.406677779	0.228	0.431	6.18E-11	12	SNX29
3.42E-15	0.268884902	0.303	0.556	6.37E-11	12	CD79B
5.85E-15	0.334469904	0.195	0.372	1.09E-10	12	MDM4
6.62E-15	0.311128962	0.298	0.542	1.23E-10	12	ADTRP
8.08E-15	0.259404885	0.108	0.227	1.51E-10	12	CREBZF
1.40E-14	0.336433585	0.343	0.653	2.62E-10	12	SP100
2.67E-14	0.332384398	0.251	0.461	4.98E-10	12	AC004687.1
6.04E-14	0.301908305	0.119	0.234	1.13E-09	12	EXOC4
1.09E-13	0.26710153	0.124	0.241	2.03E-09	12	ADAM19
1.10E-13	0.365683103	0.374	0.691	2.04E-09	12	SEC62
1.12E-13	0.274592597	0.111	0.237	2.09E-09	12	DMTF1
1.60E-13	0.393100742	0.153	0.301	2.98E-09	12	PHTF2
3.40E-13	0.416126216	0.326	0.574	6.34E-09	12	G3BP2
3.57E-13	0.296897168	0.121	0.235	6.65E-09	12	MRNIP
4.65E-13	0.352164166	0.255	0.481	8.66E-09	12	OGA
4.88E-13	0.338416336	0.134	0.249	9.09E-09	12	CD84
5.32E-13	0.26529578	0.093	0.194	9.92E-09	12	MAP3K14
6.21E-13	0.355867314	0.151	0.278	1.16E-08	12	RNASEH2B
6.56E-13	0.252639147	0.415	0.742	1.22E-08	12	SRSF5
1.17E-12	0.311833359	0.129	0.251	2.18E-08	12	SLC23A2
1.23E-12	0.373386627	0.179	0.34	2.29E-08	12	SPTBN1
1.46E-12	0.279515451	0.226	0.444	2.73E-08	12	CLK1
1.60E-12	0.289435609	0.12	0.225	2.97E-08	12	GAB1
1.78E-12	0.353997134	0.142	0.259	3.31E-08	12	TNFAIP3
2.34E-12	0.255861208	0.164	0.326	4.37E-08	12	MZB1
3.11E-12	0.420160066	0.224	0.424	5.79E-08	12	PHF3

3.95E-12	0.413337002	0.163	0.302	7.36E-08	12	NSF
5.74E-12	0.391111208	0.288	0.514	1.07E-07	12	MEF2C
8.46E-12	0.398242765	0.266	0.476	1.58E-07	12	TUT4
1.01E-11	0.361379418	0.807	0.95	1.88E-07	12	DDX5
1.40E-11	0.47447926	0.699	0.844	2.62E-07	12	FCMR
2.31E-11	0.308277113	0.197	0.357	4.30E-07	12	GABPB1-AS1
2.33E-11	0.419519187	0.193	0.332	4.35E-07	12	DOCK10
4.77E-11	0.364476486	0.138	0.28	8.89E-07	12	LHPP
6.01E-11	0.425898749	0.272	0.48	1.12E-06	12	ITGB1
7.44E-11	0.286091641	0.201	0.358	1.39E-06	12	PHACTR1
1.05E-10	0.415812724	0.202	0.347	1.95E-06	12	MCTP2
1.67E-10	0.348391416	0.104	0.205	3.10E-06	12	TGFBR3
3.24E-10	0.448592098	0.161	0.266	6.03E-06	12	BTLA
3.98E-10	0.489838353	0.171	0.294	7.42E-06	12	ZNF266
4.59E-10	0.267386275	0.119	0.226	8.55E-06	12	AC119396.1
5.33E-10	0.299740332	0.328	0.561	9.94E-06	12	PELI1
8.22E-10	0.378222141	0.142	0.26	1.53E-05	12	LYST
1.13E-09	0.288942486	0.381	0.635	2.12E-05	12	HSP90B1
2.66E-09	0.436806178	0.24	0.404	4.96E-05	12	SKAP1
3.82E-09	0.487322889	0.205	0.355	7.12E-05	12	LEF1
5.81E-09	0.3394301	0.452	0.777	0.000108374	12	Sep-07
6.67E-09	0.464725639	0.271	0.469	0.000124408	12	VPS13C
7.77E-09	0.354034374	0.406	0.705	0.000144893	12	HNRNPU
1.55E-08	0.438337304	0.173	0.317	0.000288571	12	CD46
1.92E-08	0.422640658	0.377	0.634	0.000357343	12	RCSD1
4.97E-08	0.480982987	0.167	0.283	0.00092607	12	METTL7A
8.70E-08	0.370874042	0.227	0.368	0.001621745	12	CAMK2D
1.12E-07	0.795079009	0.47	0.753	0.002088062	12	MT-ND6
1.25E-07	0.426395607	0.312	0.503	0.002338163	12	INPP5F
2.33E-07	0.251591868	0.489	0.831	0.004341808	12	SRP14
6.45E-07	0.262987613	0.407	0.647	0.012024413	12	CCDC88A
2.47E-06	0.29929206	0.717	0.88	0.045998865	12	HSP90AB1
5.35E-06	0.289790258	0.479	0.781	0.099798918	12	VOPP1
5.62E-06	0.340894973	0.466	0.8	0.104764777	12	GRB2
5.73E-06	0.428385156	0.348	0.559	0.106861394	12	HSPA5
6.22E-06	0.425963019	0.332	0.541	0.115868847	12	STX7
6.27E-06	0.445089562	0.403	0.672	0.116861671	12	ARGLU1
6.34E-06	0.454089138	0.198	0.312	0.118171172	12	AC020916.1
7.11E-06	0.304462381	0.446	0.722	0.13252313	12	SMCHD1
9.59E-06	0.409150334	0.663	0.874	0.178688701	12	FOXP1
1.08E-05	0.353552	0.396	0.646	0.201977603	12	RUBCNL
1.45E-05	0.480677458	0.332	0.573	0.269854244	12	IFT57
1.70E-05	0.472636415	0.325	0.523	0.317288989	12	OGT
1.96E-05	0.464673735	0.354	0.574	0.365376522	12	IKZF3
7.67E-05	0.284240818	0.51	0.81	1	12	ATP5MC2
8.60E-05	0.349817415	0.458	0.759	1	12	Sep-09

0.000201257	0.34010755	0.461	0.745	1	12	PNISR
0.000916464	0.424978712	0.588	0.819	1	12	PTPRC
0.001007284	0.303732699	0.527	0.85	1	12	SON
0.001205448	0.461503526	0.392	0.594	1	12	ABCA6
0.004192802	0.460636816	0.588	0.829	1	12	PNRC1
0.008249904	0.482749111	0.419	0.64	1	12	RIPOR2
8.90E-295	1.604653652	0.869	0.757	1.66E-290	13	RALGPS2
7.68E-201	1.365963629	0.796	0.685	1.43E-196	13	DDX17
2.31E-75	1.178674227	0.52	0.407	4.31E-71	13	PARP15
6.21E-49	0.7261215	0.701	0.82	1.16E-44	13	RBM39
8.11E-49	0.761531733	0.736	0.842	1.51E-44	13	TCF4
2.70E-31	1.045133907	0.349	0.246	5.03E-27	13	AC007952.4
8.85E-31	0.269230035	0.194	0.416	1.65E-26	13	PPP2R5C
2.32E-29	0.268527117	0.161	0.337	4.32E-25	13	HSD17B11
5.42E-29	0.282358274	0.19	0.4	1.01E-24	13	DUT
6.02E-29	0.285894251	0.182	0.398	1.12E-24	13	MED10
6.99E-28	0.275568209	0.176	0.386	1.30E-23	13	FAM133B
1.56E-27	0.297886173	0.221	0.463	2.90E-23	13	RBM17
2.09E-27	0.261562201	0.177	0.376	3.90E-23	13	RIN3
1.45E-26	0.255700087	0.181	0.404	2.70E-22	13	SNX6
1.70E-26	0.273945435	0.137	0.285	3.16E-22	13	SNX5
6.02E-26	1.135912268	0.212	0.106	1.12E-21	13	XIST
8.60E-26	0.270307907	0.186	0.394	1.60E-21	13	BCAS4
1.02E-25	0.268644336	0.138	0.302	1.91E-21	13	PABPN1
1.30E-25	0.825174528	0.208	0.103	2.41E-21	13	TRIM73
5.87E-25	0.251910768	0.152	0.334	1.10E-20	13	HERPUD2
1.13E-24	0.267663686	0.174	0.36	2.10E-20	13	DRAM2
2.07E-24	0.32191021	0.151	0.304	3.86E-20	13	ATG12
3.36E-24	0.266200023	0.164	0.363	6.25E-20	13	YY1
9.37E-24	0.265414585	0.184	0.395	1.75E-19	13	DNAJC15
9.53E-24	0.284711316	0.155	0.332	1.78E-19	13	SUMF2
9.87E-24	0.25935414	0.255	0.52	1.84E-19	13	HNRNPR
1.21E-23	0.319436243	0.207	0.415	2.26E-19	13	RNF10
1.80E-23	0.258625972	0.172	0.375	3.36E-19	13	MTCH1
1.98E-23	0.293626602	0.178	0.378	3.70E-19	13	FAM49B
2.03E-23	0.250685555	0.18	0.388	3.79E-19	13	RTF1
2.55E-23	0.337152682	0.181	0.369	4.76E-19	13	RASGRP2
3.37E-23	0.329423083	0.241	0.49	6.28E-19	13	ARHGAP45
4.34E-23	0.277743649	0.219	0.447	8.08E-19	13	MCUB
8.98E-23	0.869540101	0.559	0.664	1.67E-18	13	MBNL1
1.11E-22	0.292470909	0.189	0.4	2.08E-18	13	EAPP
1.24E-22	0.280462127	0.161	0.327	2.31E-18	13	UBQLN1
1.37E-22	0.292938659	0.13	0.277	2.56E-18	13	EPRS
1.77E-22	0.257107605	0.211	0.433	3.30E-18	13	SYPL1
1.81E-22	0.288043034	0.151	0.315	3.37E-18	13	MAP3K2
2.62E-22	0.260501089	0.135	0.298	4.88E-18	13	COPB1

2.92E-22	0.259660198	0.12	0.261	5.45E-18	13	GPBP1L1
7.63E-22	0.260801338	0.135	0.291	1.42E-17	13	RNF4
9.96E-22	0.266873247	0.143	0.302	1.86E-17	13	IST1
1.71E-21	0.250908887	0.273	0.549	3.18E-17	13	CDC42SE1
2.87E-21	0.254951766	0.189	0.379	5.36E-17	13	KDM2A
3.35E-21	0.285187409	0.248	0.502	6.25E-17	13	STARD7
3.47E-21	0.252600426	0.105	0.249	6.47E-17	13	DNM2
5.64E-21	0.256489738	0.25	0.49	1.05E-16	13	B4GALT1
5.69E-21	0.266401038	0.12	0.263	1.06E-16	13	CCM2
1.33E-20	0.252755674	0.138	0.292	2.48E-16	13	COMMD1
2.41E-20	0.269286586	0.101	0.21	4.49E-16	13	MRPS5
2.87E-20	0.279683959	0.187	0.392	5.35E-16	13	RAB2A
2.93E-20	0.332150444	0.212	0.416	5.47E-16	13	GSTK1
3.03E-20	0.279935412	0.177	0.363	5.65E-16	13	VPS35
3.29E-20	0.28262933	0.152	0.313	6.12E-16	13	SND1
3.40E-20	0.284926754	0.215	0.438	6.33E-16	13	STK17A
4.86E-20	0.256142276	0.235	0.511	9.06E-16	13	SYF2
5.72E-20	0.332419051	0.225	0.447	1.07E-15	13	STAT6
5.96E-20	0.320892393	0.316	0.578	1.11E-15	13	MTPN
7.62E-20	0.274031526	0.158	0.331	1.42E-15	13	RAB14
1.22E-19	0.290625187	0.234	0.47	2.27E-15	13	LTA4H
2.18E-19	0.279019927	0.145	0.311	4.07E-15	13	ASAH1
2.19E-19	0.292244986	0.173	0.361	4.09E-15	13	ZFR
2.97E-19	0.307384806	0.194	0.407	5.54E-15	13	DPP7
3.41E-19	0.26257032	0.128	0.249	6.36E-15	13	TGS1
5.95E-19	0.253039278	0.166	0.344	1.11E-14	13	DHX9
6.12E-19	0.27007577	0.137	0.302	1.14E-14	13	RAB10
6.71E-19	0.263524382	0.179	0.369	1.25E-14	13	SPTAN1
6.91E-19	0.255937453	0.123	0.26	1.29E-14	13	PDPK1
7.81E-19	0.265772847	0.221	0.446	1.46E-14	13	PARP1
8.65E-19	0.270055511	0.192	0.405	1.61E-14	13	CANX
1.13E-18	0.332494318	0.213	0.405	2.10E-14	13	RNMT
1.25E-18	0.292925688	0.244	0.478	2.33E-14	13	RAD21
1.40E-18	0.294505706	0.206	0.416	2.61E-14	13	RBBP6
1.42E-18	0.268517892	0.13	0.27	2.64E-14	13	GRSF1
1.43E-18	0.31609154	0.164	0.324	2.67E-14	13	SMARCE1
1.60E-18	0.322890191	0.227	0.434	2.98E-14	13	CSNK1A1
1.71E-18	0.289733874	0.104	0.218	3.19E-14	13	CCDC186
2.09E-18	0.329007	0.228	0.434	3.90E-14	13	FGR
2.20E-18	0.290495637	0.162	0.323	4.09E-14	13	RBBP7
2.28E-18	0.32317947	0.201	0.401	4.25E-14	13	DDX46
2.46E-18	0.348176665	0.167	0.307	4.59E-14	13	SDHA
3.18E-18	0.399743957	0.281	0.513	5.93E-14	13	PAPOLA
3.52E-18	0.340215912	0.216	0.426	6.55E-14	13	ARPC5
3.54E-18	0.726041093	0.534	0.658	6.60E-14	13	SRSF11
4.51E-18	0.26432389	0.142	0.3	8.40E-14	13	LYPLA1

4.67E-18	0.274293356	0.131	0.259	8.70E-14	13	EFCAB14
7.17E-18	0.266254708	0.114	0.232	1.34E-13	13	LMBR1L
7.26E-18	0.292877192	0.151	0.287	1.35E-13	13	SCIMP
8.15E-18	0.268860993	0.117	0.239	1.52E-13	13	DCAF11
9.03E-18	0.358633149	0.812	0.95	1.68E-13	13	DDX5
9.86E-18	0.325448141	0.173	0.341	1.84E-13	13	CCDC32
1.05E-17	0.32032334	0.211	0.413	1.96E-13	13	ANKRD11
1.07E-17	0.27139102	0.125	0.257	2.00E-13	13	TFEB
1.19E-17	0.302438353	0.158	0.33	2.22E-13	13	UBTF
1.23E-17	0.32152658	0.188	0.371	2.28E-13	13	CEBPZ
1.41E-17	0.327543613	0.16	0.316	2.63E-13	13	HADHB
1.58E-17	0.347069425	0.181	0.374	2.94E-13	13	SUPT5H
2.00E-17	0.276019987	0.138	0.281	3.73E-13	13	RBPJ
2.22E-17	0.296846991	0.233	0.42	4.15E-13	13	PLEKHA2
2.91E-17	0.33467713	0.247	0.469	5.42E-13	13	LSM14A
3.35E-17	0.769555986	0.555	0.678	6.24E-13	13	SF3B1
3.66E-17	0.334210541	0.214	0.413	6.83E-13	13	HSPA4
3.93E-17	0.327778073	0.181	0.353	7.32E-13	13	ADPGK
4.01E-17	0.275070211	0.146	0.29	7.48E-13	13	MFF
4.04E-17	0.285244823	0.155	0.302	7.54E-13	13	PIK3IP1
4.05E-17	0.320701656	0.246	0.479	7.55E-13	13	PRPF40A
5.23E-17	0.323130222	0.184	0.349	9.74E-13	13	TM9SF2
5.34E-17	0.33282558	0.132	0.267	9.96E-13	13	MICAL1
6.89E-17	0.315906761	0.118	0.223	1.28E-12	13	ANKRD17
7.46E-17	0.253144435	0.107	0.224	1.39E-12	13	RMC1
7.95E-17	0.29801176	0.155	0.306	1.48E-12	13	HPS1
8.17E-17	0.265921172	0.162	0.336	1.52E-12	13	TMF1
8.64E-17	0.376551132	0.212	0.385	1.61E-12	13	HIVEP1
8.90E-17	0.324269491	0.154	0.293	1.66E-12	13	EIF2AK1
8.99E-17	0.336745387	0.205	0.386	1.67E-12	13	BAZ1A
9.44E-17	0.31261941	0.274	0.542	1.76E-12	13	RBMX
1.03E-16	0.291868243	0.28	0.564	1.92E-12	13	C11orf58
1.18E-16	0.348440524	0.328	0.578	2.21E-12	13	TAF1D
1.28E-16	0.278722979	0.112	0.221	2.39E-12	13	ESCO1
1.36E-16	0.280826317	0.153	0.309	2.53E-12	13	RAB6A
1.52E-16	0.775075688	0.547	0.667	2.84E-12	13	ARGLU1
1.85E-16	0.324013798	0.203	0.383	3.45E-12	13	NUCKS1
1.88E-16	0.304916154	0.167	0.333	3.50E-12	13	SAFB2
1.91E-16	0.286388051	0.138	0.272	3.56E-12	13	SNAP23
2.16E-16	0.362005454	0.186	0.362	4.03E-12	13	PTPN7
2.32E-16	0.264261471	0.2	0.375	4.33E-12	13	ELF2
2.38E-16	0.347959918	0.181	0.333	4.43E-12	13	CYBC1
2.41E-16	0.288120473	0.118	0.236	4.50E-12	13	ILKAP
2.82E-16	0.266437997	0.392	0.703	5.26E-12	13	CSDE1
2.99E-16	0.250287069	0.125	0.247	5.57E-12	13	DBF4
3.44E-16	0.302124832	0.132	0.263	6.42E-12	13	ADH5

3.70E-16	0.348791355	0.12	0.243	6.90E-12	13	NKAP
3.76E-16	0.280288062	0.208	0.387	7.01E-12	13	CCDC191
3.88E-16	0.279344577	0.136	0.29	7.24E-12	13	SRP54
3.90E-16	0.316071138	0.19	0.379	7.26E-12	13	TMC6
5.11E-16	0.401359006	0.233	0.414	9.53E-12	13	YTHDC1
5.43E-16	0.368673567	0.198	0.371	1.01E-11	13	DDX18
5.49E-16	0.252690491	0.141	0.296	1.02E-11	13	WASHC1
5.84E-16	0.261667902	0.12	0.246	1.09E-11	13	USP10
6.77E-16	0.269734414	0.142	0.281	1.26E-11	13	CEP57
8.51E-16	0.271599522	0.162	0.32	1.59E-11	13	VMP1
1.06E-15	0.290677933	0.131	0.249	1.98E-11	13	CDK17
1.19E-15	0.263013492	0.113	0.232	2.22E-11	13	ADSS
1.26E-15	0.299081324	0.148	0.301	2.34E-11	13	MECP2
1.40E-15	0.37009306	0.245	0.455	2.62E-11	13	BNIP2
1.43E-15	0.326173013	0.263	0.493	2.67E-11	13	HNRNPH3
1.61E-15	0.322140928	0.156	0.298	3.00E-11	13	REV3L
1.65E-15	0.274127542	0.123	0.26	3.07E-11	13	LARP7
2.16E-15	0.312903237	0.157	0.31	4.03E-11	13	UBR4
2.78E-15	0.341846242	0.16	0.303	5.18E-11	13	SSR1
2.98E-15	0.293228828	0.212	0.4	5.55E-11	13	G3BP1
3.13E-15	0.279942546	0.102	0.204	5.84E-11	13	GNPTG
3.24E-15	0.330481653	0.217	0.423	6.04E-11	13	TRAM1
3.31E-15	0.339877214	0.289	0.546	6.17E-11	13	HP1BP3
3.53E-15	0.283766143	0.12	0.238	6.58E-11	13	EIF4A1
4.33E-15	0.287752736	0.133	0.264	8.07E-11	13	HM13
5.44E-15	0.759693776	0.503	0.635	1.01E-10	13	SRSF10
5.51E-15	0.252130041	0.127	0.266	1.03E-10	13	BCCIP
5.69E-15	0.309705612	0.13	0.262	1.06E-10	13	RABEP1
5.81E-15	0.302997968	0.136	0.262	1.08E-10	13	CARS2
5.88E-15	0.279034601	0.221	0.429	1.10E-10	13	UBE2J1
6.58E-15	0.350717573	0.145	0.277	1.23E-10	13	DEF6
7.10E-15	0.290404507	0.115	0.235	1.32E-10	13	PHTF1
8.05E-15	0.252231481	0.101	0.208	1.50E-10	13	PSMD1
8.26E-15	0.317319039	0.146	0.283	1.54E-10	13	FOXN3
8.32E-15	0.321643301	0.265	0.481	1.55E-10	13	HVCN1
9.14E-15	0.276757777	0.127	0.252	1.70E-10	13	CREBBP
9.15E-15	0.266815527	0.113	0.224	1.71E-10	13	ZNF274
9.30E-15	0.342546876	0.209	0.379	1.73E-10	13	GNPTAB
1.02E-14	0.340049725	0.254	0.469	1.90E-10	13	CAPZA1
1.09E-14	0.326451806	0.186	0.358	2.03E-10	13	NUMA1
1.13E-14	0.252102888	0.107	0.217	2.10E-10	13	ZNF106
1.18E-14	0.296504218	0.136	0.249	2.19E-10	13	CTSC
1.21E-14	0.330267498	0.181	0.36	2.26E-10	13	SH3GLB1
1.30E-14	0.299680577	0.299	0.535	2.42E-10	13	ST6GAL1
1.38E-14	0.393054126	0.163	0.304	2.56E-10	13	DNMBP
1.45E-14	0.322616348	0.181	0.345	2.70E-10	13	NFX1

1.55E-14	0.301280775	0.167	0.334	2.88E-10	13	PMPCB
1.57E-14	0.280175632	0.131	0.264	2.92E-10	13	CCDC91
1.63E-14	0.359639355	0.166	0.306	3.03E-10	13	TROVE2
1.81E-14	0.323348443	0.178	0.329	3.38E-10	13	OSBPL8
2.53E-14	0.618823135	0.601	0.795	4.72E-10	13	GRB2
3.71E-14	0.340944545	0.152	0.273	6.91E-10	13	SMARCC1
3.72E-14	0.319450947	0.183	0.354	6.93E-10	13	STK10
3.78E-14	0.326474234	0.183	0.36	7.05E-10	13	PRMT2
4.16E-14	0.300847666	0.136	0.269	7.75E-10	13	MYO1G
4.49E-14	0.258740957	0.098	0.2	8.37E-10	13	USP7
4.63E-14	0.345156196	0.232	0.442	8.64E-10	13	RTN4
4.82E-14	0.255652954	0.149	0.313	8.99E-10	13	TMED5
5.38E-14	0.256467177	0.132	0.257	1.00E-09	13	TRPC4AP
5.79E-14	0.26976902	0.118	0.243	1.08E-09	13	LYRM2
6.06E-14	0.280577952	0.155	0.311	1.13E-09	13	SYNCRIP
7.25E-14	0.354271402	0.16	0.295	1.35E-09	13	WNK1
7.63E-14	0.295590731	0.315	0.586	1.42E-09	13	VCP
8.15E-14	0.355057512	0.26	0.454	1.52E-09	13	CD19
9.00E-14	0.31457824	0.125	0.238	1.68E-09	13	SDR39U1
1.23E-13	0.301578728	0.198	0.389	2.30E-09	13	UPF3A
1.63E-13	0.281656827	0.123	0.227	3.04E-09	13	EFR3A
2.10E-13	0.311744649	0.137	0.27	3.92E-09	13	BCL10
2.16E-13	0.255898637	0.097	0.206	4.02E-09	13	NUDT5
2.17E-13	0.443640369	0.258	0.453	4.04E-09	13	USP16
2.19E-13	0.309499485	0.191	0.347	4.08E-09	13	PPP1R10
2.46E-13	0.345342538	0.246	0.461	4.58E-09	13	SLTM
2.67E-13	0.308337435	0.169	0.305	4.98E-09	13	ARL4C
2.75E-13	0.30866343	0.141	0.276	5.13E-09	13	PHF20L1
2.78E-13	0.446977204	0.263	0.46	5.17E-09	13	RSF1
3.03E-13	0.349442458	0.295	0.536	5.65E-09	13	CDC42SE2
3.40E-13	0.269873097	0.19	0.374	6.34E-09	13	ANXA6
4.16E-13	0.324922455	0.132	0.257	7.76E-09	13	OSGEP
4.35E-13	0.25724268	0.095	0.198	8.10E-09	13	YARS
4.95E-13	0.312059722	0.327	0.584	9.22E-09	13	PDCD4
5.87E-13	0.252377679	0.099	0.202	1.10E-08	13	NOL11
6.16E-13	0.361277268	0.156	0.289	1.15E-08	13	SPSB3
7.76E-13	0.342887782	0.134	0.244	1.45E-08	13	MYO9B
8.22E-13	0.378414531	0.174	0.311	1.53E-08	13	PPP4R3A
8.46E-13	0.33120546	0.35	0.616	1.58E-08	13	PDIA3
9.47E-13	0.318307061	0.125	0.234	1.76E-08	13	TUBGCP2
1.02E-12	0.291168291	0.118	0.235	1.91E-08	13	FAM53B
1.04E-12	0.34552843	0.139	0.244	1.94E-08	13	RNF13
1.11E-12	0.380137043	0.169	0.294	2.06E-08	13	ANKLE2
1.30E-12	0.336608587	0.123	0.23	2.42E-08	13	RPAIN
1.30E-12	0.26187271	0.105	0.213	2.43E-08	13	SDAD1
1.31E-12	0.375963815	0.249	0.445	2.44E-08	13	YME1L1

1.42E-12	0.267297738	0.113	0.229	2.64E-08	13	TAF3
1.50E-12	0.35400393	0.157	0.29	2.80E-08	13	TIAL1
1.52E-12	0.435996019	0.216	0.386	2.83E-08	13	TBC1D10C
1.54E-12	0.335548523	0.167	0.309	2.86E-08	13	SFT2D2
1.58E-12	0.264088017	0.132	0.262	2.95E-08	13	CDC73
1.59E-12	0.412377272	0.26	0.464	2.96E-08	13	NDFIP1
1.60E-12	0.384026313	0.142	0.281	2.98E-08	13	MARS
1.82E-12	0.288617761	0.122	0.234	3.40E-08	13	RAB5A
1.96E-12	0.350754176	0.185	0.326	3.66E-08	13	RAB30
1.97E-12	0.301476608	0.26	0.455	3.67E-08	13	MBP
1.97E-12	0.277924877	0.126	0.265	3.68E-08	13	ARID1A
2.01E-12	0.359878269	0.152	0.275	3.75E-08	13	TCERG1
2.22E-12	0.345492041	0.147	0.249	4.13E-08	13	C16orf87
2.23E-12	0.697410429	0.527	0.641	4.16E-08	13	RUBCNL
2.51E-12	0.325412254	0.141	0.271	4.68E-08	13	MAP4K1
2.83E-12	0.330967332	0.157	0.286	5.28E-08	13	CLTC
3.30E-12	0.353816048	0.191	0.367	6.15E-08	13	AKNA
3.40E-12	0.281679332	0.124	0.23	6.34E-08	13	IMMT
5.98E-12	0.309510407	0.146	0.26	1.12E-07	13	FUBP1
6.04E-12	0.294924475	0.144	0.281	1.13E-07	13	TNPO1
6.41E-12	0.364458785	0.168	0.307	1.20E-07	13	GINM1
6.92E-12	0.379993399	0.142	0.247	1.29E-07	13	NUTM2B-AS1
8.28E-12	0.282566499	0.118	0.234	1.54E-07	13	CUL1
8.63E-12	0.347530909	0.198	0.369	1.61E-07	13	HSH2D
1.19E-11	0.31349761	0.131	0.247	2.22E-07	13	KIF2A
1.27E-11	0.401066991	0.224	0.367	2.36E-07	13	KIAA0040
1.32E-11	0.335504433	0.139	0.247	2.47E-07	13	PNKP
1.49E-11	0.301007632	0.148	0.287	2.77E-07	13	ATXN10
1.66E-11	0.393503006	0.213	0.383	3.09E-07	13	CELF1
1.67E-11	0.340477548	0.136	0.257	3.11E-07	13	MTERF4
1.68E-11	0.329914109	0.384	0.654	3.12E-07	13	HLA-DMB
1.80E-11	0.267204306	0.117	0.226	3.35E-07	13	EPSTI1
1.88E-11	0.264018342	0.124	0.251	3.51E-07	13	CHMP7
2.13E-11	0.388024289	0.26	0.455	3.97E-07	13	GCC2
2.67E-11	0.385502252	0.15	0.267	4.98E-07	13	PSMC6
2.87E-11	0.327125129	0.122	0.223	5.35E-07	13	PAFAH1B2
3.00E-11	0.342437343	0.354	0.644	5.60E-07	13	SRRM2
3.01E-11	0.272040601	0.137	0.288	5.62E-07	13	WDR74
3.18E-11	0.63098618	0.527	0.69	5.92E-07	13	EPC1
3.38E-11	0.366221781	0.149	0.264	6.29E-07	13	CCDC88C
4.01E-11	0.306498429	0.181	0.34	7.47E-07	13	SNX18
4.17E-11	0.269033924	0.137	0.255	7.78E-07	13	STAM
5.03E-11	0.326843897	0.128	0.239	9.38E-07	13	FNTA
5.65E-11	0.283441593	0.29	0.511	1.05E-06	13	EHMT1
6.00E-11	0.358963741	0.169	0.308	1.12E-06	13	ARID4A
6.22E-11	0.491813468	0.203	0.318	1.16E-06	13	CPSF6

6.26E-11	0.293700088	0.115	0.22	1.17E-06	13	THUMPD1
6.92E-11	0.286851601	0.125	0.232	1.29E-06	13	ZEB1
8.44E-11	0.383286815	0.173	0.303	1.57E-06	13	TMOD3
9.26E-11	0.29856255	0.123	0.251	1.73E-06	13	TCIRG1
9.67E-11	0.283724759	0.104	0.205	1.80E-06	13	ACSL3
9.80E-11	0.370499415	0.158	0.282	1.83E-06	13	TMEM87A
1.01E-10	0.436525819	0.231	0.406	1.88E-06	13	BPTF
1.16E-10	0.329549235	0.143	0.252	2.15E-06	13	ZBTB38
1.23E-10	0.366153438	0.143	0.251	2.30E-06	13	CD2AP
1.31E-10	0.382579477	0.197	0.342	2.44E-06	13	CDC25B
1.35E-10	0.360983827	0.158	0.27	2.51E-06	13	USP9X
1.52E-10	0.346754354	0.253	0.443	2.82E-06	13	CCDC69
1.52E-10	0.379312237	0.166	0.289	2.83E-06	13	SYNRG
1.52E-10	0.267124525	0.117	0.231	2.84E-06	13	SEMA4B
1.69E-10	0.473106032	0.222	0.398	3.15E-06	13	ARHGAP4
1.77E-10	0.350810295	0.105	0.209	3.31E-06	13	TMEM259
1.81E-10	0.337919976	0.157	0.281	3.37E-06	13	ZNF394
2.40E-10	0.422676562	0.304	0.543	4.48E-06	13	MOB1A
2.59E-10	0.348592342	0.302	0.526	4.83E-06	13	WSB1
2.61E-10	0.351564219	0.323	0.567	4.87E-06	13	SFPQ
2.87E-10	0.353256056	0.276	0.477	5.36E-06	13	ZC3HAV1
3.12E-10	0.303000222	0.164	0.301	5.82E-06	13	PIK3AP1
3.39E-10	0.361545695	0.172	0.3	6.31E-06	13	HOOK3
3.46E-10	0.35575259	0.179	0.317	6.44E-06	13	STAG2
3.74E-10	0.277070345	0.124	0.241	6.97E-06	13	CACUL1
3.89E-10	0.269272861	0.127	0.247	7.25E-06	13	CNOT6L
4.43E-10	0.39861612	0.187	0.32	8.26E-06	13	CNOT2
4.48E-10	0.726799376	0.513	0.628	8.36E-06	13	JMJD1C
4.74E-10	0.331075717	0.173	0.329	8.84E-06	13	PNPLA8
5.34E-10	0.386970734	0.197	0.331	9.96E-06	13	RB1CC1
5.67E-10	0.42552778	0.263	0.466	1.06E-05	13	TPR
7.22E-10	0.384728242	0.217	0.392	1.35E-05	13	CYLD
8.64E-10	0.338099764	0.143	0.259	1.61E-05	13	PSPC1
9.45E-10	0.291671491	0.139	0.267	1.76E-05	13	NAA50
9.70E-10	0.37750046	0.143	0.253	1.81E-05	13	FARP2
1.06E-09	0.351321043	0.148	0.268	1.98E-05	13	ACADM
1.06E-09	0.514210759	0.226	0.347	1.98E-05	13	CCDC50
1.08E-09	0.369025322	0.229	0.415	2.02E-05	13	ATP2A3
1.18E-09	0.483188756	0.221	0.357	2.19E-05	13	OCIAD1
1.23E-09	0.441829364	0.249	0.448	2.29E-05	13	NT5C
1.58E-09	0.301527369	0.312	0.543	2.95E-05	13	GGA2
1.69E-09	0.360980075	0.155	0.276	3.16E-05	13	VHL
2.29E-09	0.404007512	0.163	0.283	4.27E-05	13	RNF115
2.46E-09	0.391411082	0.151	0.273	4.58E-05	13	WHAMM
2.48E-09	0.407522866	0.202	0.338	4.62E-05	13	STAT1
2.59E-09	0.320869449	0.152	0.271	4.82E-05	13	PARVG

2.71E-09	0.321072529	0.241	0.417	5.05E-05	13	SLC38A2
2.98E-09	0.307448541	0.155	0.267	5.55E-05	13	MBNL2
3.94E-09	0.415939995	0.25	0.438	7.35E-05	13	SPCS2
4.74E-09	0.348757419	0.17	0.313	8.84E-05	13	MAP4
5.12E-09	0.420639509	0.175	0.311	9.54E-05	13	DHX36
5.69E-09	0.392126979	0.182	0.313	0.000106106	13	PUM1
6.20E-09	0.424156409	0.225	0.359	0.000115525	13	EPS15
6.46E-09	0.48396807	0.199	0.34	0.000120365	13	SYTL1
6.62E-09	0.290247094	0.294	0.525	0.000123446	13	GPBP1
6.79E-09	0.432319716	0.301	0.527	0.000126599	13	KTN1
8.24E-09	0.5012413	0.245	0.406	0.000153665	13	BDP1
8.58E-09	0.432481057	0.238	0.421	0.000159853	13	UPF2
8.60E-09	0.367265576	0.155	0.256	0.000160379	13	PPP6R3
8.90E-09	0.421382877	0.192	0.325	0.000165937	13	CCAR1
9.79E-09	0.276957521	0.122	0.23	0.000182413	13	YLPM1
1.08E-08	0.275012968	0.115	0.216	0.000202237	13	GLYR1
1.12E-08	0.403417707	0.214	0.378	0.000207926	13	WDR33
1.13E-08	0.324205146	0.131	0.235	0.00021128	13	HDAC2
1.26E-08	0.345775817	0.153	0.282	0.000234808	13	GMFB
1.26E-08	0.444102821	0.154	0.258	0.000235793	13	ASXL1
1.61E-08	0.474412016	0.57	0.776	0.000300451	13	STK4
1.78E-08	0.259183417	0.121	0.236	0.000331697	13	GAB2
1.88E-08	0.339784228	0.135	0.243	0.000350539	13	CAPN2
2.08E-08	0.261418431	0.197	0.318	0.000388303	13	LINC01480
2.18E-08	0.337097909	0.213	0.388	0.000407045	13	USP11
2.38E-08	0.466567868	0.193	0.327	0.000443684	13	BOD1L1
2.39E-08	0.34601115	0.142	0.254	0.000446142	13	STX12
2.41E-08	0.464631347	0.217	0.342	0.000449811	13	TRIM22
2.59E-08	0.371315444	0.401	0.675	0.000482233	13	Sep-06
2.76E-08	0.250551796	0.115	0.238	0.000514989	13	RAPGEF1
3.07E-08	0.298739008	0.214	0.384	0.000571626	13	FBXO21
3.71E-08	0.452425069	0.187	0.297	0.000691633	13	RAB3GAP1
4.13E-08	0.270171453	0.13	0.252	0.000770747	13	VPS26A
4.27E-08	0.442320245	0.177	0.307	0.000796435	13	GON4L
4.47E-08	0.381253682	0.354	0.607	0.000832937	13	JAK1
5.59E-08	0.403767451	0.213	0.373	0.001042357	13	HDAC7
6.17E-08	0.404462522	0.173	0.297	0.001149664	13	NDE1
6.24E-08	0.395272597	0.368	0.618	0.001162278	13	PPP1CC
6.36E-08	0.48483688	0.282	0.461	0.001185329	13	APPL1
6.69E-08	0.308194862	0.163	0.297	0.001246576	13	FAM3C
7.71E-08	0.395025585	0.186	0.292	0.00143648	13	Mar-03
8.68E-08	0.346906608	0.145	0.257	0.001618184	13	ORMDL1
9.33E-08	0.289246639	0.114	0.215	0.001739678	13	NAAA
9.98E-08	0.715707746	0.46	0.579	0.001860711	13	SYK
1.03E-07	0.400492554	0.311	0.551	0.001924281	13	IQGAP1
1.24E-07	0.417071244	0.155	0.273	0.002308693	13	AP1G2

1.40E-07	0.465496647	0.186	0.311	0.002606594	13	ARHGEF2
1.43E-07	0.464688244	0.276	0.448	0.00267307	13	TAF15
1.65E-07	0.299816939	0.113	0.214	0.003069485	13	NSRP1
1.91E-07	0.406652982	0.296	0.454	0.003565592	13	ZEB2
1.91E-07	0.445041437	0.219	0.382	0.003567388	13	LSM8
2.45E-07	0.455430448	0.18	0.304	0.004563161	13	GIT2
2.74E-07	0.395351828	0.17	0.277	0.005111385	13	NAA15
2.75E-07	0.446515918	0.277	0.468	0.005128971	13	GGNBP2
2.86E-07	0.370495613	0.185	0.338	0.00532782	13	NAP1L4
2.88E-07	0.449466627	0.27	0.454	0.005371725	13	ADAR
2.89E-07	0.328033085	0.146	0.252	0.005391631	13	DCK
3.16E-07	0.544759288	0.632	0.847	0.005886586	13	SON
3.24E-07	0.454182722	0.247	0.411	0.0060444	13	SEC31A
3.29E-07	0.274696642	0.481	0.789	0.00613492	13	HNRNPDL
3.45E-07	0.382051081	0.167	0.276	0.0064293	13	KAT6B
3.45E-07	0.379029782	0.141	0.253	0.006432661	13	FCRL5
3.69E-07	0.548057183	0.607	0.785	0.006885566	13	KMT2E
3.75E-07	0.450411152	0.282	0.472	0.006992412	13	IFI16
3.95E-07	0.42244945	0.166	0.27	0.00736014	13	ANTXR2
4.37E-07	0.337299281	0.36	0.601	0.00815282	13	BCLAF1
4.76E-07	0.423102867	0.171	0.284	0.008874669	13	COL9A2
4.82E-07	0.633725141	0.499	0.653	0.008982647	13	CYTH1
4.85E-07	0.470594389	0.257	0.42	0.009041799	13	KDM5A
4.94E-07	0.442328047	0.27	0.448	0.009211977	13	CBX3
4.95E-07	0.401748693	0.198	0.324	0.009229916	13	CCNH
6.62E-07	0.422064377	0.179	0.309	0.012347426	13	EP400
6.74E-07	0.346264189	0.128	0.229	0.012556643	13	FAM69A
6.82E-07	0.486174845	0.246	0.391	0.01271935	13	UBE3A
7.27E-07	0.392066833	0.365	0.59	0.013549131	13	ARID4B
7.70E-07	0.395078163	0.188	0.318	0.01434523	13	CREBRF
7.71E-07	0.421941549	0.26	0.435	0.0143692	13	PRPF38B
7.91E-07	0.398116587	0.19	0.331	0.014737729	13	CAND1
8.08E-07	0.390098581	0.174	0.286	0.015056191	13	CENPC
9.08E-07	0.26494385	0.36	0.525	0.016916731	13	HIST1H1E
1.11E-06	0.409366851	0.194	0.332	0.020733857	13	UHMK1
1.18E-06	0.3330902	0.141	0.244	0.022039797	13	ZNF326
1.40E-06	0.408480247	0.176	0.281	0.026116425	13	NT5C3A
1.46E-06	0.456707528	0.16	0.264	0.027190495	13	CARD11
1.58E-06	0.317308385	0.416	0.715	0.02949673	13	UBE2D2
1.63E-06	0.371532393	0.168	0.288	0.030390761	13	ETS1
2.13E-06	0.654318101	0.484	0.648	0.039745318	13	SP100
2.46E-06	0.43756281	0.219	0.358	0.04582276	13	RIOK3
2.63E-06	0.448544428	0.185	0.301	0.048971038	13	ATF6B
3.18E-06	0.420311463	0.214	0.32	0.059194863	13	RALGAPA1
3.33E-06	0.373806305	0.223	0.372	0.062071122	13	TMEM154
3.59E-06	0.367884841	0.152	0.262	0.066925478	13	FGD3

3.90E-06	0.459775519	0.217	0.329	0.072738812	13	FAM13B
4.32E-06	0.490729538	0.223	0.358	0.080494371	13	SPEN
4.34E-06	0.416061818	0.263	0.437	0.080840456	13	PPP1R12A
4.95E-06	0.436142059	0.225	0.365	0.092222096	13	PDXDC1
5.41E-06	0.434704853	0.252	0.401	0.100901821	13	PAFAH1B1
5.64E-06	0.440526411	0.199	0.321	0.105189483	13	TMEM165
5.69E-06	0.400643792	0.193	0.319	0.106021857	13	PIKFYVE
6.12E-06	0.425233794	0.28	0.475	0.114035496	13	KIF5B
6.31E-06	0.448529108	0.319	0.542	0.117622713	13	EWSR1
6.59E-06	0.445118473	0.213	0.362	0.122807143	13	CNOT1
6.68E-06	0.425003241	0.17	0.287	0.124531222	13	TRIM44
7.29E-06	0.471585135	0.204	0.329	0.135896079	13	PHYKPL
7.29E-06	0.421291747	0.244	0.407	0.135925718	13	SMARCA5
9.52E-06	0.341471883	0.408	0.679	0.177391355	13	DDX24
9.80E-06	0.476551798	0.226	0.351	0.182773153	13	RSBN1L
1.18E-05	0.419280487	0.294	0.498	0.219148744	13	STAT3
1.33E-05	0.350903509	0.412	0.681	0.248833326	13	CTSS
1.37E-05	0.505884876	0.24	0.363	0.254457607	13	FCGR2B
1.49E-05	0.47265454	0.244	0.401	0.277764084	13	ACIN1
1.52E-05	0.405026834	0.159	0.263	0.282842763	13	SIN3A
1.95E-05	0.515756756	0.279	0.456	0.364336955	13	PTPN2
1.96E-05	0.674358694	0.475	0.632	0.365296923	13	SLC38A1
1.99E-05	0.522173556	0.355	0.546	0.370056882	13	HMGN3
2.00E-05	0.598666875	0.176	0.292	0.372998229	13	KCNN4
2.08E-05	0.353660708	0.146	0.249	0.388656411	13	C5orf24
2.19E-05	0.524303326	0.574	0.778	0.409076106	13	VOPP1
2.29E-05	0.460847562	0.196	0.31	0.426285147	13	TBC1D1
2.51E-05	0.413834147	0.168	0.269	0.467174582	13	PLEKHF2
2.99E-05	0.407262232	0.181	0.282	0.557414054	13	METTL7A
3.45E-05	0.759736077	0.501	0.63	0.643665075	13	RCSD1
3.55E-05	0.435421972	0.206	0.341	0.661468047	13	SAFB
3.83E-05	0.616682347	0.304	0.478	0.714452527	13	ARHGEF1
4.02E-05	0.467707068	0.252	0.399	0.749809064	13	ADK
4.06E-05	0.440771593	0.256	0.42	0.757412253	13	RBBP4
4.12E-05	0.374891949	0.282	0.451	0.76785102	13	SMIM14
5.02E-05	0.398468401	0.281	0.447	0.935726697	13	PTPN22
5.05E-05	0.466498818	0.24	0.37	0.941776122	13	PRPF8
5.44E-05	0.494183736	0.23	0.367	1	13	USP8
6.13E-05	0.403428316	0.246	0.404	1	13	TRA2A
6.29E-05	0.399242782	0.204	0.341	1	13	RNF149
6.33E-05	0.504199255	0.31	0.478	1	13	EPB41
6.50E-05	0.509992228	0.246	0.386	1	13	ANAPC5
7.15E-05	0.500313741	0.228	0.37	1	13	PRRC2B
7.78E-05	0.468927604	0.257	0.402	1	13	BTK
8.40E-05	0.496365475	0.231	0.37	1	13	CDC40
8.62E-05	0.458208196	0.339	0.56	1	13	IL10RA

9.46E-05	0.42599079	0.176	0.277	1	13	BSDC1
0.000107565	0.420922128	0.181	0.303	1	13	FIP1L1
0.000113251	0.388044542	0.176	0.284	1	13	Mar-07
0.00012812	0.457859013	0.232	0.367	1	13	ROR1
0.000128943	0.428919511	0.19	0.301	1	13	GPATCH8
0.000160864	0.464559245	0.255	0.399	1	13	OFD1
0.000165754	0.515994877	0.248	0.384	1	13	SNRNP200
0.000192738	0.497687593	0.238	0.366	1	13	SMARCC2
0.000197911	0.419383506	0.194	0.312	1	13	FGD2
0.000211113	0.464569152	0.183	0.314	1	13	MAPK8IP3
0.000215232	0.537387536	0.29	0.441	1	13	MAP3K1
0.000250083	0.386135697	0.179	0.294	1	13	KLHL24
0.000267517	0.35149646	0.163	0.279	1	13	SPAG9
0.000291412	0.466559673	0.34	0.543	1	13	CYFIP2
0.00031185	0.436449255	0.396	0.619	1	13	CAST
0.000368043	0.574177648	0.276	0.411	1	13	SRSF4
0.000380884	0.520477724	0.286	0.448	1	13	TGOLN2
0.000434122	0.468522934	0.223	0.338	1	13	SRSF1
0.000660753	0.259002911	0.464	0.769	1	13	EIF4G2
0.000694626	0.481342693	0.225	0.352	1	13	BBX
0.000731326	0.463227597	0.202	0.313	1	13	TMPO
0.000912243	0.547922498	0.214	0.319	1	13	STRBP
0.000929672	0.486302723	0.214	0.327	1	13	TMED4
0.000945452	0.627046333	0.443	0.606	1	13	RBM25
0.001007135	0.513262997	0.289	0.445	1	13	DYNC1H1
0.001166683	0.534974953	0.212	0.326	1	13	CDK12
0.001281246	0.501066296	0.207	0.314	1	13	SLC25A36
0.001376864	0.769654657	0.42	0.532	1	13	TNRC6B
0.001513906	0.280693719	0.467	0.684	1	13	FCER2
0.001552559	0.631266125	0.427	0.577	1	13	DDX6
0.001582187	0.634286828	0.393	0.516	1	13	UVRAG
0.001663415	0.273399232	0.382	0.581	1	13	AC016831.7
0.001991793	0.524615809	0.239	0.369	1	13	ADD1
0.002042177	0.551672617	0.29	0.451	1	13	TBRG1
0.002428133	0.405077833	0.368	0.552	1	13	AGPAT5
0.002606123	0.403332605	0.392	0.632	1	13	SH3BP5
0.002641192	0.553082946	0.464	0.637	1	13	AKAP13
0.002692774	0.455250806	0.207	0.311	1	13	VAMP2
0.002692956	0.738113069	0.379	0.489	1	13	AKAP9
0.002725769	0.514902648	0.35	0.552	1	13	BAZ2A
0.003062013	0.650641299	0.457	0.616	1	13	SCAF11
0.003144573	0.541461071	0.249	0.369	1	13	GOLGA4
0.003738167	0.560466181	0.249	0.353	1	13	THUMPD3-AS1
0.003747228	0.494612369	0.34	0.533	1	13	ITSN2
0.004289319	0.465951699	0.283	0.464	1	13	TTC3
0.004903986	0.532967515	0.255	0.377	1	13	PAX5

0.004937227	0.549332147	0.266	0.393	1	13	NDUFV1
0.005648772	0.419529984	0.356	0.569	1	13	ARHGAP25
0.006047494	0.444514999	0.402	0.647	1	13	MTDH
0.006370089	0.489450057	0.255	0.382	1	13	AFTPH
0.007042112	0.27116187	0.461	0.741	1	13	SRSF5
0.007843637	0.51684434	0.318	0.495	1	13	AFF4
0.00891326	0.538290735	0.377	0.571	1	13	IFT57
1.72E-77	0.693057278	0.731	0.571	3.21E-73	14	RPS4Y1
2.58E-199	1.587857447	0.413	0.022	4.81E-195	15	ANXA1
4.71E-161	1.498001081	0.347	0.02	8.78E-157	15	GNLY
1.21E-150	0.801312856	0.884	0.709	2.26E-146	15	SRGN
1.23E-131	1.227138966	0.321	0.028	2.29E-127	15	NKG7
2.30E-120	0.565785564	0.95	0.799	4.28E-116	15	TAGLN2
1.73E-98	1.107415123	0.316	0.067	3.23E-94	15	CCL5
1.76E-89	0.637006891	0.733	0.504	3.29E-85	15	RGCC
4.55E-87	1.863016689	0.464	0.245	8.48E-83	15	AL138963.3
4.34E-76	0.358054506	0.713	0.468	8.09E-72	15	GPR183
3.99E-74	0.699675264	0.53	0.308	7.43E-70	15	CREM
2.65E-69	0.744284482	0.196	0.026	4.95E-65	15	IL32
5.24E-68	0.665731454	0.175	0.013	9.77E-64	15	IL7R
2.65E-67	0.49746761	0.744	0.636	4.94E-63	15	PDE4B
1.01E-64	0.411936877	0.81	0.682	1.88E-60	15	CD55
1.93E-61	0.494458963	0.633	0.517	3.60E-57	15	HIST1H1E
3.69E-56	0.542856144	0.123	0.005	6.87E-52	15	GZMB
9.46E-54	0.568647091	0.33	0.138	1.76E-49	15	MYADM
4.98E-49	0.778143573	0.403	0.251	9.29E-45	15	TNFAIP3
1.24E-48	0.599451127	0.153	0.019	2.32E-44	15	CD8A
1.76E-48	0.538187904	0.134	0.014	3.29E-44	15	CD3E
6.56E-46	0.47281738	0.133	0.02	1.22E-41	15	CD7
2.43E-45	0.721486842	0.028	0.147	4.52E-41	15	JCHAIN
1.53E-44	0.445151299	0.115	0.009	2.86E-40	15	CTSW
5.32E-41	0.697443012	0.283	0.14	9.91E-37	15	SAMSN1
3.23E-35	0.439746535	0.129	0.025	6.01E-31	15	CD2
3.50E-34	0.553750578	0.44	0.334	6.52E-30	15	S100A11
1.16E-29	0.317096371	0.572	0.422	2.17E-25	15	ZNF331
1.20E-27	0.490537039	0.377	0.267	2.24E-23	15	SLC2A3
2.39E-23	0.364959972	0.37	0.246	4.45E-19	15	AC007952.4
0.001607586	0.345511659	0.44	0.541	1	15	HNRNPF
0.009351111	0.993856971	0.592	0.748	1	15	MT-ND6
5.31E-306	1.212905738	0.998	0.846	9.90E-302	16	GAPDH
1.54E-263	1.056105854	0.997	0.851	2.87E-259	16	ACTG1
5.02E-252	1.157881	0.968	0.624	9.36E-248	16	DBI
1.95E-229	0.902457187	0.801	0.295	3.64E-225	16	PTMS
4.73E-224	0.927686533	0.742	0.224	8.82E-220	16	LAG3
9.25E-208	0.965301656	0.652	0.154	1.72E-203	16	LILRB4
2.57E-198	0.756883675	0.968	0.712	4.80E-194	16	CLIC1

7.78E-181	1.105751304	0.571	0.13	1.45E-176	16	LILRA4
1.28E-163	0.739682596	0.717	0.266	2.38E-159	16	PIGR
3.04E-163	0.699111976	0.932	0.598	5.66E-159	16	CD99
6.26E-151	0.626486719	0.882	0.486	1.17E-146	16	RNH1
2.27E-146	0.514640343	0.989	0.818	4.24E-142	16	RHOA
1.05E-143	0.604853196	0.81	0.398	1.96E-139	16	RGS10
2.99E-141	0.606686197	0.989	0.831	5.57E-137	16	PFN1
4.26E-140	0.804233427	0.986	0.883	7.95E-136	16	VIM
4.79E-136	0.690640657	0.852	0.513	8.93E-132	16	GRN
6.46E-134	0.761885109	0.852	0.466	1.20E-129	16	TUBB
2.09E-127	0.571262397	0.802	0.413	3.91E-123	16	NME2
3.49E-126	0.982282813	0.494	0.137	6.50E-122	16	FABP5
1.84E-124	0.600670334	0.949	0.709	3.44E-120	16	COTL1
4.05E-123	0.487214352	0.934	0.66	7.54E-119	16	UQCRH
5.71E-122	0.517193753	0.481	0.132	1.06E-117	16	PDCD1
8.66E-121	0.420410791	0.617	0.223	1.61E-116	16	ABRACL
9.01E-121	0.596130444	0.99	0.843	1.68E-116	16	SH3BGRL3
2.52E-120	0.525216009	0.994	0.891	4.70E-116	16	HNRNPA1
4.94E-120	0.520187561	0.859	0.494	9.22E-116	16	COX5A
5.10E-120	0.484406705	0.622	0.236	9.50E-116	16	IMPDH2
9.18E-120	0.609762632	0.479	0.122	1.71E-115	16	CST7
1.05E-118	0.576240875	0.708	0.315	1.96E-114	16	YWHAH
2.26E-118	0.520444743	0.979	0.7	4.22E-114	16	RAC2
3.02E-118	0.522957517	0.996	0.873	5.63E-114	16	CFL1
4.38E-118	0.501564841	0.803	0.389	8.16E-114	16	NOP10
3.71E-116	0.993813482	0.825	0.526	6.92E-112	16	LGALS1
1.47E-115	0.482881186	0.941	0.66	2.73E-111	16	MYL12B
1.17E-112	0.54062813	0.987	0.853	2.19E-108	16	NPM1
4.71E-111	0.416548618	0.979	0.837	8.79E-107	16	SLC25A6
7.36E-110	0.368768894	0.496	0.152	1.37E-105	16	WSB2
1.55E-109	0.430978393	0.743	0.335	2.88E-105	16	AP2S1
5.22E-108	0.390540834	0.786	0.402	9.73E-104	16	ARPC1B
5.56E-108	0.491797511	0.875	0.534	1.04E-103	16	PTPN6
6.63E-108	0.500081249	0.989	0.816	1.24E-103	16	HINT1
1.07E-107	0.685398051	0.894	0.581	1.99E-103	16	PKM
3.08E-107	0.533273994	0.815	0.427	5.73E-103	16	ATOX1
5.59E-107	0.484528535	0.513	0.155	1.04E-102	16	COCH
8.26E-105	0.333253984	0.459	0.134	1.54E-100	16	PARVB
8.88E-105	0.527847425	0.858	0.525	1.66E-100	16	ANXA2
1.79E-103	0.768770792	0.683	0.306	3.33E-99	16	LINC01480
6.13E-103	0.682300752	0.848	0.497	1.14E-98	16	ENO1
2.68E-102	0.461772231	0.819	0.457	5.00E-98	16	APOBEC3G
6.07E-102	0.389129654	0.989	0.852	1.13E-97	16	BTF3
8.57E-101	0.870210784	0.879	0.633	1.60E-96	16	S100A4
2.20E-100	0.423619083	0.759	0.399	4.09E-96	16	CSTB
1.84E-97	0.37467696	0.688	0.321	3.44E-93	16	VDAC1

3.23E-97	0.438513325	0.702	0.334	6.03E-93	16	BANF1
8.30E-97	0.355213157	0.674	0.302	1.55E-92	16	TWF2
1.37E-96	0.462116294	0.594	0.25	2.55E-92	16	SIT1
2.16E-96	0.586425422	0.962	0.72	4.02E-92	16	MIF
2.58E-96	0.396465595	0.581	0.245	4.80E-92	16	RGS19
8.25E-96	0.582968553	0.882	0.556	1.54E-91	16	TPI1
2.55E-95	0.565560309	0.825	0.471	4.76E-91	16	PGAM1
2.03E-93	0.41829649	0.97	0.756	3.79E-89	16	SYNGR2
1.38E-90	0.362041677	0.69	0.341	2.58E-86	16	SEM1
1.64E-90	0.309873618	0.542	0.202	3.07E-86	16	PPA1
1.42E-89	0.378697575	0.714	0.353	2.65E-85	16	APOBEC3C
2.16E-89	0.301963517	0.687	0.346	4.02E-85	16	MPG
6.56E-89	0.393432271	0.382	0.103	1.22E-84	16	DRAIC
2.36E-88	0.428334643	0.905	0.6	4.41E-84	16	GPX4
9.57E-88	0.313222897	0.786	0.425	1.78E-83	16	PGLS
7.33E-87	0.327801721	0.478	0.163	1.37E-82	16	RHOC
1.27E-86	0.336034448	0.997	0.879	2.37E-82	16	ATP5F1E
1.59E-86	0.475825527	0.942	0.728	2.97E-82	16	CORO1A
3.85E-86	0.434572194	0.568	0.224	7.18E-82	16	DNPH1
3.93E-86	0.394373323	0.826	0.462	7.33E-82	16	GNG5
1.81E-85	0.326941809	0.604	0.272	3.38E-81	16	C1QBP
2.80E-85	0.387401346	0.784	0.433	5.21E-81	16	GNB2
3.94E-85	0.32375492	0.779	0.445	7.34E-81	16	ATP5MD
3.98E-85	0.283367844	0.432	0.128	7.42E-81	16	SH3BP2
1.60E-84	0.334105146	0.835	0.458	2.98E-80	16	CSK
2.01E-84	0.266288363	0.448	0.151	3.74E-80	16	PRDX3
1.18E-83	0.316899897	0.799	0.468	2.20E-79	16	VAMP8
2.32E-83	0.341310804	0.663	0.33	4.32E-79	16	FKBP1A
1.36E-82	0.519596611	0.973	0.793	2.54E-78	16	YBX1
3.60E-82	0.362801807	0.628	0.312	6.72E-78	16	ZBTB32
9.14E-82	0.323422023	0.782	0.46	1.70E-77	16	ATP5MF
1.02E-81	0.25659334	0.433	0.145	1.91E-77	16	SPN
3.47E-81	0.445617993	0.937	0.684	6.46E-77	16	RAN
4.94E-81	0.362590097	0.625	0.294	9.21E-77	16	TXN
5.93E-81	0.302903889	0.568	0.244	1.11E-76	16	TP53I11
8.86E-81	0.279027171	0.301	0.06	1.65E-76	16	C3orf14
2.04E-80	0.395097415	0.897	0.618	3.80E-76	16	SLC25A5
3.64E-80	0.416502286	0.88	0.575	6.79E-76	16	PRDX1
8.70E-80	0.422135511	0.848	0.512	1.62E-75	16	NDUFV2
1.15E-79	0.278624384	0.524	0.218	2.14E-75	16	FERMT3
1.52E-79	0.41612017	0.79	0.46	2.83E-75	16	CAPG
1.63E-79	0.287434975	0.466	0.161	3.03E-75	16	DCTPP1
2.08E-79	0.363592898	0.961	0.682	3.87E-75	16	PCBP1
4.21E-79	0.545494085	0.867	0.628	7.84E-75	16	PLP2
6.43E-79	0.334440641	0.748	0.405	1.20E-74	16	TBCB
9.59E-79	0.299927726	0.721	0.376	1.79E-74	16	SHMT2

1.57E-77	0.354293066	0.984	0.796	2.93E-73	16	ATP5MC2
2.31E-77	0.383527449	0.705	0.39	4.30E-73	16	CTSZ
6.29E-77	0.388024418	0.376	0.118	1.17E-72	16	MYL9
7.73E-77	0.263274674	0.504	0.199	1.44E-72	16	TRAF7
1.54E-76	0.402482579	0.606	0.305	2.86E-72	16	ATF5
2.31E-76	0.413656647	0.749	0.436	4.31E-72	16	LDHB
2.73E-76	0.254460773	0.532	0.227	5.09E-72	16	IRF5
2.90E-76	0.290572637	0.967	0.757	5.40E-72	16	ATP5MG
3.16E-76	0.887732298	0.273	0.057	5.88E-72	16	CCL3
3.51E-76	0.303377269	0.76	0.422	6.54E-72	16	ARF6
6.69E-76	0.308951943	0.735	0.392	1.25E-71	16	PRDX5
1.78E-75	0.312351575	0.55	0.225	3.33E-71	16	PYCARD
3.74E-75	0.347245833	0.6	0.278	6.97E-71	16	WARS
6.45E-75	0.620442159	0.248	0.039	1.20E-70	16	IL4I1
2.42E-74	0.26984096	0.856	0.551	4.52E-70	16	ATP5F1D
1.26E-72	0.281955343	0.726	0.395	2.35E-68	16	MDH2
1.57E-72	0.281630402	0.715	0.371	2.93E-68	16	APEX1
1.68E-72	0.294606532	0.481	0.19	3.14E-68	16	CCND2
2.26E-72	0.254662009	0.251	0.047	4.22E-68	16	PDPN
2.37E-72	0.452303708	0.971	0.785	4.42E-68	16	PPDPF
2.66E-72	0.312574118	0.636	0.29	4.95E-68	16	MRPL51
3.21E-72	0.377711819	0.26	0.052	5.99E-68	16	MGLL
1.21E-71	0.426732853	0.64	0.317	2.26E-67	16	NHP2
1.64E-71	0.314844684	0.782	0.451	3.05E-67	16	DAD1
2.57E-71	0.277751308	0.509	0.201	4.79E-67	16	PRKCD
2.83E-71	0.398103313	0.922	0.673	5.28E-67	16	MYL12A
4.39E-71	0.594012175	0.334	0.094	8.18E-67	16	MS4A6A
4.45E-71	0.374325638	0.907	0.636	8.29E-67	16	COX6C
4.56E-71	0.576953561	0.965	0.799	8.50E-67	16	S100A6
1.96E-70	0.391108979	0.992	0.874	3.66E-66	16	MYL6
2.10E-70	0.312415965	0.75	0.414	3.91E-66	16	RBX1
2.20E-70	0.296557154	0.766	0.42	4.10E-66	16	BRK1
5.03E-70	0.342326641	0.655	0.326	9.38E-66	16	ATP5MC1
6.13E-70	1.09469947	0.794	0.485	1.14E-65	16	APH1A
4.17E-69	0.277999653	0.602	0.279	7.77E-65	16	NDUFAB1
5.01E-69	0.267646194	0.597	0.274	9.35E-65	16	GBP2
9.94E-68	0.375804151	0.203	0.03	1.85E-63	16	CD1C
2.03E-66	0.348885239	0.84	0.54	3.78E-62	16	PARK7
6.69E-66	0.271961977	0.73	0.402	1.25E-61	16	ATP6V1F
1.94E-65	0.331979371	0.788	0.449	3.62E-61	16	NDUFB2
2.02E-65	0.280612742	0.682	0.337	3.76E-61	16	C19orf70
3.36E-65	0.306488743	0.939	0.72	6.27E-61	16	SLC25A3
6.58E-65	0.280610625	0.813	0.478	1.23E-60	16	ARF5
2.25E-64	0.309731311	0.82	0.506	4.20E-60	16	COX8A
2.33E-64	0.316169818	0.866	0.546	4.34E-60	16	PPP1CA
4.07E-64	0.310099965	0.551	0.234	7.58E-60	16	TKT

4.98E-64	0.284165303	0.719	0.401	9.28E-60	16	CCT3
1.54E-63	0.29877648	0.739	0.426	2.87E-59	16	ATP5PF
2.18E-63	0.985511166	0.782	0.48	4.06E-59	16	ENSA
6.05E-63	0.294017998	0.721	0.387	1.13E-58	16	SEC61G
7.74E-63	0.37586246	0.714	0.409	1.44E-58	16	TSPO
8.23E-63	0.289248461	0.406	0.157	1.53E-58	16	SEMA7A
1.37E-62	0.336381025	0.679	0.373	2.56E-58	16	NFATC1
1.70E-62	0.419605504	0.961	0.784	3.17E-58	16	FXYD5
1.55E-61	0.331010467	0.817	0.512	2.90E-57	16	RAC1
2.48E-61	0.307828255	0.907	0.613	4.62E-57	16	COX6B1
3.41E-61	0.258405396	0.578	0.277	6.36E-57	16	PDCD5
7.59E-61	0.259520708	0.736	0.415	1.42E-56	16	UQCRQ
1.63E-60	0.377300017	0.727	0.42	3.04E-56	16	RHOB
1.91E-60	0.410462046	0.687	0.383	3.57E-56	16	PSME2
2.42E-60	0.264255682	0.512	0.218	4.50E-56	16	PHB
2.52E-60	0.373134958	0.448	0.211	4.71E-56	16	CD72
3.24E-60	0.364571451	0.799	0.495	6.04E-56	16	SELENOH
6.82E-60	0.274302481	0.684	0.373	1.27E-55	16	VASP
2.08E-59	0.324199879	0.772	0.435	3.88E-55	16	APRT
3.22E-59	0.308914002	0.81	0.488	6.00E-55	16	PRELID1
2.21E-58	0.25001579	0.449	0.17	4.12E-54	16	SLC35B2
6.46E-58	0.330451751	0.862	0.591	1.20E-53	16	SSR4
2.66E-57	0.292276861	0.26	0.067	4.96E-53	16	BIK
2.79E-57	0.483428155	0.858	0.68	5.21E-53	16	EMP3
2.80E-57	0.276510106	0.836	0.55	5.21E-53	16	PSMA7
9.10E-57	0.288477847	0.747	0.446	1.70E-52	16	PSMB3
1.07E-56	0.284426302	0.649	0.353	2.00E-52	16	FDFT1
1.49E-56	0.292951855	0.95	0.766	2.78E-52	16	ARPC2
2.44E-56	0.306904237	0.982	0.863	4.54E-52	16	UCP2
1.02E-55	0.251663608	0.843	0.523	1.91E-51	16	CUTA
2.35E-55	0.259944285	0.755	0.437	4.38E-51	16	AP2M1
7.56E-55	0.290405778	0.742	0.4	1.41E-50	16	DDOST
8.79E-55	0.323206048	0.603	0.288	1.64E-50	16	RANBP1
4.92E-54	0.274383987	0.807	0.516	9.17E-50	16	ATP5MC3
5.56E-54	0.263700471	0.165	0.023	1.04E-49	16	ACY3
1.86E-53	0.292709557	0.812	0.483	3.46E-49	16	ALDOA
2.38E-53	0.919641244	0.269	0.075	4.44E-49	16	CCL4
3.17E-53	0.277272302	0.741	0.411	5.92E-49	16	NPC2
7.29E-53	0.251570643	0.373	0.152	1.36E-48	16	CD68
4.65E-52	0.254896728	0.883	0.62	8.67E-48	16	EIF3E
1.58E-51	0.270049281	0.949	0.729	2.94E-47	16	OST4
3.09E-51	0.433549648	0.591	0.333	5.76E-47	16	MIR155HG
5.77E-51	0.256642585	0.897	0.62	1.08E-46	16	HIGD2A
9.17E-51	0.326374275	0.875	0.588	1.71E-46	16	COX6A1
1.15E-50	0.29106955	0.784	0.494	2.15E-46	16	MRPS21
2.17E-50	0.273325436	0.827	0.536	4.05E-46	16	TRMT112

2.21E-50	0.275735399	0.864	0.558	4.12E-46	16	ELOB
3.68E-50	0.386746103	0.841	0.577	6.85E-46	16	CD27
9.25E-50	0.255761349	0.668	0.342	1.72E-45	16	TALDO1
9.28E-50	0.281100776	0.751	0.455	1.73E-45	16	IFITM2
1.27E-49	0.252828502	0.886	0.631	2.36E-45	16	SOD1
6.10E-49	0.285591066	0.862	0.589	1.14E-44	16	GDI2
3.82E-48	0.255890223	0.805	0.482	7.12E-44	16	WDR83OS
4.61E-48	0.398014969	0.966	0.848	8.59E-44	16	HLA-DRB5
5.35E-48	0.268160494	0.934	0.688	9.96E-44	16	PPIB
3.55E-47	0.300153094	0.712	0.408	6.61E-43	16	LDHA
5.78E-46	0.256368324	0.962	0.775	1.08E-41	16	CHCHD2
1.99E-44	0.260356434	0.629	0.355	3.71E-40	16	CDK2AP2
4.23E-43	0.586336574	0.332	0.15	7.89E-39	16	SNAPC3
9.12E-43	0.263384662	0.984	0.82	1.70E-38	16	ARPC3
1.95E-41	0.283797471	0.984	0.881	3.63E-37	16	HLA-DQA1
1.04E-40	0.269281889	0.716	0.44	1.94E-36	16	SMIM14
1.20E-40	0.381527793	0.382	0.18	2.25E-36	16	TOR1AIP2
2.42E-38	0.266189204	0.578	0.359	4.51E-34	16	SPIB
3.65E-38	0.256980057	0.88	0.642	6.81E-34	16	SUB1
3.52E-37	0.306097464	0.812	0.558	6.56E-33	16	LBH
8.26E-37	0.282829824	0.223	0.077	1.54E-32	16	ITM2C
1.16E-36	0.449642168	0.979	0.872	2.16E-32	16	HSP90AB1
3.27E-36	0.262510053	0.794	0.523	6.10E-32	16	PDLIM1
8.66E-36	0.307096741	0.902	0.674	1.61E-31	16	TUBA1B
1.28E-35	0.290770257	0.17	0.041	2.38E-31	16	KLK4
1.88E-35	0.314825649	0.198	0.067	3.51E-31	16	AQP3
2.01E-35	0.373677363	0.484	0.287	3.76E-31	16	HLA-DQA2
5.05E-35	0.326802014	0.94	0.78	9.41E-31	16	LSP1
5.06E-31	0.250539194	0.845	0.593	9.44E-27	16	GPSM3
1.05E-30	0.326578794	0.504	0.333	1.97E-26	16	S100A11
1.58E-28	0.280806431	0.958	0.784	2.94E-24	16	PEBP1
4.56E-25	0.295918815	0.415	0.265	8.49E-21	16	RPRD2
1.30E-24	0.435972139	0.874	0.684	2.42E-20	16	MCL1
1.53E-20	0.999910774	0.512	0.373	2.85E-16	16	PSIP1
0	2.607987205	0.996	0.494	0	17	TESC
0	1.928880866	0.989	0.515	0	17	S100A10
0	1.873176014	0.98	0.288	0	17	RHOF
0	1.845875345	0.98	0.346	0	17	CKAP4
0	1.655011825	0.761	0.029	0	17	TNFRSF4
0	1.63205745	1	0.887	0	17	RPS26
0	1.625488079	0.977	0.294	0	17	MAD1L1
0	1.606041082	0.877	0.03	0	17	TNFRSF18
0	1.534440542	0.895	0.167	0	17	CXCL16
0	1.504599033	0.937	0.323	0	17	S100A11
0	1.438395945	0.999	0.777	0	17	SQSTM1
0	1.430054882	0.795	0.146	0	17	DUSP4

0	1.428404894	0.982	0.35	0	17	KDM6B
0	1.420948529	0.901	0.1	0	17	NINJ1
0	1.383017907	0.925	0.3	0	17	CREM
0	1.365946727	0.92	0.164	0	17	NFKB1
0	1.251197436	0.938	0.229	0	17	ECE1
0	1.222122563	0.996	0.707	0	17	SRGN
0	1.168424468	0.968	0.528	0	17	NR3C1
0	1.144116247	0.978	0.453	0	17	FNBP1
0	1.109792443	0.901	0.227	0	17	SLC7A5
0	1.101520839	0.707	0.093	0	17	AKAP12
0	1.050909115	0.962	0.41	0	17	TGFB1
0	1.050686361	0.98	0.383	0	17	PIM3
0	1.049801976	0.968	0.34	0	17	NFKB2
0	1.049692131	0.962	0.406	0	17	SLC3A2
0	1.047993333	0.929	0.313	0	17	LDLRAD4
0	1.037249547	0.909	0.334	0	17	SLBP
0	1.03671928	0.958	0.429	0	17	HSPD1
0	1.02392889	0.991	0.564	0	17	GNG2
0	1.017408593	0.891	0.283	0	17	BHLHE40
0	1.014733896	1	0.883	0	17	VIM
0	0.992645554	0.998	0.756	0	17	SYNGR2
0	0.989042531	0.884	0.248	0	17	KDM2B
0	0.988097357	1	0.798	0	17	TAGLN2
0	0.979496363	0.902	0.276	0	17	ANKLE2
0	0.97369262	0.943	0.301	0	17	MAP2K3
0	0.934507817	0.854	0.141	0	17	SLCO4A1
0	0.923995629	1	0.876	0	17	EZR
0	0.919254124	0.884	0.273	0	17	MARCKSL1
0	0.893677295	0.828	0.176	0	17	CD58
0	0.881002349	0.685	0.058	0	17	TCF7
0	0.880541924	0.84	0.197	0	17	NCOR2
0	0.878201154	0.76	0.102	0	17	PDE4A
0	0.85368442	0.877	0.21	0	17	SLC16A3
0	0.852337451	0.822	0.164	0	17	RFTN1
0	0.834357794	0.864	0.199	0	17	ST14
0	0.818898427	0.782	0.149	0	17	SEMA7A
0	0.817880977	0.788	0.128	0	17	MYADM
0	0.809252191	0.913	0.352	0	17	CMTM6
0	0.802425879	0.85	0.252	0	17	RUNX3
0	0.729044766	0.711	0.074	0	17	BICDL1
1.19E-306	1.015332219	0.993	0.463	2.22E-302	17	LMNA
1.11E-304	0.808080986	0.854	0.234	2.06E-300	17	BCL2L11
2.29E-300	0.976769906	0.904	0.364	4.27E-296	17	HMGA1
2.92E-298	0.861686814	0.964	0.464	5.45E-294	17	SNX9
9.97E-297	1.062442328	0.992	0.66	1.86E-292	17	CCR7
8.55E-296	0.732421222	0.54	0.014	1.59E-291	17	ATP6V1C2

2.00E-294	0.680188797	0.723	0.129	3.72E-290	17	SH3PXD2A
3.24E-288	0.847014872	0.923	0.361	6.05E-284	17	KDM4B
1.27E-285	0.750518354	0.692	0.109	2.37E-281	17	ARHGAP31
1.90E-285	0.772525651	0.867	0.284	3.53E-281	17	GNA13
2.16E-285	0.613183038	0.655	0.084	4.02E-281	17	IRAK2
2.19E-285	0.920456295	0.988	0.615	4.08E-281	17	LRRFIP1
1.75E-283	1.19702886	0.727	0.166	3.27E-279	17	NMB
4.81E-283	0.747271506	0.689	0.117	8.96E-279	17	TACC3
1.98E-282	0.814960838	0.593	0.05	3.70E-278	17	CCND1
4.90E-277	0.770343857	0.771	0.194	9.14E-273	17	TLE3
1.58E-276	0.841498874	0.871	0.294	2.95E-272	17	PPP1CB
4.57E-275	0.606441178	0.747	0.173	8.53E-271	17	HGSNAT
2.88E-274	0.696472087	0.749	0.166	5.38E-270	17	ITPKB
5.86E-269	0.584581051	0.526	0.021	1.09E-264	17	SIRPA
1.17E-268	0.648125307	0.884	0.295	2.18E-264	17	RARA
2.72E-268	0.675956919	0.903	0.278	5.07E-264	17	HLA-DQA2
1.01E-267	0.642621786	0.489	0.004	1.88E-263	17	RAMP1
4.65E-267	0.679890479	0.908	0.367	8.67E-263	17	RHOG
4.46E-266	0.801787503	0.968	0.494	8.31E-262	17	EHMT1
6.75E-263	0.894122336	0.959	0.464	1.26E-258	17	GPR183
8.78E-262	0.569677578	0.691	0.154	1.64E-257	17	IRF2BPL
2.12E-258	0.837073846	0.938	0.465	3.96E-254	17	HSPE1
4.75E-258	0.642864399	0.798	0.221	8.86E-254	17	RAPGEF1
4.32E-257	0.641664334	0.872	0.283	8.06E-253	17	ARID5A
3.75E-256	0.579669418	0.568	0.062	6.99E-252	17	ZFHX3
1.66E-252	0.722903615	0.975	0.619	3.10E-248	17	NEAT1
3.07E-250	0.582667631	0.668	0.132	5.71E-246	17	RHBDF2
4.34E-250	0.775818545	0.974	0.599	8.09E-246	17	GPX4
1.37E-246	0.555215747	0.664	0.125	2.56E-242	17	INF2
8.65E-246	0.880754604	0.871	0.332	1.61E-241	17	SERPINB9
6.87E-245	0.601547463	0.769	0.2	1.28E-240	17	ADAM8
2.87E-244	0.620153751	0.748	0.166	5.35E-240	17	JOSD1
6.67E-244	0.725358387	0.934	0.438	1.24E-239	17	MBP
1.85E-243	0.545790386	0.619	0.098	3.45E-239	17	CERK
7.51E-242	0.996895628	0.483	0.013	1.40E-237	17	CD7
1.16E-241	0.646437392	0.822	0.259	2.17E-237	17	SNX8
5.38E-240	0.769201628	0.538	0.053	1.00E-235	17	RASSF6
1.67E-238	0.503215593	0.642	0.125	3.11E-234	17	AGO2
1.53E-237	0.619040913	0.857	0.259	2.86E-233	17	SKIL
7.41E-237	0.536909553	0.653	0.122	1.38E-232	17	SH2B3
3.03E-236	0.537765395	0.674	0.139	5.65E-232	17	TARS
5.45E-234	0.479518787	0.492	0.023	1.02E-229	17	SLC12A7
1.07E-233	0.633236129	0.709	0.165	1.99E-229	17	ARID3A
3.02E-232	0.690680565	0.985	0.625	5.63E-228	17	ATP5F1B
2.85E-231	0.493617295	0.699	0.161	5.32E-227	17	SNED1
4.46E-229	0.55867165	0.777	0.208	8.31E-225	17	ZHX2

5.21E-229	0.568565458	0.627	0.113	9.71E-225	17	SOCS3
1.29E-227	0.588556045	0.861	0.339	2.40E-223	17	RASSF5
1.41E-227	0.766594237	0.792	0.253	2.63E-223	17	NR4A3
2.60E-227	0.621297408	0.715	0.17	4.84E-223	17	ELL2
1.55E-226	0.512075943	0.708	0.188	2.89E-222	17	TNIP2
1.04E-225	0.458009251	0.618	0.117	1.93E-221	17	SKI
2.37E-225	0.545278785	0.983	0.682	4.41E-221	17	MCL1
1.28E-224	0.543724337	0.775	0.227	2.38E-220	17	MANBA
2.46E-224	0.896745233	0.985	0.691	4.59E-220	17	LITAF
2.96E-224	0.602840575	0.667	0.128	5.51E-220	17	FAM49A
3.65E-224	0.696353702	0.664	0.154	6.81E-220	17	PPIF
1.40E-223	0.562181668	0.756	0.218	2.62E-219	17	GALNT2
4.82E-222	0.650284834	0.886	0.376	8.99E-218	17	CD5
7.67E-222	0.728815622	0.67	0.173	1.43E-217	17	TRAF1
1.40E-221	0.495716554	0.628	0.12	2.61E-217	17	RANGAP1
8.70E-220	0.463844203	0.603	0.105	1.62E-215	17	VAV2
1.06E-219	0.484556005	0.523	0.073	1.98E-215	17	ELK3
1.31E-219	0.635761813	0.811	0.273	2.44E-215	17	LPXN
1.56E-218	0.591899054	0.75	0.203	2.91E-214	17	NDRG1
2.98E-218	0.402689776	0.482	0.041	5.55E-214	17	VASH1
3.99E-218	0.522962228	0.609	0.104	7.44E-214	17	PLEKHG2
2.31E-216	0.610717201	0.959	0.482	4.31E-212	17	TUBB4B
7.07E-216	0.495812833	0.709	0.183	1.32E-211	17	FLNB
1.97E-215	0.701482308	0.972	0.596	3.68E-211	17	ARID5B
1.49E-214	0.872564455	0.848	0.355	2.78E-210	17	IGFBP4
1.51E-214	0.386348219	0.414	0.008	2.82E-210	17	CRIM1
5.59E-213	0.616162085	0.996	0.719	1.04E-208	17	SLC25A3
1.75E-211	0.595412734	0.82	0.305	3.26E-207	17	EHD1
2.19E-211	0.766247202	0.919	0.468	4.08E-207	17	RILPL2
4.41E-211	0.412848907	0.521	0.058	8.22E-207	17	GRK5
8.67E-210	0.655459352	0.801	0.275	1.62E-205	17	TYMP
5.08E-209	0.506314476	0.643	0.126	9.48E-205	17	RALGDS
5.54E-209	0.711780518	0.984	0.717	1.03E-204	17	REL
5.98E-208	0.51452144	0.981	0.444	1.11E-203	17	CDKN1A
3.23E-207	0.534871623	0.815	0.295	6.02E-203	17	SDF4
4.00E-207	0.613833535	0.801	0.258	7.45E-203	17	SLC2A3
1.01E-206	0.695058278	0.795	0.305	1.89E-202	17	SPI1
1.55E-206	0.597803932	0.634	0.139	2.88E-202	17	AGPAT2
2.21E-205	0.681968259	0.959	0.523	4.12E-201	17	ANXA2
2.91E-205	0.445215878	0.454	0.033	5.42E-201	17	TRPV3
7.05E-205	0.713041403	0.89	0.387	1.31E-200	17	SYAP1
4.17E-203	0.600553976	0.764	0.248	7.77E-199	17	CHMP4B
1.95E-202	0.5198214	0.653	0.159	3.64E-198	17	LAT2
3.55E-200	0.528663458	0.735	0.206	6.61E-196	17	TCP11L2
8.93E-200	0.56285182	0.994	0.677	1.66E-195	17	EMP3
1.25E-198	0.509000467	0.661	0.186	2.33E-194	17	CCND2

4.07E-198	0.68218948	0.981	0.632	7.58E-194	17	CD44
5.46E-197	0.442254867	0.501	0.059	1.02E-192	17	GRAMD4
1.52E-196	0.533332007	0.729	0.216	2.83E-192	17	PRNP
2.42E-195	0.50147957	0.794	0.267	4.52E-191	17	CYSTM1
3.31E-195	0.467934603	0.695	0.2	6.17E-191	17	RASSF2
4.77E-195	0.671738511	0.859	0.396	8.89E-191	17	COL9A3
2.20E-194	1.03520503	0.7	0.257	4.10E-190	17	MX1
1.02E-193	0.489201181	0.701	0.218	1.89E-189	17	MTHFD2
4.90E-193	0.413133342	0.447	0.052	9.13E-189	17	CCR6
1.59E-192	0.767955001	0.97	0.744	2.96E-188	17	HIST1H4C
6.32E-192	0.711672756	0.859	0.343	1.18E-187	17	PLEC
2.71E-191	0.547811725	0.953	0.492	5.05E-187	17	RAP1B
1.71E-190	0.553506424	0.987	0.624	3.20E-186	17	HERPUD1
5.77E-190	0.439166721	0.658	0.176	1.08E-185	17	ARRDC2
1.21E-189	0.532261388	0.88	0.376	2.25E-185	17	FAM177A1
1.78E-189	0.443858938	0.574	0.101	3.32E-185	17	SLC7A1
2.12E-189	0.44770548	0.781	0.266	3.96E-185	17	MARS
2.73E-188	0.44039247	0.808	0.28	5.09E-184	17	SIPA1L1
1.92E-186	0.404083207	0.56	0.101	3.58E-182	17	TMEM245
2.32E-186	0.866717914	0.761	0.302	4.33E-182	17	ACP5
2.41E-186	0.590247363	0.873	0.359	4.49E-182	17	NFE2L2
2.66E-186	0.452476935	0.737	0.233	4.95E-182	17	PLEKHB2
2.56E-182	0.363563322	0.456	0.06	4.76E-178	17	SGPP2
2.98E-182	0.506254062	0.714	0.209	5.55E-178	17	GGA3
4.03E-182	0.519023528	0.998	0.799	7.51E-178	17	SARAF
5.75E-182	0.584955466	0.81	0.308	1.07E-177	17	TACC1
2.40E-181	0.408862466	0.588	0.11	4.47E-177	17	ABR
3.40E-181	0.354158548	0.481	0.062	6.35E-177	17	GNA12
3.60E-180	0.605791673	0.79	0.298	6.72E-176	17	FAM107B
4.86E-180	0.436119992	0.862	0.367	9.05E-176	17	CSNK1D
3.32E-179	0.431798608	0.65	0.178	6.19E-175	17	BORCS5
1.44E-178	0.397426898	0.648	0.167	2.69E-174	17	MTMR6
2.28E-178	0.449909088	0.924	0.461	4.26E-174	17	PLEKHG1
2.78E-177	0.447162176	0.573	0.126	5.18E-173	17	CBX6
2.82E-177	0.454006581	0.687	0.197	5.26E-173	17	TUBA1C
2.89E-177	0.326285583	0.998	0.671	5.38E-173	17	CD83
1.13E-176	0.372123973	0.445	0.046	2.10E-172	17	UBE2F
1.17E-176	0.459971425	0.562	0.108	2.18E-172	17	HRK
1.67E-176	0.406697747	0.816	0.31	3.11E-172	17	WASHC4
5.59E-175	0.369036071	0.371	0.016	1.04E-170	17	FAAH2
9.03E-175	0.608231653	0.98	0.718	1.68E-170	17	ISCU
1.23E-174	0.547518406	0.707	0.235	2.29E-170	17	CEP170
2.73E-174	0.693526031	0.518	0.105	5.09E-170	17	GEM
3.96E-174	0.446890339	0.444	0.04	7.38E-170	17	COL18A1
5.29E-174	0.472383194	0.764	0.283	9.86E-170	17	SFT2D1
2.47E-173	0.436743504	0.395	0.022	4.61E-169	17	CMTM7

6.60E-173	0.341866376	0.467	0.073	1.23E-168	17	SLC15A4
9.20E-173	0.328017584	0.399	0.037	1.72E-168	17	SLC41A2
3.21E-172	0.353921142	0.406	0.036	5.99E-168	17	CDK5R1
5.92E-172	0.360869337	0.472	0.064	1.10E-167	17	ZSWIM6
7.47E-172	0.451149574	0.874	0.384	1.39E-167	17	G3BP1
1.54E-171	0.391054145	0.677	0.201	2.87E-167	17	MED13L
1.57E-171	0.440357145	0.611	0.181	2.93E-167	17	MALT1
3.87E-171	0.38837181	0.648	0.182	7.22E-167	17	RAB21
9.45E-170	0.504947251	0.802	0.311	1.76E-165	17	MKNK2
1.05E-169	0.517149082	0.888	0.398	1.95E-165	17	ATP2A3
7.58E-169	0.39407805	0.623	0.164	1.41E-164	17	RASA3
3.74E-168	0.448416674	0.85	0.373	6.97E-164	17	CHD4
3.05E-166	0.411682986	0.389	0.025	5.69E-162	17	CHAC1
1.91E-165	0.349485623	0.633	0.191	3.56E-161	17	IL21R
6.03E-165	0.6300033	0.956	0.574	1.12E-160	17	PRDX1
5.54E-164	0.451065704	0.699	0.229	1.03E-159	17	HIVEP2
7.45E-164	0.422085129	0.747	0.267	1.39E-159	17	CHPT1
4.45E-163	0.434945938	0.761	0.293	8.30E-159	17	NAMPT
1.16E-162	0.434871844	0.823	0.321	2.17E-158	17	PAK1
3.95E-162	0.294650281	0.686	0.244	7.36E-158	17	ATXN1
5.32E-162	0.348508201	0.555	0.133	9.92E-158	17	STK40
9.15E-162	0.732465856	0.989	0.722	1.71E-157	17	SAT1
3.69E-161	0.471035361	0.845	0.37	6.87E-157	17	VASP
6.06E-161	0.753446429	0.649	0.221	1.13E-156	17	MX2
8.81E-161	0.419275603	0.945	0.523	1.64E-156	17	LGALS1
1.03E-160	0.326279599	0.609	0.164	1.93E-156	17	GPR132
4.89E-160	0.528774616	0.947	0.624	9.12E-156	17	AKAP13
5.50E-160	0.393003582	0.397	0.034	1.02E-155	17	CHAD
1.02E-159	0.426827083	0.75	0.28	1.91E-155	17	NFATC2
1.86E-159	0.407825014	0.772	0.315	3.47E-155	17	OSBPL8
5.62E-159	0.3995808	0.635	0.198	1.05E-154	17	UBE2D1
6.51E-159	0.367485129	0.616	0.162	1.21E-154	17	POR
1.05E-158	0.528450621	0.901	0.463	1.96E-154	17	HNRNPUL1
1.22E-158	0.41500152	0.522	0.1	2.28E-154	17	HIPK2
1.56E-158	0.463096285	0.653	0.199	2.90E-154	17	KCTD20
9.81E-158	0.449807862	0.739	0.256	1.83E-153	17	GARS
2.32E-157	0.469697597	0.865	0.376	4.32E-153	17	TGIF1
2.35E-157	0.388789067	0.664	0.215	4.39E-153	17	BCL3
1.46E-156	0.403476382	0.824	0.333	2.71E-152	17	FYTTD1
1.57E-155	0.452334139	0.631	0.194	2.93E-151	17	IRF4
1.60E-155	0.715264333	0.968	0.672	2.98E-151	17	GSTP1
1.66E-155	0.337095353	0.409	0.055	3.09E-151	17	TMEM120B
2.61E-155	0.441235524	0.579	0.145	4.87E-151	17	TES
2.77E-155	0.402079985	0.682	0.218	5.17E-151	17	ZEB1
3.23E-155	0.432228464	0.676	0.212	6.02E-151	17	LSR
1.90E-154	0.367055501	0.65	0.191	3.54E-150	17	EDEM1

2.85E-154	0.467134358	0.688	0.224	5.32E-150	17	MRPS6
9.42E-154	0.427832542	0.789	0.295	1.76E-149	17	APLP2
4.05E-153	0.400492036	0.837	0.367	7.55E-149	17	TRAF4
8.01E-153	0.430200695	0.833	0.37	1.49E-148	17	HIVEP1
1.73E-152	0.445149344	0.698	0.225	3.23E-148	17	GSPT1
8.93E-152	0.483045664	0.889	0.433	1.66E-147	17	ADGRE5
2.65E-150	0.371811551	0.573	0.135	4.93E-146	17	C15orf39
5.94E-150	0.461828118	0.888	0.43	1.11E-145	17	STAT6
1.04E-149	0.403419109	0.759	0.266	1.93E-145	17	NRROS
3.42E-149	0.482995384	0.515	0.121	6.37E-145	17	CST7
2.83E-147	0.495392081	0.51	0.126	5.28E-143	17	INSIG2
3.33E-147	0.29219024	0.443	0.069	6.20E-143	17	SELENOO
5.86E-147	0.329472135	0.582	0.159	1.09E-142	17	ZZEF1
2.05E-146	0.336818948	0.711	0.253	3.83E-142	17	PARP14
8.17E-146	0.366920537	0.558	0.143	1.52E-141	17	HYOU1
2.69E-145	0.458662235	0.67	0.215	5.01E-141	17	RALA
5.16E-145	0.328915882	0.362	0.027	9.61E-141	17	ZMIZ1
6.83E-145	0.393712655	0.493	0.098	1.27E-140	17	C12orf49
1.60E-144	0.340688416	0.798	0.319	2.98E-140	17	VDAC1
5.14E-144	0.296230555	0.355	0.028	9.59E-140	17	SMAD3
5.40E-144	0.334461364	0.44	0.072	1.01E-139	17	KLHL21
8.35E-144	0.369290879	0.616	0.199	1.56E-139	17	TRRAP
1.49E-143	0.306102618	0.509	0.132	2.78E-139	17	SEMA4D
8.99E-143	0.408085058	0.849	0.411	1.68E-138	17	DENND4A
3.06E-142	0.264869392	0.386	0.053	5.70E-138	17	IQCN
3.50E-142	0.434503408	0.776	0.32	6.53E-138	17	PEA15
7.96E-142	0.35965229	0.516	0.11	1.48E-137	17	ZC3H7B
1.37E-141	0.668230151	0.343	0.02	2.55E-137	17	RRAD
3.29E-141	0.436327089	0.992	0.719	6.13E-137	17	TMBIM6
4.86E-140	0.494573731	0.949	0.607	9.05E-136	17	ORAI2
6.41E-140	0.353924442	0.778	0.324	1.19E-135	17	SF3B4
9.84E-140	0.362938702	0.604	0.179	1.83E-135	17	HERC2
1.30E-139	0.484494958	0.941	0.558	2.42E-135	17	DDX21
5.05E-139	0.33552557	0.647	0.199	9.42E-135	17	CCSER2
3.31E-138	0.464670776	0.722	0.276	6.17E-134	17	WARS
4.30E-138	0.621959635	0.913	0.544	8.01E-134	17	ERH
1.59E-137	0.306662787	0.313	0.015	2.97E-133	17	FGFR1
1.60E-137	0.358927788	0.747	0.284	2.98E-133	17	JPT1
1.28E-136	0.292688347	0.29	0.007	2.38E-132	17	GNG4
1.29E-136	0.365193827	0.828	0.369	2.41E-132	17	FBXO21
1.40E-136	0.316058849	0.499	0.116	2.62E-132	17	HELZ2
1.89E-136	0.375810268	0.628	0.211	3.52E-132	17	LAP3
1.03E-135	0.368682339	0.634	0.208	1.91E-131	17	LYSMD2
1.26E-135	0.422507861	0.983	0.684	2.36E-131	17	RAN
3.55E-135	0.37383544	0.83	0.397	6.63E-131	17	ANKRD11
3.61E-134	0.281276605	0.404	0.062	6.73E-130	17	TPCN2

2.29E-133	0.311689831	0.433	0.087	4.27E-129	17	BID
2.37E-133	0.320509257	0.523	0.133	4.42E-129	17	WNT10A
2.97E-133	0.325162444	0.488	0.119	5.53E-129	17	IFIH1
4.47E-133	0.375634731	0.606	0.182	8.33E-129	17	BANP
7.32E-133	0.37790343	0.644	0.228	1.36E-128	17	RNF145
2.49E-132	0.444453436	0.427	0.091	4.64E-128	17	OAS2
2.63E-132	0.35841441	0.503	0.125	4.91E-128	17	MYO1C
3.86E-132	0.306852083	0.682	0.257	7.20E-128	17	GNB1
9.33E-132	0.266336929	0.455	0.106	1.74E-127	17	CTDP1
1.03E-131	0.597445755	0.711	0.29	1.93E-127	17	HMOX1
1.92E-131	0.359054113	0.944	0.521	3.59E-127	17	RELB
2.04E-131	0.332717816	0.602	0.183	3.80E-127	17	ZNF267
3.87E-131	0.334042563	0.558	0.154	7.22E-127	17	CHST11
9.44E-131	0.460421102	0.466	0.099	1.76E-126	17	MARCKS
1.09E-130	0.415702997	0.686	0.273	2.04E-126	17	IRF7
1.25E-130	0.407613259	0.802	0.34	2.33E-126	17	RANBP2
1.77E-130	0.343704639	0.793	0.353	3.30E-126	17	SPTAN1
5.03E-130	0.553207555	0.667	0.233	9.38E-126	17	CEMIP2
2.19E-129	0.28226922	0.645	0.227	4.09E-125	17	ZBTB43
3.55E-129	0.269000215	0.294	0.013	6.62E-125	17	ANKRD33B
4.01E-129	0.429162309	0.74	0.305	7.48E-125	17	PIKFYVE
5.88E-129	0.46577557	0.965	0.641	1.10E-124	17	CYTH1
7.24E-128	0.287060012	0.435	0.078	1.35E-123	17	HIP1R
1.10E-126	0.571833695	0.843	0.457	2.05E-122	17	APOBEC3G
1.23E-126	0.282054767	0.451	0.103	2.29E-122	17	N4BP3
1.48E-126	0.266471411	0.494	0.117	2.75E-122	17	BAIAP3
1.13E-125	0.292455009	0.525	0.145	2.11E-121	17	DUSP5
2.30E-125	0.258957564	0.351	0.048	4.29E-121	17	JSRP1
3.21E-125	0.29607105	0.682	0.236	5.99E-121	17	CDK17
5.96E-125	0.274919487	0.442	0.094	1.11E-120	17	PRKAG2
6.29E-125	0.435793638	0.95	0.632	1.17E-120	17	PDE4B
1.01E-124	0.419317439	0.761	0.336	1.88E-120	17	PTP4A1
3.70E-124	0.412718915	0.943	0.566	6.90E-120	17	FLNA
5.10E-124	0.276886945	0.515	0.137	9.51E-120	17	CLCN3
1.14E-123	0.250570778	0.337	0.039	2.13E-119	17	GPR137B
1.18E-123	0.328618546	0.87	0.433	2.21E-119	17	SMG1
1.75E-123	0.272545535	0.524	0.136	3.27E-119	17	RAB3IP
3.14E-123	0.276348178	0.344	0.053	5.85E-119	17	ADAP2
4.54E-123	0.349419197	0.82	0.377	8.46E-119	17	CYLD
8.51E-123	0.40064072	0.95	0.58	1.59E-118	17	SEC61B
1.65E-122	0.359076432	0.937	0.58	3.07E-118	17	PKM
3.42E-122	0.301546764	0.765	0.336	6.37E-118	17	PSMB4
4.79E-122	0.254681206	0.485	0.125	8.94E-118	17	PRDM4
8.95E-122	0.408140986	0.732	0.301	1.67E-117	17	ATP1B3
3.00E-121	0.284180714	0.63	0.211	5.59E-117	17	ANKRD13A
5.08E-121	0.294698183	0.604	0.201	9.47E-117	17	TUBB6

5.20E-121	0.262431476	0.666	0.249	9.70E-117	17	WHRN
8.05E-121	0.298660617	0.426	0.086	1.50E-116	17	FOSL2
8.72E-121	0.376456435	0.418	0.078	1.63E-116	17	GRAMD1A
9.99E-121	0.300211673	0.634	0.216	1.86E-116	17	CLIC4
1.33E-120	0.277397922	0.396	0.055	2.48E-116	17	SREBF1
1.84E-120	0.355440617	0.824	0.368	3.43E-116	17	SEC14L1
2.02E-120	0.41243491	0.975	0.656	3.76E-116	17	EIF5A
5.99E-120	0.402537996	0.625	0.208	1.12E-115	17	CPEB4
7.07E-120	0.543998056	0.89	0.495	1.32E-115	17	TNFRSF1B
1.34E-119	0.259519327	0.429	0.093	2.49E-115	17	TIMP2
3.30E-119	0.274413744	0.489	0.117	6.16E-115	17	GOT1
5.08E-119	0.283136372	0.464	0.118	9.48E-115	17	ORAI1
5.38E-119	0.674167823	0.959	0.767	1.00E-114	17	ZFP36L1
3.45E-118	0.271447787	0.391	0.069	6.43E-114	17	AMPD3
5.12E-118	0.408441446	0.892	0.493	9.55E-114	17	TNIP1
2.26E-117	0.391237394	0.846	0.439	4.22E-113	17	ADAR
1.53E-116	0.385300795	0.564	0.177	2.85E-112	17	TUBB2A
2.53E-116	0.489120079	0.479	0.13	4.72E-112	17	AL133415.1
1.46E-115	0.369443841	0.502	0.152	2.72E-111	17	RAB9A
3.04E-115	0.42460157	0.29	0.03	5.66E-111	17	OASL
5.94E-115	0.255564444	0.311	0.031	1.11E-110	17	CYB561
6.74E-115	0.403568491	0.829	0.405	1.26E-110	17	PLEKHA2
8.89E-115	0.25676254	0.458	0.119	1.66E-110	17	ST8SIA4
9.88E-115	0.380637253	0.843	0.405	1.84E-110	17	LDHA
1.38E-114	0.363588162	1	0.883	2.57E-110	17	COX4I1
2.46E-114	0.26021639	0.594	0.2	4.59E-110	17	ORMDL2
4.40E-114	0.256260032	0.397	0.081	8.19E-110	17	SLC1A4
8.64E-114	0.284943954	0.496	0.133	1.61E-109	17	TXNRD1
4.26E-113	0.330791133	0.621	0.225	7.94E-109	17	IRF5
7.32E-113	0.338371008	0.369	0.076	1.36E-108	17	CYTOR
2.34E-112	0.258452177	0.488	0.127	4.35E-108	17	SRD5A1
2.71E-112	0.323303244	0.786	0.346	5.05E-108	17	FMNL1
3.71E-112	0.275378338	0.725	0.3	6.92E-108	17	MAP3K2
4.75E-112	0.278925072	0.607	0.211	8.85E-108	17	CBFA2T3
6.98E-112	0.343555539	0.819	0.385	1.30E-107	17	EIF2S2
2.68E-111	0.267463097	0.54	0.164	5.00E-107	17	PRR7
4.75E-111	0.347827268	0.844	0.421	8.85E-107	17	CD63
1.35E-110	0.261083522	0.633	0.227	2.52E-106	17	SS18
8.97E-110	0.29813661	0.837	0.387	1.67E-105	17	TMED2
1.90E-109	0.278797806	0.816	0.41	3.55E-105	17	POLR2A
2.25E-108	0.265104975	0.394	0.076	4.20E-104	17	GRASP
3.97E-108	0.308911682	0.662	0.254	7.40E-104	17	SOD2-ENSG00000112096
2.81E-107	0.490334839	0.852	0.478	5.23E-103	17	TUBA4A
2.12E-106	0.2997134	0.805	0.383	3.95E-102	17	RIPOR1
6.21E-106	0.387838409	0.943	0.597	1.16E-101	17	CD99
6.79E-106	0.262182115	0.724	0.316	1.27E-101	17	ANXA7

1.09E-105	0.413011716	0.933	0.579	2.04E-101	17	MYH9
1.63E-105	0.310909239	0.774	0.353	3.03E-101	17	SBNO1
4.52E-105	0.309438502	0.869	0.435	8.43E-101	17	UBE2N
1.01E-104	0.255533359	0.487	0.132	1.88E-100	17	ACSL1
3.36E-104	0.349331469	0.904	0.498	6.26E-100	17	BIRC3
7.11E-104	0.258589492	0.622	0.219	1.33E-99	17	ADSS
7.33E-104	0.270217203	0.683	0.266	1.37E-99	17	SPAG9
1.30E-103	0.289924616	0.682	0.25	2.41E-99	17	CS
3.45E-103	0.325910031	0.597	0.212	6.43E-99	17	CTSB
6.10E-103	0.265723334	0.695	0.296	1.14E-98	17	SEL1L3
8.23E-103	0.369283834	0.863	0.476	1.53E-98	17	WIPF1
2.64E-102	0.284855052	0.54	0.165	4.93E-98	17	STX11
2.97E-102	0.381229969	0.825	0.448	5.53E-98	17	CD82
6.43E-102	0.256077755	0.529	0.173	1.20E-97	17	NEK1
1.17E-101	0.283834644	0.353	0.074	2.18E-97	17	CMSS1
2.36E-101	0.346551422	0.855	0.431	4.40E-97	17	LAPTM4A
4.00E-101	0.260619256	0.567	0.2	7.46E-97	17	PRKCD
6.86E-101	0.281528216	0.804	0.401	1.28E-96	17	SPINT2
8.46E-101	0.283457319	0.501	0.16	1.58E-96	17	PDCL3
2.63E-100	0.261781066	0.6	0.231	4.91E-96	17	GLIPR1
9.48E-100	0.263275503	0.33	0.05	1.77E-95	17	L1CAM
1.11E-99	0.446595559	0.856	0.511	2.07E-95	17	IFNGR2
1.18E-99	0.250364822	0.746	0.321	2.21E-95	17	UBE2A
1.21E-99	0.319417887	0.887	0.461	2.26E-95	17	GNG5
2.70E-99	0.300746478	0.981	0.765	5.04E-95	17	STK4
1.71E-98	0.254778147	0.283	0.032	3.18E-94	17	TNFRSF9
9.65E-98	0.337237493	0.543	0.195	1.80E-93	17	GUSB
2.61E-97	0.31647523	0.957	0.612	4.87E-93	17	SRSF2
2.95E-97	0.309183725	0.785	0.353	5.50E-93	17	ATP6V0D1
3.87E-97	0.250049563	0.629	0.25	7.21E-93	17	DLGAP4
7.10E-97	0.256287626	0.422	0.097	1.32E-92	17	MIR22HG
7.30E-97	0.298500423	0.719	0.312	1.36E-92	17	CTNNB1
1.12E-96	0.260776895	0.465	0.135	2.08E-92	17	PRDX2
1.66E-96	0.277208095	0.255	0.022	3.09E-92	17	APOBEC3B
3.93E-96	0.259260496	0.791	0.384	7.33E-92	17	WBP11
4.36E-95	0.290594325	0.872	0.473	8.12E-91	17	JUND
5.49E-95	0.343418628	0.696	0.323	1.02E-90	17	RAB29
1.49E-94	0.290286919	0.834	0.432	2.79E-90	17	R3HDM4
6.15E-94	0.307187019	0.787	0.391	1.15E-89	17	TMEM123
1.20E-93	0.352745783	0.452	0.132	2.25E-89	17	PEG10
1.69E-93	0.29969936	0.948	0.598	3.15E-89	17	SPOCK2
3.50E-93	0.310494344	0.853	0.44	6.53E-89	17	ZEB2
1.69E-91	0.277256863	0.265	0.028	3.15E-87	17	HES4
3.03E-91	0.634746317	0.537	0.212	5.65E-87	17	ISG15
4.04E-91	0.309835227	0.806	0.399	7.53E-87	17	PBXIP1
7.23E-91	0.862288986	0.38	0.094	1.35E-86	17	RMRP

1.67E-90	0.275887228	0.215	0.009	3.11E-86	17	MAP1B
1.72E-90	0.279896918	0.786	0.406	3.21E-86	17	ANXA5
6.61E-90	0.29348916	0.285	0.046	1.23E-85	17	PLSCR1
9.17E-90	0.787439905	0.26	0.03	1.71E-85	17	RGS12
3.19E-89	0.314696991	0.971	0.679	5.94E-85	17	ATP6V0C
1.14E-88	0.276557351	0.831	0.422	2.13E-84	17	STK17A
4.81E-88	0.253846111	0.342	0.062	8.96E-84	17	PFKFB3
8.51E-87	0.270456476	0.796	0.39	1.59E-82	17	TENT5C
1.04E-86	0.39187566	0.623	0.257	1.94E-82	17	SESN3
1.37E-86	0.29351275	0.454	0.149	2.55E-82	17	CXCR3
1.27E-85	0.264476633	0.867	0.483	2.37E-81	17	GUK1
4.49E-81	0.254147356	0.537	0.2	8.38E-77	17	HIST2H2AC
1.89E-80	0.255229831	0.84	0.46	3.52E-76	17	TPM4
1.17E-79	0.27033294	0.84	0.459	2.18E-75	17	IL16
4.23E-77	0.51185571	0.87	0.574	7.88E-73	17	ISG20
9.20E-77	0.33313446	0.658	0.293	1.71E-72	17	TXN
2.71E-75	0.258196222	0.585	0.253	5.06E-71	17	BACE2
9.08E-74	0.253348679	0.983	0.711	1.69E-69	17	CALM2
2.50E-73	0.30345842	0.877	0.539	4.67E-69	17	AGPAT5
9.88E-72	0.351939926	0.471	0.192	1.84E-67	17	DDIT4
1.50E-71	0.252144119	0.976	0.737	2.79E-67	17	PRRC2C
1.45E-66	0.649693724	0.351	0.113	2.71E-62	17	MT2A
1.50E-66	0.385880813	0.762	0.423	2.80E-62	17	LY9
2.04E-65	0.384782488	0.296	0.081	3.81E-61	17	GK
1.49E-63	0.282255744	0.935	0.637	2.77E-59	17	CDC37
1.04E-62	0.322658933	0.346	0.095	1.94E-58	17	LGALS3
3.72E-59	0.257419216	0.939	0.651	6.93E-55	17	TUBA1A
3.05E-55	0.252158983	0.757	0.436	5.68E-51	17	SERPINB1
1.74E-52	0.372665442	0.568	0.27	3.24E-48	17	MGAT1
3.30E-52	0.28206437	0.874	0.531	6.15E-48	17	GABARAPL2
3.47E-49	0.443562492	0.193	0.044	6.47E-45	17	IFIT2
4.08E-46	0.337983934	0.824	0.497	7.61E-42	17	PLCG2
4.92E-307	1.696595727	0.843	0.308	9.17E-303	18	LINC01480
1.54E-265	1.141539163	0.961	0.722	2.87E-261	18	MIF
3.53E-265	1.033420803	0.998	0.873	6.58E-261	18	HSP90AB1
1.64E-240	1.200159257	0.878	0.5	3.06E-236	18	ENO1
3.29E-230	0.824402107	0.727	0.226	6.14E-226	18	DNPH1
6.17E-225	0.907440459	0.844	0.416	1.15E-220	18	NME2
3.15E-220	0.872771557	0.784	0.319	5.87E-216	18	NHP2
3.49E-219	0.943100161	0.818	0.385	6.51E-215	18	PSME2
2.66E-217	0.843830629	0.981	0.833	4.96E-213	18	PFN1
6.34E-202	0.887482984	0.864	0.498	1.18E-197	18	SELENOH
3.00E-196	0.860250846	0.968	0.795	5.59E-192	18	YBX1
6.97E-190	0.792864926	0.756	0.328	1.30E-185	18	ATP5MC1
7.24E-188	0.84546306	0.983	0.855	1.35E-183	18	NPM1
9.12E-179	0.800645382	0.706	0.274	1.70E-174	18	C1QBP

5.76E-178	0.846887139	0.928	0.687	1.07E-173	18	RAN
2.29E-176	0.86531856	0.919	0.659	4.28E-172	18	EIF5A
4.52E-170	0.84317174	0.876	0.527	8.43E-166	18	RPL22L1
9.57E-164	0.801463089	0.789	0.439	1.78E-159	18	LDHB
4.44E-163	0.652121531	0.714	0.311	8.28E-159	18	SNRPE
1.06E-162	0.803824314	0.869	0.56	1.97E-158	18	TPI1
3.86E-161	0.752006283	0.646	0.24	7.19E-157	18	IMPDH2
1.51E-156	0.753694062	0.829	0.518	2.82E-152	18	ATP5MC3
1.09E-148	0.762174155	0.922	0.628	2.04E-144	18	DBI
4.05E-146	0.738960415	0.81	0.431	7.56E-142	18	ATOX1
5.40E-145	0.652496225	0.804	0.439	1.01E-140	18	APRT
2.37E-144	1.07862939	0.724	0.335	4.42E-140	18	MIR155HG
3.90E-144	1.034717602	0.801	0.471	7.27E-140	18	TUBB
2.92E-141	0.661141988	0.656	0.29	5.45E-137	18	RANBP1
3.50E-138	0.638295165	0.74	0.338	6.53E-134	18	BANF1
1.03E-137	0.62747273	0.817	0.498	1.91E-133	18	COX5A
1.08E-135	0.649953529	0.739	0.374	2.02E-131	18	PRMT1
3.53E-134	0.647631871	0.609	0.227	6.58E-130	18	ABRACL
3.73E-133	0.602553828	0.905	0.604	6.96E-129	18	GPX4
6.77E-128	0.572046804	0.685	0.328	1.26E-123	18	PSMB6
1.11E-127	0.618065978	0.891	0.639	2.07E-123	18	COX6C
3.28E-125	0.582119804	0.798	0.464	6.11E-121	18	ATP5MF
1.90E-122	0.461209829	0.405	0.083	3.54E-118	18	PAICS
3.07E-118	0.563052402	0.859	0.561	5.73E-114	18	ANP32B
1.00E-116	0.642918778	0.857	0.591	1.87E-112	18	COX6A1
2.06E-116	0.535219444	0.578	0.22	3.85E-112	18	PHB
1.39E-114	0.401050432	0.42	0.101	2.59E-110	18	MRPL24
1.41E-114	0.480946362	0.986	0.874	2.64E-110	18	CFL1
1.46E-114	0.69957312	0.646	0.297	2.72E-110	18	TXN
2.60E-112	0.585228863	0.759	0.429	4.85E-108	18	ATP5PF
4.85E-111	0.498497243	0.961	0.798	9.05E-107	18	ATP5MC2
1.37E-110	0.476301585	0.978	0.872	2.55E-106	18	RPL26
1.93E-110	0.487901393	0.955	0.746	3.60E-106	18	TMA7
2.84E-110	0.51864882	0.669	0.335	5.29E-106	18	MRPL52
1.81E-108	0.527644123	0.685	0.359	3.38E-104	18	CCT7
4.68E-107	0.513533341	0.773	0.453	8.72E-103	18	NDUFB2
1.12E-104	0.713590696	0.843	0.585	2.08E-100	18	PKM
1.59E-103	0.569695046	0.861	0.57	2.96E-99	18	SET
3.26E-102	0.601212528	0.725	0.418	6.08E-98	18	UQCRQ
2.28E-101	0.502584852	0.961	0.786	4.25E-97	18	PEBP1
5.23E-101	0.499911613	0.838	0.561	9.74E-97	18	ELOB
4.33E-100	0.406342652	0.558	0.24	8.07E-96	18	MRPL4
6.36E-100	0.481457933	0.742	0.441	1.19E-95	18	ATP5MPL
1.77E-98	0.508880012	0.521	0.206	3.30E-94	18	PPA1
3.72E-98	0.425671556	0.956	0.783	6.93E-94	18	HSPA8
7.25E-98	0.47930288	0.502	0.17	1.35E-93	18	TIMM13

1.29E-96	0.418988729	0.539	0.211	2.40E-92	18	NDUFAF8
1.44E-96	0.608006127	0.82	0.486	2.69E-92	18	IGLL5
2.51E-96	0.416529875	0.667	0.352	4.68E-92	18	SNRPC
3.60E-96	0.496910701	0.756	0.449	6.71E-92	18	PSMB3
5.43E-96	0.377560853	0.431	0.134	1.01E-91	18	TRMT1
2.44E-94	0.443253453	0.492	0.16	4.55E-90	18	PHPT1
1.67E-92	0.446528594	0.668	0.341	3.12E-88	18	C19orf70
4.62E-92	0.285690625	0.249	0.022	8.62E-88	18	NME1
1.92E-90	0.328560859	0.349	0.086	3.58E-86	18	MCRIP2
1.97E-90	0.523625995	0.634	0.326	3.67E-86	18	VDAC1
5.90E-90	0.430565383	0.974	0.853	1.10E-85	18	BTF3
6.09E-90	0.444485536	0.663	0.338	1.13E-85	18	NDUFB7
2.93E-89	0.49368355	0.319	0.064	5.47E-85	18	L1TD1
3.05E-89	0.541014847	0.867	0.634	5.68E-85	18	SOD1
9.88E-89	0.50027924	0.708	0.408	1.84E-84	18	SNRPF
2.21E-88	0.479123887	0.935	0.777	4.12E-84	18	CHCHD2
6.85E-88	0.402315884	0.648	0.342	1.28E-83	18	GADD45GIP1
2.25E-87	0.357997626	0.51	0.201	4.19E-83	18	PFDN6
7.10E-87	0.437164343	0.472	0.17	1.32E-82	18	CDK4
8.89E-87	0.411819051	0.579	0.253	1.66E-82	18	NUTF2
1.09E-86	0.45393733	0.752	0.446	2.03E-82	18	FBL
4.13E-86	0.488221351	0.706	0.405	7.70E-82	18	CCT3
4.14E-86	0.463421165	0.605	0.3	7.73E-82	18	NDUFS6
6.37E-86	0.427853437	0.732	0.455	1.19E-81	18	TUFM
9.80E-86	0.497675046	0.724	0.444	1.83E-81	18	COX7B
1.24E-85	0.605832794	0.677	0.391	2.32E-81	18	SEC61G
2.99E-85	0.418118997	0.705	0.398	5.58E-81	18	MDH2
6.05E-85	0.428374492	0.587	0.283	1.13E-80	18	NDUFAB1
6.73E-85	0.691855802	0.878	0.669	1.25E-80	18	CALR
1.04E-84	0.547694898	0.975	0.853	1.93E-80	18	ACTG1
1.18E-84	0.396869516	0.468	0.167	2.20E-80	18	EBNA1BP2
1.35E-84	0.475606244	0.597	0.28	2.52E-80	18	PDCD5
1.35E-84	0.499368215	0.848	0.614	2.52E-80	18	NDUFA4
2.12E-84	0.681097972	0.774	0.501	3.94E-80	18	MS4A1
2.98E-84	0.369269041	0.437	0.165	5.55E-80	18	DCTPP1
5.60E-84	0.393841573	0.986	0.881	1.04E-79	18	ATP5F1E
8.12E-84	0.384691687	0.764	0.491	1.51E-79	18	UQCR10
1.20E-83	0.339745919	0.348	0.087	2.25E-79	18	ISOC2
7.86E-83	0.490184896	0.419	0.142	1.46E-78	18	FABP5
1.09E-82	0.463207653	0.823	0.543	2.04E-78	18	PARK7
1.20E-82	0.395175963	0.703	0.419	2.24E-78	18	PSMB10
1.04E-81	0.417682072	0.51	0.193	1.94E-77	18	ATIC
1.18E-81	0.447293208	0.749	0.461	2.21E-77	18	ROMO1
1.38E-81	0.41245185	0.827	0.579	2.57E-77	18	NDUFA1
2.81E-81	0.492967722	0.89	0.681	5.24E-77	18	RBM3
2.89E-81	0.463753225	0.683	0.381	5.39E-77	18	PRDX6

3.25E-81	0.466654341	0.665	0.369	6.06E-77	18	PA2G4
4.76E-81	0.338369659	0.502	0.21	8.88E-77	18	CCDC124
6.13E-81	0.431657136	0.792	0.539	1.14E-76	18	TRMT112
4.49E-80	0.2616126	0.296	0.068	8.37E-76	18	EXOSC5
6.50E-80	0.39025683	0.488	0.19	1.21E-75	18	AHCY
1.20E-79	0.460405653	0.719	0.429	2.24E-75	18	ATP5ME
1.49E-79	0.524567223	0.839	0.579	2.77E-75	18	PRDX1
2.47E-79	0.449668474	0.763	0.492	4.60E-75	18	PRELID1
2.58E-79	0.395328684	0.525	0.234	4.82E-75	18	NDUFB3
6.01E-79	0.457937955	0.768	0.51	1.12E-74	18	COX8A
1.06E-78	0.485877405	0.781	0.521	1.98E-74	18	ATP5IF1
2.99E-78	0.447972228	0.814	0.554	5.58E-74	18	ATP5F1D
3.73E-78	0.427131319	0.68	0.375	6.96E-74	18	APEX1
9.54E-78	0.368101403	0.561	0.246	1.78E-73	18	MRPS34
1.94E-77	0.560674511	0.546	0.255	3.62E-73	18	ARHGAP44
3.43E-77	0.475889612	0.644	0.349	6.40E-73	18	HSPB1
8.13E-77	0.421314672	0.78	0.488	1.51E-72	18	LSM7
8.89E-77	0.402220033	0.596	0.28	1.66E-72	18	CYC1
1.45E-76	0.438612686	0.765	0.499	2.69E-72	18	POLR2L
4.67E-75	0.325157812	0.949	0.818	8.71E-71	18	SRP14
6.87E-75	0.405502247	0.735	0.455	1.28E-70	18	DAD1
9.04E-75	0.34063486	0.765	0.486	1.68E-70	18	WDR83OS
5.39E-73	0.297966483	0.352	0.101	1.00E-68	18	RUVBL2
9.66E-73	0.36718421	0.791	0.537	1.80E-68	18	PHB2
1.67E-72	0.450905462	0.516	0.224	3.10E-68	18	FMOD
4.99E-72	0.342747017	0.467	0.175	9.31E-68	18	FAM173A
5.82E-72	0.563882166	0.616	0.332	1.09E-67	18	PDIA6
1.13E-71	0.389855845	0.664	0.363	2.11E-67	18	NDUFA2
2.78E-71	0.344447502	0.689	0.442	5.18E-67	18	PSMD8
6.07E-71	0.548158822	0.341	0.105	1.13E-66	18	SDF2L1
2.21E-70	0.392220987	0.713	0.424	4.12E-66	18	BRK1
2.44E-70	0.43898915	0.845	0.617	4.56E-66	18	COX6B1
3.21E-70	0.373914846	0.508	0.211	5.99E-66	18	TMEM147
3.99E-70	0.456891505	0.828	0.598	7.44E-66	18	COX5B
6.46E-69	0.424182398	0.788	0.549	1.20E-64	18	PSMB1
9.02E-69	0.275649324	0.315	0.086	1.68E-64	18	BOLA3
9.41E-69	0.348333251	0.653	0.387	1.75E-64	18	NDUFA3
1.21E-68	0.315337756	0.486	0.205	2.25E-64	18	MRPL11
1.30E-68	0.361713491	0.695	0.414	2.42E-64	18	SSBP1
1.47E-68	0.622735611	0.524	0.255	2.74E-64	18	MYDGF
1.78E-68	0.376844339	0.553	0.25	3.32E-64	18	AC243960.1
1.89E-68	0.391372553	0.506	0.229	3.52E-64	18	PKIG
2.81E-68	0.36077456	0.619	0.31	5.23E-64	18	AKR1A1
8.59E-68	0.422599846	0.777	0.507	1.60E-63	18	UQCR11
1.69E-67	0.312137516	0.363	0.108	3.15E-63	18	TRAP1
3.75E-67	0.288588664	0.336	0.106	6.98E-63	18	MRTO4

5.51E-67	0.397363643	0.752	0.502	1.03E-62	18	SNRPB
1.01E-66	0.450839965	0.834	0.538	1.89E-62	18	PTPN6
2.10E-66	0.533946907	0.562	0.273	3.91E-62	18	PIGR
2.67E-66	0.393255217	0.932	0.765	4.98E-62	18	Sep-07
3.69E-66	0.29976155	0.357	0.128	6.88E-62	18	TESPA1
1.35E-65	0.352802799	0.562	0.275	2.52E-61	18	SRI
2.53E-65	0.358178064	0.762	0.5	4.72E-61	18	ARL6IP4
2.70E-65	0.336921518	0.78	0.549	5.03E-61	18	ERH
5.16E-65	0.43968612	0.807	0.543	9.61E-61	18	LRMP
5.57E-65	0.298451237	0.525	0.245	1.04E-60	18	NDUFS8
6.23E-65	0.336466142	0.595	0.321	1.16E-60	18	PSMA6
2.59E-64	0.350429018	0.728	0.458	4.83E-60	18	EIF3I
7.64E-64	0.360838456	0.609	0.331	1.42E-59	18	SNRPD1
8.83E-64	0.344545147	0.402	0.138	1.65E-59	18	PARVB
9.41E-64	0.460008439	0.847	0.621	1.75E-59	18	SLC25A5
1.08E-63	0.304153345	0.635	0.367	2.01E-59	18	C8orf59
1.41E-63	0.377012747	0.441	0.182	2.63E-59	18	LCK
1.49E-63	0.363965417	0.597	0.31	2.78E-59	18	RPS17
1.80E-63	0.353670029	0.716	0.456	3.35E-59	18	BSG
2.19E-63	0.366159146	0.703	0.436	4.08E-59	18	NDUFB9
2.30E-63	0.351339616	0.651	0.372	4.28E-59	18	POLR2E
4.02E-63	0.340243117	0.676	0.386	7.50E-59	18	FIS1
5.32E-63	0.308631093	0.472	0.199	9.92E-59	18	NAA38
8.31E-63	0.388759093	0.776	0.54	1.55E-58	18	ATP5F1A
8.73E-63	0.396241694	0.681	0.404	1.63E-58	18	RGS10
1.78E-62	0.441034561	0.808	0.585	3.32E-58	18	SERBP1
2.38E-62	0.390407231	0.282	0.069	4.44E-58	18	SUSD1
2.45E-62	0.338622573	0.71	0.436	4.57E-58	18	PARP1
3.07E-62	0.302678249	0.558	0.277	5.73E-58	18	PDAP1
4.46E-62	0.354125258	0.305	0.08	8.31E-58	18	SRM
4.52E-62	0.293579119	0.707	0.44	8.42E-58	18	CBX3
7.00E-62	0.309036511	0.378	0.141	1.30E-57	18	TOMM40
1.34E-61	0.301433167	0.311	0.098	2.49E-57	18	IFRD2
1.39E-61	0.288341942	0.548	0.287	2.59E-57	18	LSM3
1.61E-61	0.522463223	0.291	0.09	3.00E-57	18	FKBP11
3.26E-61	0.295318117	0.302	0.091	6.07E-57	18	GPATCH4
5.67E-61	0.397202005	0.546	0.276	1.06E-56	18	SLIRP
7.17E-61	0.292029558	0.557	0.303	1.34E-56	18	BAX
7.29E-61	0.322104922	0.286	0.078	1.36E-56	18	PDGFD
1.67E-60	0.309413558	0.552	0.273	3.12E-56	18	UQCRC1
3.41E-60	0.356883355	0.968	0.838	6.35E-56	18	SLC25A6
3.69E-60	0.306039784	0.445	0.192	6.87E-56	18	MRPL3
9.19E-60	0.266087912	0.316	0.091	1.71E-55	18	VARS
1.06E-59	0.265562085	0.377	0.143	1.98E-55	18	ADSL
2.73E-59	0.7383054	0.964	0.848	5.09E-55	18	GAPDH
2.99E-59	0.283193459	0.422	0.168	5.58E-55	18	POLD2

6.07E-59	0.343363291	0.849	0.626	1.13E-54	18	UBL5
6.94E-59	0.364392416	0.665	0.37	1.29E-54	18	ATP5PD
9.33E-59	0.346341175	0.716	0.464	1.74E-54	18	COPE
1.36E-58	0.303871545	0.975	0.853	2.54E-54	18	RPL23
1.53E-58	0.40118945	0.795	0.554	2.85E-54	18	PSMA7
1.77E-58	0.397555945	0.499	0.239	3.30E-54	18	FKBP2
2.26E-58	0.280179705	0.482	0.217	4.21E-54	18	ITPA
2.60E-58	0.321725633	0.464	0.2	4.86E-54	18	MRPS12
2.74E-58	0.381988041	0.73	0.476	5.12E-54	18	PGAM1
2.98E-58	0.278990813	0.493	0.233	5.55E-54	18	ERCC1
3.24E-58	0.306414149	0.645	0.373	6.04E-54	18	NDUFB10
3.39E-58	0.427942085	0.758	0.513	6.31E-54	18	CHCHD10
4.71E-58	0.292047362	0.399	0.154	8.79E-54	18	PRDX3
5.52E-58	0.258156796	0.345	0.126	1.03E-53	18	WDR46
5.88E-58	0.47494182	0.757	0.502	1.10E-53	18	SPCS1
7.00E-58	0.388881116	0.922	0.76	1.31E-53	18	ATP5MG
8.71E-58	0.33958158	0.655	0.397	1.62E-53	18	PRDX5
2.65E-57	0.339809161	0.634	0.396	4.95E-53	18	CANX
3.19E-57	0.324232223	0.562	0.291	5.95E-53	18	REX1BD
3.33E-57	0.339622455	0.597	0.334	6.21E-53	18	FKBP1A
7.70E-57	0.325648019	0.578	0.32	1.44E-52	18	ANAPC11
1.23E-56	0.43749276	0.7	0.461	2.29E-52	18	TMEM258
2.16E-56	0.88163916	0.258	0.065	4.03E-52	18	APOD
2.40E-56	0.260533715	0.505	0.237	4.48E-52	18	TMEM256
3.01E-56	0.353226918	0.463	0.198	5.61E-52	18	C19orf24
4.01E-56	0.323593749	0.63	0.38	7.47E-52	18	CCT6A
4.47E-56	0.315699035	0.608	0.367	8.33E-52	18	CCT8
4.69E-56	0.284159408	0.505	0.256	8.74E-52	18	PSMA5
7.15E-56	0.295927562	0.506	0.236	1.33E-51	18	HSD17B10
8.04E-56	0.319502715	0.382	0.148	1.50E-51	18	RCC1
8.35E-56	0.293595768	0.781	0.54	1.56E-51	18	NDUFB11
9.29E-56	0.343248792	0.486	0.238	1.73E-51	18	TKT
3.07E-55	0.283961126	0.651	0.389	5.73E-51	18	SNRPD3
3.35E-55	0.279218015	0.641	0.363	6.24E-51	18	TRAPPC1
4.21E-55	0.390262284	0.703	0.438	7.85E-51	18	LY6E
6.48E-55	0.336231759	0.938	0.778	1.21E-50	18	HNRNPDL
1.70E-54	0.370131297	0.863	0.666	3.17E-50	18	PSME1
2.09E-54	0.339156795	0.619	0.369	3.89E-50	18	TOMM5
2.39E-54	0.255299463	0.581	0.332	4.45E-50	18	PSMC5
3.68E-54	0.368196864	0.541	0.283	6.85E-50	18	CCT5
4.13E-54	0.260025854	0.521	0.276	7.70E-50	18	MRPL57
7.31E-54	0.254378807	0.309	0.099	1.36E-49	18	UQCC2
8.39E-54	0.388802964	0.18	0.036	1.56E-49	18	TNFRSF17
8.39E-54	0.497396941	0.541	0.282	1.56E-49	18	WARS
1.67E-53	0.256151368	0.533	0.273	3.11E-49	18	NDUFS7
2.52E-53	0.418637982	0.657	0.411	4.69E-49	18	LDHA

4.17E-53	0.284494509	0.594	0.325	7.78E-49	18	NEDD8
8.95E-53	0.288657293	0.785	0.523	1.67E-48	18	ANAPC16
1.23E-52	0.320362986	0.774	0.541	2.30E-48	18	JTB
1.41E-52	0.311461515	0.308	0.118	2.63E-48	18	PVT1
1.59E-52	0.339354254	0.512	0.252	2.96E-48	18	NDUFB6
1.81E-52	0.318946715	0.341	0.132	3.37E-48	18	FKBP4
3.43E-52	0.301050758	0.564	0.303	6.40E-48	18	NDUFA12
3.46E-52	0.285436274	0.566	0.311	6.46E-48	18	PSMA4
3.48E-52	0.381812667	0.814	0.612	6.48E-48	18	COX7A2
5.39E-52	0.279807083	0.329	0.119	1.01E-47	18	TIMM8B
6.52E-52	0.277184463	0.97	0.858	1.22E-47	18	COX7C
8.86E-52	0.319695034	0.751	0.495	1.65E-47	18	C19orf53
1.35E-51	0.314137736	0.72	0.467	2.52E-47	18	GNG5
1.51E-51	0.316864184	0.757	0.513	2.81E-47	18	HNRNPM
2.66E-51	0.279671541	0.505	0.258	4.96E-47	18	CARD11
2.83E-51	0.312673105	0.67	0.407	5.27E-47	18	ARPC1B
4.59E-51	0.274939693	0.715	0.473	8.56E-47	18	HSPE1
5.54E-51	0.475737191	0.432	0.194	1.03E-46	18	CCND2
6.52E-51	0.295096372	0.518	0.256	1.21E-46	18	GYPC
6.87E-51	0.30343968	0.588	0.33	1.28E-46	18	RAP1A
7.17E-51	0.301369221	0.921	0.756	1.34E-46	18	SNRPD2
7.96E-51	0.356303404	0.735	0.485	1.48E-46	18	LCP1
1.58E-50	0.267951979	0.4	0.183	2.95E-46	18	TIMM10
1.78E-50	0.348335044	0.925	0.768	3.31E-46	18	ARPC2
2.18E-50	0.256771427	0.411	0.173	4.07E-46	18	STOML2
5.17E-50	0.286530479	0.46	0.228	9.63E-46	18	PHTF1
1.29E-49	0.267867544	0.515	0.266	2.41E-45	18	PSMC3
1.54E-49	0.279325736	0.609	0.35	2.88E-45	18	MPG
3.48E-49	0.251080054	0.499	0.25	6.48E-45	18	ASNA1
3.81E-49	0.300839843	0.789	0.538	7.10E-45	18	GMFG
1.05E-48	0.355544242	0.825	0.637	1.96E-44	18	MTDH
1.42E-48	0.292107587	0.787	0.55	2.65E-44	18	HMGN1
1.95E-48	0.776110752	0.815	0.595	3.64E-44	18	SSR4
2.46E-48	0.250933875	0.932	0.77	4.59E-44	18	UBB
2.47E-48	0.267930855	0.526	0.296	4.60E-44	18	PSMB2
4.48E-48	0.253476637	0.863	0.658	8.35E-44	18	HNRNPA3
6.59E-48	0.298928349	0.372	0.157	1.23E-43	18	WSB2
7.06E-48	0.284342977	0.906	0.711	1.32E-43	18	RPL36A
9.84E-48	0.256336095	0.488	0.258	1.83E-43	18	PSMA3
1.04E-47	0.304232857	0.558	0.302	1.94E-43	18	GPI
1.86E-47	0.906708267	0.836	0.625	3.47E-43	18	HSP90B1
2.11E-47	0.308708856	0.652	0.397	3.94E-43	18	DPP7
2.39E-47	0.292526003	0.594	0.346	4.45E-43	18	SEM1
2.73E-47	0.469614552	0.625	0.402	5.09E-43	18	P4HB
3.04E-47	0.257133055	0.486	0.253	5.66E-43	18	SLC25A39
3.98E-47	0.25868563	0.577	0.336	7.42E-43	18	MRPL20

6.25E-47	0.255066482	0.499	0.25	1.16E-42	18	TXN2
1.58E-46	0.465954472	0.929	0.782	2.95E-42	18	NCL
1.59E-46	0.275184392	0.622	0.396	2.97E-42	18	NOP10
2.12E-46	0.276961274	0.654	0.423	3.95E-42	18	CCT4
2.24E-46	0.28198023	0.71	0.467	4.18E-42	18	PSMB8
5.57E-46	0.258395931	0.54	0.279	1.04E-41	18	BST2
6.38E-46	0.293939549	0.67	0.45	1.19E-41	18	ATP5MD
7.72E-46	0.272218786	0.576	0.333	1.44E-41	18	AURKAIP1
9.42E-46	0.25425308	0.426	0.202	1.76E-41	18	CTSA
2.71E-45	0.2508133	0.471	0.224	5.05E-41	18	THOC7
2.72E-45	0.296801246	0.831	0.615	5.07E-41	18	NAP1L1
3.91E-45	0.294403639	0.523	0.295	7.29E-41	18	MRPL51
8.18E-45	0.282285994	0.55	0.301	1.52E-40	18	GTF3C6
1.79E-44	0.262231988	0.704	0.473	3.33E-40	18	VAMP8
2.32E-44	0.281918412	0.645	0.391	4.32E-40	18	ANP32A
2.54E-44	0.292862354	0.726	0.463	4.73E-40	18	CSK
3.25E-44	0.258360794	0.601	0.355	6.06E-40	18	COPS9
3.91E-44	0.269316902	0.6	0.358	7.29E-40	18	MDH1
7.63E-44	0.288069627	0.654	0.43	1.42E-39	18	POMP
9.67E-44	0.333255138	0.911	0.704	1.80E-39	18	RAC2
1.12E-43	0.269778676	0.884	0.71	2.09E-39	18	EDF1
1.33E-43	0.258612495	0.721	0.48	2.48E-39	18	RSL1D1
1.76E-43	0.254371794	0.673	0.416	3.28E-39	18	LAMTOR1
2.29E-43	0.250343071	0.442	0.215	4.26E-39	18	RPA3
3.71E-43	0.307402454	0.688	0.433	6.92E-39	18	CCDC85B
1.57E-42	0.264319178	0.901	0.732	2.93E-38	18	OST4
2.39E-42	0.284906919	0.639	0.429	4.45E-38	18	SPCS2
3.26E-42	0.250013208	0.513	0.29	6.08E-38	18	NDUFAF3
5.12E-42	0.332210802	0.631	0.406	9.55E-38	18	CCT2
6.22E-42	0.884859727	0.533	0.318	1.16E-37	18	MZB1
7.20E-42	0.501092085	0.34	0.149	1.34E-37	18	PDIA4
1.06E-41	0.317428244	0.683	0.459	1.97E-37	18	IFITM2
1.03E-40	0.75662281	0.492	0.291	1.92E-36	18	SEC11C
1.04E-40	0.262205826	0.735	0.492	1.93E-36	18	RNH1
1.65E-40	0.253693263	0.65	0.407	3.08E-36	18	ATP6V1F
2.76E-40	0.268107225	0.525	0.286	5.14E-36	18	UBE2L6
3.22E-40	0.395309746	0.463	0.257	6.01E-36	18	HM13
3.61E-40	0.265829142	0.656	0.416	6.73E-36	18	RAD23A
3.62E-40	0.33680104	0.847	0.664	6.74E-36	18	UQCRH
7.26E-40	0.263117423	0.78	0.559	1.35E-35	18	ST13
1.14E-39	0.260418057	0.621	0.42	2.13E-35	18	TMED9
1.44E-39	0.326061767	0.809	0.631	2.68E-35	18	ATP5F1B
2.95E-39	0.893058935	0.868	0.692	5.50E-35	18	PPIB
9.06E-39	0.251868486	0.729	0.517	1.69E-34	18	PGK1
1.29E-38	0.252234993	0.542	0.307	2.41E-34	18	RNF181
2.97E-38	0.260684552	0.733	0.519	5.53E-34	18	NDUFS5

3.63E-38	0.266968995	0.319	0.139	6.77E-34	18	PRDX4
3.97E-38	0.345791271	0.453	0.246	7.40E-34	18	OSTC
7.79E-38	0.257754714	0.58	0.356	1.45E-33	18	NDUFC1
2.66E-37	0.279074926	0.702	0.476	4.95E-33	18	ILF2
1.15E-35	0.253578238	0.451	0.248	2.15E-31	18	RRP7A
1.72E-35	0.253879389	0.278	0.119	3.21E-31	18	CCDC167
1.92E-35	0.476137047	0.767	0.586	3.58E-31	18	SEC61B
1.53E-34	0.27809849	0.54	0.345	2.85E-30	18	RPN2
2.92E-34	0.322340584	0.873	0.707	5.44E-30	18	HMGN2
3.25E-34	0.298703586	0.595	0.374	6.06E-30	18	HMGA1
1.86E-33	0.727991081	0.806	0.646	3.47E-29	18	SUB1
2.82E-32	0.264597969	0.823	0.641	5.26E-28	18	GABARAP
5.05E-32	0.300736729	0.773	0.573	9.41E-28	18	RPS4Y1
3.22E-30	0.27386939	0.872	0.675	6.01E-26	18	FCER2
4.39E-30	0.419954264	0.831	0.678	8.18E-26	18	TUBA1B
8.31E-29	0.562533132	0.233	0.107	1.55E-24	18	TXNDC5
2.54E-28	0.260857618	0.558	0.357	4.73E-24	18	FDFT1
3.14E-27	0.31067818	0.284	0.14	5.84E-23	18	PRDX2
7.03E-26	0.318545336	0.289	0.142	1.31E-21	18	MANF
1.13E-23	0.295660982	0.603	0.405	2.11E-19	18	DDOST
2.46E-20	0.459531176	0.586	0.421	4.59E-16	18	UBE2J1
7.86E-13	0.380673545	0.501	0.349	1.47E-08	18	SSR3
1.91E-12	0.260632718	0.669	0.551	3.57E-08	18	HSPA5
3.16E-204	0.687625622	0.984	0.759	5.90E-200	19	RALGPS2
4.81E-196	0.71630909	0.97	0.686	8.96E-192	19	DDX17
1.08E-169	0.713708876	0.836	0.407	2.01E-165	19	PARP15
2.33E-163	0.740403534	0.907	0.542	4.34E-159	19	MSI2
8.07E-161	0.741079663	0.905	0.531	1.50E-156	19	STX7
8.02E-137	0.539880661	0.93	0.655	1.50E-132	19	AFF3
1.72E-134	0.58827666	0.954	0.711	3.21E-130	19	SMCHD1
5.63E-133	0.638841503	0.881	0.514	1.05E-128	19	OGT
6.43E-132	0.581649445	0.912	0.585	1.20E-127	19	ABCA6
3.28E-124	0.566907046	0.764	0.376	6.11E-120	19	NKTR
6.16E-123	0.687693281	0.894	0.569	1.15E-118	19	TTN
1.77E-122	0.565184118	0.895	0.57	3.29E-118	19	CDK14
5.98E-122	0.66183036	0.739	0.349	1.11E-117	19	GABPB1-AS1
3.34E-119	0.713314093	0.747	0.349	6.22E-115	19	CLNK
5.72E-119	0.526357255	0.538	0.155	1.07E-114	19	POLR2J3-ENSG00000285437
8.60E-119	0.60673715	0.977	0.837	1.60E-114	19	TCF4
9.29E-118	0.66329999	0.927	0.637	1.73E-113	19	CCDC88A
1.09E-115	0.521509515	0.847	0.49	2.04E-111	19	ANKRD44
2.50E-115	0.508003952	0.94	0.72	4.65E-111	19	ARHGAP24
8.12E-111	0.50381455	0.727	0.339	1.51E-106	19	MCTP2
3.82E-109	0.638495847	0.84	0.505	7.12E-105	19	FAM129C
5.22E-108	0.475964547	0.605	0.218	9.73E-104	19	GAB1
3.39E-107	0.504321838	0.91	0.631	6.31E-103	19	RIPOR2

3.86E-106	0.437379196	0.687	0.292	7.19E-102	19	RNPC3
4.67E-106	0.53401175	0.742	0.36	8.71E-102	19	CAMK2D
6.66E-105	0.641565381	0.564	0.204	1.24E-100	19	SERINC5
1.64E-104	0.5617906	0.776	0.401	3.06E-100	19	ATM
2.28E-104	0.442667404	0.819	0.46	4.25E-100	19	VPS13C
5.49E-104	0.444811502	0.688	0.313	1.02E-99	19	PHC3
4.48E-103	0.425896806	0.881	0.565	8.35E-99	19	PNN
6.35E-103	0.508927777	0.74	0.368	1.18E-98	19	ARID1B
1.70E-100	0.506478664	0.95	0.734	3.17E-96	19	PNISR
1.37E-99	0.498713035	0.629	0.246	2.55E-95	19	CCDC141
8.69E-97	0.395374518	0.928	0.664	1.62E-92	19	RSRP1
1.37E-95	0.495600902	0.832	0.529	2.56E-91	19	BCL2
4.27E-94	0.40378417	0.788	0.429	7.95E-90	19	TMEM131L
9.26E-94	0.427205439	0.608	0.261	1.73E-89	19	UTY
1.16E-93	0.398610333	0.673	0.325	2.15E-89	19	DOCK10
2.08E-93	0.388671831	0.833	0.533	3.88E-89	19	N4BP2L2
3.66E-93	0.421802162	0.764	0.423	6.82E-89	19	ZNF292
5.20E-93	0.427835599	0.718	0.363	9.69E-89	19	MDM4
8.48E-92	0.520520109	0.761	0.385	1.58E-87	19	Mar-01
1.70E-91	0.46497883	0.712	0.373	3.17E-87	19	WDR11
1.73E-90	0.391015773	0.755	0.421	3.23E-86	19	SNX29
2.47E-90	0.423729104	0.547	0.208	4.60E-86	19	ADAMTS6
2.55E-90	0.401174669	0.578	0.236	4.76E-86	19	GOLGA8B
9.11E-90	0.33358284	0.414	0.104	1.70E-85	19	TRIM73
2.43E-89	0.404599171	0.708	0.359	4.52E-85	19	CREB3L2
8.89E-89	0.488854358	0.866	0.564	1.66E-84	19	IKZF3
3.59E-88	0.436772836	0.58	0.234	6.68E-84	19	ADAM19
6.60E-88	0.42776447	0.802	0.468	1.23E-83	19	SNRNP70
3.83E-87	0.505457452	0.784	0.482	7.14E-83	19	BCL11A
2.22E-86	0.368158519	0.465	0.152	4.14E-82	19	FTX
3.34E-86	0.3152843	0.55	0.22	6.22E-82	19	CREBZF
1.60E-85	0.449110258	0.821	0.494	2.99E-81	19	INPP5F
2.14E-85	0.470277894	0.811	0.471	3.98E-81	19	OGA
7.41E-85	0.422531896	0.77	0.413	1.38E-80	19	ZRANB2
2.58E-84	0.462469847	0.836	0.528	4.80E-80	19	LUC7L3
3.13E-84	0.479016774	0.638	0.297	5.83E-80	19	TTC14
1.53E-83	0.355767666	0.544	0.208	2.85E-79	19	KHDRBS2
5.57E-83	0.382439366	0.671	0.322	1.04E-78	19	TLE4
4.86E-82	0.396873857	0.777	0.467	9.06E-78	19	TUT4
5.54E-82	0.50635431	0.847	0.544	1.03E-77	19	LRMP
7.62E-82	0.424767774	0.988	0.866	1.42E-77	19	FOXP1
1.27E-80	0.457605874	0.753	0.395	2.36E-76	19	TRAF3IP3
4.89E-80	0.384097776	0.884	0.602	9.11E-76	19	NCOA3
4.96E-79	0.345932532	0.964	0.789	9.25E-75	19	FUS
5.80E-79	0.338192229	0.973	0.835	1.08E-74	19	SF1
1.41E-78	0.370667663	0.571	0.255	2.62E-74	19	DNAJC10

8.91E-78	0.483699903	0.582	0.243	1.66E-73	19	PCDH9
1.06E-77	0.335093433	0.858	0.55	1.98E-73	19	SSH2
2.79E-77	0.410059501	0.837	0.551	5.19E-73	19	PELI1
2.82E-77	0.395899982	0.812	0.526	5.25E-73	19	TNRC6B
4.69E-77	0.350897717	0.557	0.254	8.73E-73	19	DDHD1
1.85E-76	0.395303906	0.688	0.37	3.45E-72	19	GTF2I
2.39E-76	0.386935447	0.647	0.313	4.45E-72	19	SLC9A7
9.72E-76	0.361869402	0.958	0.81	1.81E-71	19	PTPRC
1.08E-75	0.400218856	0.9	0.662	2.02E-71	19	ARGLU1
3.66E-75	0.366231524	0.533	0.243	6.83E-71	19	CD84
9.07E-75	0.452042049	0.518	0.199	1.69E-70	19	HIBCH
1.63E-74	0.390972615	0.702	0.382	3.04E-70	19	ZBTB20
9.48E-74	0.333778671	0.958	0.815	1.77E-69	19	RBM39
9.77E-74	0.320627919	0.741	0.446	1.82E-69	19	ARHGAP15
7.59E-73	0.398403933	0.698	0.383	1.41E-68	19	ZNF107
2.49E-71	0.312439023	0.702	0.397	4.64E-67	19	SKAP1
3.59E-71	0.340370208	0.547	0.245	6.70E-67	19	SLC23A2
8.76E-71	0.437041541	0.868	0.624	1.63E-66	19	RCSD1
9.79E-71	0.43166004	0.529	0.238	1.83E-66	19	LINC02397
1.36E-70	0.339033017	0.715	0.389	2.53E-66	19	ASH1L
1.58E-70	0.349859436	0.51	0.197	2.95E-66	19	AC012368.1
5.42E-70	0.348844442	0.563	0.258	1.01E-65	19	PHKB
9.15E-70	0.517639916	0.578	0.288	1.71E-65	19	ZNF266
3.10E-68	0.370874066	0.767	0.463	5.77E-64	19	ZCCHC7
5.57E-68	0.289274741	0.662	0.35	1.04E-63	19	UTRN
2.29E-67	0.265833506	0.377	0.12	4.27E-63	19	PPP1R3E
6.63E-67	0.317140454	0.691	0.381	1.24E-62	19	LENG8
7.38E-67	0.396650999	0.687	0.37	1.38E-62	19	CIITA
1.10E-66	0.358052725	0.88	0.622	2.05E-62	19	JMJD1C
2.94E-66	0.322320015	0.9	0.652	5.47E-62	19	SRSF11
3.49E-66	0.299715211	0.554	0.263	6.51E-62	19	RBM5
4.37E-66	0.346465855	0.765	0.474	8.15E-62	19	PCM1
4.48E-66	0.387619348	0.821	0.541	8.34E-62	19	LINC00926
4.50E-66	0.303093793	0.63	0.329	8.40E-62	19	SECISBP2
5.00E-66	0.279063693	0.494	0.218	9.32E-62	19	CEP95
8.47E-66	0.370259044	0.961	0.788	1.58E-61	19	TXNIP
8.81E-66	0.306453359	0.33	0.098	1.64E-61	19	LINC02363
1.93E-65	0.330617012	0.576	0.273	3.60E-61	19	MCOLN2
2.13E-65	0.333352026	0.402	0.139	3.97E-61	19	HDAC9
2.46E-65	0.325060588	0.542	0.245	4.58E-61	19	CBLB
2.65E-65	0.295907645	0.568	0.289	4.95E-61	19	BRWD1
4.23E-65	0.381993932	0.84	0.573	7.88E-61	19	SYK
5.12E-65	0.259816334	0.397	0.157	9.55E-61	19	NPIPB5
8.76E-65	0.285666245	0.447	0.163	1.63E-60	19	LRRK2
1.51E-64	0.306990433	0.401	0.142	2.81E-60	19	ZDHHC21
2.14E-64	0.322839516	0.661	0.35	3.98E-60	19	ACSM3

3.20E-64	0.37753279	0.826	0.543	5.97E-60	19	CELF2
4.80E-64	0.356614296	0.529	0.22	8.95E-60	19	AC119396.1
1.34E-63	0.330625126	0.635	0.327	2.50E-59	19	AL158850.1
1.87E-63	0.320343557	0.736	0.447	3.48E-59	19	HNRNPH1
2.29E-63	0.296711177	0.424	0.158	4.28E-59	19	MBD5
2.94E-63	0.300799745	0.571	0.264	5.48E-59	19	GSAP
4.67E-63	0.3322022	0.462	0.19	8.71E-59	19	ZNF101
1.04E-62	0.347265855	0.822	0.561	1.94E-58	19	USP15
1.19E-62	0.268637616	0.328	0.095	2.22E-58	19	AL445673.1
3.54E-62	0.282214062	0.598	0.283	6.61E-58	19	RIC1
3.69E-62	0.349770162	0.487	0.203	6.88E-58	19	RASA1
3.93E-62	0.296124746	0.605	0.294	7.33E-58	19	PHTF2
4.12E-62	0.373906544	0.86	0.641	7.68E-58	19	SP100
7.81E-62	0.335295699	0.567	0.283	1.46E-57	19	WDFY1
9.14E-62	0.27373533	0.505	0.231	1.70E-57	19	DMTF1
9.19E-62	0.301249626	0.445	0.186	1.71E-57	19	FBXL20
9.24E-62	0.326581824	0.901	0.683	1.72E-57	19	EPC1
1.08E-61	0.300786427	0.61	0.326	2.01E-57	19	LNPEP
1.11E-61	0.280469703	0.545	0.261	2.06E-57	19	PRKCE
1.66E-61	0.309574127	0.378	0.121	3.10E-57	19	ZNF439
3.08E-61	0.343436245	0.802	0.509	5.75E-57	19	UVRAG
4.11E-61	0.347675772	0.688	0.4	7.65E-57	19	CHD9
8.98E-61	0.273447682	0.581	0.285	1.67E-56	19	TBC1D5
1.10E-60	0.325640517	0.499	0.21	2.05E-56	19	KHDC4
2.37E-60	0.326530932	0.519	0.229	4.42E-56	19	MRNIP
6.14E-60	0.324939275	0.604	0.327	1.14E-55	19	USP34
6.17E-60	0.321470035	0.57	0.295	1.15E-55	19	NSF
8.15E-60	0.301375594	0.829	0.579	1.52E-55	19	TMEM243
9.02E-60	0.366007056	0.532	0.241	1.68E-55	19	CLEC2D
1.32E-59	0.321530924	0.484	0.196	2.46E-55	19	STAMBPL1
1.46E-59	0.326475808	0.567	0.286	2.72E-55	19	CDK13
1.67E-59	0.331482311	0.798	0.519	3.12E-55	19	ZNF207
1.91E-59	0.267402826	0.524	0.255	3.57E-55	19	RABEP2
2.17E-59	0.329428024	0.764	0.483	4.04E-55	19	AKAP9
3.00E-59	0.297588437	0.635	0.349	5.59E-55	19	NFAT5
4.21E-59	0.295363125	0.621	0.343	7.85E-55	19	BIRC6
5.81E-59	0.275335812	0.474	0.199	1.08E-54	19	MAML2
7.76E-59	0.288664671	0.581	0.32	1.45E-54	19	BTAF1
1.36E-58	0.358885849	0.75	0.467	2.53E-54	19	ADAM28
1.59E-58	0.292248479	0.595	0.304	2.97E-54	19	FRYL
1.69E-58	0.300894161	0.801	0.529	3.14E-54	19	ATRX
2.81E-58	0.252384781	0.56	0.286	5.25E-54	19	MAN2A1
3.26E-58	0.259450065	0.402	0.158	6.09E-54	19	SUGP2
3.49E-58	0.299466303	0.558	0.274	6.51E-54	19	KANSL1
4.81E-58	0.293697169	0.622	0.319	8.97E-54	19	TTC17
5.03E-58	0.313058271	0.54	0.261	9.38E-54	19	PARP14

6.40E-58	0.309629786	0.85	0.609	1.19E-53	19	SCAF11
7.36E-58	0.285681262	0.383	0.139	1.37E-53	19	KDM5D
8.53E-58	0.31507559	0.57	0.295	1.59E-53	19	ADD3
8.66E-58	0.366283907	0.726	0.429	1.61E-53	19	EBLN3P
1.00E-57	0.327619467	0.541	0.244	1.87E-53	19	JAK2
1.32E-57	0.330353721	0.734	0.44	2.45E-53	19	SMG1
1.69E-57	0.317811301	0.789	0.528	3.15E-53	19	CD47
1.91E-57	0.299478578	0.759	0.479	3.56E-53	19	TLK1
2.56E-57	0.351650301	0.557	0.277	4.78E-53	19	SLC12A6
2.96E-57	0.336613343	0.555	0.26	5.52E-53	19	BTLA
3.24E-57	0.273417288	0.426	0.178	6.03E-53	19	NHLRC3
3.58E-57	0.332525526	0.636	0.348	6.67E-53	19	RNF19A
6.56E-57	0.33719674	0.757	0.468	1.22E-52	19	PLEKHG1
7.58E-57	0.311008271	0.864	0.628	1.41E-52	19	SRSF10
7.69E-57	0.342798666	0.702	0.424	1.43E-52	19	SP140
9.40E-57	0.296259559	0.63	0.355	1.75E-52	19	MORC3
2.31E-56	0.311663068	0.543	0.26	4.31E-52	19	GLS
3.24E-56	0.293081182	0.657	0.389	6.03E-52	19	PPP4R3B
4.76E-56	0.484967164	0.753	0.502	8.86E-52	19	IL4R
6.47E-56	0.295734688	0.56	0.264	1.21E-51	19	TRAF5
1.50E-55	0.293701079	0.564	0.298	2.80E-51	19	LUC7L
2.73E-55	0.258370739	0.561	0.289	5.09E-51	19	FCHSD2
2.90E-55	0.330204642	0.64	0.354	5.41E-51	19	SREK1
3.02E-55	0.303547314	0.478	0.228	5.62E-51	19	SMC6
3.10E-55	0.40869655	0.333	0.112	5.77E-51	19	TSHZ2
3.14E-55	0.303271177	0.609	0.325	5.85E-51	19	LPP
3.39E-55	0.550837938	0.478	0.213	6.32E-51	19	AC063949.2
5.70E-55	0.286641035	0.373	0.137	1.06E-50	19	CCDC14
1.17E-54	0.276266474	0.538	0.248	2.18E-50	19	MON2
2.21E-54	0.301195493	0.44	0.198	4.12E-50	19	OSBPL10
2.45E-54	0.294473595	0.749	0.498	4.56E-50	19	FNBP4
3.71E-54	0.399925092	0.865	0.654	6.92E-50	19	PRKCB
4.57E-54	0.294159709	0.549	0.281	8.52E-50	19	SPG7
1.07E-53	0.292570154	0.703	0.433	2.00E-49	19	PPM1K
1.09E-53	0.255422062	0.477	0.22	2.03E-49	19	CCNT2
1.75E-53	0.281738488	0.508	0.245	3.25E-49	19	BICD1
1.94E-53	0.288083807	0.416	0.166	3.62E-49	19	IL6ST
3.08E-53	0.274761398	0.488	0.227	5.73E-49	19	DGKD
3.24E-53	0.310108533	0.694	0.423	6.03E-49	19	TNFAIP8
3.33E-53	0.41183053	0.854	0.595	6.21E-49	19	POU2F2
3.53E-53	0.257242179	0.755	0.518	6.58E-49	19	ABI1
5.78E-53	0.276597601	0.56	0.302	1.08E-48	19	PCMTD1
7.72E-53	0.299468532	0.871	0.636	1.44E-48	19	RUBCNL
8.03E-53	0.252388262	0.584	0.321	1.50E-48	19	ZNF638
1.01E-52	0.289024046	0.553	0.281	1.88E-48	19	CLEC17A
5.57E-52	0.282288575	0.697	0.448	1.04E-47	19	MYCBP2

5.95E-52	0.295569683	0.241	0.055	1.11E-47	19	AC245060.5
8.05E-52	0.312046613	0.353	0.128	1.50E-47	19	ZNF37A
1.22E-51	0.359334642	0.573	0.327	2.27E-47	19	DMD
2.55E-51	0.279061201	0.63	0.361	4.75E-47	19	TGFBR2
3.22E-51	0.270076282	0.584	0.326	5.99E-47	19	MIS18BP1
3.24E-51	0.302320939	0.84	0.602	6.03E-47	19	SYNE2
3.60E-51	0.267283152	0.692	0.42	6.70E-47	19	NEMF
3.73E-51	0.259022687	0.446	0.194	6.95E-47	19	NUP88
3.98E-51	0.324957602	0.579	0.32	7.41E-47	19	BOD1L1
5.50E-51	0.322064956	0.875	0.672	1.03E-46	19	SF3B1
6.56E-51	0.305792932	0.523	0.262	1.22E-46	19	STIM2
6.73E-51	0.269038062	0.542	0.273	1.25E-46	19	IMMP2L
1.28E-50	0.282676731	0.584	0.319	2.39E-46	19	MZB1
1.41E-50	0.288730537	0.66	0.383	2.63E-46	19	HECTD1
2.08E-50	0.267621283	0.398	0.159	3.87E-46	19	ANKRD36C
2.22E-50	0.278251784	0.433	0.191	4.14E-46	19	DCLK2
2.65E-50	0.27533271	0.356	0.124	4.94E-46	19	ZMAT1
8.13E-50	0.257940722	0.512	0.264	1.52E-45	19	UBR5
9.36E-50	0.268440649	0.703	0.454	1.74E-45	19	INPP5D
9.95E-50	0.264744453	0.391	0.158	1.85E-45	19	TMEM63A
1.62E-49	0.270880332	0.504	0.242	3.01E-45	19	XRN1
2.12E-49	0.251265995	0.422	0.18	3.95E-45	19	ZNF431
2.44E-49	0.250221099	0.536	0.272	4.55E-45	19	RNASEH2B
2.48E-49	0.325138489	0.812	0.57	4.61E-45	19	KIAA1551
2.86E-49	0.310653638	0.407	0.166	5.34E-45	19	KSR2
3.15E-49	0.257279011	0.331	0.114	5.86E-45	19	GMDS-DT
3.33E-49	0.289741779	0.619	0.333	6.20E-45	19	SPTBN1
3.46E-49	0.275303531	0.736	0.474	6.45E-45	19	BLNK
3.98E-49	0.314170757	0.512	0.254	7.42E-45	19	LYST
5.43E-49	0.302958597	0.57	0.29	1.01E-44	19	ZMYM2
9.13E-49	0.31575718	0.7	0.437	1.70E-44	19	CFLAR
2.01E-48	0.252348727	0.553	0.296	3.75E-44	19	ZFC3H1
2.90E-48	0.275587339	0.86	0.622	5.40E-44	19	SH3BP5
4.34E-48	0.256278243	0.532	0.271	8.10E-44	19	AP1G1
4.43E-48	0.25993368	0.416	0.17	8.25E-44	19	ZNF493
7.49E-48	0.320295524	0.94	0.769	1.40E-43	19	STK4
3.86E-47	0.269792624	0.567	0.317	7.20E-43	19	RBM33
4.88E-47	0.325774499	0.646	0.374	9.09E-43	19	SETX
1.57E-46	0.346156992	0.513	0.257	2.93E-42	19	ARHGAP44
2.12E-46	0.262466409	0.664	0.424	3.95E-42	19	PHIP
3.30E-46	0.378050273	0.635	0.36	6.15E-42	19	KIAA0040
3.33E-46	0.298595884	0.64	0.391	6.20E-42	19	CLINT1
4.73E-46	0.304419918	0.659	0.408	8.81E-42	19	NCKAP1L
7.90E-46	0.254421287	0.472	0.239	1.47E-41	19	ZNF506
9.95E-46	0.545286858	0.712	0.489	1.85E-41	19	IGLL5
1.03E-45	0.285676691	0.67	0.421	1.93E-41	19	ZNF800

1.45E-45	0.25017861	0.404	0.165	2.70E-41	19	ANKRD36
1.87E-45	0.36188014	0.739	0.502	3.48E-41	19	MS4A1
7.18E-45	0.364877705	0.715	0.446	1.34E-40	19	ATF7IP
8.79E-45	0.270872727	0.8	0.549	1.64E-40	19	EVL
1.17E-44	0.272097345	0.228	0.064	2.19E-40	19	WNT16
1.86E-44	0.284988065	0.585	0.326	3.46E-40	19	DGKA
2.48E-44	0.2846163	0.864	0.658	4.63E-40	19	HNRNPA3
2.92E-44	0.262364052	0.461	0.238	5.43E-40	19	RASGRP3
9.05E-44	0.291295034	0.633	0.379	1.69E-39	19	CCDC191
1.06E-43	0.257546633	0.865	0.646	1.97E-39	19	CYTH1
1.75E-43	0.302558935	0.661	0.389	3.26E-39	19	DOCK8
2.53E-43	0.270467898	0.47	0.23	4.71E-39	19	PSMA3-AS1
2.99E-43	0.261740242	0.481	0.232	5.58E-39	19	ITPR1
1.33E-42	0.263228756	0.391	0.163	2.49E-38	19	PMS1
2.11E-42	0.250802744	0.604	0.373	3.93E-38	19	TAOK3
2.72E-42	0.301419141	0.856	0.625	5.07E-38	19	SLC38A1
2.94E-42	0.255767995	0.58	0.347	5.48E-38	19	PCF11
8.49E-42	0.289671103	0.49	0.265	1.58E-37	19	ZNF92
8.75E-42	0.283741612	0.759	0.506	1.63E-37	19	RABGAP1L
9.41E-42	0.324154921	0.757	0.505	1.75E-37	19	MEF2C
1.22E-40	0.270331997	0.619	0.376	2.27E-36	19	CDK5RAP3
2.04E-40	0.254260893	0.409	0.2	3.80E-36	19	TGFBR3
2.06E-40	0.322251418	0.677	0.448	3.85E-36	19	PTPN2
2.55E-40	0.258821569	0.707	0.46	4.75E-36	19	ACAP2
4.10E-40	0.258763016	0.329	0.133	7.65E-36	19	SLC16A1-AS1
5.00E-40	0.254568218	0.429	0.208	9.33E-36	19	PLCL2
5.35E-40	0.282505536	0.833	0.601	9.97E-36	19	SWAP70
1.00E-39	0.256240338	0.406	0.19	1.87E-35	19	NFATC2IP
1.10E-39	0.274245357	0.217	0.058	2.05E-35	19	ZNF804A
2.72E-39	0.28650651	0.438	0.219	5.07E-35	19	ARRDC3
8.08E-39	0.288951455	0.37	0.161	1.51E-34	19	SESTD1
8.86E-39	0.265478751	0.543	0.289	1.65E-34	19	ERICH1
1.37E-38	0.339374253	0.698	0.469	2.56E-34	19	BACH2
4.33E-38	0.257309451	0.465	0.241	8.07E-34	19	QRSL1
5.68E-38	0.25606117	0.5	0.278	1.06E-33	19	AIM2
8.64E-38	0.25831787	0.469	0.238	1.61E-33	19	LONP2
3.42E-37	0.253229738	0.532	0.287	6.38E-33	19	Mar-03
7.54E-37	0.31984244	0.891	0.676	1.41E-32	19	FCER2
8.91E-37	0.267163525	0.416	0.198	1.66E-32	19	FAM214A
1.16E-36	0.258376514	0.498	0.268	2.17E-32	19	ARHGEF3
1.21E-36	0.260983355	0.52	0.282	2.26E-32	19	ETS1
1.53E-36	0.251407039	0.622	0.363	2.86E-32	19	TBC1D22A
2.04E-36	0.270446951	0.88	0.677	3.80E-32	19	BLK
3.97E-36	0.31466204	0.691	0.471	7.41E-32	19	EPB41
4.62E-36	0.304837629	0.674	0.452	8.61E-32	19	AC004687.1
5.11E-36	0.273390928	0.771	0.563	9.52E-32	19	IFT57

1.17E-35	0.256886181	0.864	0.694	2.19E-31	19	HNRNPU
1.53E-35	0.254509656	0.547	0.304	2.84E-31	19	NSD1
8.16E-35	0.282993233	0.826	0.638	1.52E-30	19	MTDH
4.06E-34	0.255645087	0.412	0.201	7.56E-30	19	ENTPD1
6.94E-34	0.250009547	0.584	0.342	1.29E-29	19	PDCD6IP
7.90E-34	0.268005824	0.537	0.302	1.47E-29	19	SEL1L3
1.09E-33	0.254695768	0.53	0.319	2.03E-29	19	RRBP1
1.13E-33	0.25375323	0.379	0.174	2.10E-29	19	GPM6A
6.64E-33	0.257625277	0.43	0.221	1.24E-28	19	PCSK7
3.27E-32	0.259204555	0.338	0.139	6.09E-28	19	KLF8
2.17E-31	0.538978607	0.379	0.189	4.05E-27	19	SFTPB
3.54E-30	0.270142958	0.438	0.248	6.61E-26	19	FCRL5
3.81E-27	0.252744038	0.898	0.733	7.10E-23	19	ANKRD12
2.10E-26	0.274344225	0.838	0.644	3.91E-22	19	HLA-DMB
6.21E-24	0.320990403	0.464	0.269	1.16E-19	19	RHEX
3.48E-19	0.382821496	0.284	0.157	6.49E-15	19	COBLL1
0	2.192187404	0.816	0.137	0	20	MYADM
0	1.474076529	0.817	0.206	0	20	BANK1
6.28E-286	1.53562342	0.697	0.103	1.17E-281	20	MARCKS
6.43E-194	0.966335564	0.402	0.006	1.20E-189	20	PDE4D
1.82E-182	0.997469271	0.891	0.501	3.39E-178	20	MS4A1
8.64E-179	1.110820111	0.731	0.252	1.61E-174	20	TNFAIP3
2.09E-176	0.597298077	0.366	0.003	3.90E-172	20	EBF1
6.29E-162	0.680418231	0.94	0.67	1.17E-157	20	NFKBIA
3.35E-157	0.977439529	0.913	0.643	6.25E-153	20	LTB
3.55E-157	0.649521917	0.999	0.897	6.63E-153	20	RPS20
2.94E-156	1.235297842	0.585	0.159	5.48E-152	20	BCL2A1
2.08E-151	0.734494762	0.39	0.033	3.87E-147	20	FAS
3.61E-150	0.575589034	0.33	0.008	6.73E-146	20	CD80
5.99E-147	0.644335788	0.306	0.002	1.12E-142	20	EBI3
2.57E-142	0.626367066	0.565	0.141	4.79E-138	20	JCHAIN
3.06E-139	0.792364621	0.782	0.361	5.70E-135	20	CMTM6
1.11E-137	0.799258868	0.473	0.091	2.08E-133	20	BASP1
4.81E-131	0.57501656	0.458	0.076	8.96E-127	20	CYBB
1.36E-128	0.62076581	0.993	0.801	2.54E-124	20	TAGLN2
1.68E-119	0.717615492	0.693	0.266	3.13E-115	20	SLC2A3
5.51E-116	0.437538002	0.266	0.015	1.03E-111	20	CR1
1.26E-115	0.711875062	0.928	0.676	2.35E-111	20	CD83
3.03E-114	0.617127245	0.468	0.109	5.64E-110	20	ITGA4
6.58E-112	0.561133402	0.587	0.209	1.23E-107	20	GNG7
6.10E-111	0.409792886	0.242	0.006	1.14E-106	20	PAG1
1.03E-110	0.646828553	0.392	0.072	1.92E-106	20	VPS37B
2.44E-110	0.51654487	0.24	0.005	4.55E-106	20	HOPX
7.06E-109	0.734059782	0.731	0.361	1.32E-104	20	KDM6B
1.81E-108	0.693610226	0.726	0.376	3.38E-104	20	RHOG
1.29E-106	0.604755443	0.911	0.615	2.41E-102	20	TAGAP

1.11E-105	0.541498872	0.501	0.156	2.07E-101	20	COBLL1
1.70E-105	0.637565292	0.632	0.276	3.17E-101	20	HIF1A
4.07E-105	0.592148096	0.638	0.261	7.60E-101	20	PARP14
3.45E-104	0.638222125	0.222	0.002	6.43E-100	20	LINC01781
9.69E-103	0.596437801	0.763	0.418	1.81E-98	20	DENND4A
1.25E-99	0.489088266	0.378	0.078	2.33E-95	20	IQSEC1
1.17E-95	0.341726988	0.208	0.004	2.18E-91	20	CSGALNACT1
1.85E-94	0.778442701	0.752	0.454	3.46E-90	20	CD82
4.93E-92	0.550215882	0.992	0.882	9.18E-88	20	HLA-DQA1
1.11E-91	0.634560621	0.69	0.358	2.07E-87	20	MOB3A
5.66E-91	0.65820537	0.819	0.526	1.05E-86	20	ATP2B1
5.39E-89	0.399820798	0.239	0.019	1.01E-84	20	NEIL1
9.02E-88	0.529047999	0.88	0.59	1.68E-83	20	CYTIP
8.99E-86	0.545881694	0.655	0.312	1.68E-81	20	MAP3K8
9.98E-85	0.306166465	0.2	0.01	1.86E-80	20	SNX22
1.22E-83	0.352708348	0.227	0.018	2.27E-79	20	ANKRD33B
2.52E-83	0.672598055	0.877	0.63	4.69E-79	20	HERPUD1
3.39E-83	0.433981048	0.285	0.04	6.32E-79	20	GPR65
3.86E-81	0.519446713	0.422	0.119	7.19E-77	20	TMEM156
9.50E-80	0.318942105	0.175	0.002	1.77E-75	20	PPP1R14A
1.02E-79	0.382662174	0.264	0.036	1.90E-75	20	PIK3R5
3.75E-79	0.319283476	0.194	0.011	6.99E-75	20	SSPN
4.58E-79	0.605278848	0.643	0.327	8.55E-75	20	CD40
2.52E-78	0.456695913	0.342	0.079	4.69E-74	20	ITM2C
1.08E-77	0.312333255	0.181	0.005	2.01E-73	20	TEX9
1.88E-77	0.516660719	0.906	0.721	3.50E-73	20	REL
2.70E-76	0.381583357	0.257	0.042	5.04E-72	20	GRAMD1C
3.45E-76	0.555111007	0.302	0.062	6.43E-72	20	RASSF6
4.79E-74	0.518565737	0.845	0.581	8.92E-70	20	SNX2
1.03E-73	0.49351759	0.867	0.573	1.92E-69	20	RPS4Y1
1.36E-73	0.363828295	0.33	0.084	2.53E-69	20	HIP1R
2.04E-73	0.435250851	0.817	0.548	3.81E-69	20	NFKBID
2.37E-72	0.416906422	0.334	0.083	4.41E-68	20	ITGB2
5.20E-72	0.439581997	0.398	0.12	9.69E-68	20	ARHGAP31
4.13E-71	0.37860395	0.179	0.008	7.69E-67	20	TIAM2
6.61E-71	0.585795967	0.686	0.375	1.23E-66	20	TRAF4
1.05E-70	0.413829629	0.82	0.505	1.96E-66	20	BIRC3
1.49E-70	0.313914344	0.231	0.029	2.79E-66	20	CMTM7
2.98E-69	0.450563155	0.484	0.184	5.55E-65	20	LY86
5.58E-69	0.445957883	0.334	0.081	1.04E-64	20	GRASP
1.30E-68	0.269824584	0.176	0.012	2.43E-64	20	SMAGP
1.63E-68	0.292083901	0.192	0.01	3.04E-64	20	C12orf75
1.52E-66	0.450250544	0.151	0.003	2.83E-62	20	MAL
4.30E-66	0.383261995	0.894	0.665	8.01E-62	20	CCR7
6.19E-66	0.598385078	0.522	0.239	1.15E-61	20	TKT
1.61E-65	0.344337079	0.306	0.08	3.00E-61	20	SNX11

1.29E-64	0.401572883	0.559	0.281	2.41E-60	20	ZFAND6
5.63E-64	0.351600618	0.284	0.055	1.05E-59	20	SCPEP1
6.58E-64	0.271100213	0.184	0.016	1.23E-59	20	DENND3
9.63E-64	0.407108722	0.706	0.441	1.80E-59	20	BACH1
2.87E-63	0.420643623	0.893	0.682	5.35E-59	20	RBM3
8.14E-63	0.253605323	0.143	0.003	1.52E-58	20	AK8
6.09E-62	0.39827407	0.395	0.138	1.14E-57	20	FAM49A
6.49E-62	0.478771525	0.647	0.367	1.21E-57	20	ANXA6
1.21E-61	0.317045203	0.522	0.22	2.25E-57	20	AC119396.1
3.24E-61	0.315778188	0.349	0.107	6.03E-57	20	WDFY2
7.13E-59	0.392794499	0.369	0.116	1.33E-54	20	ICAM1
3.31E-58	0.361825298	0.87	0.621	6.17E-54	20	LRRFIP1
7.14E-58	0.382553399	0.432	0.175	1.33E-53	20	MTMR6
4.92E-57	0.395958767	0.877	0.673	9.17E-53	20	TAPBP
1.39E-56	0.374940398	0.847	0.624	2.59E-52	20	EIF3E
6.23E-56	0.532483991	0.473	0.216	1.16E-51	20	CPNE5
9.16E-56	0.421537439	0.953	0.811	1.71E-51	20	ARHGDIB
1.52E-55	0.345596754	0.61	0.317	2.83E-51	20	RASGEF1B
4.76E-55	0.44066115	0.644	0.351	8.86E-51	20	NFKB2
6.64E-55	0.382448065	0.956	0.839	1.24E-50	20	SLC25A6
1.13E-54	0.357756639	0.982	0.848	2.11E-50	20	TOMM7
1.03E-53	0.376656293	0.362	0.125	1.92E-49	20	C7orf50
5.65E-53	0.375882717	0.43	0.176	1.05E-48	20	RFTN1
9.45E-53	0.371809507	0.577	0.293	1.76E-48	20	PER1
1.62E-52	0.368505377	0.924	0.731	3.01E-48	20	UQCRB
8.20E-52	0.474880239	0.969	0.833	1.53E-47	20	PFN1
1.04E-50	0.453545003	0.393	0.161	1.94E-46	20	SEMA7A
1.59E-50	0.589058102	0.493	0.249	2.96E-46	20	PLEK
1.89E-49	0.448831955	0.219	0.05	3.52E-45	20	SGK1
2.35E-49	0.319158196	0.369	0.142	4.38E-45	20	RHBDF2
4.89E-49	0.251882221	0.186	0.033	9.12E-45	20	IFNG-AS1
6.26E-49	0.357263089	0.681	0.441	1.17E-44	20	ADGRE5
7.41E-48	0.317806969	0.474	0.22	1.38E-43	20	CAMK1D
2.42E-47	0.297514133	0.262	0.084	4.50E-43	20	NEK6
6.10E-47	0.376406762	0.367	0.152	1.14E-42	20	KYNU
8.26E-47	0.377313684	0.331	0.131	1.54E-42	20	MYO1C
1.74E-45	0.318333251	0.748	0.5	3.24E-41	20	RAP1B
2.64E-45	0.326319625	0.564	0.302	4.92E-41	20	RHOF
3.12E-44	0.312974281	0.98	0.853	5.82E-40	20	RPL23
5.35E-44	0.344208608	0.383	0.168	9.98E-40	20	LAT2
8.14E-44	0.38035849	0.316	0.124	1.52E-39	20	ANXA4
9.93E-44	0.26313973	0.231	0.056	1.85E-39	20	LPIN1
1.84E-43	0.325742077	0.613	0.362	3.43E-39	20	SPIB
4.15E-43	0.258582451	0.869	0.638	7.74E-39	20	CD44
1.35E-41	0.260609633	0.213	0.059	2.51E-37	20	RASGRP1
3.47E-41	0.302001776	0.803	0.616	6.47E-37	20	NAP1L1

9.01E-41	0.286013413	0.345	0.142	1.68E-36	20	SAMSN1
4.42E-40	0.406799162	0.793	0.586	8.23E-36	20	MYH9
5.85E-40	0.323197331	0.399	0.183	1.09E-35	20	S1PR1
6.63E-40	0.306775708	0.416	0.206	1.24E-35	20	EMB
7.62E-40	0.379946968	0.842	0.646	1.42E-35	20	SUB1
1.74E-39	0.2577554	0.274	0.094	3.24E-35	20	TP53INP1
2.36E-39	0.301353883	0.717	0.516	4.40E-35	20	PTPN1
8.93E-39	0.330876857	0.457	0.23	1.67E-34	20	DAPP1
4.43E-38	0.331788102	0.531	0.294	8.26E-34	20	ARID5A
6.55E-38	0.260143893	0.182	0.048	1.22E-33	20	GSN
9.72E-38	0.346504711	0.698	0.487	1.81E-33	20	LCP1
1.09E-36	0.263336141	0.446	0.238	2.04E-32	20	GLIPR1
1.63E-36	0.307069096	0.309	0.122	3.05E-32	20	RARRES3
2.86E-36	0.29992384	0.954	0.788	5.33E-32	20	PPDPF
8.89E-35	0.254181321	0.659	0.441	1.66E-30	20	LDHB
4.91E-33	0.337798522	0.673	0.481	9.16E-29	20	CAPZB
1.15E-32	0.289479229	0.533	0.331	2.14E-28	20	SASH3
2.13E-32	0.28209751	0.274	0.12	3.96E-28	20	CCDC167
2.75E-32	0.280846504	0.474	0.26	5.13E-28	20	KDM2B
3.55E-31	0.274580412	0.39	0.208	6.61E-27	20	PPA1
8.90E-31	0.264945258	0.975	0.854	1.66E-26	20	BTF3
1.06E-30	0.251016699	0.358	0.173	1.97E-26	20	GPR132
1.37E-30	0.2886047	0.768	0.564	2.55E-26	20	DDX21
3.70E-30	0.253909375	0.251	0.108	6.89E-26	20	HIPK2
4.90E-30	0.267160547	0.728	0.518	9.13E-26	20	PGK1
1.59E-28	0.254389193	0.352	0.179	2.97E-24	20	NFKB1
1.92E-28	0.411738852	0.576	0.408	3.57E-24	20	GSTK1
2.68E-28	0.272110523	0.458	0.248	4.99E-24	20	TMBIM1
3.77E-28	0.298880605	0.708	0.511	7.02E-24	20	MAPK1IP1L
1.00E-27	0.259707011	0.853	0.661	1.86E-23	20	EIF5A
9.39E-27	0.250077424	0.93	0.76	1.75E-22	20	SYNGR2
3.44E-25	0.267868284	0.838	0.688	6.42E-21	20	YWHAB
1.32E-24	0.271085043	0.663	0.482	2.46E-20	20	RSL1D1
1.22E-21	0.250619931	0.474	0.307	2.28E-17	20	COX17
2.24E-21	0.261776341	0.881	0.732	4.17E-17	20	CORO1A
8.15E-19	0.366175784	0.217	0.097	1.52E-14	20	CD70
1.66E-16	0.357368263	0.222	0.112	3.09E-12	20	MYC
2.88E-13	0.310566771	0.306	0.183	5.37E-09	20	TRAF1

Supplementary Table 2. Probes for rapid capture hybridization sequencing (RaCH-seq). Probe panel was designed to target the exons of the BCL2 family members.The xGen Lockdown Probes were individually synthesized 5′-biotinylated oligos.

ID	Sequence
BAD-201_exon1	CGGCAGGCCCGGGTCAGGGGCCTCGAGATCGGGCTTGGGCCCAGAGCATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGCAGAGAGGGGCCTGGGCCCCA
BAD-201_exon2	CCCAGAGCATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGCAGAGAGGGGCCTGGGCCCCAGCCCCGCAGGGGACGGGCCCTCAGGCTCCGGCAAGCATC
BAD-201_exon4	GGCGGAAGTACTTCCCTCAGGCCTATGCAAAAAGAGGATCCGTGCTGTCTCCTTTGGAGGGAGGGCTGACCCAGATTCCCTTCCGGTGCGTGTGAAGCCACGGAAGGCTTGGTCCCATCG
BAD-202_exon1	GGGGCCTCGAGATCGGGCTTGGGCCCAGAGCATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGCAGAGAGGGGCCTGGGCCCCAGCCCCGCAGGGGACGG
BAD-202_exon3	GGAGAACTTCGTATTCTCCTTCTTGGGAATCTGAGGACTCTGAAAATCCCAGTGCAGGGATGCTCGCGGAAGCATCAGCAGGGATGTCCGCCCCAGCCGCTGACTCAGAAGCCCAACACG
BAD-202_exon5	CTCCGGAGGATGAGTGACGAGTTTGTGGACTCCTTTAAGAAGGGACTTCCTCGCCCGAAGAGCGCGGGCACAGCAACGCAGATGCGGCAAAGCTCCAGCTGGACGCGAGTCTTCCAGTCC
BAD-203_exon1	AGCTGTGCCTTGACTACGTAACATCTTGTCCTCACAGCCCAGAGCATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGCAGAGAGGGGCCTGGGCCCCAGC
BAD-203_exon2	GGGGAGGAGCCCAGCCCCTTTCGGGGCCGCTCGCGCTCGGCGCCCCCCAACCTCTGGGCAGCACAGCGCTATGGCCGCGAGCTCCGGAGGATGAGTGACGAGTTTGTGGACTCCTTTAAG
BAD-203_exon3	CGGAAGTACTTCCCTCAGGCCTATGCAAAAAGAGGATCCGTGCTGTCTCCTTTGGAGGGAGGGCTGACCCAGATTCCCTTCCGGTGCGTGTGAAGCCACGGAAGGCTTGGTCCCATCGGA
BAD-204_exon1	GGACACAGGCTAAGAGAGTCGAAGGCTGGCTAGACAAGGGGAGAGACACAGAGCTCCGCTGATCATCACTGGACTCTGGATTCCACCAAACCTTTGGAACCTTCCAGCCTCAGGCCTCCA
BAD-204_exon3	TCGCGCTCGGCGCCCCCCAACCTCTGGGCAGCACAGCGCTATGGCCGCGAGCTCCGGAGGATGAGTGACGAGTTTGTGGACTCCTTTAAGAAGGGACTTCCTCGCCCGAAGAGCGCGGGC
BAD-205_exon1	GGCAGGGCCAGGGGCTTAGAGGAGCTGAGATTAACGTCGCCCCCCTACCCACTGACCCTCTGCAGGCGCTGGGGCTGTGGAGATCCGGAGTCGCCACAGCTCCTACCCCGCGGGGACGGA
BAD-205_exon2	CTATGGCCGCGAGCTCCGGAGGATGAGTGACGAGTTTGTGGACTCCTTTAAGAAGGGACTTCCTCGCCCGAAGAGCGCGGGCACAGCAACGCAGATGCGGCAAAGCTCCAGCTGGACGCG
BAD-206_exon1	AACTAGGGCCCGGAGCCCGGGGTGCTGGAGGGAGGCGGCAGGCCCGGGTCAGGGGCCTCGAGATCGGGCTTGGGCCCAGAGCATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAGGA
BAD-207_exon1	CATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGCAGAGAGGGGCCTGGGCCCCAGCCCCGCAGGGGACGGGCCCTCAGGCTCCGGCAAGCATCATCGCCA
BAD-207_exon2	ATGCAAAAAGAGGATCCGTGCTGTCTCCTTTGGAGGGAGGGCTGACCCAGATTCCCTTCCGGTGCGTGTGAAGCCACGGAAGGCTTGGTCCCATCGGAAGTTTTGGGTTTTCCGCCCACA
BAK1-201_exon1	TGATCACTGGAGTCTCGCGGGTCCCTCGGGCTGCACAGGGACAAGTAAAGGCTACATCCAGATGCCGGGAATGCACTGACGCCCATTCCTGGAAACTGGGCTCCCACTCAGCCCCTGGGA
BAK1-201_exon2	TTGGGCCAGGATCCCGGCAGGCTGATCCCGTCCTCCACTGAGACCTGAAAAATGGCTTCGGGGCAAGGCCCAGGTCCTCCCAGGCAGGAGTGCGGAGAGCCTGCCCTGCCCTCTGCTTCT
BAK1-201_exon2	GCTGATCCCGTCCTCCACTGAGACCTGAAAAATGGCTTCGGGGCAAGGCCCAGGTCCTCCCAGGCAGGAGTGCGGAGAGCCTGCCCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCCAGGA
BAK1-201_exon3	GGCCCAGGTCCTCCCAGGCAGGAGTGCGGAGAGCCTGCCCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCCAGGACACAGAGGAGGTTTTCCGCAGCTACGTTTTTTACCGCCATCAGCAG
BAK1-201_exon3	AGGAGCAGGTAGCCCAGGACACAGAGGAGGTTTTCCGCAGCTACGTTTTTTACCGCCATCAGCAGCAACCTAGCAGCACCATGGGGCAGGTGGGACGGCAGCTCGCCATCATCGGGGACG
BAK1-201_exon4	TCCCAGGCAGGAGTGCGGAGAGCCTGCCCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCCAGGACACAGAGGAGGTTTTCCGCAGCTACGTTTTTTACCGCCATCAGCAGCAACCTAGCAG
BAK1-201_exon4	CAACCTAGCAGCACCATGGGGCAGGTGGGACGGCAGCTCGCCATCATCGGGGACGACATCAACCGACGCTATGACTCAGAGTTCCAGACCATGTTGCAGCACCTGCAGCCCACGGCAGAG
BAK1-201_exon5	GCTCGCCATCATCGGGGACGACATCAACCGACGCTATGACTCAGAGTTCCAGACCATGTTGCAGCACCTGCAGCCCACGGCAGAGAATGCCTATGAGTACTTCACCAAGATTGCCACCAG
BAK1-201_exon6	CCTGTTTGAGAGTGGCATCAATTGGGGCCGTGTGGTGGCTCTTCTGGGCTTCGGCTACCGTCTGGCCCTACACGTCTACCAGCATGGCCTGACTGGCTTCCTAGGCCAGGTGACCCGCTT
BAK1-201_exon7	GGTGCCCTTTGGGGTCCCGGTTCAGACCCCTGCCTGGACTTAAGCGAAGTCTTTGCCTTCTCTGTTCCCTTGCAGGGGTCCCCCCTCAAGAGTACAGAAGCTTTAGCAAGTGTGCACTCC
BAK1-201_exon7	TGTGAATACTTGAACTCTGTTCCCCCACCCTCCATGCTCCTCACCTGTCTAGGTCTCCTCAGGGTGGGGGGTGACAGTGCCTTCTCTATTGGGCACAGCCTAGGGTCTTGGGGGTCAGGG
BAK1-202_exon1	ACAGAGCAACTTCCTCTAGAGGGAGCTGATTGGAGCCGGGTGCCGCTGGCACCTCTATGATCACTGGAGTCTCGCGGGTCCCTCGGGCTGCACAGGGACAAGTAAAGGCTACATCCAGAT
BAK1-202_exon6	GGGTGCCCTTTGGGGTCCCGGTTCAGACCCCTGCCTGGACTTAAGCGAAGTCTTTGCCTTCTCTGTTCCCTTGCAGGGGTCCCCCCTCAAGAGTACAGAAGCTTTAGCAAGTGTGCACTC
BAK1-202_exon6	ATTCTGGAAGATCAGCACCCTAAGAGATGGGACTAGGACCTGAGCCTGGTCCTGGCCGTCCCTAAGCATGTGTCCCAGGAGCAGGACCTACTAGGAGAGGGGGGCCAAGGTCCTGCTCAA
BAK1-203_exon3	GGACACAGAGGAGGTTTTCCGCAGCTACGTTTTTTACCGCCATCAGCAGGAACAGGAGGCTGAAGGGGTGGCTGCCCCTGCCGACCCAGAGATGGTCACCTTACCTCTGCAACCTAGCAG
BAK1-203_exon5	ACATCAACCGACGCTATGACTCAGAGTTCCAGACCATGTTGCAGCACCTGCAGCCCACGGCAGAGAATGCCTATGAGTACTTCACCAAGATTGCCACCAGGCCAGCAGCAACACCCACAG
BAK1-203_exon5	GCCAGCAGCAACACCCACAGCCTGTTTGAGAGTGGCATCAATTGGGGCCGTGTGGTGGCTCTTCTGGGCTTCGGCTACCGTCTGGCCCTACACGTCTACCAGCATGGCCTGACTGGCTTC
BAX-201_exon5	GCCCTGTGCACCAAGGTGCCGGAACTGATCAGAACCATCATGGGCTGGACATTGGACTTCCTCCGGGAGCGGCTGTTGGGCTGGATCCAAGACCAGGGTGGTTGGGTGAGACTCCTCAAG
BAX-202_exon1	GCGCTGCGGCCGCCCGCGCGGACCCGGCGAGAGGCGGCGGCGGGAGCGGCGGTGATGGACGGGTCCGGGGAGCAGCCCAGAGGCGGGGGGCCCACCAGCTCTGAGCAGATCATGAAGACA
BAX-202_exon2	GACCCGGCGAGAGGCGGCGGCGGGAGCGGCGGTGATGGACGGGTCCGGGGAGCAGCCCAGAGGCGGGGGGCCCACCAGCTCTGAGCAGATCATGAAGACAGGGGCCCTTTTGCTTCAGGG
BAX-202_exon2	GGCCCACCAGCTCTGAGCAGATCATGAAGACAGGGGCCCTTTTGCTTCAGGGTTTCATCCAGGATCGAGCAGGGCGAATGGGGGGGGAGGCACCCGAGCTGGCCCTGGACCCGGTGCCTC
BAX-202_exon6	CTCACTCACCATCTGGAAGAAGATGGGCTGAGGCCCCCAGCTGCCTTGGACTGTGTTTTTCCTCCATAAATTATGGCATTTTTCTGGGAGGGGTGGGGATTGGGGGACGTGGGCATTTTT
BAX-203_exon1	ATGGACGGGTCCGGGGAGCAGCCCAGAGGCGGGGGGCCCACCAGCTCTGAGCAGATCATGAAGACAGGGGCCCTTTTGCTTCAGGGGATGATTGCCGCCGTGGACACAGACTCCCCCCGA

BAX-203_exon2	GGCCCACCAGCTCTGAGCAGATCATGAAGACAGGGGCCCTTTTGCTTCAGGGGATGATTGCCGCCGTGGACACAGACTCCCCCCGAGAGGTCTTTTTCCGAGTGGCAGCTGACATGTTTT
BAX-203_exon5	ACCAGGGTGGTTGGGACGGCCTCCTCTCCTACTTTGGGACGCCCACGTGGCAGACCGTGACCATCTTTGTGGCGGGAGTGCTCACCGCCTCACTCACCATCTGGAAGAAGATGGGCTGAG
BAX-204_exon1	ATGGACGGGTCCGGGGAGCAGCCCAGAGGCGGGGGGCCCACCAGCTCTGAGCAGATCATGAAGACAGGGGCCCTTTTGCTTCAGGGTTTCATCCAGGATCGAGCAGGGCGAATGGGGGGG
BAX-204_exon5	TGCCAGCAAACTGGTGCTCAAGGCTGGCGTGAAATGGCGTGATCTGGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCGATTCACCTGCCTCAGCATCCCAAGGAGCTGGGATTACAG
BAX-204_exon5	GCTGGCGTGAAATGGCGTGATCTGGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCGATTCACCTGCCTCAGCATCCCAAGGAGCTGGGATTACAGGCCCTGTGCACCAAGGTGCCGG
BAX-204_exon6	GAGCTGGGATTACAGGCCCTGTGCACCAAGGTGCCGGAACTGATCAGAACCATCATGGGCTGGACATTGGACTTCCTCCGGGAGCGGCTGTTGGGCTGGATCCAAGACCAGGGTGGTTGG
BAX-204_exon7	GACCAGGGTGGTTGGGACGGCCTCCTCTCCTACTTTGGGACGCCCACGTGGCAGACCGTGACCATCTTTGTGGCGGGAGTGCTCACCGCCTCACTCACCATCTGGAAGAAGATGGGCTGA
BAX-205_exon1	ATGGACGGGTCCGGGGAGCAGCCCAGAGGCGGGGGTTTCATCCAGGATCGAGCAGGGCGAATGGGGGGGAGGCACCCGAGCTGGCCCTGGACCCGGTGCCTCAGGATGCGTCCACCAAG
BAX-205_exon2	TTTCATCCAGGATCGAGCAGGGCGAATGGGGGGGAGGCACCCGAGCTGGCCCTGGACCCGGTGCCTCAGGATGCGTCCACCAAGAAGCTGAGCGAGTGTCTCAAGCGCATCGGGGACGAA
BAX-205_exon3	TGGGGGGGAGGCACCCGAGCTGGCCCTGGACCCGGTGCCTCAGGATGCGTCCACCAAGAAGCTGAGCGAGTGTCTCAAGCGCATCGGGGACGAACTGGACAGTAACATGGAGCTGCAGAG
BAX-205_exon3	GGGGGGGAGGCACCCGAGCTGGCCCTGGACCCGGTGCCTCAGGATGCGTCCACCAAGAAGCTGAGCGAGTGTCTCAAGCGCATCGGGGACGAACTGGACAGTAACATGGAGCTGCAGAGG
BAX-205_exon6	GCCTCACTCACCATCTGGAAGAAGATGGGCTGAGGCCCCCAGCTGCCTTGGACTGTGTTTTTCCTCCATAAATTATGGCATTTTTCTGGGAGGGGTGGGGATTGGGGGACGTGGGCATTT
BAX-206_exon5	GCCCTGTGCACCAAGGTGCCGGAACTGATCAGAACCATCATGGGCTGGACATTGGACTTCCTCCGGGAGCGGCTGTTGGGCTGGATCCAAGACCAGGGTGGTTGGACCGTGACCATCTTT
BAX-206_exon6	TTGGACTTCCTCCGGGAGCGGCTGTTGGGCTGGATCCAAGACCAGGGTGGTTGGACCGTGACCATCTTTGTGGCGGGAGTGCTCACCGCCTCACTCACCATCTGGAAGAAGATGGGCTGA
BAX-207_exon1	CTCCACAGTCTCCTGATCCCCTAGAACCCAAGAGTCCAGGTACCTCTTCCCTTCCTTTCTCCTCTAGGGCCCACCAGCTCTGAGCAGATCATGAAGACAGGGGCCCTTTTGCTTCAGGG
BAX-207_exon2	TTTCATCCAGGATCGAGCAGGGCGAATGGGGGGGGAGGCACCCGAGCTGGCCCTGGACCCGGTGCCTCAGGATGCGTCCACCAAGAAGCTGAGCGAGTGTCTCAAGCGCATCGGGGACGA
BAX-207_exon3	GATGATTGCCGCCGTGGACACAGACTCCCCCCGAGAGGTCTTTTTCCGAGTGGCAGCTGACATGTTTTCTGACGGCAACTTCAACTGGGGCCGGGTTGTCGCCCTTTTCTACTTTGCCAG
BAX-207_exon4	CAAACTGGTGCTCAAGGCCCTGTGCACCAAGGTGCCGGAACTGATCAGAACCATCATGGGCTGGACATTGGACTTCCTCCGGGAGCGGCTGTTGGGCTGGATCCAAGACCAGGGTGGTTG
BAX-207_exon4	GCCCTGTGCACCAAGGTGCCGGAACTGATCAGAACCATCATGGGCTGGACATTGGACTTCCTCCGGGAGCGGCTGTTGGGCTGGATCCAAGACCAGGGTGGTTGGGACGGCCTCCTCTCC
BAX-207_exon5	TGTGGCGGGAGTGCTCACCGCCTCACTCACCATCTGGAAGAAGATGGGCTGAGGCCCCCAGCTGCCTTGGACTGTGTTTTTCCTCCATAAATTATGGCATTTTTCTGGGAGGGGTGGGGA
BAX-208_exon1	GTCTGATTATTGTGGCACAGATTTGAGGAGTGACACCCCGTTCTGATTCTGCACCCTCACTCCATCCCCACTCTAGTTTCATCCAGGATCGAGCAGGGCGAATGGGGGGGGAGGCACCCG
BAX-208_exon3	TTTCCGAGTGGCAGCTGACATGTTTTCTGACGGCAACTTCAACTGGGGCCGGGTTGTCGCCCTTTTCTACTTTGCCAGCAAACTGGTGCTCAAGGCCCTGTGCACCAAGGTGCCGGAACT
BAX-209_exon4	CAGGGTGGTTGGGACGGCCTCCTCTCCTACTTTGGGACGCCCACGTGGCAGACCGTGACCATCTTTGTGGCGGGAGTGCTCACCGCCTCACTCACCATCTGGAAGAAGATGGGCTGAGGC
BAX-210_exon1	CAGAAGTCCAGCCACTGGGCTCCTTCAGGACACAGGACTCTCAGCCCCGCATTCTCCTCCTCCCCTAAGAACTAGGAGTCTGGGCCCCACAACTCAGCGCAAACATTCCGGACTCCCAGC
BAX-210_exon2	CCGCCACTCCTCTGGGACCCTGGGCCTTCTGGAGCAGGTCACAGTGGTGCCCTCTCCCCATCTTCAGATCATCAGATGTGGTCTATAATGCGTTTTCCTTACGTGTCTGATCAATCCCCG
BAX-211_exon1	CCCGGCGAGAGGCGGCGGCGGGAGCGGCGGTGATGGACGGGTCCGGGGAGCAGCCCAGAGGCGGGGGGCCCACCAGCTCTGAGCAGATCATGAAGACAGGGGCCCTTTTGCTTCAGGGGT
BAX-211_exon2	ATTTGAGGAGTGACACCCCGTTCTGATTCTGCACCCTCACTCCATCCCCACTCTAGTTTCATCCAGGATCGAGCAGGGCGAATGGGGGGGGAGGCACCCGAGCTGGCCCTGGACCCGGTG
BAX-211_exon5	AGTGCTCACCGCCTCACTCACCATCTGGAAGAAGATGGGCTGAGGCCCCCAGCTGCCTTGGACTGTGTTTTTCCTCCATAAATTATGGCATTTTTCTGGGAGGGGTGGGGATTGGGGGAC
BAX-212_exon1	ATGGACGGGTCCGGGGAGCAGCCCAGAGGCGGGGTTTCATCCAGGATCGAGCAGGGCGAATGGGGGGGGAGGCACCCGAGCTGGCCCTGGACCCGGTGCCTCAGGATGCGTCCACCAAGA
BAX-212_exon3	GGATGATTGCCGCCGTGGACACAGACTCCCCCCGAGAGGTCTTTTTCCGAGTGGCAGCTGACATGTTTTCTGACGGCAACTTCAACTGGGGCCGGGTTGTCGCCCTTTTCTACTTTGCCA
BAX-213_exon1	ATGGACGGGTCCGGGGAGCAGCCCAGAGGCGGGGGATGATTGCCGCCGTGGACACAGACTCCCCCCGAGAGGTCTTTTTCCGAGTGGCAGCTGACATGTTTTCTGACGGCAACTTCAACT
BAX-213_exon3	TCCCTGCCCCCCGCCACTCCTCTGGGACCCTGGGCCTTCTGGAGCAGGTCACAGTGGTGCCCTCTCCCCATCTTCAGATCATCAGATGTGGTCTATAATGCGTTTTCCTTACGTGTCTGA
BBC3-203_exon1	ACGCGGACGCGCCTGCGGCCCGGGGAGCAGCAGCAGCCACAGCCACAGCAGCCGCCACTGCAGTTAGAGCGGCAGCAGCAGCGACAGCCACAGCAGCAGCCGCCGCGGAGAGCGGCGCTC
BBC3-204_exon1	AAAAGAAACGGAATGGAAAGCTATGAGACAGGATGAAATTTGGCATGGGGTCTGCCCAGGCATGTCCATGCCAGGTGCCCAGGGCTGCTTCCACGACGTGGGTCCCCTGCCAGATTTGTG
BBC3-204_exon2	CCCTTCCCGCTCGGCCGCCTGGTGCCCTCGGCAGTGTCCTGCGGCCTCTGCGAGCCCGGCCTGGCTGCCGCCCCCGCCGCCCCCACCCTGCTGCCCGCTGCCTACCTCTGCGCCCCCACC
BBC3-204_exon3	GCGGGCGGTCCCACCCAGGCGGCCCCGGGAGTCCGCGGGGAGGAGGAACAGTGGGCCCGGGAGATCGGGGCCCAGCTGCGGCGGATGGCGGACGACCTCAACGCACAGTACGAGCGGCGG
BBC3-204_exon4	AGACAAGAGGAGCAGCAGCGGCACCGCCCCTCACCCTGGAGGGTCCTGTACAATCTCATCATGGGACTCCTGCCCTTACCCAGGGGCCACAGAGCCCCCGAGATGGAGCCCAATTAGGTG
BBC3-204_exon4	TGCCCGTGACCGCCCCCCGCCCCATCAATCCCATTGCATAGGTTTAGAGAGAGCACGTGTGACCACTGGCATTCATTTGGGGGGTGGGAGATTTTGGCTGAAGCCGCCCCAGCCTTAGTC
BBC3-205_exon1	GCCTGTCACATGGAAAAGGCAAAATGTGGCCCCTTTGGAAAATAGAGGTCGTTAAGCCTGACCACCCCCGGGGTCACCTCTCTGGCCGTCTACCTTCCACACTGACAAGGGCCGTGGGGA
BBC3-206_exon1	GGTCCTAGAGACCACCTTGTTTTCATCCTGCCACTGGAGAGGGGGCAGGGGTTTCACTCGGCGTTGCCTAGAGGTGCTTCTGTTGAAGCCTCTGCAATGGGGGGGGCTCTTCCCAGTTCT
BBC3-206_exon1	TGAATCCTGTGCTCTGCCCGTGACCGCCCCCCGCCCCATCAATCCCATTGCATAGGTTTAGAGAGAGCACGTGTGACCACTGGCATTCATTTGGGGGGTGGGAGATTTTGGCTGAAGCCG
BCL2-201_exon1	ACCCCTCGCCGCACCACACACAGCGCGGGCTTCTAGCGCTCGGCACCGGCGGGCCAGGCGCGTCCTGCCTTCATTTATCCAGCAGCTTTTCGGAAAATGCATTTGCTGTTCGGAGTTTAA
BCL2-201_exon2	GGGTCATGTGTGTGGAGAGCGTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCT

BCL2-201_exon3	GATGCCTTTGTGGAACTGTACGGCCCCAGCATGCGGCCTCTGTTTGATTTCTCCTGGCTGTCTCTGAAGACTCTGCTCAGTTTGGCCCTGGTGGGAGCTTGCATCACCCTGGGTGCCTAT
BCL2-201_exon3	CCAGGGATGATCAACAGGGCAGTGTGGTCTCCGAATGTCTGGAAGCTGATGGAGCTCAGAATTCCACTGTCAAGAAAGAGCAGTAGAGGGGTGTGGCTGGGCCTGTCACCCTGGGGCCCT
BCL2-201_exon3	ATGGTGGTTTGACCTTTAGAGAGTTGCTTTACGTGGCCTGTTTCAACACAGACCCACCCAGAGCCCTCCTGCCCTCCTTCCGCGGGGGCTTTCTCATGGCTGTCCTTCAGGGTCTTCCTG
BCL2-201_exon3	TGAAATGCAGTGGTGCTTACGCTCCACCAAGAAAGCAGGAAACCTGTGGTATGAAGCCAGACCTCCCCGGCGGGCCTCAGGGAACAGAATGATCAGACCTTTGAATGATTCTAATTTTTA
BCL2-201_exon3	CTGAGAACCTCCTCGGCCCTCCCAGTCCCTCGCTGCACAAATACTCCGCAAGAGAGGCCAGAATGACAGCTGACAGGGTCTATGGCCATCGGGTCGTCTCCGAAGATTTGGCAGGGGCAG
BCL2-201_exon3	CCTGTATTGGGGTCGATGTGATGCCTCTGCGAAGAACCTTGTGTGACAAATGAGAAACATTTTGAAGTTTGTGGTACGACCTTTAGATTCCAGAGACATCAGCATGGCTCAAAGTGCAGC
BCL2-202_exon1	AAAATGCATTTGCTGTTCGGAGTTTAATCAGAAGAGGATTCCTGCCTCCGTCCCCGGCTCCTTCATCGTCCCCTCTCCCCTGTCTCTCTCCTGGGGAGGCGTGAAGCGGTCCCGTGGATA
BCL2-202_exon1	GTGGATAGAGATTCATGCCTGTGCCCGCGCGTGTGTGCGCGCGTGTAAATTGCCGAGAAGGGGAAAACATCACAGGACTTCTGCGAATACCGGACTGAAAATTGTAATTCATCTGCCGCC
BCL2-202_exon1	CCAATAAAATAGCTGGATTATAACTCCTCTTCTTTCTCTGGGGGCCGTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTTGGCCCCCGTTGCTTTTCCTCTGGGAAGGATGGCGCACGCTGG
BCL2-203_exon1	CTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGCGTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCA
BCL2-203_exon1	TGAGCAGCTTGTTGGAACCGGAGGGAGGTTTCAGGGACTGCTTATGAACCAGATACCAGGTTGGGTCTTGACAGTCTGCATCCCAAACAAGCTCCCCTGAAACAAGCCCGTTGTACACTA
BCL2-203_exon1	ATCTTTGAAAAACAGGATGCAATTCAGTGCTTCCTTTTATAGCCTCTTGGGAGAATGACTAATGTCATTATTTTATAGGACCTAACAGGAGCAAAAAGCCTAGAAATTACTGCAAGTGGA
BCL2-203_exon1	CTGCACTGTCCCCAGGGCTCCGTGGATTAGCCCATCTCCTGAATACTACACTGAATACTCCAGGCTTTAGACTGCAAGTCATTTCTTTTTCTTTGCTGCTGCTCGTAGAAAATTGGAACC
BCL2-203_exon1	ATGTGGATACCTTGCTGCTCAGTGTGGCTTATAGACAGTAGCACATGCATCCCCCGGAGCTTTGTAGAGATGCTAAAGCTCAGCTCCCACCCCAGAGCTACTGAGTCAGAATATGTGGTT
BCL2-203_exon1	CAGGTGATGGAGAGTGACCCTCTAAACTGGGAACTGTGACGACATTCAGCTTCATGTCTTAGGAGAGAGTGAGATAGGAGCCACTAGAAGAATGAGATGATTCAGACAAGAGATTGTAGG
BCL2-204_exon1	AGAGTGGTTGGCTTACACATGGAGGATGCCTTTGTGGAACTGTACGGCCCCAGCATGCGGCCTCTGTTTGATTTCTCCTGGCTGTCTCTGAAGACTCTGCTCAGTTTGGCCCTGGTGGGA
BCL2A1-201_exon1	AGTGAGCATTCTCAGCACATTGCCTCAACAGCTTCAAGGTGAGCCAGCTCAAGACTTTGCTCTCCACCAGGCAGAAGATGACAGACTGTGAATTTGGATATATTTACAGGCTGGCTCAGG
BCL2A1-202_exon1	ACAGCTTCAAGGTGAGCCAGCTCAAGACTTTGCTCTCCACCAGGCAGAAGATGACAGACTGTGAATTTGGATATATTTACAGGCTGGCTCAGGACTATCTGCAGTGCGTCCTACAGATAC
BCL2A1-202_exon2	ATTTTGTTGCGGAGTTCATAATGAATAACACAGGAGAATGGATAAGGCAAAACGGAGGCTGGGGGAAATGGCACAATCACACACCTATGCTGGTAGAGTCAGTGGCCCACAAGAAGAG
BCL2A1-202_exon2	GGGAAATGGCACAATCACACACCTATGCTGGTAGAGTCAGTGGCCCACAAGAAGAGGAAAATGGCTTTGTAAAGAAGTTTGAACCTAAATCTGGCTGGATGACTTTTCTAGAAGTTACAG
BCL2A1-202_exon3	GAAAATGGCTTTGTAAAGAAGTTTGAACCTAAATCTGGCTGGATGACTTTTCTAGAAGTTACAGGAAAGATCTGTGAAATGCTATCTCTCCTGAAGCAATACTGTTGACCAGAAAGGACA
BCL2L1-201_exon2	CACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGG
BCL2L1-201_exon3	CTCACTCTTCAGTCGGAAATGACCAGACACTGACCATCCACTCTACCCTCCCACCCCCTTCTCTGCTCCACCACATCCTCCGTCCAGCCGCCATTGCCACCAGGAGAACCACTACATGCA
BCL2L1-201_exon3	CCCAGAGCTGTTTATGGCCTCAGCTGCCTCACTTCCTACAAGAGCAGCCTGTGGCATCTTTGCCTTGGGCTGCTCCTCATGGTGGGTTCAGGGGACTCAGCCCTGAGGTGAAAGGGAGCT
BCL2L1-202_exon1	GCCACCGCGAGGCCGGCTGAGTTACCGGCATCCCCGCAGCCACCTCCTCTCCCGACCTGTGATACAAAAGATCTTCCGGGGGCTGCACCTGCCTGCCTTTGCCTAAGGCGGATTTGAAT
BCL2L1-202_exon2	AGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACA
BCL2L1-203_exon1	GGAGTGGGGCGGGGGGGACTGCCCAGGGAGTGACTTTCCGAGGAAGGCATTTCGGAGAAGACGGGGGTAGAAAAGGCTGGTGGGAGATTCAGAGTCCACTGGTGCTTTCGATTTGACTTA
BCL2L1-203_exon2	TCACTCTTCAGTCGGAAATGACCAGACACTGACCATCCACTCTACCCTCCCACCCCCTTCTCTGCTCCACCACATCCTCCGTCCAGCCGCCATTGCCACCAGGAGAACCACTACATGCAG
BCL2L1-203_exon2	TGTTTATGGCCTCAGCTGCCTCACTTCCTACAAGAGCAGCCTGTGGCATCTTTGCCTTGGGCTGCTCCTCATGGTGGGTTCAGGGGACTCAGCCCTGAGGTGAAAGGGAGCTATCAGGAA
BCL2L1-204_exon1	CTTTGCGTCTCGGGCTCGCGCGCGTTGCCGCGGCACCGGAAGTGACTGAGCTTGCAAGTTCCCCTGTCTCTTCAGGGGAAACTGAGGCCGGCTTGTTCGGGAGAGACGGCGCGAGCAGTC
BCL2L1-205_exon1	CAGCCACCGCGAGGCCGGCTGAGTTACCGGCATCCCCGCAGCCACCTCCTCTCCCGACCTGTGATACAAAAGATCTTCCGGGGGCTGCACCTGCCTGCCTTTGCCTAAGGCGGATTTGAA
BCL2L1-206_exon1	TTTCGGAGAAGACGGGGGTAGAAAAGGCTGGTGGGAGATTCAGAGTCCACTGGTGCTTTCGATTTGACTTAAGTGAAGTATCTTGGAACCTAGACCCAGACCTTCCTCTTTCTCTCCCTT
BCL2L1-206_exon2	GGTTGACTTTCTCTCCTACAAGCTTTCCCAGAAAGGATACAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAGAAGGGACTGAATCGGAGATGGAGACCCCCAG
BCL2L1-207_exon2	GCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGG
BCL2L1-208_exon1	GGCTTGTTCGGGAGAGACGGCGCGAGCAGTCAGCCAGGTAGGCCGGCAGCCAGGTAGGCCGGCCCGGGTCCGCGGCGCGGAACTCGGCCGCGAAGAGCTCTTGCGTCTGGAAGCTACCGG
BCL2L1-208_exon2	GGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTG
BCL2L1-208_exon3	GATCGCAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAA
BCL2L1-209_exon1	CCGGAAGTGACTGAGCTTGCAAGTTCCCCTGTCTCTTCAGGGGAAACTGAGGCCGGCTTGTTCGGGAGAGACGGCGCGAGCAGTCAGCCAGGTAGGCCGGCAGCCAGGTAGGCCGGCCCG
BCL2L11-201_exon3	ACAGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCTTCCATGAGGCAGGCTGAACCTGCAGATA
BCL2L11-201_exon4	TATCTCAGTGCAATGGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGG
BCL2L11-201_exon4	CTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGGGTATTTTTGAATAATT
BCL2L11-201_exon5	GCCGAGATACCATGCAGACATTTTGCTTGTTCAAACCAACAAGACCCAGCACCGCGGTCTCCTGGTGCCATTATTATGCAGCCAGCGGTTCTCTTGTGGAGGGGGCAGGTGACGTTTCAG
BCL2L11-202_exon1	GCGATCGCATCATCGCGGTATTCGGTTCGCTGCGTTCCCGCCGCCACCGCCTCGGCGCCCTTTCTTGGCCCTTGTTCCCCCAAATGTCTGACTCTGACTCTCGGACTGAGAAACGCAAG

BCL2L11-202_exon2	CAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGGCCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCTACAGACAGAGCCACAAG
BCL2L11-202_exon3	CCCCTACCTCCCTACAGACAGAGCCACAAGACAGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGG
BCL2L11-202_exon3	ACAGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGTAGTCATCCTAGAGGATATAGGTGATCTTT
BCL2L11-202_exon4	TAGTCATCCTAGAGGATATAGGTGATCTTTCACTGTGCTTTGGATTTATATTTACTGGCTTAGATTTGTATGGCCACCACCATAGTCAAGATACAGAACAACTCAACCACAAGGATTTCT
BCL2L11-203_exon3	ACAGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGATGACTCCGCTGGATCCTCCCTCAGAATTG
BCL2L11-203_exon4	TCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGATGACTCCGCTGGATCCTCCCTCAGAATTGCCCTTCATAGGGAAGTTCAGTGGCCACTCAAGTGGTTAGCAAAATCAAG
BCL2L11-203_exon4	ATGACTCCGCTGGATCCTCCCTCAGAATTGCCCTTCATAGGGAAGTTCAGTGGCCACTCAAGTGGTTAGCAAAATCAAGCTAACTGGGACTAGAAACAGCTCCATCACCCAGTAAAGAGA
BCL2L11-203_exon5	TGCAATGGATGACTCCGCTGGATCCTCCCTCAGAATTGCCCTTCATAGGGAAGTTCAGTGGCCACTCAAGTGGTTAGCAAAATCAAGCTAACTGGGACTAGAAACAGCTCCATCACCCAG
BCL2L11-203_exon5	CTAACTGGGACTAGAAACAGCTCCATCACCCAGTAAAGAGAAAGAAAACATGGATCTGCCTAGGAAGTCACCTCTGCCTGAGTCTGCTACTTGCAGGATTGGAGCTTTTGCTGCAGATTA
BCL2L11-203_exon6	TAAAGAGAAAGAAAACATGGATCTGCCTAGGAAGTCACCTCTGCCTGAGTCTGCTACTTGCAGGATTGGAGCTTTTGCTGCAGATTACAGCTTTGAAGTCACTTTACCTCAAGAGCAGTT
BCL2L11-204_exon2	AAGTCTCACTCTGTCACCCAGGCTGGAGTGCACTGGTGCGATCTTGGCTCACTGCAACCTCCAACTCCCAAGTTCAAGCGGTTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAG
BCL2L11-204_exon2	TCTCACTCTGTCACCCAGGCTGGAGTGCACTGGTGCGATCTTGGCTCACTGCAACCTCCAACTCCCAAGTTCAAGCGGTTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGCTTC
BCL2L11-204_exon3	GTAGCTGGGATTACAGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGG
BCL2L11-204_exon4	AACGCTTACTATGCAAGGAGGGTATTTTTGAATAATTACCAAGCAGCCGAAGACCACCCACGAATGGTTATCTTACGACTGTTACGTTACATTGTCCGCCTGGTGTGGAGAATGCATTGA
BCL2L11-205_exon1	GCGGGCTGGCGGGAAGGCGCGGGCTTTGCGCTGCGCCGGGGACTCTGAACCCGAGTCCCGGGCTTTGTCTCCTGCGCTGCTTTCGTGGTGACGGTCAGGGGGCGCCCGGTCGGCGAAGGG
BCL2L11-206_exo4	CAAGTGAATGGGTGGGACAGGTGGCTCCTGCCTAAGGACCACCTCAGGCCACTAACCCCTTGTGGACAACTGTGAGTAGCTGGGTTTTCCCCCACCTGCTGTGCAACTTCCTGTGCTTTG
BCL2L11-206_exon2	TCAGGGCCCGCTGGCCCCACCTGCCAGCCCTGGCCCTTTTGCTACCAGATCCCCGCTTTTCATCTTTATGAGAAGATCCTCCCTGCTGTCTCGATCCTCCAGTGGGTATTTCTCTTTTGA
BCL2L11-206_exon3	ATCTCAGTGCAATGGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGG
BCL2L11-206_exon4	ATACCATGCAGACATTTTGCTTGTTCAAACCAACAAGACCCAGCACCGCGGTCTCCTGGTGCCATTATTATGCAGCCAGCGGTTCTCTTGTGGAGGGGGCAGGTGACGTTTCAGAAGACA
BCL2L11-206_exon4	TTGTGCTGCTGGCTTTTCTGGTTGCAGGCTTTCCCATGGTCACAGGATGCACTGTCAGCATCAGGTCCCAGAGGGCCACCGTGTCCATTACAGCAGAGTCCAGCTGCAGCATCCAGCTCA
BCL2L11-206_exon4	GGATCTGGGCACCCCCTCCCAGGATCCCTGTACTCACGTGCCAGTCTCCTGACTAGAGCACTTTACTCTGTTTCCTCAGCCCTGCAGCCCCTGGGAGCACACACTGGGTGCAGCCCTGGG
BCL2L11-206_exon4	AAGTATTAACATCCCTGTCTCCCACTCCCCTGCCGTCCCATGAAGTTAACTCCTGAGAGTTGTCGGGGGTGACTGGAGAGCTCATTGCAGACCACGTGGTCCTCCAGGGTGGCTCTCCAC
BCL2L11-207_exon1	ATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGGCCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCTACAGACAGAGCCA
BCL2L11-208_exon2	ACAGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGTTAGAGAAATAGAGGAAGTTGTCGTGTAGT
BCL2L11-208_exon4	GAGGAGGTGAGAGAGGCACAGGTATTTTTGAATAATTACCAAGCAGCCGAAGACCACCCACGAATGGTTATCTTACGACTGTTACGTTACATTGTCCGCCTGGTGTGGAGAATGCATTGA
BCL2L11-209_exon2	AGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCTAACTGGGACTAGAAACAGCTCCATCACCCA
BCL2L11-209_exon5	AGGTTCTTTGCGGAGCCGAGATACCATGCAGACATTTTGCTTGTTCAAACCAACAAGACCCAGCACCGCGGTCTCCTGGTGCCATTATTATGCAGCCAGCGGTTCTCTTGTGGAGGGGGC
BCL2L11-210_exon1	CTGAGACTTTGGCATGGGGCTGCGCTGTGTCCCACTGACGTTACAGAAGCGCTTATGAATTTAAAAACTGCTCCAGGCGGCCGGACGGCGGGACAACGCCTCCTCACTTGCTCCTCTACG
BCL2L11-210_exon2	AAAAAAAGACCAAATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGGCCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCT
BCL2L11-211_exon1	TCTCCTGCGCTGCTTTCGTGGTGACGGTCAGGGGGCGCCCGGTCGGCGAAGGGCGCGGGCCGGACGCCGCGGGGCTTGGTCCCTGGCCCGGACGCTGCGCTCTGAAGGGAAGGCGCGGAC
BCL2L11-211_exon6	ACAGGTTCTTTGCGGAGCCGAGATACCATGCAGACATTTTGCTTGTTCAAACCAACAAGACCCAGCACCGCGGTCTCCTGGTGCCATTATTATGCAGCCAGCGGTTCTCTTGTGGAGGGG
BCL2L11-213_exon2	ACTATCTCAGTGCAATGGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGA
BCL2L11-213_exon4	CTGCTGATGATCCGCTTATGGGTATTTTTGAATAATTACCAAGCAGCCGAAGACCACCCACGAATGGTTATCTTACGACTGTTACGTTACATTGTCCGCCTGGTGTGGAGAATGCATTGA
BCL2L11-214_exon1	AAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGGCCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCTACAGACAGAGCCACAAGAC
BCL2L11-218_exon3	ACAGACAGAGCCACAAGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAG
BCL2L11-218_exon3	CTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGGCTGGCAAAACTCCTGG
BCL2L11-218_exon4	GAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGGCTGGCAAAACTCCTGGCATCCTCCACCTGACATAAACCAGTTCACAGAACATTCCAGCCTAGATCTGAAATG
BCL2L11-218_exon4	CTGGCAAAACTCCTGGCATCCTCCACCTGACATAAACCAGTTCACAGAACATTCCAGCCTAGATCTGAAATGTTAGAGAAATAGAGGAAGTTGTCGTGTAGTTGTCATGTATTCAGTCCA
BCL2L11-219_exon3	GAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCTAACTGGGACTAGAAACAGCTCCATCACCCAG
BCL2L11-219_exon3	CTAACTGGGACTAGAAACAGCTCCATCACCCAGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACG
BCL2L11-219_exon4	CAGCTCCATCACCCAGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGG
BCL2L11-221_exo4	GAAATAGAGGAAGTTGTCGTGTAGTTGTCATGTATTCAGTCCACTTAAGGGCAGTGGGGAAGCGTTTGAGACGGAGCTGTGGAGGCTGAATCCTTGAAGGAGGAGGTGAGAGAGGCACAG
BCL2L11-221_exon3	CTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGGTTAGAGAAATAGAGGA

BCL2L11-222_exon3	CTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGGATGCCTCTTCCACCTG
BCL2L11-222_exon4	ATGCCTCTTCCACCTGATTAAGAACCACTGTAGCAGACGCAGACTTATTGGACACTAGGCGGGAGGCCAGCTCTGCAGACAGCAGGTCTCAGGAAGACGGTCAAGGCATGGCTGCTGATG
BCL2L11-224_exon3	ACAGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGTTAGAGAAATAGAGGAAGTTGTCGTGTAG
BCL2L11-225_exon2	CAGACAGAGCCACAAGCTTCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGG
BCL2L11-225_exon3	ATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAACGCTTACTATGCAAGGAGGATGCCTCTTCCACCTGATTAA
BCL2L2-201_exon1	ATCACCCGGCGCCGGGCCCTCCCTCTGCCCCCCCCTTTCTCCTCCCTCCTTCCTTCCCTCCCTTCCTCCCTCTCTCCCTCCCTCCCAGCTCCTGCACCAGGAAACGGCCCGGATCCCGGC
BCL2L2-201_exon2	AAACGGCCCGGATCCCGGCAGCGGCCTGACCCGGCTCCACGCTGGCCAGGAGGATGAAAGGCCCCAGCTGGGGGCTCCTTGCCACCAGTGCTGTGTCTTAAGAGCTGCCATCCCGGCTGG
BCL2L2-201_exon3	TGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTTGTCTTTGGGGCTGCACTGTGTGCTGA
BCL2L2-201_exon4	TGGCAAGTTTAGGGGCACAGGAGATGTAGTCGTTCCAGGGCTGGGGGAGGTGGGAGGGATCACGCCTATAGGTGTGGGCACATGAAACGACCTGGAACTTGCTTCACAGCCCTGAGGAAG
BCL2L2-201_exon4	TCTGATAGAAGGGCAGGGCTGTTGAGCCTGGATGGGTGGAGGCTTAGGTAGCCGGACCTGCCTGCCACCCTCCTCTCCCACTCAGGCACAATGGTGCCTAAAGTGTTTCCAATCTCTGGG
BCL2L2-201_exon4	AACTAGGCCAGTGGTTTTCAAACTGCTTGGCAGAGCCCTGAAGTTTCCTAGGGGTTGCCTCAGGAGTCCTTGGGGAGATGAAGGGGGTGGGGAGCTGAGCAGGCTGGGCAATTTGCCCTC
BCL2L2-202_exon4	TCTGGTGGCAGACTTTGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGA
BCL2L2-202_exon1	GTTTTCTTCACAAGACAAGGATGATGTTTAAATGGGCATTTGTTTGCGGAATGACTTGGAGAGTTCCTCTCTTTCAGCCATCTTTTCTCAAAGACTAAGGCTGTGGACAGGATGGGCATG
BCL2L2-202_exon2	AAGACTGTCAAGGAGCCCGAGTGAGGGAAGCAGACCAACCATGGTCTTGGAGAAAAGAAAATAGGGTTTCCATCCCTTCTGGAGGGAGAAGGAATAGCAGAGATGAACATGAATGAAGAA
BCL2L2-202_exon3	GAAGGAAACAAATGGAAATAAACAAAATGAAGGGCTCCACGCTGGCCAGGAGGATGAAAGGCCCCAGCTGGGGGCTCCTTGCCACCAGTGCTGTGTCTTAAGAGCTGCCATCCCGGCTGG
BCL2L2-202_exon3	GGCTCCACGCTGGCCAGGAGGATGAAAGGCCCCAGCTGGGGGCTCCTTGCCACCAGTGCTGTGTCTTAAGAGCTGCCATCCCGGCTGGCCGCCCGGATGGCGACCCCAGCCTCGGCCCCA
BCL2L2-203_exon1	AGCTGGGCCTTTGGGCTGCACTAGGGGGAACCGGGAATAGAGATGGTGTCGGCAGGAAGCCCTTGGCCTTGGGTTTCCCGGGAGGACAGTCATTAAACATGGATTCGGCCACACAGCTGG
BCL2L2-203_exon2	CCGCCCGGATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAG
BCL2L2-204_exon1	CACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGCAGTGGGGGCTGG
BCL2L2-204_exon2	CTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCT
BCL2L2-204_exon2	GCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGTA
BCL2L2-204_exon3	GTATGGAGCACACTCTTCACCCTACCCTCTACCACAGGACACATATCCCTGTTAGCATTCCCCGGGACCTTTAGCCAAGAGGAGCTGCAGGGACCATGGCCAGGTTACCAAAATGCCCTG
BCL2L2-205_exon1	AGGAAACGGCCCGGATCCCGGCAGCGGCCTGACCCGTGAGATCCCTAACCTGGCAGGCGGGCGGGGTTGGAGACTGGCTGAGGTGGGGGGCTCCACGCTGGCCAGGAGGATGAAAGGCCC
BCL2L2-205_exon2	GCGGGCGGGGTTGGAGACTGGCTGAGGTGGGGGGCTCCACGCTGGCCAGGAGGATGAAAGGCCCCAGCTGGGGGCTCCTTGCCACCAGTGCTGTGTCTTAAGAGCTGCCATCCCGGCTGG
BCL2L2-205_exon4	GTGTCAACAAGGAGATGGAACCACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGCAGTGGGGGCTGGGCGGAGTTCACAGCT
BCL2L2-206_exon1	ATCCCGGCAGCGGCCTGACCCGTGAGATCCCTAACCTGGCAGGCGGGCGGGGTTGGAGACTGGCTGAGGGCTCCACGCTGGCCAGGAGGATGAAAGGCCCCAGCTGGGGGCTCCTTGCCA
BCL2L2-206_exon2	TGGCAGGCGGGCGGGGTTGGAGACTGGCTGAGGGCTCCACGCTGGCCAGGAGGATGAAAGGCCCCAGCTGGGGGCTCCTTGCCACCAGTGCTGTGTCTTAAGAGCTGCCATCCCGGCTGG
BCL2L2-PABPN1-201_exon1	CTCCCTCCCTCCCAGCTCCTGCACCAGGAAACGGCCCGGATCCCGGCAGCGGCCTGACCCGGCTCCACGCTGGCCAGGAGGATGAAAGGCCCCAGCTGGGGGCTCCTTGCCACCAGTGCT
BCL2L2-PABPN1-201_exon4	CTGGGAGCTGGAAGCTATCAAAGCTCGAGTCAGGGAGATGGAGGAAGAAGCTGAGAAGCTAAAGGAGCTACAGAACGAGGTAGAGAAGCAGATGAATATGAGTCCACCTCCAGGCAATG
BCL2L2-PABPN1-201_exon4	GAGCTGGAAGCTATCAAAGCTCGAGTCAGGGAGATGGAGGAAGAAGCTGAGAAGCTAAAGGAGCTACAGAACGAGGTAGAGAAGCAGATGAATATGAGTCCACCTCCAGGCAATGCTGGC
BCL2L2-PABPN1-201_exon5	CTACAGAACGAGGTAGAGAAGCAGATGAATATGAGTCCACCTCCAGGCAATGCTGGCCCGGTGATCATGTCCATTGAGGAGAAGATGGAGGCTGATGCCCGTTCCATCTATGTTGGCAAT
BCL2L2-PABPN1-201_exon5	CTGGCCCGGTGATCATGTCCATTGAGGAGAAGATGGAGGCTGATGCCCGTTCCATCTATGTTGGCAATGTGGACTATGGTGCAACAGCAGAAGAGCTGGAAGCTCACTTTCATGGCTGTG
BCL2L2-PABPN1-201_exon6	CTATGTTGGCAATGTGGACTATGGTGCAACAGCAGAAGAGCTGGAAGCTCACTTTCATGGCTGTGGTTCAGTCAACCGTGTTACCATACTGTGTGACAAATTTAGTGGCCATCCCAAAGG
BCL2L2-PABPN1-201_exon6	GTGGACTATGGTGCAACAGCAGAAGAGCTGGAAGCTCACTTTCATGGCTGTGGTTCAGTCAACCGTGTTACCATACTGTGTGACAAATTTAGTGGCCATCCCAAAGGGTTTGCGTATATA
BCL2L2-PABPN1-201_exon7	CTGTGTGACAAATTTAGTGGCCATCCCAAAGGGTTTGCGTATATAGAGTTCTCAGACAAAGAGTCAGTGAGGACTTCCTTGGCCTTAGATGAGTCCCTATTTAGAGGAAGGCAAATCAAG
BCL2L2-PABPN1-201_exon7	TTTGCGTATATAGAGTTCTCAGACAAAGAGTCAGTGAGGACTTCCTTGGCCTTAGATGAGTCCCTATTTAGAGGAAGGCAAATCAAGGTGATCCCAAAACGAACCAACAGACCAGGCATC
BCL2L2-PABPN1-201_exon8	GTGATCCCAAAACGAACCAACAGACCAGGCATCAGCACAACAGACCGGGGTTTTCCACGAGCCCGCTACCGCGCCCGGACCACCAACTACAACAGCTCCCGCTCTCGATTCTACAGTGGT
BCL2L2-PABPN1-201_exon9	GGGCCGGGCTAGAGCGACATCATGGTATTCCCCTTACTAAAAAAAGTGTGTATTAGGAGGAGAGAGAGGAAAAAAAGAGGAAAGAAGGAAAAAAAAAAGAATTAAAAAAAAAAAAAAAGAA
BCL2L2-PABPN1-202_exon1	CTCCTGCACCAGGAAACGGCCCGGATCCCGGCAGCGGCCTGACCCGGCTCCACGCTGGCCAGGAGGATGAAAGGCCCCAGCTGGGGGCTCCTTGCCACCAGTGCTGTGTCTTAAGAGCTG
BCL2L2-PABPN1-202_exon4	GACGCAGCTGGCTGACTGGATCCACAGCAGTGGGGGCTGGTTATCCCAGATCACTGAAGCTGAGATGGCTGATGAAGTAATTTGCAGTGAAATTTTAAGCGACTGTGACTCTGCTGCAAG
BCL2L2-PABPN1-203_exon1	TTTGGGCTGCACTAGGGGGAACCGGGAATAGAGATGGTGTCGGCAGGAAGCCCTTGGCCTTGGGTTTCCCGGGAGGACAGTCATTAAACATGGATTCGGCCACACAGCTGGTAGAGCGTT
BCL2L2-PABPN1-203_exon8	GTGGTTTTAACAGCAGGCCCCGGGGTCGCGTCTACAGGGGCCGGGCTAGAGCGACATCATGGTATTCCCCTTACTAAAAAAAGTGTGTATTAGGAGGAGAGAGAGGAAAAAAAGAGGAAA
BID-201_exon1	GGGCTGGCAAGGGTTCATTCATTCATTCAACAAATACGAATGTGCAGCGGTGCTGGGGTCATGATGGCTCGGTGGGCAGCGAGGGGCCGGGCCGGCTGGAGGAGCACAGTGCGGATTCT

BID-201_exon2	CGGTGGGCAGCGAGGGGCCGGGCCGGCTGGAGGAGCACAGTGCGGATTCTGTCGCCACTGGGACACTGTGAACCAGGAGTGAGTCGGAGCTGCCGCGCTGCCCAGGCCATGGACTGTGAG
BID-201_exon2	GTCGCCACTGGGACACTGTGAACCAGGAGTGAGTCGGAGCTGCCGCGCTGCCCAGGCCATGGACTGTGAGGTCAACAACGGTTCCAGCCTCAGGGATGAGTGCATCACAAACCTACTGGT
BID-201_exon3	GTCAACAACGGTTCCAGCCTCAGGGATGAGTGCATCACAAACCTACTGGTGTTTGGCTTCCTCCAAAGCTGTTCTGACAACAGCTTCCGCAGAGAGCTGGACGCACTGGGCCACGAGCTG
BID-201_exon4	ATTCTGAAAGTCAAGAAGACATCATCCGGAATATTGCCAGGCACCTCGCCCAGGTCGGGGACAGCATGGACCGTAGCATCCCTCCGGGCCTGGTGAACGGCCTGGCCCTGCAGCTCAGGA
BID-201_exon5	GACCGGAACAGGGACCTGGCCACTGCCCTGGAGCAGCTGCTGCAGGCCTACCCTAGAGACATGGAGAAGGAGAAGACCATGCTGGTGCTGGCCCTGCTGCTGGCCAAGAAGGTGGCCAGT
BID-201_exon6	GGGATGGACTGAACGGACAGTTCCAGAAGTGTGACTGGCTAAAGCTCGATGTGGTCACAGCTGTATAGCTGCTTCCAGTGTAGACGGAGCCCTGGCATGTCAACAGCGTTCCTAGAGAAG
BID-201_exon6	TTCCATGACATCAAGACTTTGCTAAAGACATGAAGCCACGGGTGCCAGAAGCTACTGCGATGCCCCGGGAGTTAGCCCCCTGGTAATAGCTGTAAACTTCCAATTTCTAGCCATACGCTC
BID-202_exon1	GGACGCGCCCGCGCCCCCGCGGCTGGAGGGTGGTCGCCACTGGGACACTGTGAACCAGGAGTGAGTCGGAGCTGCCGCGCTGCCCAGGCCATGGACTGTGAGGTCAACAACGGTTCCAGC
BID-202_exon4	TCCCGCTTGGGAAGAATAGAGGCAGGGGCGTCAGACAATAACACAGCAAGTGCTGAGGAAGAAACGGAGGCGGCAGGGAGCGTGGCAGTTGAGCGTGGCCTTCATGGAGCTGCGACAGTG
BID-202_exon4	GGGCGTCAGACAATAACACAGCAAGTGCTGAGGAAGAAACGGAGGCGGCAGGGAGCGTGGCAGTTGAGCGTGGCCTTCATGGAGCTGCGACAGTGATTCTGAAAGTCAAGAAGACATCAT
BID-202_exon7	ACCTACGTGAGGAGCTTAGCCAGAAATGGGATGGACTGAACGGACAGTTCCAGAAGTGTGACTGGCTAAAGCTCGATGTGGTCACAGCTGTATAGCTGCTTCCAGTGTAGACGGAGCCCT
BID-203_exon1	GGAAGCGCGCGGGGCGCCATAAGGAGGAAGCGGGTAGTCGACCGTGTCCGCGCGCCTGGGAGACGCTGCCTCGGCCCGGACGCGCCCGCGCCCCCGCGGCTGGAGGGTGATTCTGAAAGT
BID-204_exon1	GAAGGAGGAAGCGCGCGGGGCGCCATAAGGAGGAAGCGGGTAGTCGACCGTGTCCGCGCGCCTGGGAGACGCTGCCTCGGCCCGGACGCGCCCGCGCCCCCGCGGCTGGAGGGTGGTCAA
BID-205_exon1	GGAGGAAGCGCGCGGGGCGCCATAAGGAGGAAGCGGGTAGTCGACCGTGTCCGCGCGCCTGGGAGACGCTGCCTCGGCCCGGACGCGCCCGCGCCCCCGCGGCTGGAGGGTGGTCGCCAC
BID-205_exon6	AGCTACTGCGATGCCCCGGGAGTTAGCCCCCTGGTAATAGCTGTAAACTTCCAATTTCTAGCCATACGCTCAGCTCATCCATGCCTCAGAAGTGCATCTGGAGAGAACAGGTTTCTAAGC
BID-206_exon4	CTAGAGACATGGAGAAGGAGAAGACCATGCTGGTGCTGGCCCTGCTGCTGGCCAAGAAGGTGGCCAGTCACACGCCGTCCTTGCTCCGTGATGTCTTTCACACAACAGTGAATTTTATTA
BID-207_exon1	GACTGGACGGCAGGGAGTGGGGCTGTCATCATCAGATGAGAGCTAAGGGGACCCCCACCAGGGTGGCGGCAATGGCAGAGGGTAGGCAAAACGCTTGTATTTGCAACATAAGGTGAGATT
BID-207_exon1	CGGACCTGTCCTTTCCCGGGGCAGGGTGGTGTGGGAGAGGGTATCAGGGACATTTTCTGAGTCTGCTCTGTCTCTGCCGCCCCTGCCTGAACACAGATTCTGAAAGTCAAGAAGACATCA
BID-208_exon4	CGCGGACCTGTCCTTTCCCGGGGCAGGGTGGTGTGGGAGAGGGTATCAGGGACATTTTCTGAGTCTGCTCTGTCTCTGCCGCCCCTGCCTGAACACAGATTCTGAAAGTCAAGAAGACAT
BID-208_exon6	TTGCTCCGTGATGTCTTTCACACAACAGTGAATTTTATTAACCAGAACCTACGCACCTACGTGAGGAGCTTAGCCAGAAATGGGATGGACTGAACGGACAGTTCCAGAAGTGTGACTGGC
BID-209_exon1	CACTGTCTGAAACAGTCGCGTAAGGGGTCGCCACTGGGACACTGTGAACCAGGAGTGAGTCGGAGCTGCCGCGCTGCCCAGGCCATGGACTGTGAGGTCAACAACGGTTCCAGCCTCAGG
BID-210_exon1	CCAGACTGTTCCAGAAACAGCCTGGGGATTCTGAATGTTTCCCAGAGAATCATTAGGAATTATCCCAGCGGCGCTGGAGTCAACAACGGTTCCAGCCTCAGGGATGAGTGCATCACAAAC
BID-210_exon3	CCCCAGTGGGAGGGCTACGATGAGCTGCAGACTGATGGCAACCGCAGCAGCCACTCCCGCTTGGGAAGAATAGAGGCAGATTCTGAAAGTCAAGAAGACATCATCCGGAATATTGCCAGG
BID-211_exon1	CACTGTCTGAAACAGTCGCGTAAGGGATTCTGAAAGTCAAGAAGACATCATCCGGAATATTGCCAGGCACCTCGCCCAGGTCGGGGACAGCATGGACCGTAGCATCCCTCCGGGCCTGGT
BID-212_exon2	GTCGCCACTGGGACACTGTGAACCAGGAGTGAGTCGGAGCTGCCGCGCTGCCCAGGCCATGGACTGTGAGATTCTGAAAGTCAAGAAGACATCATCCGGAATATTGCCAGGCACCTCGCC
BID-213_exon1	CTGGGCTGGCAAGGGTTCATTCATTCATTCAACAAATACGAATGTGCAGCGGTGCTGGGGTCATGATGGCTCGGTGGGCAGCGAGGGGCCGGGCCGGCTGGAGGAGCACAGTGCGGATTC
BID-214_exon4	GGGCGTCAGACAATAACACAGCAAGTGCTGAGGAAGAAACGGAGGCGGCAGGGAGCGTGGCAGTTGAGCGTGGCCTTCATGGAGCTGCGACAGTGGTACTCGGGCAGGGGCAGCACGGAG
BID-215_exon1	GAAGGAGGAAGCGCGCGGGGCGCCATAAGGAGGAAGCGGGTAGTCGACCGTGTCCGCGCGCCTGGGAGACGCTGCCTCGGCCCGGACGCGCCCGCGCCCCCGCGGCTGGAGGGTGGTCGC
BID-215_exon2	GAGACGCTGCCTCGGCCCGGACGCGCCCGCGCCCCCGCGGCTGGAGGGTGGTCGCCACTGGGACACTGTGAACCAGGAGTGAGTCGGAGCTGCCGCGCTGCCCAGGCCATGGACTGTGAG
BIK-201_exon1	AGACACGAAGCCTCCCGGGTGGCTTACAGACGCTGCCAGCATCGCCGCCGCCAGAGGAGAAATGTCTGAAGTAAGACCCCTCTCCAGAGACATCTTGATGGAGACCCTCCTGTATGAGCA
BIK-201_exon2	GACCCTCCTGTATGAGCAGCTCCTGGAACCCCCGACCATGGAGGTTCTTGGCATGACTGACTCTGAAGAGGACCTGGACCCTATGGAGGACTTCGATTCTTTGGAATGCATGGAGGGCAG
BIK-201_exon3	TTGGAATGCATGGAGGGCAGTGACGCATTGGCCCTGCGGCTGGCCTGCATCGGGGACGAGATGGACGTGAGCCTCAGGGCCCCGCGCCTGGCCCAGCTCTCCGAGGTGGCCATGCACAG
BIK-201_exon3	TGACGCATTGGCCCTGCGGCTGGCCTGCATCGGGGACGAGATGGACGTGAGCCTCAGGGCCCCGCGCCTGGCCCAGCTCTCCGAGGTGGCCATGCACAGCCTGGGTCTGGCTTTCATCTA
BIK-201_exon4	GCTTTCATCTACGACCAGACTGAGGACATCAGGGATGTTCTTAGAAGTTTCATGGACGGTTTCACCACACTTAAGGAGAACATAATGAGGTTCTGGAGATCCCCGAACCCCGGGTCCTGG
BIK-201_exon5	CCCCGGCGGCTCAGGGCGGGGCTGGCCCCACCCCCATGACCACTGCCCTGGAGGTGGCGGCCTGCTGCTGTTATCTTTTTAACTGTTTTCTCATGATGCCTTTTTATATTTAAACCCCGA
BOK-201_exon1	GGCGCCGGGGCGGGGCGCGCGTCCTCGCGGGTCTGAATGGAAGGGTCGAGGTCGTCGTCGGCGGCGAGCAGATCCTGAAGCCAGAACTCCACCCCGGCGCCCGCGCCATGCGGCGGGAGA
BOK-201_exon2	CGAGATCATGGACGCCTTTGACCGCTCGCCCACAGACAAGGAGCTGGTGGCCCAGGCCAAGGCGCTGGGCCGGGAGTACGTGCACGCGCGGCTGCTGCGCGCCGGCCTCTCCTGGAGCGC
BOK-201_exon4	GCATCACGTGGGGCAAGGTGGTGTCCCTGTATGCGGTGGCCGCGGGGCTGGCCGTGGACTGTGTGAGGCAGGCCCAGCCTGCCATGGTCCACGCCCTCGTGGACTGCCTGGGGGAGTTCG
BOK-201_exon5	GACCCTCCCCGCTTGTGTCCCTTCTCCTGTGATCTCTGTGTTTTCCCTTTTCTTTCTGGGGCCAGGAAGTCAGGGTCAACTCCCAGGCCTCAGATGCAGGGGCCCAGAACACCTGCTCTC
BOK-201_exon5	GGTGGGCCATGTGCCAGGACAGGAGGGTCCCGGCGGAAAGCCAGCCCCGGACTCATCGTGACATTGAGATCCCACTGGAGGGTAGGGGTGGTAATAAACTTCTCCAAACGATCGTTGTCA
BOK-202_exon1	CGTGAGGCTGCTTTTCTGTGACTCGGAACCAGCGCACCCCATCGCTCACTGCAGGCGATGAGCTGGAGATGATCCGGCCCAGCGTCTACCGCAACGTGGCGCGTCAGCTGCACATCTCCC
BOK-202_exon2	TGGAGATGATCCGGCCCAGCGTCTACCGCAACGTGGCGCGTCAGCTGCACATCTCCCTGCAGTCTGAGCCTGTGGTGACCGATGCGTTCCTGGCCGTGGCTGGCCACATCTTCTCTGCAG
BOK-AS1-201_exon1	CGCGGGCGCCGGGGTGGAGTTCTGGCTTCAGGATCTGCTCGCCGCCGACGACGACCTCGACCCTTCCATTCAGACCCGCGAGGACGCGCGCCCCGCCCCGGCGCCCGCCCCGTCCACGCC

BOK-AS1-201_exon2	GGCCTCCAGAGGAACCAGCGCTGCCGACTCCTTGATTCTAACCCACTGAGGCCTATTTTGGATTTCTGCACCCCAGAACTGTGGGAGAGTAAATTGTGCTGTTGAAGCCACCACATTTGT
HRK-201_exon1	GGCTGTGCGCGGCCGCGCAGGTGGCGGCGCTGGCGGCCTGGCTGCTCGGCAGGCGGAACTTGTAGGAACGCGGGGCTTCTTGGTGGGGCCGGAGCCGAGACCCAGCCGGAGCGAGCAACA
HRK-201_exon2	GTTGGTGAAAACCCTGTGTCCTTGGAGAAAGCTGGTTCCCGTTTTCCAGAGGGGGAGCCCAGAGCTTGAAAGGCCGCGGTTGGCACTTCGAGAAGGAAGTGGAGAGTAAAGACAGCGCCT
HRK-201_exon2	TCTGTGCAGGATACCACACACTGCCATTTTCAAAGCCGAGGTGGCGAGGTGTCAGGCTGCAGATTCGGACGGTCATTCTCCAAGGCTGGATTTGCAGGTCACCACCCGGTACCTATAGAC
HRK-201_exon2	TTCCCCTGGAGGATACAAACTCCAAACGCTGGGGTTGGCATTTTGGGTGATTTTGATTTCAATGAAGCCACTTTGCTGAGAGAACTGGGGCACCCACGACCTCCTGATAGAGCTTCTCAG
HRK-201_exon2	AGATGAAGAGACTTTTGCCTCTTCATTTCTGATGGTGCTGCTTGCTCTCAGAGAGTGGGGAGCCAGGAACCGCTGGGACTGGAGCCCCCGGGACTTCAACACTCCGAATGAGATCCAGTC
HRK-201_exon2	TCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCGAGCTCAGCTCACTGCAACCTCCACCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCAC
HRK-201_exon2	AAGGTCTTTGCACTATAAGCGCCAAGGAGCCCGTGTGCGTGGCAGGGGCGGCTGGGAGGGTATCTGGAGAACCTTAGTGAGGCCTCTGGCCTAGCCAGAGAGGCAATAAGCTTGGGGACG
HRK-202_exon1	GCGGCCGCGCAGGTGGCGGCGCTGGCGGCCTGGCTGCTCGGCAGGCGGAACTTGTAGGAACGCGGGGCTTCTTGGTGGGGCCGGAGCCGAGACCCAGCCGGAGCGAGCAACAGCCTACAT
HRK-202_exon2	CCGGAGCCGAGACCCAGCCGGAGCGAGCAACAGCCTACATCTGACCTCAGAATACCAGCCGCTCCGGCCTTTCTTGTGCTTTTGATTTAATTTGGGGAAACTCATTTTTTCCCAGCTCTG
HRK-202_exon2	CCTACATCTGACCTCAGAATACCAGCCGCTCCGGCCTTTCTTGTGCTTTTGATTTAATTTGGGGAAACTCATTTTTTCCCAGCTCTGAGCCCCAGGGGAGGCTCCTCTGAGGCTGGGGAG
HRK-202_exon3	CCCAGCTCTGAGCCCCAGGGGAGGCTCCTCTGAGGCTGGGGAGGCCTGGAGGAGGATGGGTATGATTTAACCAGTCAATACTCAAAGATACAGGAGAGAGGGAACAAAAGACGCTTTATG
HRK-202_exon3	AGCCCCAGGGGAGGCTCCTCTGAGGCTGGGGAGGCCTGGAGGAGGATGGGTATGATTTAACCAGTCAATACTCAAAGATACAGGAGAGAGGGAACAAAAGACGCTTTATGGTGGTTGAGA
HRK-202_exon4	GTGGTTGAGATCTTCCCATGTCAACACGCAAAGGTTTTCCTCATCCTTTTTAATGGCTGCATGATGTTCTGTTGCTTGGATGAACCAGGATTTCCTTATATGGTCACTTCCTTGGGAACA
HRK-202_exon5	TGTGTCCTTGGAGAAAGCTGGTTCCCGTTTTCCAGAGGGGGAGCCCAGAGCTTGAAAGGCCGCGGTTGGCACTTCGAGAAGGAAGTGGAGAGTAAAGACAGCGCCTGGAGCGATCGTAGA
HRK-203_exon1	GCTGCCCAATCCCAGGGACAGGAAGAACATTTTGGATGGATCGCGGGGTGCAGAAAAAGGAAGTTGAGCGACAGACGCGAAGCCCAAAGCGTGGAATTTGGGAAGAGGCAGAAAAAAAGT
HRK-204_exon1	TTTGATTTAATTTGGGGAAACTCATTTTTTCCCAGCTCTGAGCCCCAGGGGAGGCTCCTCTGAGGCTGGGGAGGCCTGGAGGAGGATGGGTATGATTTAACCAGTCAATACTCAAAGATA
HRK-204_exon2	AGCCCCAGGGGAGGCTCCTCTGAGGCTGGGGAGGCCTGGAGGAGGATGGGTATGATTTAACCAGTCAATACTCAAAGATACAGGAGAGAGGGAACAAAAGACGCTTTATGGGAAGCTTCA
HRK-204_exon3	GGAAGCTTCATGGAAAGGGACATGAATTTTGGAGTCAGGCCGACTTTCACATCACTTTCTCCATCTCGCATTTGCCAGTTGTGTGACCTTAGGCCGATCCCATTACCTTCTGAGCCTTGG
MCL1-201_exon1	AACACCAGTACGGACGGGTCACTACCCTCGACGCCGCCGCCAGCAGAGGAGGAGGAGGACGAGTTGTACCGGCAGTCGCTGGAGATTATCTCTCGGTACCTTCGGGAGCAGGCCACCGGC
MCL1-202_exon1	ACTTCTCACTTCCGCTTCCTTCCAGTAAGGAGTCGGGGTCTTCCCCAGTTTTCTCAGCCAGGCGGCGGCGGCGACTGGCAATGTTTGGCCTCAAAAGAAACGCGGTAATCGGACTCAACC
MCL1-202_exon3	ATTATAAAATGATGGCTTGGAAAAGCAGGCTAGTCTAACCATGGTGCTATTATTAGGCTTGCTTGTTACACACACAGGTCTAAGCCTAGTATGTCAATAAAGCAAATACTTACTGTTTTG
MCL1-202_exon3	AGTGGTGGGTTTATAGGGGGAGGAGGAGGCAGGTGGTCTAAGTGCTGACTGGCTACGTAGTTCGGGCAAATCCTCCAAAAGGGAAAGGGAGGATTTGCTTAGAAGGATGGCGCTCCCAGT
MCL1-203_exon1	CGCCGCGGGTGGGCAGGCGAATCTTGCGCCGGTTTAGACAAAGGAGGCCGTGAGGACCTGCATGCTTTTCTTTCTCAGGCATGCTTCGGAAACTGGACATCAAAAACGAAGACGATGTGA
MCL1-204_exon1	CCTAAAACCGTGATAAAGGAGCTGCTCGCCACTTCTCACTTCCGCTTCCTTCCAGTAAGGAGTCGGGGTCTTCCCCAGTTTTCTCAGCCAGGCGGCGGCGGCGACTGGCAATGTTTGGCC
MCL1-204_exon2	GCCACCGGCGCCAAGGACACAAAGCCAATGGGCAGGTCTGGGGCCACCAGCAGGAAGGCGCTGGAGACCTTACGACGGGTTGGGGATGGCGTGCAGCGCAACCACGAGACGGCCTTCCAA
MCL1-204_exon3	GCATGCTTCGGAAACTGGACATCAAAAACGAAGACGATGTGAAATCGTTGTCTCGAGTGATGATCCATGTTTTCAGCGACGGCGTAACAAACTGGGGCAGGATTGTGACTCTCATTTCTT
MCL1-204_exon4	GATGGGTTTGTGGAGTTCTTCCATGTAGAGGACCTAGAAGGTGGCATCAGGAATGTGCTGCTGGCTTTTGCAGGTGTTGCTGGAGTAGGAGCTGGTTTGGCATATCTAATAAGATAGCCT
MCL1-204_exon4	TGGCTTGGAAAAGCAGGCTAGTCTAACCATGGTGCTATTATTAGGCTTGCTTGTTACACACACAGGTCTAAGCCTAGTATGTCAATAAAGCAAATACTTACTGTTTTGTTTCTATTAATG
MCL1-204_exon4	GACTGTGGAAATACAGACAAGGATCTTAGTTGATATTTTGGGCTTGGGGCAGTGAGGGCTTAGGACACCCCAAGTGGTTTGGGAAAGGAGGAGGGGAGTGGTGGGTTTATAGGGGGAGGA
PMAIP1-201_exon1	CGTGTGTAGTTGGCATCTCCGCGCGTCCGGACACCCGATCCCAGCATCCCTGCCTGCAGGACTGTTCGTGTTCAGCTCGCGTCCTGCAGCTGTCCGAGGTGCTCCAGTTGGAGGCTGAGG
PMAIP1-201_exon2	CCAAGCCGGATTTGCGATTGGGATGCAGCTGCGTTTCACCAGGGGCAAAAAGCTCCTTTCCTCCTCTCTTTCCTCCTCGCCACTTGCCCTTCCCCGGGGCCACGAGGAACAAGTGCAAGT
PMAIP1-201_exon3	GCCTACTGTGAAGGGAGATGACCTGTGATTAGACTGGGCGGCTGGGGAGAAACAGTTCAGTGCATTGTTGTTGTTGCTGTTTTTGGTGTTTTGCTTTTCAGTGCCAACTCAGCACATTGT
PMAIP1-202_exon1	AGGGAAGTTCTCACTGGACAAAAGCGTGGTCTCTGGCGCGGGGATCTCAGAGTTTCCCGGGCACTCACCGTGTGTAGTTGGCATCTCCGCGCGTCCGGACACCCGATCCCAGCATCCCTG
PMAIP1-202_exon2	AGCTGGAAGTCGAGTGTGCTACTCAACTCAGGAGATTTGGAGACAAACTGAACTTCCGGCAGAAACTTCTGAATCTGATATCCAAACTCTTCTGCTCAGGAACCTGACTGCATCAAAAAC
PMAIP1-202_exon2	CAGATGATCTTTCATTCAATGTGTTCCTGTTGGGCGTTACTAGAAACTATGGAAAACTGGAAAATAACTTTGAAAAAATTGGATAAAGTATAGGAGGGTTACTTGGGGCCAGTAAATCAG
PMAIP1-203_exon1	GCGCGTCCGGACACCCGATCCCAGCATCCCTGCCTGCAGGACTGTTCGTGTTCAGCTCGCGTCCTGCAGCTGTCCGAGGTGCTCCAGTTGGAGGCTGAGGTTCCCGGGCTCTGTAGCTGA
PMAIP1-203_exon2	TCCTTTCCTCCTCTCTTTCCTCCTCGCCACTTGCCCTTCCCCGGGGCCACGAGGAACAAGTGCAAGTGTAGGCGGCTGTCTCTAGGAGAAAGTCATTGTCGCGGCAGAAGGGGCAGGAGA