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Supplementary Information for

SF3B1 mutant-induced missplicing of MAP3K7 causes anemia in myelodysplastic syndromes

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Supplementary Information Text

Supplemental Materials and Methods

Generation of knock-in cell lines using CRISPR/Cas9 genome editing

The SF3B1 K700E and U2AF1 S34F mutations along with silent mutations were knocked into K562 cells using CRISPR/Cas9 technology as previously described (33). For true isogenic controls, only the silent mutations were knocked into K562 cells to generate independent WT control cell lines. The human SF3B1 CRISPR guide RNA was 5'-TGGATGAGCAGCAGAAAGTTcgg-3'. The singlestranded oligodeoxynucleotides (ssODNs, Integrated DNA Technologies) for WT and K700E SF3B1were 5’-AATGTTGGGGCATAGTTAAAACCTGTGTTTGGTTTTGTAGGTCTTGTGGATGAGCAGCAGAAAGTGCGCACCATCAGTGCTTTGGCCATTGCTGCCTTGGCTGAAGCAGCAACTCCTTATGGTATCGAAT-3’ and 5’-AATGTTGGGGCATAGTTAAAACCTGTGTTTGGTTTTGTAGGTCTTGTGGATGAGCAGCAGGAAGTGCGCACCATCAGTGCTTTGGCCATTGCTGCCTTGGCTGAAGCAGCAACTCCTTATGGTATCGAAT-3’, respectively. SF3B1 mutation knock-in was confirmed using PCR amplification of genomic DNA (forward primer:5’-GTTGATATATTGAGAGAATCTGGATG-3’; and reverse primer: 5’-AAATCAAAAGGTAATTGGTGGA-3’) and DNA sequencing. The human U2AF1 CRISPR guide RNA was 5’-AAAATTGGAGCATGTCGTCATGG-3’ and the mutant ssODN was 5’-ttacagagtc aac tgt tca ttt tat ttc aaa att gga gca tgt cgt cat gga gac Cgg tgc tTt cgg ttg cac aat aaac cgacgtttag ccaggtttgt ttgccttttttcatgtaaa ttataaaaac-3’. U2AF1 mutation knock-in was confirmed using PCR amplification of genomic DNA (forward primer: 5’- TGCTGCTGACATATTCCATGT-3’; and reverse primer: 5’-AGTCGATCACCTGCCTCACT -3’) and DNA sequencing.

MAP3K7 expression constructs

5’ hemagglutinin (HA) tag-containing MAP3K7 forward primer (5’-cagtGGGCCCaccATGTACCCATACGATGTTCCAGATTACGCTAGCGGCCGCATGTCTACAGCCTCTGCCG-3’) and its reverse primer (5’-ATAggatccTCATGAAGTGCCTTGTCGTTTC-3’) were used to amplify MAP3K7 from pDONR223-MAP3K7 plasmid (Addgene plasmid #23693) and cloned into the NotI and BamHI sites of lentiviral vector pHIV-Zsgreen (Addgene plasmid #18121) to generate the pHIV-Zsgreen-5’HA tagged MAP3K7 construct. pLKO.1-eGFP was generated from pLKO.1-puro (Sigma) by replacing the coding sequence of the puromycin resistance gene with that of eGFP using restriction sites BamHI and KpnI (5’CGCGGATCCACCGGAGCTTACCATGGTGAGCAAGGGCGA-3’; 5’- GGGGCGGGCGTTACTTGTACAGCTCGTCCATG-3’). Short hairpin RNAs (shRNAs) for negative controls and for targeting mRNAs of MAP3K7 were each cloned into pLKO.1-eGFP plasmid. The shRNA sequences were: shNegative Control #1, 5’-ccgg CAACAAGATGAAGAGCACCcctctcaacactggGGTGCTCTTCATCTTGTTGtttttg-3’; shNegative Control #2, 5’-ccggTTCTCCGAACGTGTCACGTcctctcaacactgg ACGTGACACGTTCGGAGAAtttttg-3’; shMAP3K7 #1, 5’-ccgg CCTGAAACCACCAAACTTAcctctcaacactggTAAGTTTGGTGGTTTCAGGtttttg-3’; shMAP3K7 #2, 5’-ccggCATGCAACCCAAAGCGCTAcctctcaacactgg TAGCGCTTTGGGTTGCATGtttttg-3’; shMAP3K7 #3, 5’-ccggGTGTTTACAGTGTTCCCAA cctctcaacactggTTGGGAACACTGTAAACACtttttg-3’; shMAP3K7 #4, 5’-ccggTGGCTTATCTTACACTGGAcctctcaacactgg TCCAGTGTAAGATAAGCCAtttttg-3’; shMAP3K7 #5, 5’-ccgg GAGGAAAGCGTTTATTGTAcctctcaacactggTACAATAAACGCTTTCCTCtttttg-3’; shMAP3K7 #6, 5’-ccggCCCAATGGCTTATCTTACAcctctcaacactgg TGTAAGATAAGCCATTGGGtttttg-3’. All PCR-amplified products were confirmed by DNA sequencing, and all plasmids were validated by digestion with multiple restriction enzymes and partial DNA sequencing.

Viral production

For the re-expression and KD studies, lentiviral pHIV-Zsgreen encoding MAP3K7 and pLKO.1_eGFP lentiviral vectors containing the six MAP3K7 shRNAs or negative control shRNAs were constructed as described above. Lentiviral vectors, along with the packaging plasmid PsPAX2 (Addgene #12260) and the envelope plasmid pCMV-VSV-G (Addgene #8454), were co-transfected into HEK293T cells that were cultured in Dulbecco’s Modified Eagle’s Medium (Gibco, cat # 11965092) supplemented with 10% FBS (VWR Seradigm, cat # 89510-186) in a 37ºC, 5% CO_2 incubator. Viral supernatant was harvested at 48h and 72h to transduce cell lines and human CD34+ cells using standard protocols. Cells were sorted for GFP positivity before proceeding with the assays (see more details below).

Purification, erythroid induction culture, and transduction of human CD34+ cells

Human CD34+ cells were purified from adult peripheral whole blood (LeukoPaks) by positive selection using microbeads magnetic cell separation system (Miltenyi Biotec, Cat # 130-100-453), according to the manufacturer’s instructions. The purity of the isolated CD34+ cells was greater than

95%. CD34+ cells were induced to erythroid differentiation using three phase-culture media cocktails, containing various amount of erythropoietin, as previously described (2). Transduction of human CD34+ cells with viruses was performed using a method we previously published(3). The cells were cultured in a 37ºC, 5% CO_2 incubator.

Erythroblast staging analysis

Healthy and MDS BM aspirates were analyzed for the four erythroblast stages (proerythroblast, basophilic normoblast, polychromatophilic normoblast, and orthochromatic normoblast) using a previously published method(2). Briefly, BM aspirates were separated on a Ficoll (GE Healthcare) density gradient, and the purified mononuclear cells were incubated with CD45 microbeads (STEMCELL Technologies) for negative selection according to the manufacturer's instructions. CD45 negative cells were stained with antibodies to detect three erythroid surface markers (GPA, Integrin Alpha4, Band 3), then flow cytometric analyzed, and quantified as previously described (2).

Fluorescence-activated cell sorting of cultured and CD34+ cells

Cells were washed and resuspended in PBS containing 0.5% BSA. The virally-transduced human CD34+ were sorted for GFP reporter expresssion on a MoFlo high-speed cell sorter (Beckman-Coulter) located at the New York Blood Center, NY. Transduced cultured cells were sorted for GFP on an Influx cell sorter (BD Biosciences) or BD FACSAriaII sorter (BD Biosciences) at Columbia University Irving Medical Center.

Western blot analysis

Whole-cell lysates of cultured cells or MDS BM MNCs were prepared with standard radioimmunoprecipitation assay buffer in the presence of protease (Sigma, cOmplete) and phosphatase (Sigma, PhosSTOP) inhibitor cocktails. Protein concentration was measured using Bio-Rad Protein Assay. Protein lysates (15-25 ug) were run on Novex Tris-Glycine gels (Invitrogen) and transferred to nitrocellulose membranes (Bio-Rad), followed by immunoblotting with primary and secondary antibodies using standard methods. Bands were measured and quantified using ImageJ (NIH) or ImageQuant (Molecular Dynamics) softwares. All antibodies used were as follow: anti-

MAP3K7 (Cell Signaling, 4505S), anti-p38 MAPK (Cell Signaling, 8690T), anti-p-p38 MAPK (T180) (Cell Signaling, 4511S), anti-p-NF-kappaB p65 (Cell Signaling, 3033P), anti-GATA-1 (Cell Signaling, 3535T), anti-p-HSP27 (Cell Signaling, 9709T), anti-p-MAPKAPK-2 (MK2; T334) (Cell Signaling, 9595T), anti- α-Tubulin (Cell Signaling, 3007T), anti-p-SAPK/JNK (T183/Y185) (Cell Signaling, 9255S), anti-p-ERK1/2 (Bethyl, A303-608A-T), anti-K700E SF3B1 (Bethyl, custom made), anti-SF3B1 (Bethyl, A300-996A), anti-beta-Actin (Sigma, A3853), anti-GAPDH (Sigma, G9545), and anti-HA (Sigma, H3663)

RT-PCR and qPCR

One microgram of RNA was used for reverse transcription using Invitrogen's SuperScript III First-Strand kit with the provided oligo-dT (ThermoFisher, cat # 18080-051). For qPCR, transcript levels were measured using SYBR Green qPCR (Applied Biosystems, cat # 4367659). Relative RNA levels in whole-cell lysates were determined by normalizing expression levels of the target genes to expression levels of GAPDH. For RT-PCR, PCR was carried out using EconoTaq PLUS GREEN 2x master mixes (Lucigen) and primers for target genes and control housekeeping genes. RT-PCR primers used are the following: SF3B1 5'-gctgtgtgcaaaagcaagaa-3' and 5'-agccaaaccctttcctctgt-3'; MAP3K7 5'-GTGAGATGATCGAAGCCCCT-3' and 5'- CAGCACCATGCAGCACATTA-3'. qPCR primers used are as follow: GAPDH 5'-CTGACTTCAACAGCGACACC-3' and 5'-CCCTGTTGCTGTAGCCAAAT-3'; LDB1 5'-TGTCACGCCACAAGACCTAC-3' and 5'-GGAGAGGGCGAAGGTGCTA-3'; HSPA5 5'-GAAAGAAGGTTACCCATGCAGTTG-3' and 5'-CATTTAGGCCAGCAATAGTTCCAG-3'; c-MYC 5' -CGTCTCCACACATCAGAGCACAA-3' and 5'-GCAGCAGGATAGTCCTT-3'; c-MYB 5'-GAAAGCGTCACTTGGGGAAAA-3' and 5'-TGTTCGATTCGGGAGATAATTGG-3'; and EKLF1 5'-ATGACTTCCTCAAGTGGTGG-3' and 5'-CTCTCATCGTCCTCTTCCTC-3'.

siRNA transfection

siRNA transfections of K562, TF1a, and K052 suspension cells were carried out using the Neon Transfection System (Thermo Fisher Sci) with the Neon 100uL tip kit that includes the R buffer for electroporation (Thermo Fisher Sci). One million cells were resuspended in 100uL of R buffer, containing 1uL of 100uM siRNAs. Transfection was performed following the manufacture's protocol. Electroporated cells were immediately placed in 2mL complete media for 24h. After 24h, an additional 8mL of complete media was added to the 2mL cells for 24h. Cells were harvested for subsequent assays. For GATA1 KD, 17.5-18.5h hemin (50uM final)-pretreated K562 cells were used for electroporation. Transfected cells were immediately put into 2mL complete media containing 50uM hemin for 24h. After 24h, an additional 13mL of 50uM hemin complete media was added to the cells for 32h before cells were harvested for analysis. The siRNA sequences used are as follow: Negative Control siC1 from Sigma Universal Negative Control #1 (SIC001); Negative Control siC2 from mit.edu/sirna (GL3 #1008); Negative Control siC3 from mit.edu/sirna (siRL3 #1001); siMAP3K7#1 from Sigma, NM_003188 SASI_Hs01_00234777 CCTGAAACCACCAAACTTAdTdT; siMAP3K7#2 from Sigma, NM_003188 SASI_Hs01_00234778 CATGCAACCCAAAGCGCTAdTdT; siMAP3K7#3 from Sigma, NM_003188 SASI_Hs02_00335227 GTGTTTACAGTGTTCCCAAdTdT; siGATA1#1 from Sigma, NM_002049 SASI_Hs01_00092060 GGAUGGUAUUCAGACUCGAdTdT; siGATA1#2 from Sigma, NM_002049 SASI_Hs01_00092059 CCAAGAAGCGCCUGAUUGUdTdT.

Flow cytometric analysis

Cells were washed with PBS containing 0.5% bovine serum albumin (BSA). After blocking with 0.4% human AB serum for 10 minutes on ice, cells were stained with fluorochrome-conjugated antibodies in PBS/0.5% BSA for 15 minutes at 4°C. Cells were washed once with PBS/0.5% BSA before analysis. When Annexin V analysis was performed, cells were washed with 1x Annexin V binding buffer (Biolegend, Cat #422201) instead. Cells were subsequently stained with Fluorochrome-conjugated Annexin V in 1x Annexin V binding buffer according to manufacturer's protocol. Cells were immediately analyzed on a FACSCalibur (Becton Dickinson) or LSRFortessa (BD Biosciences) cell analyzer. FACS files were analyzed using FlowJo software (FlowJo, LLC). FACS antibodies used were the following: anti-human CD235a (GPA) PE (Biolegend, 349106), anti-Annexin V APC (Biolegend, 640941), anti-CD45 APC-Cy7 (Biolegend, 304014), anti-human CD71 (Biolegend, 151204), anti-Annexin V Pacific Blue (Biolegend, 640917), anti-Ki67 AF488 (Biolegend, 151204), 7AAD (BD

Pharmingen, 559925), anti-alpha4 integrin/CD49d PE (Miltenyi Biotec, 130-118-548), anti-CD235a-PC7 (PE-Cy7) (Beckman Coulter, A71564), and anti-Band 3 APC (made by Xiuli An's lab[26]).

Gene ontology analysis

To determine gene ontology pathways that could potentially be affected by abnormal splicing in *SF3B1* mutant cells. To this end, we first performed standard enrichment analysis using GO David online tools. The input is a list of genes associated with significant aberrant splicing events between mutant and wild-type by satisfying: 1) significantly more frequently used in mutant with *q*-value <0.05; and 2) associated with a distance <50 bp upstream of the canonical 3'ss.

RNAseq coverage plots of cryptic 3'ss

We used Integrative Genomics Viewer (IGV) (1) to visualize usage of cryptic 3'ss of gene junctions. For different *SF3B1* mutation comparisons, we downloaded MDS RNASeq data from NCBI Sequence Read Archive (GSE85712 (2); GSE63569 (3)).

Intracellular Ki67 staining

Day 3- hemin-treated cells were washed and stained with GPA-PE surface marker as described above. Cells were then washed, fixed and stained for intracellular Ki67 following BD Pharmingen's procedure for FITC BrdU Flow Kit with two modifications: DNase treatment step was omitted and Ki67-AlexaFluor488 (Biolegend) was used instead of anti-BrdU FITC.

Supplemental Figures and Legends

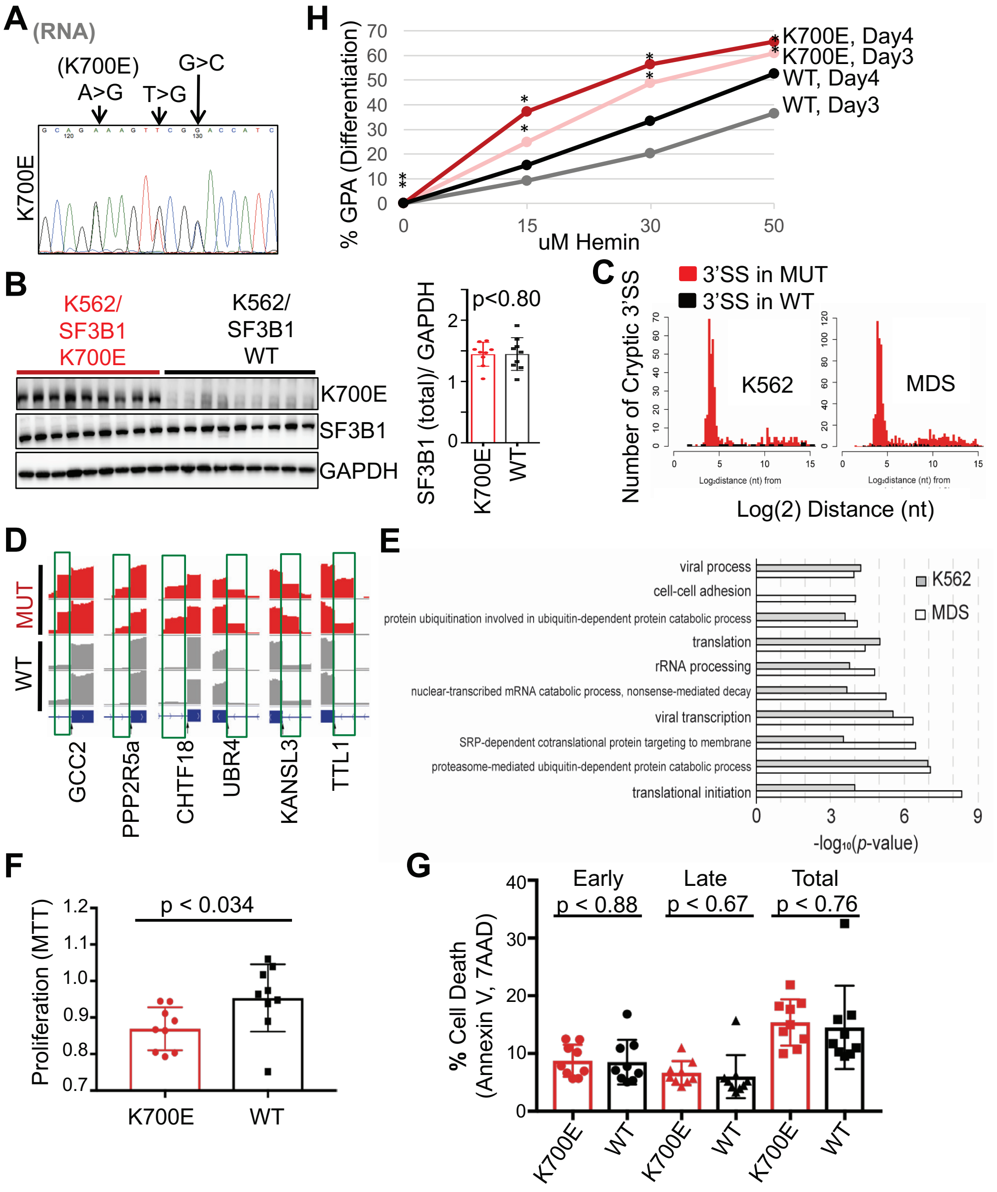

Fig. S1. Characteristics of K562/SF3B1 K700E and WT CRISPR clones (A) DNA chromatogram of RT-PCR products from a representative K562/SF3B1 mutant clone, demonstrating the stable expression of K700E and two silent mutations in *SF3B1* mRNA. (B) Left panel, representative WB images showing expression of total SF3B1, K700E mutant SF3B1, and loading control GAPDH in the nine independent K700E mutant and nine independent WT K562/SF3B1 clones. Right panel, bar graph displaying the results of ImageJ-quantified, GAPDH-normalized total SF3B1 band intensity and p-value from t-test. (C) Image showing Log_2 distance in nucleotides from cryptic 3'ss to corresponding canonical 3'ss from K562 cells (left panel) and MDS patients (right panel). (D) RNA-seq coverage plots of some examples of cryptic 3'ss-containing transcripts in two K562/SF3B1 K700E and two WT clones: (from left to right) *GCC2*, *PPP2R5A*, *CHTF18*, *UBR4*, *KANSL3* and *TTI1*. (E) Image displaying comparison of the top 10 enriched GO pathways determined from misspliced transcripts from SF3B1 mutant K562 cells (grey bar) and SF3B1 mutant MDS patients (white bar). Representative bar graphs quantifying (F) the relative proliferative capacity as measured by MTT assay (n=3 independent experiments) and (G) cell death as measured by FACS using AnnexinV and 7AAD (n=3 independent experiments) in SF3B1 mutant and WT K562 cells under normal growth conditions. p-values from t-tests are shown. (H) Bar graph showing the normalized percent GPA of Fig. 1E to 0 uM hemin. *, $p < 0.05$.

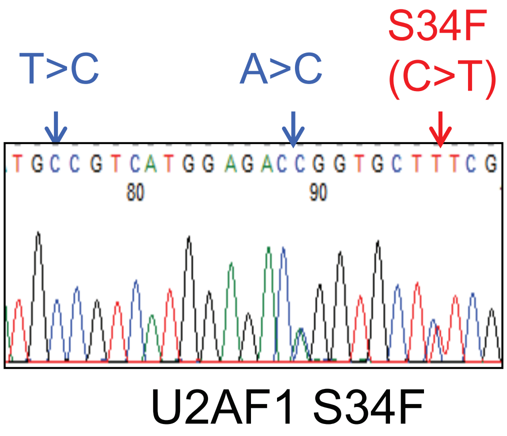

Fig. S2. Introduction of the hotspot *U2AF1* S34F mutation into K562 cells using CRISPR/Cas9. DNA chromatogram of representative K562/U2AF1 mutant clone, showing hotspot S34F and two silent mutations in the *U2AF1* gene by CRISPR.

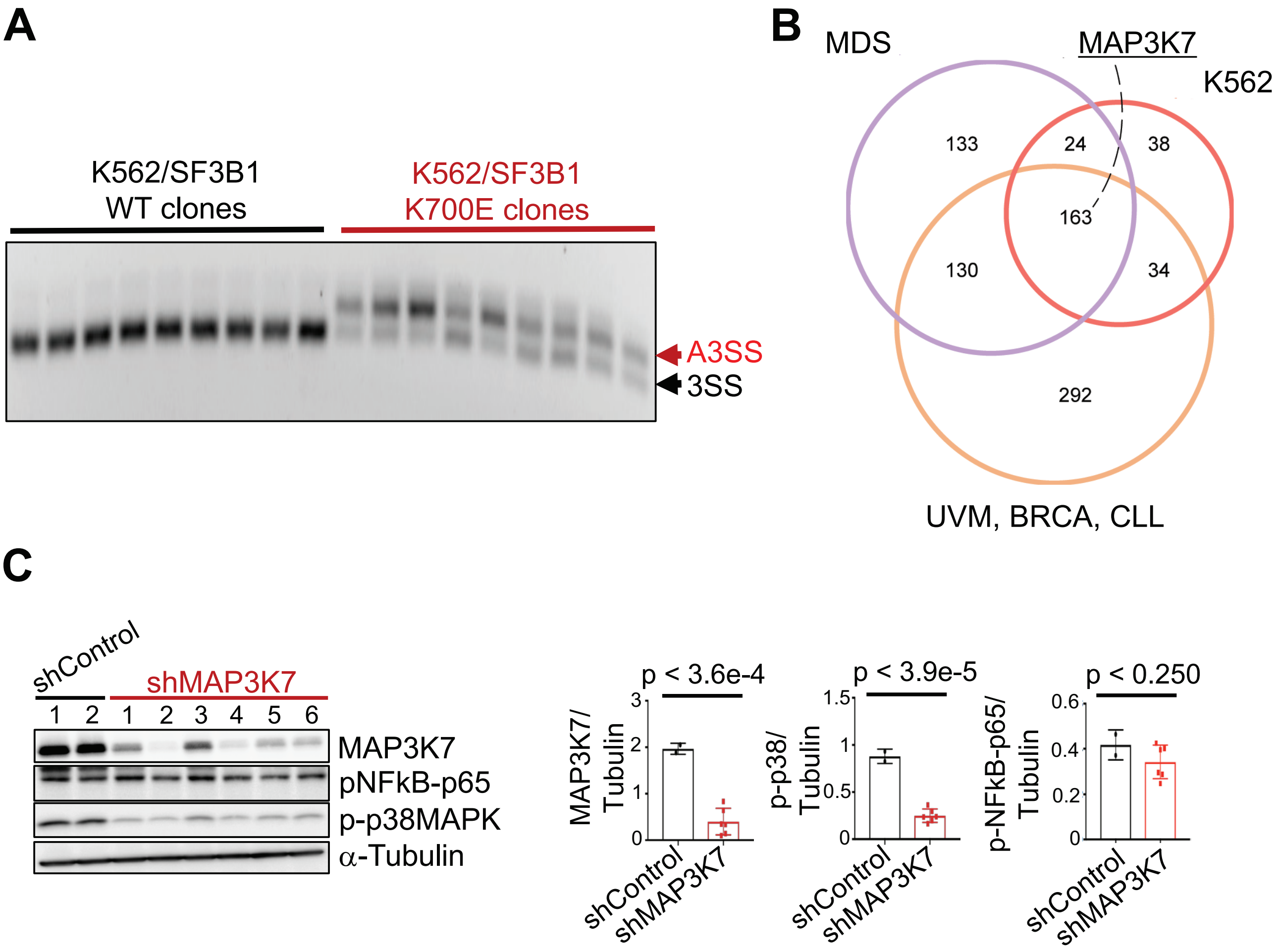

Fig. S3. *MAP3K7* is misspliced in mutant *SF3B1* cells from K562, MDS, and other cancers. (A) Image of RT-PCR gel showing 3'ss usage in mutant K562/SF3B1 cells. (B) Venn diagram showing the numbers of differentially spliced transcripts in mutant *SF3B1* samples from MDS, K562/SF3B1 and other cancers: uveal melanoma (UVM), breast carcinoma (BRCA), and chronic lymphocytic leukemia (CLL) (gene list of other cancers (4)). (C) Images (left) of representative WB analysis of GFP-sorted, shRNA-mediated MAP3K7 KD (two different negative control and six different MAP3K7 shRNAs) in parental K562 cells, and bar graphs (right) displaying the results of ImageJ-quantified, α-Tubulin-normalized phospho-NFkBp65, MAP3K7, and p-p38 band intensities in WB analysis are shown. p-values from t-tests are labelled on all bar graphs. n= 2 independent experiments.

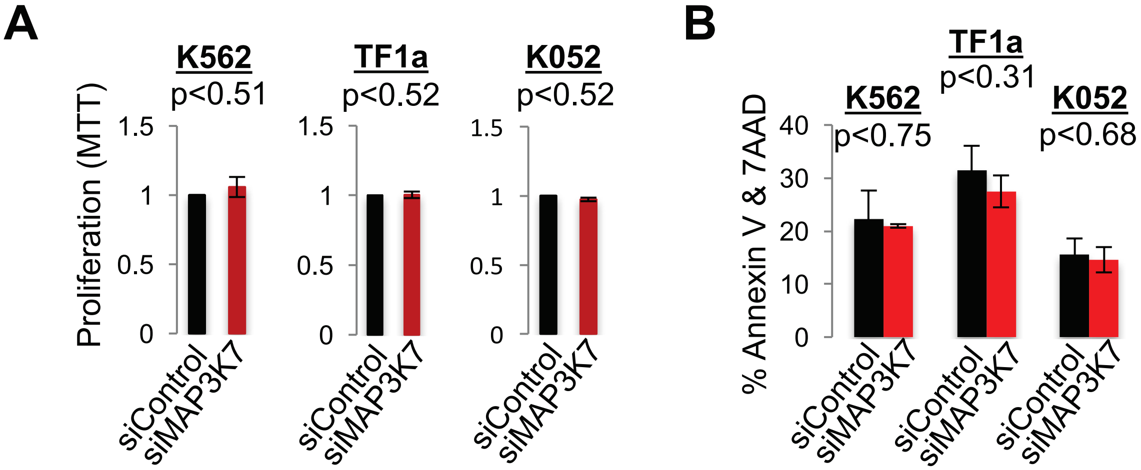

Fig. S4. Knockdown of *MAP3K7* in K562, TF1a, and K052 cells has no effects on proliferation and cell death under normal growth conditions but leads to increased erythroid development and erythroid cell death. Bar graphs quantifying (A) proliferation via MTT assay and (B) cell death via AnnexinV and 7AAD by FACS analysis of K562, TF1a, and K052 cells at 48h post-transfection with control (siControl #1) or MAP3K7 (siMAP3K7 #2) siRNAs under normal growth conditions. p-values from t-tests are shown. n=3 independent experiments.

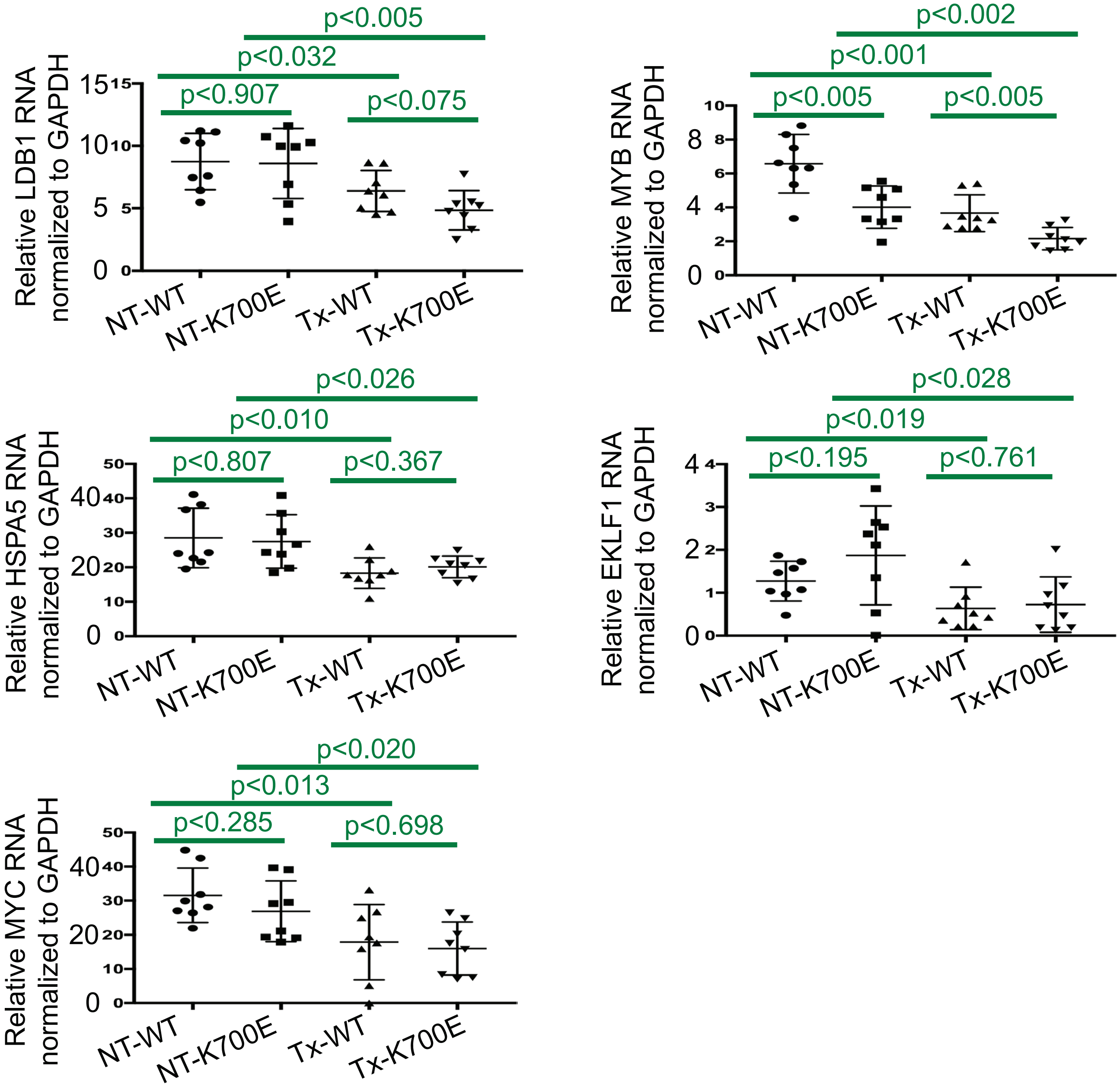

Fig. S5. Expression of several major transcription factors in erythroid differentiation of K562/SF3B1 cells. qPCR showing expression of several transcription factors (*LDB1*, *MYB*, *HSPA5*, *EKLF1*, *MYC*) that are known to play a role in erythroid differentiation. p-values from t-tests are shown.

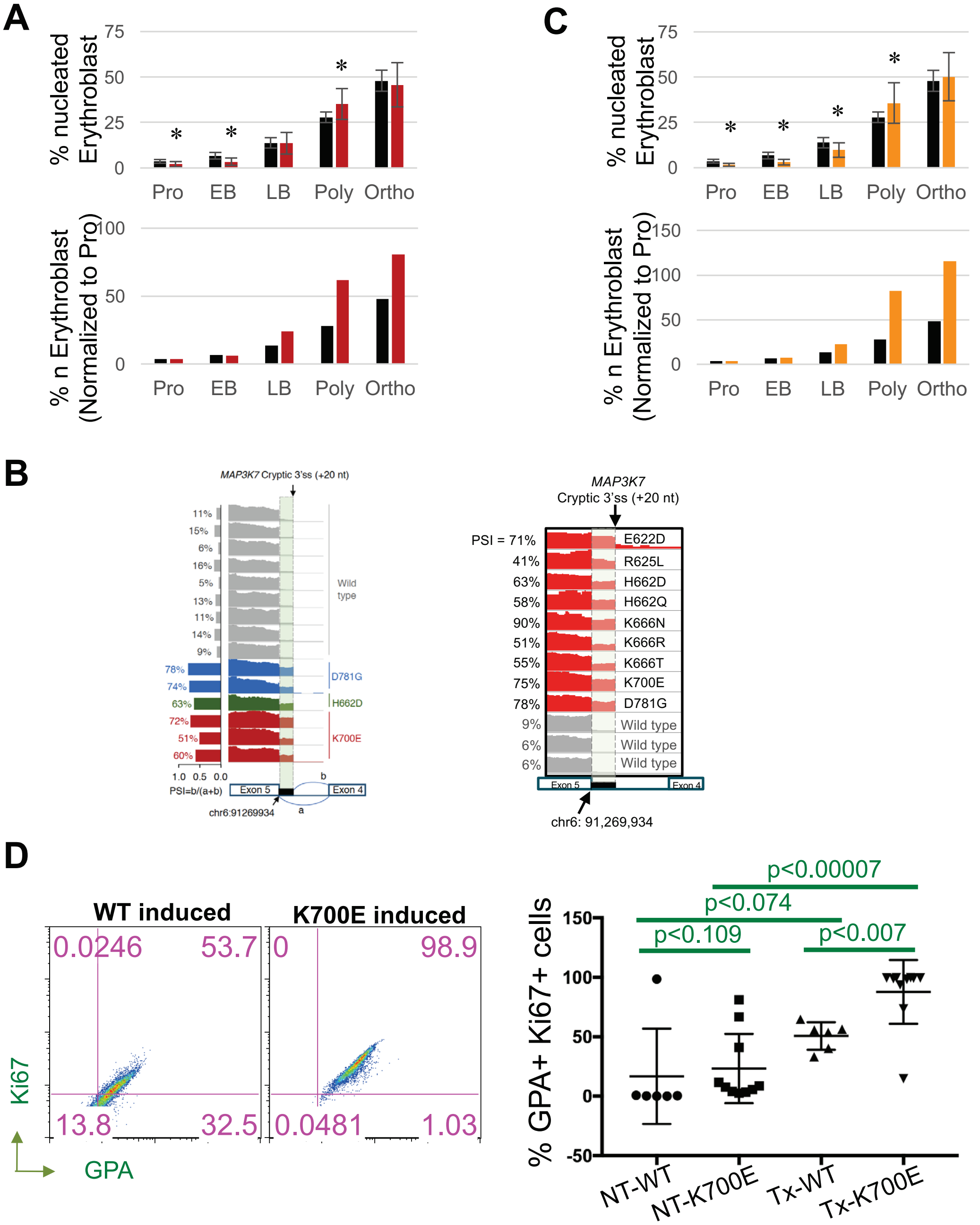

Fig. S6. Other MDS SF3B1 mutations, besides K700E, also cause *MAP3K7* missplicing and accelerated erythroid differentiation. Re-plotted MDS erythroblast profile data (5) using only normal healthy samples (n=16) and MDS samples (A) with K700E (n=15) and (C) with non-K700E SF3B1 mutations (n=14). The percentages of nucleated erythroid cells in each erythroblast stage are illustrated in the bar graphs. *, $p < 0.05$. Normalized-to-proerythroblast (Pro)-staged bar graphs are also shown for comparison. Pro, proethroblasts; EB, early basophilic erythroblasts; LB, late basophilic erythroblasts; Poly, polychromatic erythroblasts; and Ortho, orthochromatic erythroblasts. (B) RNA-seq coverage plots of *MAP3K7* cryptic 3'ss in MDS patients with different *SF3B1* hotspot mutations (MDS RNAseq data downloaded (left panel) (6) and (right panel) (2, 3)) and with no *SF3B1* mutations (wild-type). (C) Expression of proliferative marker Ki67 in mutant and WT K562/SF3B1 erythroid cells. FACS analysis of Ki67 vs. GPA expression in representative 50 uM hemin-induced day 3 K700E and WT cells. Results of multiple K700E and WT clones are summarized graphically. p-values from t-tests are shown. n=2 independent experiments.

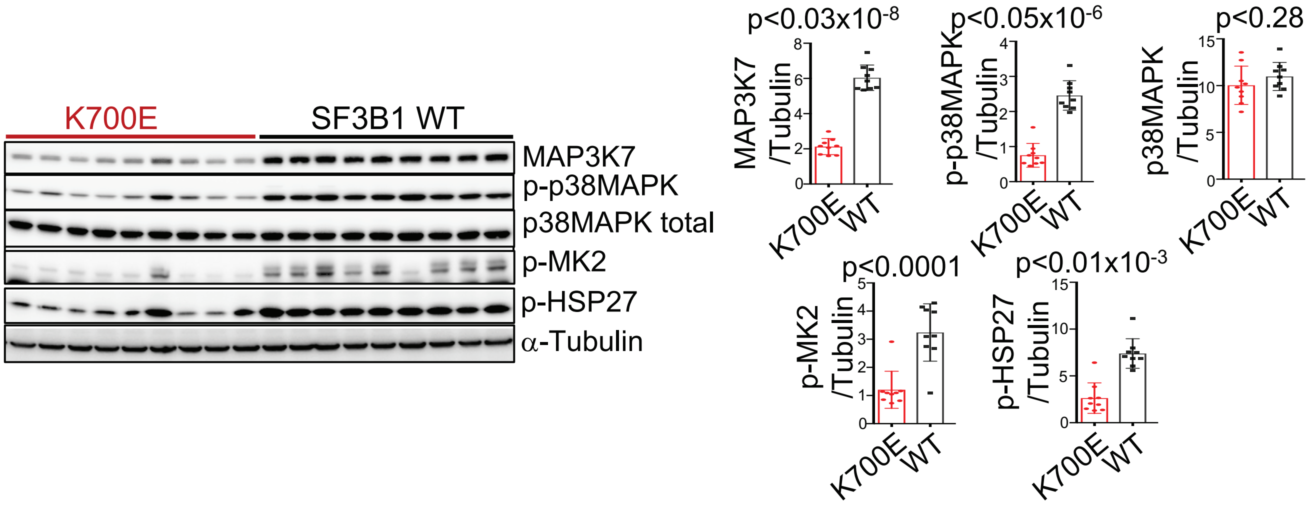

Fig. S7. Mutant SF3B1 cells display increased proliferative capacity and deactivation of p38 MAPK downstream effectors, MAPKAPK2 (MK2) and HSP27. (A) Representative WB images showing expression of p-MK2 and p-HSP27 in mutant and WT K562/SF3B1 clones. Bar graphs display the results of ImageJ-quantified, α-Tubulin-normalized protein band intensities and p-values from t-tests. n=3 independent experiments.

Table S1. Cryptic 3’ Splice Sites Differentially Used by Mutant 700E vs WT SF3B1 K562 Cells

statistics					inclusion_level			Gene	Locati	
pvalue	padj	MUT	WT	log2fold_MUT_WT	inclusion_level_WT	inclusion_level_MUT	inclu_diff_WT-MUT	Genename	transcripts	chrom
1.43E-06	0.00041	5.146	0.182	4.824	0.000	0.900	-0.900	LONP1	chr19:5717646-5719714:-	chr19
2.68E-13	2.88E-10	11.734	0.116	6.657	0.000	0.806	-0.806	PFDN5	chr12:53689726-53691607:+	chr12
6.13E-05	0.00956	4.974	1.100	2.178	0.050	0.780	-0.730	ORAI2	chr7:102074109-102076648:+	chr7
0.0002	0.02623	4.226	0.169	4.644	0.000	0.721	-0.721	CROCCP3	chr1:16803043-16803424:-	chr1
2.66E-05	0.00481	8.588	2.581	1.734	0.069	0.770	-0.701	IDUA	chr4:995352-995438:+	chr4
1.11E-05	0.00233	4.761	0.180	4.728	0.000	0.697	-0.697	NDUFB8	chr10:102276735-102286155:-	chr10
1.45E-20	3.33E-17	17.298	4.998	1.791	0.076	0.773	-0.697	MAP3K7	chr6:91269954-91271340:-	chr6
3.09E-18	6.14E-15	9.417	0.159	5.888	0.000	0.688	-0.688	SEPSECS	chr4:25158620-25160574:-	chr4
1.95E-21	5.00E-18	11.339	1.871	2.599	0.146	0.811	-0.665	CHTF18	chr16:843275-844033:+	chr16
0.0003	0.03114	5.042	1.470	1.779	0.043	0.708	-0.665	DZIP3	chr3:108403189-108405274:+	chr3
1.49E-07	5.50E-05	5.615	0.130	5.429	0.000	0.654	-0.654	EFTUD2	chr17:42929951-42930884:-	chr17
2.18E-05	0.00415	6.138	2.172	1.499	0.148	0.795	-0.647	ZNF41	chrX:47315814-47326808:-	chrX
6.03E-06	0.00139	5.003	0.121	5.371	0.000	0.635	-0.635	ADGRV1	chr5:89977272-89979392:+	chr5
6.94E-08	2.78E-05	7.800	1.606	2.280	0.044	0.673	-0.629	HERC2P2	chr15:23283431-23285704:-	chr15
4.90E-12	4.43E-09	7.412	0.162	5.514	0.000	0.616	-0.616	USP39	chr2:85848703-85850728:+	chr2
7.59E-05	0.01146	8.671	3.064	1.501	0.129	0.740	-0.611	CCDC66	chr3:56649301-56649931:+	chr3
6.29E-18	1.20E-14	11.441	2.152	2.410	0.081	0.688	-0.607	HIGD1A	chr3:42835782-42845927:-	chr3
1.11E-07	4.18E-05	7.339	1.969	1.898	0.044	0.646	-0.602	SH2D2A	chr1:156785905-156786466:-	chr1
1.92E-15	2.83E-12	9.306	0.134	6.118	0.000	0.590	-0.590	KANSL3	chr2:97285514-97297048:-	chr2
4.37E-27	1.81E-23	13.963	3.084	2.179	0.036	0.618	-0.582	VPS9D1-AS1	chr16:89778631-89779081:+	chr16
9.89E-15	1.34E-11	9.374	1.553	2.593	0.019	0.593	-0.574	GCC2	chr2:109102365-109102954:+	chr2
5.44E-14	6.59E-11	8.090	0.169	5.578	0.000	0.510	-0.510	MAN2A1	chr5:109181708-109183328:+	chr5
7.00E-90	2.09E-85	24.995	4.228	2.564	0.018	0.525	-0.507	MYL4	chr17:45300424-45300861:+	chr17
1.56E-07	5.71E-05	5.661	0.121	5.549	0.000	0.505	-0.505	ADGRV1	chr5:90000306-90001195:+	chr5
2.42E-05	0.00445	5.293	1.134	2.223	0.025	0.529	-0.504	CASD1	chr7:94157563-94162500:+	chr7
9.48E-20	2.11E-16	10.317	0.870	3.567	0.005	0.489	-0.485	TTI1	chr20:36631196-36634598:-	chr20
1.04E-28	4.94E-25	15.293	2.245	2.768	0.009	0.493	-0.484	DPH5	chr1:101458311-101460665:-	chr1
1.98E-10	1.31E-07	8.883	1.051	3.079	0.008	0.480	-0.473	ECT2	chr3:172479474-172480187:+	chr3
3.79E-08	1.62E-05	6.029	0.174	5.117	0.000	0.463	-0.463	CEP135	chr4:56874549-56875878:+	chr4
0.0001	0.01768	6.357	2.716	1.227	0.199	0.635	-0.437	SOCS2-AS1	chr12:93939175-93960519:-	chr12
0.0003	0.03667	5.401	1.044	2.372	0.012	0.442	-0.430	ZNF445	chr3:44492077-44492359:-	chr3
1.11E-08	5.36E-06	6.853	1.115	2.620	0.013	0.427	-0.414	SMURF2	chr17:62574713-62576906:-	chr17
3.52E-10	2.25E-07	7.657	0.135	5.831	0.000	0.404	-0.404	TPP2	chr13:103297360-103298629:+	chr13
3.10E-17	5.64E-14	9.818	1.331	2.883	0.006	0.404	-0.398	VARS2	chr6:30884737-30884871:+	chr6
6.93E-12	5.90E-09	7.410	0.155	5.579	0.000	0.385	-0.385	NDRG3	chr20:35282127-35284762:-	chr20
3.10E-08	1.34E-05	6.208	0.138	5.497	0.000	0.381	-0.381	UQCC1	chr20:33934265-33934966:-	chr20
1.75E-43	1.86E-39	19.202	4.096	2.229	0.017	0.398	-0.380	OXA1L	chr14:23237381-23238985:+	chr14
1.30E-09	7.29E-07	7.908	1.704	2.215	0.024	0.404	-0.379	CCDC74A	chr2:132288401-132289210:+	chr2
6.40E-07	0.0002	5.620	0.134	5.391	0.000	0.359	-0.359	TRMT2A	chr22:20101111-20101208:-	chr22
8.04E-11	5.73E-08	9.556	2.872	1.734	0.017	0.361	-0.344	CFH	chr1:196694428-196695585:+	chr1

8.88E-08	3.42E-05	5.855	0.129	5.507	0.000	0.338	-0.338	RNF38	chr9:36351217-36352738:-	chr9
1.19E-09	6.82E-07	6.616	0.189	5.128	0.000	0.336	-0.336	DIP2A	chr21:47970658-47971529:+	chr21
2.56E-06	0.00068	6.888	2.709	1.346	0.058	0.384	-0.326	FAM188B	chr7:30811173-30818033:+	chr7
0.0002	0.0204	4.976	1.146	2.118	0.013	0.338	-0.325	PLXND1	chr3:129284873-129285369:-	chr3
1.75E-26	6.85E-23	12.050	0.907	3.732	0.002	0.319	-0.317	SAFB2	chr19:5595522-5598803:-	chr19
8.22E-06	0.00179	8.458	3.923	1.108	0.063	0.380	-0.317	DLG1	chr3:196792336-196792578:-	chr3
1.64E-06	0.00046	14.022	9.359	0.583	0.304	0.620	-0.316	STARD8	chrX:67936274-67937041:+	chrX
2.85E-29	1.42E-25	17.543	6.232	1.493	0.050	0.355	-0.305	HINT2	chr9:35813154-35813262:-	chr9
1.68E-11	1.34E-08	7.361	0.128	5.847	0.000	0.303	-0.303	IQGAP3	chr1:156532467-156532925:-	chr1
2.15E-09	1.18E-06	6.898	0.157	5.457	0.000	0.299	-0.299	NFYA	chr6:41040824-41046743:+	chr6
9.10E-25	3.08E-21	12.264	2.136	2.521	0.008	0.302	-0.294	FASTKD1	chr2:170388019-170393736:-	chr2
1.04E-10	7.23E-08	8.967	2.640	1.764	0.026	0.318	-0.292	RWDD4	chr4:184577128-184580081:-	chr4
9.61E-06	0.00206	4.966	0.138	5.170	0.000	0.286	-0.286	UQCC1	chr20:33934241-33934966:-	chr20
2.63E-06	0.00069	6.057	1.206	2.328	0.007	0.291	-0.284	CCDC74A	chr2:132288401-132289224:+	chr2
1.70E-15	2.53E-12	9.853	1.798	2.454	0.010	0.289	-0.279	COL23A1	chr5:177684584-177686721:-	chr5
4.98E-12	4.47E-09	7.690	0.174	5.469	0.000	0.279	-0.279	SETD4	chr21:37416268-37417879:-	chr21
4.89E-06	0.00117	5.791	1.316	2.138	0.012	0.290	-0.278	LIG3	chr17:33319712-33321272:+	chr17
1.29E-06	0.00038	5.137	0.112	5.518	0.000	0.273	-0.273	MAP3K4	chr6:161518209-161519291:+	chr6
6.47E-06	0.00148	5.736	1.384	2.051	0.017	0.288	-0.271	NRSN2	chr20:330008-330259:+	chr20
6.00E-06	0.00139	4.879	0.164	4.892	0.000	0.269	-0.269	ZFAND5	chr9:74978548-74979611:-	chr9
3.20E-05	0.00565	4.878	0.159	4.937	0.000	0.263	-0.263	RABGAP1	chr9:125759641-125760854:+	chr9
1.71E-13	1.89E-10	9.243	1.478	2.645	0.009	0.265	-0.256	TOR1AIP2	chr1:179835005-179846373:-	chr1
1.18E-07	4.43E-05	7.014	0.965	2.861	0.005	0.252	-0.247	EML3	chr11:62376299-62376433:-	chr11
3.19E-09	1.70E-06	6.350	0.139	5.516	0.000	0.245	-0.245	NF1	chr17:29587534-29588714:+	chr17
3.06E-05	0.00545	5.976	1.782	1.746	0.018	0.252	-0.234	HTT	chr4:3142384-3144471:+	chr4
1.70E-05	0.00338	7.074	1.545	2.195	0.011	0.239	-0.228	TRIM37	chr17:57148330-57153007:-	chr17
5.96E-11	4.35E-08	8.466	1.893	2.161	0.012	0.238	-0.226	UBXN2A	chr2:24207702-24222524:+	chr2
9.63E-10	5.67E-07	6.563	0.165	5.313	0.000	0.225	-0.225	CDC7	chr1:91966506-91967193:+	chr1
7.42E-07	0.00023	5.402	0.186	4.859	0.000	0.224	-0.224	ZFYVE27	chr10:99502922-99504468:+	chr10
2.41E-08	1.07E-05	7.957	2.430	1.711	0.015	0.238	-0.223	PPP2R5A	chr1:212515623-212519131:+	chr1
5.10E-08	2.12E-05	9.201	3.910	1.235	0.049	0.272	-0.223	UBR4	chr1:19480449-19481411:-	chr1
9.38E-11	6.59E-08	10.473	3.963	1.402	0.035	0.257	-0.221	RNF2	chr1:185056773-185060696:+	chr1
5.72E-05	0.00905	4.407	0.143	4.949	0.000	0.216	-0.216	FAM126B	chr2:201853164-201857003:-	chr2
2.23E-05	0.00422	4.686	0.212	4.469	0.000	0.215	-0.215	CBY1	chr22:39064138-39066874:+	chr22
1.39E-20	3.23E-17	15.590	1.791	3.122	0.002	0.214	-0.211	NET1	chr10:5497082-5498027:+	chr10
0.0002	0.02087	4.290	0.175	4.619	0.000	0.211	-0.211	IL17RC	chr3:9960294-9962150:+	chr3
0.0004	0.03957	5.795	2.289	1.340	0.038	0.248	-0.210	DHX35	chr20:37635000-37638902:+	chr20
5.11E-33	3.31E-29	17.486	5.982	1.547	0.023	0.230	-0.208	PRPF38A	chr1:52880320-52880412:+	chr1
4.59E-06	0.00111	8.483	4.097	1.050	0.062	0.267	-0.205	TRNT1	chr3:3186395-3188099:+	chr3
0.0005	0.04959	5.433	2.047	1.408	0.026	0.227	-0.201	DHX35	chr20:37662961-37667121:+	chr20
9.84E-08	3.76E-05	6.126	0.129	5.571	0.000	0.200	-0.200	KPNA1	chr3:122152653-122156016:-	chr3
1.06E-07	4.02E-05	8.678	3.411	1.347	0.030	0.227	-0.198	KEL	chr7:142651631-142654913:-	chr7
5.60E-05	0.00891	5.542	0.191	4.861	0.000	0.197	-0.197	SCLT1	chr4:129886490-129891532:-	chr4
1.80E-10	1.21E-07	7.691	1.406	2.452	0.006	0.200	-0.195	GTF2I	chr7:74131271-74133179:+	chr7
3.72E-16	6.09E-13	13.092	0.178	6.203	0.000	0.194	-0.194	DGCR2	chr22:19044700-19050714:-	chr22
0.0003	0.02996	4.819	1.013	2.251	0.012	0.205	-0.193	BIRC6	chr2:32614012-32617091:+	chr2

0.0002	0.02847	7.445	3.769	0.982	0.099	0.286	-0.187	RGL2	chr6:33261713-33261810:-	chr6
1.17E-08	5.55E-06	7.899	1.041	2.923	0.003	0.188	-0.185	STIM1	chr11:4104213-4104471:+	chr11
1.87E-10	1.25E-07	7.740	1.273	2.604	0.005	0.188	-0.184	RDX	chr11:110128653-110128830:-	chr11
1.06E-28	4.94E-25	11.769	0.156	6.233	0.000	0.183	-0.183	TPR	chr1:186324918-186325417:-	chr1
9.66E-06	0.00207	4.737	0.157	4.919	0.000	0.179	-0.179	PRPF38B	chr1:109235490-109236193:+	chr1
0.0001	0.0168	4.671	0.120	5.280	0.000	0.174	-0.174	PFDN5	chr12:53690336-53691607:+	chr12
7.17E-07	0.00023	5.367	0.132	5.344	0.000	0.171	-0.171	FKBP15	chr9:115934003-115935732:-	chr9
1.16E-06	0.00034	6.532	1.767	1.886	0.019	0.179	-0.160	ACD	chr16:67692736-67692830:-	chr16
3.33E-09	1.76E-06	6.865	0.994	2.788	0.002	0.157	-0.155	SYVN1	chr11:64900741-64900940:-	chr11
9.26E-12	7.66E-09	7.654	0.212	5.172	0.000	0.154	-0.154	RAB4A	chr1:229407118-229422214:+	chr1
1.01E-05	0.00216	6.865	2.519	1.447	0.071	0.220	-0.149	AK2	chr1:33477744-33478807:-	chr1
1.09E-05	0.00228	6.231	1.904	1.711	0.016	0.164	-0.149	KIAA0319L	chr1:35917393-35919157:-	chr1
2.85E-06	0.00074	7.500	2.980	1.331	0.024	0.170	-0.146	ATF1	chr12:51174022-51189680:+	chr12
4.90E-06	0.00117	4.911	0.148	5.048	0.000	0.144	-0.144	SOS1	chr2:39285969-39294768:-	chr2
0.0001	0.01866	4.320	0.198	4.446	0.000	0.142	-0.142	DMXL1	chr5:118454700-118456645:+	chr5
4.62E-11	3.44E-08	7.240	0.165	5.460	0.000	0.141	-0.141	COL23A1	chr5:177669415-177672942:-	chr5
1.72E-07	6.22E-05	6.809	0.199	5.099	0.000	0.140	-0.140	TTK	chr6:80750421-80751814:+	chr6
2.09E-16	3.57E-13	9.144	0.922	3.309	0.001	0.138	-0.137	TNPO3	chr7:128645231-128655032:-	chr7
2.25E-13	2.43E-10	7.885	0.156	5.661	0.000	0.136	-0.136	PPP6R3	chr11:68363687-68367788:+	chr11
7.76E-19	1.63E-15	10.236	1.437	2.833	0.002	0.137	-0.136	SLC3A2	chr11:62648920-62649352:+	chr11
1.88E-12	1.80E-09	8.910	2.030	2.134	0.007	0.141	-0.134	ELP2	chr18:33724998-33725896:+	chr18
1.14E-08	5.43E-06	6.270	0.176	5.158	0.000	0.132	-0.132	GALK2	chr15:49531565-49574168:+	chr15
6.16E-08	2.51E-05	6.218	0.134	5.540	0.000	0.130	-0.130	UPF3B	chrX:118972032-118972329:-	chrX
4.09E-05	0.00688	4.515	0.182	4.631	0.000	0.125	-0.125	TRAPPC6B	chr14:39627620-39628686:-	chr14
3.54E-09	1.85E-06	6.286	0.166	5.240	0.000	0.124	-0.124	SOAT1	chr1:179318078-179319411:+	chr1
3.57E-10	2.27E-07	6.788	0.185	5.196	0.000	0.124	-0.124	ZMYM4	chr1:35871070-35873587:+	chr1
5.96E-09	2.97E-06	6.485	0.176	5.201	0.000	0.123	-0.123	LIN9	chr1:226485534-226488873:-	chr1
7.13E-12	6.03E-09	8.643	1.337	2.692	0.003	0.125	-0.122	C1D	chr2:68274469-68290089:-	chr2
4.30E-05	0.00719	5.509	1.529	1.850	0.011	0.130	-0.120	RPS6KA3	chrX:20194635-20195113:-	chrX
1.15E-06	0.00034	5.598	0.134	5.384	0.000	0.118	-0.118	MUT	chr6:49416665-49419178:-	chr6
5.80E-06	0.00135	4.807	0.131	5.194	0.000	0.116	-0.116	ACAP3	chr1:1233509-1233749:-	chr1
0.0005	0.04671	5.182	1.800	1.525	0.044	0.160	-0.116	USP34	chr2:61415872-61416044:-	chr2
5.61E-05	0.00891	4.964	1.004	2.306	0.004	0.118	-0.113	PRICKLE3	chrX:49036186-49040186:-	chrX
5.76E-07	0.00018	6.124	1.041	2.556	0.003	0.114	-0.111	VPS51	chr11:64877396-64877934:+	chr11
1.38E-07	5.11E-05	6.108	0.141	5.441	0.000	0.108	-0.108	HEATR1	chr1:236738219-236739518:-	chr1
1.34E-05	0.00275	6.939	2.665	1.381	0.019	0.127	-0.108	VWDE	chr7:12407145-12409170:-	chr7
8.29E-05	0.01217	7.875	4.025	0.968	0.059	0.164	-0.104	GCFC2	chr2:75929574-75933648:-	chr2
1.81E-05	0.00355	4.918	0.190	4.693	0.000	0.103	-0.103	MTFR1	chr8:66557020-66582085:+	chr8
1.64E-07	5.99E-05	6.639	1.039	2.676	0.002	0.105	-0.103	CUL4A	chr13:113915074-113917776:+	chr13
2.25E-05	0.00425	5.247	1.068	2.297	0.005	0.106	-0.101	YY1AP1	chr1:155630725-155631097:-	chr1
0.0002	0.02859	4.076	0.143	4.832	0.000	0.100	-0.100	DUSP22	chr6:348842-350802:+	chr6
5.37E-05	0.00861	6.655	2.035	1.709	0.012	0.112	-0.100	ATP8B2	chr1:154316731-154316848:+	chr1
1.40E-05	0.00287	6.036	1.588	1.926	0.009	0.108	-0.099	SLC35A3	chr1:100477090-100480840:+	chr1
6.32E-11	4.59E-08	10.922	1.122	3.283	0.001	0.101	-0.099	SF3B1	chr2:198267784-198268308:-	chr2
6.10E-06	0.0014	5.880	1.487	1.983	0.005	0.104	-0.099	HECTD3	chr1:45474012-45474207:-	chr1
3.21E-11	2.43E-08	7.115	0.123	5.859	0.000	0.098	-0.098	ITFG1	chr16:47347748-47399698:-	chr16

7.20E-06	0.00161	5.967	0.172	5.120	0.000	0.098	-0.098	BRCA1	chr17:41247961-41249260:-	chr17
0.0003	0.02915	5.273	1.613	1.709	0.012	0.109	-0.097	FBXL19	chr16:30958270-30958352:+	chr16
9.66E-05	0.0138	5.290	0.128	5.373	0.000	0.092	-0.092	RECQL	chr12:21627930-21628401:-	chr12
4.79E-06	0.00115	8.027	3.244	1.307	0.019	0.110	-0.091	NPLOC4	chr17:79556146-79563141:-	chr17
5.56E-06	0.00131	8.556	2.985	1.519	0.012	0.102	-0.090	EIF3B	chr7:2419147-2419815:+	chr7
8.19E-05	0.01205	4.299	0.180	4.575	0.000	0.089	-0.089	UBN2	chr7:138957187-138958026:+	chr7
0.0002	0.01978	4.239	0.206	4.360	0.000	0.089	-0.089	KDM4A	chr1:44132227-44132609:+	chr1
1.00E-31	5.82E-28	12.961	1.028	3.656	0.001	0.090	-0.089	GUK1	chr1:228335401-228336058:+	chr1
0.0002	0.02511	5.897	0.149	5.308	0.000	0.088	-0.088	C15orf57	chr15:40849590-40854970:-	chr15
6.66E-06	0.00151	7.455	2.913	1.356	0.019	0.106	-0.086	TRABD	chr22:50635781-50635865:+	chr22
1.76E-10	1.20E-07	6.816	0.131	5.705	0.000	0.085	-0.085	AKAP8L	chr19:15491445-15507960:-	chr19
3.58E-16	5.92E-13	9.632	1.284	2.907	0.002	0.086	-0.085	TPR	chr1:186300729-186301326:-	chr1
2.49E-07	8.69E-05	5.987	0.863	2.795	0.002	0.083	-0.081	RTF1	chr15:41762591-41763349:+	chr15
4.36E-05	0.00727	5.435	1.454	1.903	0.007	0.087	-0.081	MTOR	chr1:11272544-11272852:-	chr1
1.83E-08	8.40E-06	6.662	1.021	2.705	0.002	0.082	-0.080	CDC27	chr17:45216273-45219218:-	chr17
1.93E-06	0.00053	5.898	1.112	2.407	0.002	0.082	-0.080	FAM76B	chr11:95513113-95516228:-	chr11
2.48E-11	1.93E-08	8.295	1.699	2.288	0.004	0.084	-0.080	PDS5A	chr4:39911977-39915230:-	chr4
5.59E-09	2.81E-06	6.114	1.723	1.827	0.001	0.080	-0.079	CLEC3B	chr3:45043101-45046767:+	chr3
7.53E-08	2.97E-05	5.873	0.137	5.419	0.000	0.079	-0.079	NCAPG	chr4:17824747-17825253:+	chr4
7.77E-06	0.00171	6.814	2.459	1.471	0.011	0.089	-0.077	PDHX	chr11:34953032-34969039:+	chr11
6.40E-05	0.00992	4.950	0.117	5.402	0.000	0.077	-0.077	STK24	chr13:99127257-99127503:-	chr13
2.60E-09	1.40E-06	6.825	0.905	2.914	0.001	0.076	-0.074	SLC5A6	chr2:27428395-27428893:-	chr2
0.0001	0.01552	4.267	0.182	4.548	0.000	0.074	-0.074	TMEM179B	chr11:62555000-62556481:+	chr11
5.70E-07	0.00018	7.629	2.248	1.763	0.005	0.079	-0.074	MRPS9	chr2:105713783-105716106:+	chr2
1.61E-06	0.00045	5.769	1.037	2.476	0.002	0.075	-0.073	NUP98	chr11:3697620-3697738:-	chr11
6.74E-06	0.00152	5.428	0.950	2.515	0.003	0.075	-0.072	SNW1	chr14:78203439-78205120:-	chr14
6.55E-08	2.65E-05	5.936	0.209	4.831	0.000	0.071	-0.071	TTC3	chr21:38570327-38572514:+	chr21
5.22E-12	4.58E-09	13.593	6.857	0.987	0.022	0.092	-0.070	GATA1	chrX:48651705-48652184:+	chrX
1.44E-06	0.00041	5.151	0.147	5.128	0.000	0.069	-0.069	ATAD1	chr10:89519558-89527429:-	chr10
0.0004	0.04322	11.713	8.236	0.508	0.061	0.129	-0.068	HMGCS1	chr5:43307947-43313457:-	chr5
4.67E-08	1.95E-05	5.868	0.133	5.463	0.000	0.068	-0.068	CLASRP	chr19:45572507-45573243:+	chr19
3.05E-05	0.00545	6.262	1.877	1.738	0.011	0.077	-0.066	DDIT3	chr12:57911243-57911488:-	chr12
1.82E-05	0.00355	4.673	0.161	4.855	0.000	0.064	-0.064	FAM234A	chr16:313775-313996:+	chr16
2.18E-09	1.19E-06	8.154	2.354	1.792	0.008	0.071	-0.063	IMMT	chr2:86398460-86400772:-	chr2
0.0005	0.04538	5.398	1.990	1.440	0.009	0.072	-0.062	NFE2L2	chr2:178096759-178097119:-	chr2
8.01E-10	4.83E-07	6.980	0.235	4.890	0.000	0.062	-0.062	LYPLAL1	chr1:219347324-219352471:+	chr1
1.21E-09	6.86E-07	8.178	2.073	1.980	0.004	0.065	-0.061	MRPS27	chr5:71524211-71528269:-	chr5
4.47E-05	0.00741	4.463	0.180	4.629	0.000	0.061	-0.061	JAK2	chr9:5080381-5080511:+	chr9
4.92E-84	1.22E-79	30.577	10.362	1.561	0.008	0.068	-0.061	LRRC75A-AS	chr17:16344445-16344670:+	chr17
0.0002	0.02703	4.732	1.117	2.083	0.004	0.063	-0.059	PEX3	chr6:143792587-143792673:+	chr6
1.28E-12	1.29E-09	7.816	0.174	5.487	0.000	0.059	-0.059	SF3A2	chr19:2247022-2247564:+	chr19
3.54E-05	0.00613	4.623	0.195	4.565	0.000	0.059	-0.059	ACAA2	chr18:47311743-47313660:-	chr18
0.0002	0.02114	5.187	1.517	1.774	0.006	0.064	-0.058	KCTD9	chr8:25290170-25290845:-	chr8
1.92E-07	6.87E-05	7.598	1.456	2.383	0.002	0.060	-0.057	MCM3AP	chr21:47655361-47656742:-	chr21
8.24E-08	3.22E-05	6.314	0.975	2.696	0.001	0.058	-0.057	COQ4	chr9:131087519-131088044:+	chr9
3.80E-11	2.84E-08	7.185	0.159	5.502	0.000	0.057	-0.057	GPS1	chr17:80013702-80013861:+	chr17

6.73E-07	0.00021	5.283	0.136	5.281	0.000	0.057	-0.057	CUL1	chr7:148451243-148454059:+	chr7
6.28E-09	3.11E-06	7.081	1.397	2.342	0.002	0.059	-0.056	MAN1A1	chr6:119511061-119514941:-	chr6
8.91E-11	6.29E-08	7.878	0.190	5.373	0.000	0.056	-0.056	ACSM3	chr16:20788903-20792021:+	chr16
2.94E-08	1.29E-05	9.212	1.529	2.591	0.001	0.057	-0.055	LRPPRC	chr2:44145291-44145394:-	chr2
4.23E-15	5.89E-12	9.914	0.235	5.398	0.000	0.055	-0.055	LRRC75A-AS	chr17:16343568-16344670:+	chr17
1.34E-09	7.50E-07	8.547	2.299	1.895	0.005	0.059	-0.055	COPS2	chr15:49420971-49421673:-	chr15
1.49E-06	0.00043	6.874	2.217	1.633	0.006	0.059	-0.053	USP15	chr12:62783480-62783562:+	chr12
1.92E-05	0.00371	4.604	0.128	5.172	0.000	0.052	-0.052	CDC27	chr17:45234507-45234595:-	chr17
0.0002	0.02701	5.374	1.722	1.642	0.005	0.057	-0.051	TCF25	chr16:89960267-89961424:+	chr16
8.04E-06	0.00176	4.906	0.170	4.854	0.000	0.051	-0.051	TMEM57	chr1:25815785-25817874:+	chr1
3.13E-06	0.0008	5.143	0.151	5.093	0.000	0.051	-0.051	BTK	chrX:100630322-100641049:-	chrX
1.09E-39	8.09E-36	14.414	0.999	3.851	0.000	0.050	-0.049	NONO	chrX:70516898-70517210:+	chrX
0.0002	0.02048	4.430	0.195	4.502	0.000	0.049	-0.049	PPM1M	chr3:52283339-52283671:+	chr3
1.93E-06	0.00053	5.194	0.155	5.068	0.000	0.048	-0.048	ORC5	chr7:103807348-103808920:-	chr7
2.40E-11	1.89E-08	7.872	1.141	2.787	0.001	0.048	-0.047	MRPS18C	chr4:84378112-84379477:+	chr4
4.63E-05	0.00764	6.118	1.947	1.652	0.005	0.052	-0.047	CIAO1	chr2:96934397-96934993:+	chr2
4.64E-15	6.40E-12	8.482	0.178	5.575	0.000	0.045	-0.045	NOP58	chr2:203160561-203162080:+	chr2
1.61E-12	1.57E-09	8.508	1.499	2.505	0.002	0.046	-0.044	NRD1	chr1:52293559-52299688:-	chr1
0.0002	0.02703	4.093	0.148	4.793	0.000	0.044	-0.044	ATF6B	chr6:32095540-32095893:-	chr6
########	########	36.427	2.703	3.752	0.000	0.042	-0.042	RPL24	chr3:101401354-101401614:-	chr3
4.41E-05	0.00734	5.825	1.770	1.718	0.004	0.046	-0.042	POLR1E	chr9:37501842-37503015:+	chr9
0.0002	0.01971	4.199	0.132	4.996	0.000	0.042	-0.042	FANCD2	chr3:10088408-10089567:+	chr3
6.64E-05	0.01024	4.418	0.203	4.445	0.000	0.041	-0.041	KDM3A	chr2:86705389-86705705:+	chr2
3.60E-10	2.28E-07	11.291	1.144	3.303	0.000	0.040	-0.040	GTSF1	chr12:54854276-54855892:-	chr12
1.27E-06	0.00037	5.170	0.173	4.902	0.000	0.040	-0.040	POM121C	chr7:75070414-75070709:-	chr7
3.52E-07	0.00012	6.567	1.540	2.093	0.002	0.042	-0.040	LARS	chr5:145522669-145522974:-	chr5
3.62E-10	2.28E-07	7.809	1.576	2.309	0.002	0.039	-0.038	TIMM17B	chrX:48751115-48751182:-	chrX
0.0003	0.0316	6.102	2.581	1.241	0.008	0.045	-0.037	ABCF2	chr7:150912186-150912689:-	chr7
0.0002	0.01971	6.168	1.133	2.444	0.001	0.037	-0.036	PRPF38A	chr1:52880320-52880403:+	chr1
0.0005	0.04608	4.571	1.145	1.998	0.002	0.038	-0.036	MITD1	chr2:99788124-99790377:-	chr2
0.0003	0.02908	4.568	0.982	2.217	0.002	0.037	-0.035	SUPV3L1	chr10:70955022-70956733:+	chr10
1.87E-08	8.51E-06	13.657	8.018	0.768	0.020	0.055	-0.035	AP2S1	chr19:47342878-47349249:-	chr19
2.98E-06	0.00077	5.028	0.187	4.751	0.000	0.035	-0.035	ENOPH1	chr4:83376008-83378044:+	chr4
1.50E-05	0.00302	4.634	0.126	5.196	0.000	0.034	-0.034	ELP2	chr18:33739794-33739904:+	chr18
4.27E-09	2.21E-06	19.315	13.942	0.470	0.043	0.076	-0.033		chr19:29101239-29101875:+	chr19
7.15E-14	8.52E-11	9.344	1.941	2.267	0.001	0.032	-0.030	SRSF1	chr17:56082979-56083161:-	chr17
1.58E-06	0.00045	5.734	1.014	2.499	0.001	0.031	-0.030	TCERG1	chr5:145883103-145883371:+	chr5
1.52E-07	5.60E-05	6.510	0.139	5.546	0.000	0.030	-0.030	NUDT3	chr6:34256733-34261227:-	chr6
5.85E-12	5.07E-09	7.999	1.054	2.924	0.001	0.030	-0.029	HSPA4	chr5:132439719-132439902:+	chr5
4.79E-11	3.55E-08	8.039	1.526	2.397	0.001	0.027	-0.026	HADHA	chr2:26437446-26437921:-	chr2
2.73E-06	0.00071	5.649	1.009	2.485	0.001	0.027	-0.026	FXYD5	chr19:35646515-35647729:+	chr19
1.85E-05	0.00359	5.156	0.157	5.034	0.000	0.026	-0.026	ZCCHC17	chr1:31811896-31819465:+	chr1
4.03E-07	0.00014	5.399	0.155	5.122	0.000	0.025	-0.025	HIGD2A	chr5:175815975-175816311:+	chr5
1.85E-05	0.00359	8.087	3.966	1.028	0.008	0.032	-0.024	FKBP8	chr19:18643625-18644079:-	chr19
1.12E-08	5.36E-06	6.791	1.057	2.684	0.001	0.024	-0.023	IARS	chr9:95007368-95009658:-	chr9
8.22E-06	0.00179	5.142	0.088	5.868	0.000	0.022	-0.022	PFDN5	chr12:53689424-53691607:+	chr12

1.19E-09	6.82E-07	7.431	1.409	2.399	0.001	0.023	-0.022	MAPK1	chr22:22118552-22123483:-	chr22
2.71E-06	0.00071	6.205	1.549	2.002	0.002	0.024	-0.022	MRPS30	chr5:44813385-44814996:+	chr5
9.34E-13	9.66E-10	8.307	1.129	2.880	0.000	0.022	-0.022	NHP2	chr5:177576860-177577888:-	chr5
3.70E-22	1.04E-18	10.827	0.145	6.226	0.000	0.021	-0.021	TFRC	chr3:195782191-195785154:-	chr3
0.0002	0.02351	6.333	2.576	1.298	0.005	0.025	-0.020	PABPC4	chr1:40031068-40033422:-	chr1
5.92E-05	0.00929	4.470	0.196	4.514	0.000	0.019	-0.019	PCNP	chr3:101293124-101298615:+	chr3
2.62E-08	1.15E-05	6.167	0.199	4.955	0.000	0.018	-0.018	GRHPR	chr9:37425992-37426519:+	chr9
5.80E-05	0.00913	4.452	0.170	4.715	0.000	0.018	-0.018	NDC80	chr18:2601485-2606399:+	chr18
0.0002	0.02777	4.757	1.056	2.172	0.001	0.018	-0.018	RARS	chr5:167921656-167922295:+	chr5
1.45E-05	0.00296	7.917	2.968	1.416	0.003	0.020	-0.017	CCNA2	chr4:122740084-122740526:-	chr4
1.80E-08	8.26E-06	6.448	0.213	4.918	0.000	0.016	-0.016	MGST3	chr1:165619202-165620230:+	chr1
2.88E-06	0.00075	5.704	1.015	2.490	0.001	0.016	-0.016	FBXW5	chr9:139837450-139837800:-	chr9
2.83E-11	2.17E-08	9.991	1.685	2.568	0.000	0.015	-0.014	PA2G4	chr12:56503078-56503622:+	chr12
2.31E-11	1.82E-08	9.467	2.761	1.778	0.001	0.015	-0.014	ATP5C1	chr10:7841158-7841707:+	chr10
8.90E-05	0.01289	6.047	2.205	1.455	0.002	0.016	-0.014	CLNS1A	chr11:77333735-77336007:-	chr11
0.0005	0.04801	5.478	1.823	1.587	0.001	0.015	-0.013	BRIX1	chr5:34922393-34922624:+	chr5
0.0003	0.03156	4.589	1.033	2.152	0.000	0.013	-0.013	CDC20	chr1:43826917-43827852:+	chr1
5.87E-06	0.00137	4.855	0.120	5.338	0.000	0.012	-0.012	EIF3J	chr15:44846866-44849667:+	chr15
0.0002	0.02893	4.808	1.017	2.242	0.001	0.013	-0.012	SLC3A2	chr11:62653081-62655584:+	chr11
0.0002	0.02322	4.715	0.999	2.238	0.001	0.010	-0.010	NONO	chrX:70504304-70510460:+	chrX
4.97E-07	0.00016	6.223	1.174	2.406	0.000	0.010	-0.010	PSMA7	chr20:60712019-60712419:-	chr20
0.0002	0.02423	5.016	1.203	2.060	0.001	0.009	-0.008	MRPS10	chr6:42176133-42176595:-	chr6
9.55E-12	7.86E-09	9.459	1.823	2.375	0.000	0.008	-0.008	TXN	chr9:113013761-113018691:-	chr9
2.03E-52	2.74E-48	19.598	2.806	2.804	0.000	0.008	-0.008	RPL27A	chr11:8704813-8705536:+	chr11
9.92E-05	0.01409	5.925	2.133	1.474	0.001	0.009	-0.008	CCT2	chr12:69992202-69993621:+	chr12
1.23E-08	5.79E-06	8.111	2.394	1.761	0.001	0.008	-0.008	PSMB1	chr6:170844510-170846321:-	chr6
0.0001	0.01621	8.610	4.036	1.093	0.002	0.010	-0.008	CCT5	chr5:10263427-10264749:+	chr5
1.15E-52	1.71E-48	23.663	8.096	1.547	0.001	0.008	-0.007	RPS27A	chr2:55462099-55462545:+	chr2
1.70E-32	1.05E-28	16.608	4.401	1.916	0.000	0.007	-0.007	TPT1	chr13:45911539-45912794:-	chr13
0.0003	0.03051	6.235	2.650	1.234	0.001	0.007	-0.006		chr19:29103062-29103327:+	chr19
0.0003	0.03468	5.159	1.032	2.322	0.000	0.006	-0.006	CSDE1	chr1:115263359-115266503:-	chr1
5.72E-07	0.00018	5.690	0.145	5.290	0.000	0.005	-0.005	CCT4	chr2:62095857-62096574:-	chr2
2.61E-18	5.32E-15	18.882	7.217	1.388	0.001	0.005	-0.005	RPS27A	chr2:55462099-55462548:+	chr2
2.54E-05	0.00465	4.822	0.145	5.059	0.000	0.005	-0.005	TFRC	chr3:195799040-195800800:-	chr3
6.89E-05	0.01058	5.361	0.203	4.723	0.000	0.004	-0.004	BRK1	chr3:10157504-10167295:+	chr3
6.94E-14	8.34E-11	14.150	6.551	1.111	0.001	0.004	-0.003	RPS10	chr6:34392633-34392848:-	chr6
0.0001	0.01675	4.278	0.136	4.978	0.000	0.002	-0.002	ATP5G2	chr12:54063774-54066359:-	chr12
8.09E-11	5.74E-08	8.477	1.411	2.587	0.000	0.002	-0.002	RPL9	chr4:39455867-39456152:-	chr4
1.83E-13	2.00E-10	9.967	2.510	1.989	0.000	0.002	-0.002	RPL27A	chr11:8705629-8706243:+	chr11
8.26E-10	4.96E-07	7.570	0.133	5.836	0.000	0.001	-0.001	RPL4	chr15:66792532-66792630:-	chr15
3.60E-06	0.00091	6.679	1.971	1.761	0.000	0.001	-0.001	TPT1	chr13:45912933-45913631:-	chr13
2.67E-05	0.00483	4.722	0.128	5.203	0.000	0.001	-0.001	HSPA8	chr11:122929211-122929339:-	chr11
8.85E-05	0.01284	5.451	1.340	2.024	0.000	0.001	-0.001	RPS10	chr6:34392636-34392848:-	chr6
0.0001	0.01434	4.436	0.171	4.697	0.000	0.000	0.000	RPL41	chr12:56510444-56510537:+	chr12
0.0004	0.03848	4.618	1.072	2.106	0.000	0.000	0.000	FTL	chr19:49469664-49469803:+	chr19
1.03E-09	6.07E-07	10.460	4.100	1.351	0.533	0.371	0.163	RPS15A	chr16:18799478-18800302:-	chr16

n				nclusion level WT		clusion level MU		read Conts WT		ead Conts MU	
start	end	strand	distance to canonical site	WT1 (SY061)	WT2 (SY062)	Mut1 (SY063)	Mut2 (SY064)	count Data.SY061	count Data.SY062	count Data.SY063	count Data.SY064
5717646	5719714	-	18	0.000	0.000	0.800	1.000	0	0	8	4
53689726	53691607	+	26	0.000	0.000	0.838	0.774	0	0	88	24
102074109	102076648	+	23	0.100	0.000	0.727	0.833	1	0	8	5
16803043	16803424	-	43	0.000	0.000	0.727	0.714	0	0	8	5
995352	995438	+	28	0.116	0.022	0.714	0.826	5	1	15	19
102276735	102286155	-	17	0.000	0.000	0.727	0.667	0	0	8	4
91269954	91271340	-	20	0.060	0.093	0.702	0.844	11	18	59	54
25158620	25160574	-	23	0.000	0.000	0.587	0.789	0	0	27	15
843275	844033	+	6	0.167	0.125	0.738	0.885	2	1	45	23
108403189	108405274	+	17	0.067	0.020	0.667	0.750	1	1	6	6
42929951	42930884	-	20	0.000	0.000	0.474	0.833	0	0	9	5
47315814	47326808	-	16	0.154	0.143	0.813	0.778	2	2	13	7
89977272	89979392	+	10	0.000	0.000	0.769	0.500	0	0	10	2
23283431	23285704	-	14	0.059	0.029	0.607	0.739	1	1	17	17
85848703	85850728	+	20	0.000	0.000	0.607	0.625	0	0	17	10
56649301	56649931	+	18	0.079	0.179	0.680	0.800	3	5	17	20
42835782	42845927	-	14	0.111	0.050	0.716	0.659	2	1	63	29
156785905	156786466	-	18	0.000	0.088	0.543	0.750	0	3	19	12
97285514	97297048	-	14	0.000	0.000	0.500	0.680	0	0	21	17
89778631	89779081	+	15	0.038	0.035	0.554	0.682	6	5	46	30
109102365	109102954	+	12	0.019	0.018	0.614	0.571	1	1	27	20
109181708	109183328	+	29	0.000	0.000	0.550	0.471	0	0	22	8
45300424	45300861	+	13	0.012	0.024	0.514	0.536	7	5	330	111
90000306	90001195	+	21	0.000	0.000	0.385	0.625	0	0	10	5
94157563	94162500	+	16	0.000	0.050	0.474	0.583	0	1	9	7
36631196	36634598	-	17	0.000	0.009	0.558	0.421	0	1	29	8
101458311	101460665	-	14	0.003	0.015	0.419	0.566	1	4	57	47
172479474	172480187	+	18	0.015	0.000	0.327	0.633	1	0	18	19
56874549	56875878	+	22	0.000	0.000	0.481	0.444	0	0	13	4
93939175	93960519	-	40	0.167	0.231	0.655	0.615	2	3	19	8
44492077	44492359	-	11	0.000	0.024	0.313	0.571	0	1	5	8
62574713	62576906	-	18	0.025	0.000	0.395	0.458	1	0	15	11
103297360	103298629	+	14	0.000	0.000	0.529	0.278	0	0	18	5
30884737	30884871	+	10	0.005	0.007	0.354	0.455	1	1	29	10
35282127	35284762	-	22	0.000	0.000	0.347	0.423	0	0	17	11
33934265	33934966	-	38	0.000	0.000	0.486	0.276	0	0	17	8
23237381	23238985	+	14	0.019	0.015	0.377	0.419	9	6	116	72
132288401	132289210	+	26	0.036	0.013	0.429	0.379	2	2	9	11
20101111	20101208	-	26	0.000	0.000	0.273	0.444	0	0	6	8
196694428	196695585	+	14	0.000	0.033	0.341	0.381	0	5	44	24

36351217	36352738	-		20	0.000	0.000	0.342	0.333	0	0	13	3
47970658	47971529	+		17	0.000	0.000	0.381	0.292	0	0	16	7
30811173	30818033	+		14	0.054	0.063	0.333	0.435	3	3	16	10
129284873	129285369	-		12	0.000	0.026	0.342	0.333	0	1	13	2
5595522	5598803	-		13	0.004	0.000	0.355	0.283	1	0	38	15
196792336	196792578	-		16	0.042	0.083	0.436	0.324	5	12	17	12
67936274	67937041	+		12	0.287	0.321	0.586	0.654	39	45	78	17
35813154	35813262	-		11	0.046	0.053	0.336	0.373	14	16	121	62
156532467	156532925	-		9	0.000	0.000	0.345	0.261	0	0	20	6
41040824	41046743	+		24	0.000	0.000	0.349	0.250	0	0	15	4
170388019	170393736	-		18	0.007	0.009	0.338	0.266	2	2	53	25
184577128	184580081	-		13	0.022	0.031	0.269	0.368	2	3	29	21
33934241	33934966	-		14	0.000	0.000	0.379	0.192	0	0	11	5
132288401	132289224	+		12	0.000	0.013	0.400	0.182	0	2	8	4
177684584	177686721	-		15	0.000	0.020	0.316	0.262	0	3	37	11
37416268	37417879	-		13	0.000	0.000	0.284	0.275	0	0	23	14
33319712	33321272	+		22	0.023	0.000	0.286	0.294	2	0	8	5
161518209	161519291	+		18	0.000	0.000	0.280	0.267	0	0	7	4
330008	330259	+		22	0.022	0.012	0.276	0.300	1	1	8	6
74978548	74979611	-		25	0.000	0.000	0.348	0.190	0	0	8	4
125759641	125760854	+		21	0.000	0.000	0.192	0.333	0	0	5	6
179835005	179846373	-		15	0.009	0.010	0.301	0.229	1	1	31	11
62376299	62376433	-		21	0.000	0.010	0.193	0.310	0	1	11	9
29587534	29588714	+		14	0.000	0.000	0.277	0.214	0	0	13	6
3142384	3144471	+		21	0.037	0.000	0.297	0.207	3	0	11	6
57148330	57153007	-		21	0.022	0.000	0.324	0.154	2	0	22	6
24207702	24222524	+		17	0.008	0.016	0.210	0.266	1	2	21	17
91966506	91967193	+		17	0.000	0.000	0.250	0.200	0	0	14	6
99502922	99504468	+		17	0.000	0.000	0.282	0.167	0	0	11	3
212515623	212519131	+		13	0.016	0.014	0.191	0.286	4	4	13	8
19480449	19481411	-		15	0.051	0.048	0.294	0.250	8	6	30	12
185056773	185060696	+		14	0.049	0.022	0.245	0.268	8	3	40	30
201853164	201857003	-		19	0.000	0.000	0.182	0.250	0	0	8	3
39064138	39066874	+		14	0.000	0.000	0.179	0.250	0	0	7	5
5497082	5498027	+		22	0.000	0.005	0.174	0.253	0	3	54	56
9960294	9962150	+		24	0.000	0.000	0.188	0.235	0	0	9	4
37635000	37638902	+		20	0.047	0.030	0.261	0.235	3	2	12	4
52880320	52880412	+		21	0.022	0.024	0.227	0.234	16	12	115	64
3186395	3188099	+		14	0.061	0.064	0.259	0.275	6	7	28	14
37662961	37667121	+		20	0.038	0.015	0.233	0.222	3	1	10	4
122152653	122156016	-		17	0.000	0.000	0.256	0.143	0	0	10	3
142651631	142654913	-		16	0.022	0.038	0.265	0.190	5	7	22	11
129886490	129891532	-		16	0.000	0.000	0.283	0.111	0	0	13	2
74131271	74133179	+		18	0.006	0.006	0.181	0.220	1	1	15	11
19044700	19050714	-		24	0.000	0.000	0.134	0.255	0	0	25	38
32614012	32617091	+		15	0.023	0.000	0.243	0.167	1	0	9	2

33261713	33261810	-	19	0.100	0.097	0.377	0.194	5	7	23	7
4104213	4104471	+	21	0.000	0.006	0.245	0.130	0	1	25	6
110128653	110128830	-	14	0.009	0.000	0.246	0.130	2	0	16	6
186324918	186325417	-	17	0.000	0.000	0.201	0.165	0	0	36	16
109235490	109236193	+	18	0.000	0.000	0.200	0.158	0	0	7	3
53690336	53691607	+	26	0.000	0.000	0.098	0.250	0	0	8	8
115934003	115935732	-	16	0.000	0.000	0.164	0.179	0	0	10	5
67692736	67692830	-	16	0.022	0.017	0.196	0.161	2	2	10	5
64900741	64900940	-	17	0.000	0.005	0.189	0.125	0	1	14	7
229407118	229422214	+	18	0.000	0.000	0.168	0.141	0	0	26	9
33477744	33478807	-	20	0.063	0.080	0.253	0.188	2	2	25	9
35917393	35919157	-	15	0.031	0.000	0.173	0.156	3	0	14	7
51174022	51189680	+	11	0.019	0.029	0.140	0.200	3	4	20	12
39285969	39294768	-	23	0.000	0.000	0.103	0.185	0	0	6	5
118454700	118456645	+	20	0.000	0.000	0.068	0.217	0	0	5	5
177669415	177672942	-	19	0.000	0.000	0.167	0.116	0	0	21	5
80750421	80751814	+	21	0.000	0.000	0.086	0.194	0	0	12	12
128645231	128655032	-	17	0.000	0.003	0.143	0.133	0	1	20	12
68363687	68367788	+	20	0.000	0.000	0.155	0.117	0	0	18	7
62648920	62649352	+	12	0.000	0.003	0.156	0.119	0	2	33	16
33724998	33725896	+	14	0.006	0.008	0.139	0.143	2	2	25	12
49531565	49574168	+	15	0.000	0.000	0.152	0.111	0	0	16	6
118972032	118972329	-	17	0.000	0.000	0.176	0.083	0	0	12	3
39627620	39628686	-	13	0.000	0.000	0.151	0.100	0	0	8	3
179318078	179319411	+	19	0.000	0.000	0.118	0.130	0	0	9	7
35871070	35873587	+	21	0.000	0.000	0.134	0.114	0	0	15	9
226485534	226488873	-	19	0.000	0.000	0.106	0.139	0	0	14	11
68274469	68290089	-	17	0.000	0.005	0.127	0.122	0	1	41	18
20194635	20195113	-	18	0.013	0.008	0.129	0.132	1	1	11	5
49416665	49419178	-	24	0.000	0.000	0.169	0.067	0	0	10	2
1233509	1233749	-	15	0.000	0.000	0.128	0.105	0	0	6	4
61415872	61416044	-	27	0.036	0.053	0.154	0.167	1	2	8	5
49036186	49040186	-	30	0.009	0.000	0.088	0.147	1	0	6	5
64877396	64877934	+	19	0.006	0.000	0.147	0.080	1	0	14	4
236738219	236739518	-	15	0.000	0.000	0.085	0.131	0	0	7	8
12407145	12409170	-	25	0.014	0.024	0.127	0.127	2	3	22	9
75929574	75933648	-	24	0.036	0.082	0.176	0.151	4	8	27	11
66557020	66582085	+	22	0.000	0.000	0.109	0.098	0	0	13	4
113915074	113917776	+	24	0.004	0.000	0.086	0.123	1	0	12	9
155630725	155631097	-	20	0.000	0.010	0.103	0.109	0	1	9	5
348842	350802	+	19	0.000	0.000	0.130	0.070	0	0	7	3
154316731	154316848	+	22	0.012	0.012	0.151	0.072	2	2	16	5
100477090	100480840	+	17	0.017	0.000	0.147	0.069	2	0	16	5
198267784	198268308	-	24	0.000	0.003	0.073	0.129	0	1	31	32
45474012	45474207	-	18	0.011	0.000	0.095	0.113	2	0	10	7
47347748	47399698	-	13	0.000	0.000	0.079	0.117	0	0	9	9

41247961	41249260	-	21	0.000	0.000	0.143	0.053	0	0	20	3
30958270	30958352	+	20	0.009	0.015	0.141	0.077	1	2	9	2
21627930	21628401	-	16	0.000	0.000	0.131	0.053	0	0	11	2
79556146	79563141	-	15	0.025	0.013	0.144	0.075	6	4	23	8
2419147	2419815	+	23	0.013	0.012	0.055	0.149	5	5	13	15
138957187	138958026	+	16	0.000	0.000	0.097	0.081	0	0	7	3
44132227	44132609	+	15	0.000	0.000	0.111	0.067	0	0	8	2
228335401	228336058	+	13	0.001	0.000	0.093	0.086	1	0	51	28
40849590	40854970	-	18	0.000	0.000	0.047	0.130	0	0	7	14
50635781	50635865	+	12	0.015	0.023	0.123	0.088	3	5	21	6
15491445	15507960	-	21	0.000	0.000	0.081	0.089	0	0	14	7
186300729	186301326	-	15	0.000	0.003	0.098	0.075	0	2	26	9
41762591	41763349	+	20	0.003	0.000	0.087	0.078	1	0	8	4
11272544	11272852	-	12	0.005	0.008	0.105	0.069	1	1	9	5
45216273	45219218	-	15	0.000	0.003	0.074	0.090	0	1	15	6
95513113	95516228	-	22	0.004	0.000	0.067	0.096	1	0	11	8
39911977	39915230	-	18	0.003	0.006	0.101	0.066	1	2	21	9
45043101	45046767	+	15	0.002	0.000	0.072	0.089	1	0	33	17
17824747	17825253	+	16	0.000	0.000	0.062	0.096	0	0	8	7
34953032	34969039	+	13	0.009	0.013	0.078	0.099	2	4	13	8
99127257	99127503	-	24	0.000	0.000	0.036	0.118	0	0	4	6
27428395	27428893	-	22	0.000	0.003	0.075	0.077	0	1	10	7
62555000	62556481	+	13	0.000	0.000	0.080	0.068	0	0	7	4
105713783	105716106	+	21	0.004	0.006	0.055	0.103	2	2	16	16
3697620	3697738	-	13	0.003	0.000	0.065	0.086	1	0	10	6
78203439	78205120	-	20	0.000	0.005	0.094	0.057	0	1	9	3
38570327	38572514	+	18	0.000	0.000	0.060	0.083	0	0	11	9
48651705	48652184	+	15	0.018	0.025	0.085	0.099	20	23	60	32
89519558	89527429	-	13	0.000	0.000	0.077	0.062	0	0	8	4
43307947	43313457	-	20	0.048	0.074	0.124	0.135	29	31	52	19
45572507	45573243	+	36	0.000	0.000	0.066	0.070	0	0	11	6
57911243	57911488	-	21	0.022	0.000	0.064	0.089	2	0	20	11
313775	313996	+	18	0.000	0.000	0.068	0.061	0	0	8	4
86398460	86400772	-	24	0.009	0.007	0.076	0.066	3	2	21	12
178096759	178097119	-	22	0.005	0.014	0.084	0.060	1	3	9	4
219347324	219352471	+	17	0.000	0.000	0.053	0.071	0	0	23	12
71524211	71528269	-	15	0.007	0.000	0.057	0.072	3	0	28	15
5080381	5080511	+	21	0.000	0.000	0.060	0.063	0	0	6	5
16344445	16344670	+	11	0.006	0.009	0.066	0.070	29	33	394	359
143792587	143792673	+	20	0.008	0.000	0.056	0.069	1	0	7	5
2247022	2247564	+	28	0.000	0.000	0.070	0.048	0	0	22	7
47311743	47313660	-	21	0.000	0.000	0.068	0.049	0	0	10	3
25290170	25290845	-	16	0.006	0.005	0.078	0.050	1	1	10	4
47655361	47656742	-	20	0.000	0.005	0.047	0.072	0	2	13	13
131087519	131088044	+	13	0.000	0.003	0.065	0.052	0	1	11	6
80013702	80013861	+	15	0.000	0.000	0.047	0.067	0	0	14	12

148451243	148454059	+	15	0.000	0.000	0.048	0.066	0	0	8	4
119511061	119514941	-	12	0.003	0.002	0.053	0.065	1	1	14	8
20788903	20792021	+	14	0.000	0.000	0.041	0.072	0	0	36	9
44145291	44145394	-	18	0.001	0.001	0.034	0.079	1	1	24	19
16343568	16344670	+	11	0.000	0.000	0.059	0.052	0	0	49	28
49420971	49421673	-	13	0.002	0.007	0.051	0.068	1	3	25	18
62783480	62783562	+	14	0.005	0.007	0.063	0.055	2	2	16	10
45234507	45234595	-	16	0.000	0.000	0.056	0.048	0	0	7	3
89960267	89961424	+	21	0.004	0.007	0.075	0.038	1	2	10	3
25815785	25817874	+	26	0.000	0.000	0.069	0.033	0	0	9	3
100630322	100641049	-	19	0.000	0.000	0.040	0.061	0	0	7	7
70516898	70517210	+	16	0.000	0.000	0.047	0.052	0	1	62	31
52283339	52283671	+	14	0.000	0.000	0.040	0.057	0	0	8	6
103807348	103808920	-	15	0.000	0.000	0.045	0.050	0	0	9	6
84378112	84379477	+	21	0.000	0.002	0.047	0.048	0	1	21	15
96934397	96934993	+	12	0.000	0.010	0.047	0.056	0	3	12	9
203160561	203162080	+	21	0.000	0.000	0.046	0.044	0	0	24	10
52293559	52299688	-	17	0.000	0.003	0.041	0.050	0	2	22	14
32095540	32095893	-	12	0.000	0.000	0.035	0.053	0	0	6	4
101401354	101401614	-	17	0.000	0.000	0.042	0.043	3	1	866	330
37501842	37503015	+	24	0.007	0.000	0.046	0.045	3	0	11	5
10088408	10089567	+	33	0.000	0.000	0.049	0.035	0	0	8	2
86705389	86705705	+	25	0.000	0.000	0.041	0.041	0	0	8	4
54854276	54855892	-	20	0.001	0.000	0.025	0.055	1	0	32	36
75070414	75070709	-	20	0.000	0.000	0.031	0.049	0	0	6	5
145522669	145522974	-	21	0.004	0.000	0.042	0.042	2	0	16	7
48751115	48751182	-	14	0.003	0.000	0.039	0.040	2	0	22	12
150912186	150912689	-	17	0.008	0.007	0.049	0.041	4	3	11	5
52880320	52880403	+	30	0.001	0.000	0.020	0.054	1	0	8	12
99788124	99790377	-	14	0.004	0.000	0.040	0.037	1	0	7	5
70955022	70956733	+	14	0.003	0.000	0.038	0.035	1	0	6	3
47342878	47349249	-	42	0.018	0.022	0.061	0.049	22	30	76	30
83376008	83378044	+	23	0.000	0.000	0.040	0.029	0	0	8	4
33739794	33739904	+	16	0.000	0.000	0.037	0.031	0	0	7	3
29101239	29101875	+	13	0.045	0.041	0.070	0.082	86	26	152	144
56082979	56083161	-	17	0.002	0.001	0.030	0.033	3	1	23	14
145883103	145883371	+	15	0.002	0.000	0.029	0.033	1	0	9	6
34256733	34261227	-	24	0.000	0.000	0.042	0.018	0	0	19	4
132439719	132439902	+	22	0.000	0.001	0.026	0.034	0	1	17	14
26437446	26437921	-	15	0.001	0.001	0.028	0.026	1	1	23	11
35646515	35647729	+	17	0.000	0.002	0.029	0.025	0	1	9	5
31811896	31819465	+	21	0.000	0.000	0.018	0.034	0	0	9	10
175815975	175816311	+	20	0.000	0.000	0.024	0.026	0	0	8	5
18643625	18644079	-	19	0.008	0.007	0.031	0.033	8	7	21	10
95007368	95009658	-	14	0.000	0.001	0.019	0.029	0	1	14	9
53689424	53691607	+	26	0.000	0.000	0.021	0.024	0	0	13	7

22118552	22123483	-	22	0.001	0.001	0.019	0.027	1	1	10	14
44813385	44814996	+	18	0.002	0.002	0.028	0.020	1	1	16	5
177576860	177577888	-	20	0.001	0.000	0.022	0.023	1	0	25	14
195782191	195785154	-	18	0.000	0.000	0.022	0.021	0	0	53	22
40031068	40033422	-	17	0.003	0.007	0.022	0.027	3	4	10	7
101293124	101298615	+	18	0.000	0.000	0.020	0.018	0	0	9	3
37425992	37426519	+	15	0.000	0.000	0.019	0.017	0	0	17	7
2601485	2606399	+	14	0.000	0.000	0.024	0.012	0	0	8	2
167921656	167922295	+	24	0.002	0.000	0.014	0.023	1	0	5	6
122740084	122740526	-	15	0.003	0.002	0.026	0.013	5	3	25	7
165619202	165620230	+	20	0.000	0.000	0.018	0.014	0	0	22	6
139837450	139837800	-	24	0.001	0.000	0.021	0.012	1	0	11	4
56503078	56503622	+	18	0.000	0.000	0.010	0.019	2	1	19	21
7841158	7841707	+	27	0.001	0.002	0.015	0.016	2	3	43	19
77333735	77336007	-	16	0.002	0.002	0.012	0.019	2	2	13	7
34922393	34922624	+	19	0.003	0.000	0.019	0.011	3	0	11	4
43826917	43827852	+	13	0.001	0.000	0.012	0.015	1	0	6	4
44846866	44849667	+	19	0.000	0.000	0.014	0.011	0	0	7	3
62653081	62655584	+	22	0.002	0.000	0.017	0.008	1	0	9	2
70504304	70510460	+	18	0.001	0.000	0.013	0.008	1	0	8	2
60712019	60712419	-	13	0.001	0.000	0.010	0.010	1	0	16	8
42176133	42176595	-	22	0.000	0.001	0.007	0.010	0	1	8	8
113013761	113018691	-	18	0.000	0.000	0.007	0.010	1	1	36	29
8704813	8705536	+	16	0.000	0.000	0.007	0.009	4	1	181	97
69992202	69993621	+	21	0.001	0.002	0.010	0.008	1	3	12	6
170844510	170846321	-	16	0.000	0.001	0.007	0.009	1	3	25	17
10263427	10264749	+	18	0.004	0.001	0.012	0.008	11	4	27	10
55462099	55462545	+	18	0.001	0.001	0.008	0.008	13	21	354	153
45911539	45912794	-	15	0.000	0.001	0.007	0.007	5	5	150	93
29103062	29103327	+	18	0.001	0.000	0.006	0.008	4	0	14	16
115263359	115266503	-	20	0.000	0.000	0.004	0.008	0	1	5	7
62095857	62096574	-	15	0.000	0.000	0.006	0.004	0	0	15	4
55462099	55462548	+	15	0.001	0.001	0.005	0.006	12	15	199	115
195799040	195800800	-	16	0.000	0.000	0.005	0.004	0	0	12	3
10157504	10167295	+	14	0.000	0.000	0.006	0.002	0	0	19	3
34392633	34392848	-	15	0.001	0.001	0.004	0.004	11	13	114	50
54063774	54066359	-	41	0.000	0.000	0.002	0.002	0	0	8	3
39455867	39456152	-	21	0.000	0.000	0.002	0.002	0	1	43	21
8705629	8706243	+	21	0.000	0.000	0.002	0.002	1	3	49	22
66792532	66792630	-	17	0.000	0.000	0.001	0.002	0	0	16	13
45912933	45913631	-	21	0.000	0.000	0.001	0.001	2	0	26	13
122929211	122929339	-	18	0.000	0.000	0.000	0.001	0	0	5	6
34392636	34392848	-	18	0.000	0.000	0.001	0.001	1	0	16	8
56510444	56510537	+	21	0.000	0.000	0.000	0.000	0	0	9	5
49469664	49469803	+	36	0.000	0.000	0.000	0.000	0	1	8	3
18799478	18800302	-	50	0.667	0.400	0.337	0.404	6	2	68	36

Table S2. Cryptic 3' Splice Sites Differentially Used by Mutant vs WT SF3B1 MDS Cells

statistics					inclusion_level			Gene	Locatio	
pvalue	padj	MUT	WT	log2fold_WT_MUT	inclusion_level_WT	inclusion_level_MUT	inclu_diff_WT-MUT	Genename	transcripts	chrom
3.57E-17	2.92E-14	5.408	1.146	-2.239	0.125	0.890	-0.765	FXYD5	chr19:35646515-35647729:+	chr19
3.25E-26	5.46E-23	8.073	1.328	-2.604	0.111	0.831	-0.720	ATAD1	chr10:89519558-89527429:-	chr10
1.02E-38	4.50E-35	8.121	1.759	-2.207	0.031	0.720	-0.689	ZNF91	chr19:23545542-23556543:-	chr19
8.21E-84	2.68E-79	12.504	2.107	-2.569	0.017	0.638	-0.622	ORAI2	chr7:102074109-102076648:+	chr7
1.87E-43	1.09E-39	10.832	1.773	-2.611	0.053	0.652	-0.599	PFDN5	chr12:53689726-53691607:+	chr12
6.83E-109	3.91E-104	27.400	5.087	-2.429	0.016	0.580	-0.564	CCDC88B	chr11:64119859-64120198:+	chr11
9.00E-20	9.10E-17	5.968	1.513	-1.980	0.066	0.620	-0.554	VPS9D1-AS1	chr16:89778631-89779081:+	chr16
2.04E-31	5.19E-28	11.795	4.908	-1.265	0.111	0.664	-0.553	MAP3K7	chr6:91269954-91271340:-	chr6
1.15E-16	8.67E-14	5.442	1.357	-2.004	0.127	0.676	-0.549	HIGD1A	chr3:42835782-42845927:-	chr3
1.06E-14	6.27E-12	5.947	2.057	-1.531	0.140	0.673	-0.533	MZB1	chr5:138725126-138725368:-	chr5
1.67E-29	3.60E-26	9.104	1.343	-2.761	0.018	0.551	-0.532	GCC2	chr2:109102365-109102954:+	chr2
1.28E-05	0.0017	3.496	1.172	-1.577	0.042	0.565	-0.523	NDUFV2-AS1	chr18:9133521-9136361:-	chr18
2.77E-24	4.22E-21	6.783	0.563	-3.591	0.005	0.526	-0.521	USP39	chr2:85848703-85850728:+	chr2
4.61E-17	3.72E-14	7.715	1.401	-2.462	0.034	0.549	-0.515		chr8:65716854-65718145:-	chr8
3.15E-16	2.26E-13	4.646	0.708	-2.714	0.006	0.516	-0.509	SEPSECS	chr4:25158620-25160574:-	chr4
4.19E-182	9.58E-177	23.928	5.928	-2.013	0.024	0.524	-0.501	MICAL1	chr6:109767079-109767338:-	chr6
2.75E-08	7.10E-06	5.857	3.196	-0.874	0.277	0.775	-0.498	ZNF41	chrX:47315814-47326808:-	chrX
1.83E-36	6.53E-33	10.050	1.802	-2.480	0.063	0.553	-0.490	PPM1M	chr3:52283339-52283671:+	chr3
1.57E-44	9.94E-41	8.169	1.193	-2.775	0.014	0.497	-0.483	KANSL3	chr2:97285514-97297048:-	chr2
1.20E-21	1.46E-18	6.074	1.174	-2.371	0.008	0.456	-0.448	IL17RC	chr3:9960294-9962150:+	chr3
6.09E-15	3.69E-12	4.707	0.751	-2.649	0.034	0.479	-0.446	ZNF530	chr19:58115775-58117036:+	chr19
6.57E-48	5.37E-44	19.340	7.061	-1.454	0.052	0.495	-0.443	PPP2R5A	chr1:212515623-212519131:+	chr1
8.49E-47	6.69E-43	25.165	7.538	-1.739	0.043	0.485	-0.443	OXA1L	chr14:23237381-23238985:+	chr14
1.90E-19	1.84E-16	7.185	1.965	-1.871	0.039	0.481	-0.441	CASD1	chr7:94157563-94162500:+	chr7
7.54E-17	5.84E-14	7.641	1.108	-2.786	0.017	0.456	-0.439	ZNF548	chr19:57908543-57909780:+	chr19
2.04E-07	4.36E-05	6.595	2.453	-1.427	0.123	0.552	-0.429	DOCK10	chr2:225670232-225670842:-	chr2
6.14E-30	1.35E-26	7.282	0.632	-3.527	0.003	0.431	-0.428	IQGAP3	chr1:156532467-156532925:-	chr1
2.29E-21	2.67E-18	6.605	1.501	-2.138	0.015	0.429	-0.413	VPS8	chr3:184566984-184567705:+	chr3
4.83E-14	2.71E-11	5.492	0.102	-5.746	0.000	0.410	-0.410	MYL6	chr12:56552496-56553390:+	chr12
1.03E-28	2.17E-25	17.632	4.222	-2.062	0.016	0.418	-0.402	MYL4	chr17:45300424-45300861:+	chr17
2.15E-38	8.80E-35	8.152	1.666	-2.291	0.031	0.432	-0.401	FAM134A	chr2:220044486-220044888:+	chr2
5.89E-16	4.07E-13	5.097	0.751	-2.764	0.005	0.397	-0.392	NDUFB8	chr10:102276735-102286155:-	chr10
8.73E-62	1.54E-57	11.241	0.091	-6.949	0.000	0.390	-0.390	DIP2A	chr21:47970658-47971529:+	chr21
1.01E-05	0.0014	5.142	1.976	-1.380	0.162	0.552	-0.390	ARRDC1	chr9:140508222-140508388:+	chr9
2.20E-09	6.84E-07	4.187	1.205	-1.797	0.024	0.412	-0.388	FAM188B	chr7:30811173-30818033:+	chr7
6.27E-16	4.32E-13	5.609	0.732	-2.938	0.003	0.390	-0.386	GUCY1B3	chr4:156721227-156723466:+	chr4
1.49E-22	2.01E-19	7.334	0.706	-3.377	0.003	0.385	-0.382	CEP135	chr4:56874549-56875878:+	chr4
1.95E-12	8.96E-10	4.179	0.597	-2.808	0.004	0.382	-0.377	HELLS	chr10:96305665-96306117:+	chr10
1.39E-37	5.40E-34	16.441	5.719	-1.523	0.045	0.416	-0.371	HINT2	chr9:35813154-35813262:-	chr9
6.47E-09	1.87E-06	5.254	1.178	-2.157	0.017	0.382	-0.366	HERC2P2	chr15:23283431-23285704:-	chr15
2.42E-14	1.38E-11	8.805	3.725	-1.241	0.387	0.743	-0.356	ANKRD11	chr16:89358208-89371613:-	chr16
1.37E-36	5.05E-33	10.150	3.592	-1.499	0.039	0.392	-0.353	GSAP	chr7:76943821-76950041:-	chr7
6.66E-10	2.24E-07	6.647	2.882	-1.206	0.080	0.429	-0.349	IDUA	chr4:995352-995438:+	chr4
4.62E-15	2.86E-12	8.387	2.409	-1.800	0.031	0.375	-0.344	RWDD4	chr4:184577128-184580081:-	chr4
3.66E-15	2.30E-12	6.266	2.105	-1.573	0.056	0.396	-0.341	WDR90	chr16:708345-708509:+	chr16
3.19E-08	8.13E-06	7.109	3.023	-1.234	0.085	0.421	-0.336	CCDC66	chr3:56649301-56649931:+	chr3
1.86E-27	3.46E-24	6.812	0.556	-3.614	0.005	0.338	-0.333	TRIM37	chr17:57148330-57153007:-	chr17
1.64E-17	1.38E-14	7.788	0.895	-3.121	0.004	0.333	-0.329	TBRG1	chr11:124495800-124496355:+	chr11
6.94E-12	3.02E-09	7.588	1.251	-2.600	0.010	0.338	-0.328	LIG3	chr17:33319712-33321272:+	chr17

2.77E-48	2.34E-44	8.788	0.848	-3.373	0.003	0.316	-0.313	DPH5	chr1:101458311-101460665:-	chr1
1.10E-19	1.11E-16	9.579	3.891	-1.300	0.054	0.365	-0.310	DLG1	chr3:196792336-196792578:-	chr3
6.18E-08	1.47E-05	4.228	1.614	-1.389	0.063	0.364	-0.301	RIOK1	chr6:7393537-7395239:+	chr6
3.71E-17	3.01E-14	5.377	1.080	-2.316	0.006	0.306	-0.300	COL23A1	chr5:177684584-177686721:-	chr5
7.19E-17	5.61E-14	8.846	1.300	-2.767	0.004	0.297	-0.294	CCDC125	chr5:68602750-68603777:-	chr5
1.55E-44	9.94E-41	7.780	0.549	-3.826	0.002	0.290	-0.288	NFYA	chr6:41040824-41046743:+	chr6
1.94E-22	2.61E-19	11.354	0.959	-3.566	0.002	0.284	-0.281	EML3	chr11:62376299-62376433:-	chr11
7.51E-07	0.00014	7.697	4.920	-0.646	0.308	0.583	-0.276	STARD8	chrX:67936274-67937041:+	chrX
3.16E-20	3.33E-17	5.262	0.094	-5.807	0.000	0.275	-0.275	CDK8	chr13:26970492-26971275:+	chr13
3.59E-05	0.00402	5.598	2.852	-0.973	0.130	0.392	-0.262	IFI35	chr17:41164295-41164946:+	chr17
0.00034	0.02326	4.987	3.089	-0.691	0.139	0.398	-0.259	DERL3	chr22:24177167-24179250:-	chr22
6.35E-14	3.52E-11	5.246	1.592	-1.721	0.021	0.277	-0.257	TCP11L1	chr11:33080642-33083060:+	chr11
2.21E-64	5.06E-60	20.181	2.074	-3.283	0.002	0.257	-0.255	TYMP	chr22:50966162-50966940:-	chr22
2.61E-15	1.65E-12	6.007	1.850	-1.699	0.032	0.285	-0.253	GABPA	chr21:27107890-27113871:+	chr21
1.18E-27	2.20E-24	7.710	1.286	-2.584	0.005	0.257	-0.251	FAM132B	chr2:239070358-239071364:+	chr2
8.67E-28	1.68E-24	6.184	0.751	-3.042	0.004	0.253	-0.249	HTT	chr4:3142384-3144471:+	chr4
3.92E-07	7.90E-05	6.611	3.381	-0.968	0.101	0.345	-0.244	PCNXL3	chr11:65388438-65389694:+	chr11
1.22E-08	3.38E-06	7.020	3.581	-0.971	0.105	0.348	-0.243	TTI1	chr20:36631196-36634598:-	chr20
3.25E-32	8.53E-29	7.155	0.987	-2.857	0.003	0.242	-0.238	ZMYM4	chr1:35871070-35873587:+	chr1
3.59E-18	3.13E-15	6.473	0.951	-2.767	0.003	0.241	-0.238	TPP2	chr13:103297360-103298629:+	chr13
4.73E-17	3.80E-14	4.951	0.735	-2.753	0.006	0.240	-0.234	FBN2	chr5:127624271-127624818:-	chr5
8.79E-13	4.25E-10	5.796	1.570	-1.884	0.023	0.252	-0.229	EPG5	chr18:43459193-43460039:-	chr18
1.08E-05	0.00147	8.231	2.571	-1.678	0.030	0.259	-0.229	TMC5	chr16:19498664-19499145:-	chr16
2.57E-16	1.86E-13	5.914	1.463	-2.015	0.015	0.243	-0.227	SMURF2	chr17:62574713-62576906:-	chr17
1.73E-28	3.52E-25	7.376	0.986	-2.903	0.005	0.232	-0.227	GTF2I	chr7:74131271-74133179:+	chr7
5.69E-14	3.16E-11	4.374	0.545	-3.004	0.003	0.229	-0.226	ADCY4	chr14:24788662-24788947:-	chr14
3.70E-16	2.63E-13	6.523	0.613	-3.411	0.002	0.228	-0.226	ECT2	chr3:172479474-172480187:+	chr3
2.82E-22	3.69E-19	8.779	0.578	-3.924	0.001	0.226	-0.225	C1D	chr2:68274469-68290089:-	chr2
5.03E-17	4.02E-14	6.045	0.768	-2.976	0.003	0.227	-0.224	ZFYVE27	chr10:99502922-99504468:+	chr10
2.69E-10	9.59E-08	7.167	1.548	-2.211	0.010	0.233	-0.223	FAM13A-AS1	chr4:89633169-89643287:+	chr4
1.82E-56	2.31E-52	13.043	2.077	-2.651	0.005	0.222	-0.217	SAFB2	chr19:5595522-5598803:-	chr19
8.99E-24	1.32E-20	8.214	3.319	-1.307	0.039	0.254	-0.214	RNF2	chr1:185056773-185060696:+	chr1
3.07E-11	1.25E-08	8.173	3.112	-1.393	0.027	0.240	-0.213	KIAA0196	chr8:126051219-126052036:-	chr8
2.52E-21	2.91E-18	5.986	0.785	-2.930	0.004	0.217	-0.213	TOR1AIP2	chr1:179835005-179846373:-	chr1
6.75E-23	9.30E-20	6.425	0.707	-3.184	0.002	0.214	-0.212	FASTKD1	chr2:170388019-170393736:-	chr2
8.48E-14	4.66E-11	4.831	0.851	-2.505	0.003	0.215	-0.212	CHD7	chr8:61741366-61742868:+	chr8
2.40E-06	0.0004	4.326	2.099	-1.043	0.044	0.253	-0.209	IDUA	chr4:995352-995433:+	chr4
1.01E-32	2.79E-29	7.363	1.530	-2.266	0.010	0.216	-0.206	MAN2A1	chr5:109181708-109183328:+	chr5
2.56E-07	5.34E-05	12.602	4.080	-1.627	0.058	0.264	-0.206	TMCC2	chr1:205240384-205240923:+	chr1
7.14E-08	1.68E-05	9.642	5.351	-0.849	0.099	0.303	-0.204	UBR4	chr1:19480449-19481411:-	chr1
3.77E-20	3.90E-17	6.985	1.556	-2.167	0.009	0.211	-0.203	DNAJC3	chr13:96377507-96409878:+	chr13
1.84E-13	9.78E-11	5.879	0.989	-2.571	0.004	0.205	-0.201	VARS2	chr6:30884737-30884871:+	chr6
4.44E-58	6.35E-54	10.980	2.606	-2.075	0.012	0.210	-0.198	STIM1	chr11:4104213-4104471:+	chr11
8.03E-13	3.95E-10	4.829	0.951	-2.345	0.010	0.208	-0.197	CBY1	chr22:39064138-39066874:+	chr22
2.62E-16	1.89E-13	5.870	1.281	-2.196	0.006	0.202	-0.196	FIG4	chr6:110085186-110086201:+	chr6
0.00014	0.01219	3.709	1.805	-1.039	0.055	0.250	-0.195	CDC7	chr1:91966506-91967193:+	chr1
3.62E-10	1.26E-07	8.215	1.803	-2.188	0.015	0.209	-0.195	RNF38	chr9:36351217-36352738:-	chr9
5.49E-15	3.37E-12	11.561	1.854	-2.640	0.006	0.199	-0.193	SLC7A7	chr14:23242938-23243141:-	chr14
9.71E-21	1.08E-17	5.373	0.587	-3.194	0.003	0.194	-0.192	UBXN2A	chr2:24207702-24222524:+	chr2
7.93E-10	2.63E-07	5.488	1.984	-1.468	0.027	0.218	-0.191	VPS8	chr3:184587317-184588487:+	chr3
8.31E-17	6.38E-14	5.841	0.979	-2.577	0.005	0.195	-0.190	SCLT1	chr4:129886490-129891532:-	chr4
1.11E-44	7.47E-41	9.546	2.360	-2.016	0.011	0.201	-0.190	PDLIM7	chr5:176916843-176917870:-	chr5
1.24E-15	8.13E-13	5.750	0.540	-3.413	0.002	0.192	-0.189	SUPV3L1	chr10:70955022-70956733:+	chr10
1.25E-14	7.32E-12	7.366	2.580	-1.514	0.018	0.206	-0.188	HYI	chr1:43917703-43917875:-	chr1
1.17E-13	6.41E-11	7.964	1.493	-2.415	0.008	0.195	-0.187	TMEM179B	chr11:62555000-62556481:+	chr11
5.80E-40	2.88E-36	10.072	1.851	-2.444	0.007	0.192	-0.185	PLXND1	chr3:129284873-129285369:-	chr3

9.72E-13	4.67E-10	8.267	3.213	-1.364	0.024	0.206	-0.182	RECQL	chr12:21627930-21628401:-	chr12
1.00E-12	4.78E-10	5.461	1.231	-2.150	0.005	0.186	-0.181	DOCK5	chr8:25224487-25225688:+	chr8
7.71E-39	3.46E-35	11.286	3.540	-1.673	0.019	0.199	-0.180	PRPF38A	chr1:52880320-52880412:+	chr1
2.67E-29	5.64E-26	7.348	1.448	-2.344	0.008	0.185	-0.177	OAS1	chr12:113346630-113348840:+	chr12
1.20E-22	1.63E-19	6.843	1.602	-2.094	0.007	0.183	-0.176	HYI	chr1:43917718-43917875:-	chr1
1.11E-28	2.32E-25	6.617	0.865	-2.935	0.003	0.179	-0.176	MUT	chr6:49416665-49419178:-	chr6
6.86E-19	6.28E-16	5.485	0.710	-2.949	0.003	0.178	-0.175	RDX	chr11:110128653-110128830:-	chr11
5.41E-60	8.84E-56	14.915	4.041	-1.884	0.013	0.187	-0.175	SHKBP1	chr19:41084119-41084353:+	chr19
2.84E-14	1.62E-11	5.102	1.337	-1.932	0.012	0.186	-0.174	RABGAP1	chr9:125759641-125760854:+	chr9
1.04E-10	3.97E-08	7.275	3.977	-0.871	0.695	0.865	-0.171	USP34	chr2:61415872-61416044:-	chr2
2.65E-09	8.13E-07	8.058	1.395	-2.530	0.005	0.176	-0.171	TRIM10	chr6:30124850-30125145:-	chr6
4.54E-08	1.12E-05	3.697	0.910	-2.022	0.015	0.183	-0.168	ESPL1	chr12:53666642-53668573:+	chr12
2.86E-54	3.11E-50	10.599	1.448	-2.872	0.002	0.167	-0.165	FAR2	chr12:29450134-29460566:+	chr12
2.92E-07	6.04E-05	4.840	2.310	-1.067	0.040	0.205	-0.164	SETD4	chr21:37416268-37417879:-	chr21
0.00011	0.00981	4.690	2.717	-0.787	0.075	0.237	-0.162	DHX35	chr20:37635000-37638902:+	chr20
4.54E-05	0.00486	4.202	2.089	-1.008	0.456	0.617	-0.162	PRKCSH	chr19:11546528-11546892:+	chr19
8.04E-21	8.97E-18	8.185	2.591	-1.659	0.019	0.178	-0.159	ANKRD13A	chr12:110437590-110449795:+	chr12
2.84E-11	1.17E-08	4.518	0.543	-3.057	0.003	0.160	-0.157	NDRG3	chr20:35282127-35284762:-	chr20
8.92E-19	8.09E-16	6.003	0.506	-3.569	0.001	0.154	-0.153	UPF3B	chrX:118972032-118972329:-	chrX
4.65E-06	0.00072	4.773	2.498	-0.934	0.050	0.202	-0.152	SH2D2A	chr1:156785905-156786466:-	chr1
1.25E-35	4.03E-32	7.577	0.531	-3.835	0.001	0.153	-0.152	TNPO3	chr7:128645231-128655032:-	chr7
4.25E-14	2.39E-11	5.560	0.958	-2.537	0.006	0.155	-0.149	CC2D1A	chr19:14031736-14034130:+	chr19
3.34E-31	8.29E-28	8.385	0.617	-3.765	0.001	0.149	-0.148	NET1	chr10:5497082-5498027:+	chr10
3.82E-07	7.74E-05	9.014	4.780	-0.915	0.069	0.217	-0.148	BUB1B	chr15:40493182-40494590:+	chr15
3.65E-07	7.42E-05	6.363	3.483	-0.869	0.085	0.232	-0.148	RASGRP2	chr11:64494851-64496334:-	chr11
4.20E-22	5.36E-19	7.463	2.390	-1.643	0.018	0.165	-0.147	C7orf43	chr7:99752805-99752884:-	chr7
0.00052	0.03208	6.095	2.693	-1.178	0.058	0.204	-0.145	WAC	chr10:28824687-28824838:+	chr10
2.15E-19	2.07E-16	8.318	3.925	-1.084	0.039	0.184	-0.145	UBA7	chr3:49848903-49849302:-	chr3
3.30E-09	1.00E-06	7.102	1.011	-2.812	0.002	0.146	-0.143	MRE11A	chr11:94192765-94194101:-	chr11
5.32E-13	2.66E-10	4.569	0.767	-2.574	0.010	0.147	-0.137	PRPF38B	chr1:109235490-109236193:+	chr1
2.99E-21	3.40E-18	5.976	1.187	-2.332	0.008	0.142	-0.134	ITSN2	chr2:24538115-24550920:-	chr2
1.24E-11	5.22E-09	5.220	0.100	-5.712	0.000	0.133	-0.133	NOP58	chr2:203157627-203162080:+	chr2
4.28E-39	1.96E-35	8.738	0.737	-3.567	0.001	0.133	-0.133	PPP6R3	chr11:68363687-68367788:+	chr11
2.54E-11	1.05E-08	5.779	1.995	-1.535	0.014	0.146	-0.132	ELP2	chr18:33724998-33725896:+	chr18
1.38E-34	4.18E-31	6.606	0.090	-6.204	0.000	0.132	-0.132	KPNA1	chr3:122152653-122156016:-	chr3
1.42E-21	1.70E-18	5.832	0.539	-3.436	0.006	0.138	-0.132	SOS1	chr2:39285969-39294768:-	chr2
3.81E-16	2.70E-13	5.351	0.087	-5.939	0.000	0.129	-0.129	SLC35A3	chr1:100477090-100480840:+	chr1
1.27E-25	2.10E-22	6.522	0.955	-2.771	0.003	0.130	-0.127	DGCR2	chr22:19044700-19050714:-	chr22
1.05E-11	4.45E-09	4.985	0.072	-6.108	0.000	0.126	-0.126	CCNYL1	chr2:208607067-208611755:+	chr2
5.38E-28	1.07E-24	6.925	1.098	-2.656	0.003	0.128	-0.125	RTF1	chr15:41762591-41763349:+	chr15
4.18E-07	8.31E-05	3.818	1.009	-1.920	0.016	0.141	-0.125	TEX30	chr13:103422451-103426031:-	chr13
4.16E-07	8.29E-05	4.761	0.788	-2.595	0.002	0.126	-0.124	CEP152	chr15:49044681-49048099:-	chr15
4.58E-06	0.00071	7.201	3.383	-1.090	0.042	0.165	-0.123	NDST2	chr10:75566590-75566865:-	chr10
8.75E-22	1.09E-18	7.934	0.880	-3.172	0.002	0.122	-0.120	GCLC	chr6:53381039-53385575:-	chr6
7.67E-24	1.14E-20	5.373	0.079	-6.088	0.000	0.119	-0.119	SOAT1	chr1:179318078-179319411:+	chr1
0.00011	0.00963	4.374	0.077	-5.819	0.000	0.117	-0.117	RAD18	chr3:8923170-8932072:-	chr3
0.00021	0.01639	6.791	2.195	-1.630	0.015	0.129	-0.114	ZFAND5	chr9:74978548-74979611:-	chr9
1.24E-16	9.30E-14	8.319	1.320	-2.655	0.003	0.113	-0.110	COPS2	chr15:49420971-49421673:-	chr15
2.18E-16	1.59E-13	5.605	1.597	-1.811	0.009	0.119	-0.109	PROSER1	chr13:39605783-39608267:-	chr13
1.79E-28	3.63E-25	7.072	1.444	-2.292	0.006	0.115	-0.109	SYVN1	chr11:64900741-64900940:-	chr11
9.11E-40	4.43E-36	10.839	2.856	-1.924	0.010	0.118	-0.108	SLC3A2	chr11:62648920-62649352:+	chr11
2.44E-05	0.00291	3.876	1.660	-1.224	0.023	0.131	-0.108	ITSN1	chr21:35140133-35144342:+	chr21
0.00022	0.01656	3.924	2.066	-0.925	0.034	0.141	-0.106	MITD1	chr2:99788124-99789876:-	chr2
3.01E-18	2.67E-15	5.895	1.726	-1.772	0.010	0.115	-0.106	ITFG1	chr16:47347748-47399698:-	chr16
0.00027	0.01964	4.337	2.280	-0.928	0.032	0.137	-0.106	SCMH1	chr1:41579226-41582593:-	chr1
1.50E-05	0.00193	9.736	5.831	-0.739	0.055	0.160	-0.105	UBL7	chr15:74740929-74741526:-	chr15

6.51E-18	5.51E-15	5.550	0.973	-2.512	0.005	0.110	-0.104	PFDN5	chr12:53690336-53691607:+	chr12
8.80E-13	4.25E-10	5.566	1.322	-2.074	0.006	0.110	-0.104	CCDC84	chr11:118883973-118885685:+	chr11
4.13E-10	1.43E-07	4.695	0.551	-3.090	0.002	0.106	-0.104	DUSP22	chr6:348842-350802:+	chr6
1.13E-15	7.51E-13	8.200	1.645	-2.317	0.004	0.108	-0.104	YY1AP1	chr1:155630725-155631097:-	chr1
9.81E-28	1.85E-24	11.823	6.507	-0.862	0.041	0.144	-0.103	PTPN7	chr1:202122979-202123313:-	chr1
3.72E-13	1.89E-10	7.744	1.117	-2.793	0.003	0.106	-0.103	AKAP8	chr19:15479151-15480956:-	chr19
3.30E-24	4.96E-21	5.660	0.706	-3.004	0.002	0.104	-0.102	TPR	chr1:186324918-186325417:-	chr1
1.03E-06	0.00019	4.418	1.555	-1.506	0.014	0.116	-0.102	C10orf76	chr10:103771555-103772589:-	chr10
0.00062	0.03651	8.932	6.679	-0.419	0.093	0.193	-0.100	LYST	chr1:235914679-235915304:-	chr1
1.47E-05	0.0019	9.538	6.508	-0.551	0.103	0.202	-0.099	KEL	chr7:142651631-142654913:-	chr7
1.46E-05	0.00189	4.060	1.880	-1.110	0.062	0.160	-0.099	TRMT13	chr1:100606071-100606400:+	chr1
1.65E-08	4.46E-06	6.629	3.936	-0.752	0.044	0.141	-0.097	ATF1	chr12:51174022-51189680:+	chr12
1.03E-05	0.00141	4.751	2.110	-1.171	0.020	0.117	-0.097	DHX29	chr5:54566334-54566405:-	chr5
2.84E-08	7.31E-06	5.069	1.341	-1.918	0.006	0.099	-0.093	SLC33A1	chr3:155546181-155547476:-	chr3
1.74E-10	6.42E-08	4.765	0.922	-2.370	0.004	0.095	-0.091	TMEM94	chr17:73486840-73487110:+	chr17
0.00036	0.02453	7.057	2.684	-1.394	0.013	0.103	-0.089	ADAM9	chr8:38947708-38948761:+	chr8
1.63E-07	3.58E-05	4.807	2.316	-1.054	0.025	0.114	-0.089	ACD	chr16:67692736-67692830:-	chr16
9.26E-08	2.13E-05	11.487	8.730	-0.396	0.124	0.211	-0.088	RGL2	chr6:33261713-33261810:-	chr6
1.10E-05	0.0015	6.767	3.371	-1.005	0.028	0.115	-0.087	POLG	chr15:89870311-89870397:-	chr15
2.90E-20	3.09E-17	7.304	2.883	-1.341	0.015	0.100	-0.085	TNIP1	chr5:150411956-150413168:-	chr5
2.15E-14	1.23E-11	4.953	1.162	-2.091	0.005	0.089	-0.084	C15orf57	chr15:40849590-40854970:-	chr15
2.32E-22	3.09E-19	6.369	1.532	-2.056	0.005	0.088	-0.084	PDS5A	chr4:39911977-39915230:-	chr4
5.36E-15	3.30E-12	5.525	0.913	-2.597	0.003	0.085	-0.082	ULK3	chr15:75131105-75131350:-	chr15
1.66E-44	1.02E-40	9.041	2.070	-2.127	0.004	0.086	-0.082	VPS51	chr11:64877396-64877934:+	chr11
5.85E-41	3.04E-37	16.602	5.712	-1.539	0.010	0.091	-0.081	ITGAM	chr16:31288371-31289273:+	chr16
1.78E-10	6.54E-08	7.585	2.870	-1.402	0.013	0.095	-0.081	NPLOC4	chr17:79556146-79563141:-	chr17
1.14E-10	4.30E-08	13.579	7.554	-0.846	0.034	0.115	-0.081	GATA1	chrX:48651705-48652184:+	chrX
0.0001	0.00938	5.549	2.225	-1.318	0.007	0.088	-0.081	ADAM9	chr8:38899637-38911982:+	chr8
7.98E-11	3.10E-08	4.698	1.100	-2.094	0.002	0.083	-0.080	BAZ2B	chr2:160253916-160255339:-	chr2
4.71E-07	9.24E-05	7.511	4.416	-0.766	0.110	0.190	-0.080	C20orf24	chr20:35236222-35236271:+	chr20
1.20E-14	7.09E-12	5.095	0.934	-2.448	0.003	0.083	-0.080	RIOK1	chr6:7404789-7405128:+	chr6
4.20E-27	7.63E-24	6.699	1.478	-2.181	0.004	0.084	-0.080	SNW1	chr14:78203439-78205120:-	chr14
6.50E-06	0.00096	4.024	1.815	-1.148	0.027	0.106	-0.079	RASGRP2	chr11:64494863-64496334:-	chr11
2.82E-08	7.26E-06	4.284	1.442	-1.571	0.010	0.089	-0.079	PDHX	chr11:34953032-34969039:+	chr11
9.38E-08	2.16E-05	5.747	2.599	-1.145	0.014	0.093	-0.078	RPS6KA3	chrX:20194635-20195113:-	chrX
3.29E-05	0.00373	4.868	2.414	-1.012	0.023	0.101	-0.078	ARHGAP19	chr10:99025904-99052328:-	chr10
3.08E-16	2.22E-13	6.925	1.549	-2.161	0.004	0.082	-0.078	FKBP15	chr9:115934003-115935732:-	chr9
5.60E-31	1.36E-27	9.127	0.091	-6.652	0.000	0.077	-0.077	ANPEP	chr15:90342810-90344341:-	chr15
1.07E-12	5.09E-10	4.376	0.096	-5.517	0.000	0.077	-0.077	RAB4A	chr1:229407118-229422214:+	chr1
8.04E-17	6.21E-14	7.322	1.547	-2.243	0.003	0.079	-0.076	LPCAT2	chr16:55579730-55583167:+	chr16
4.25E-15	2.65E-12	9.026	1.713	-2.398	0.003	0.078	-0.075	STK24	chr13:99127257-99127503:-	chr13
1.39E-16	1.02E-13	5.244	0.667	-2.974	0.001	0.075	-0.074	SLC27A3	chr1:153751362-153751571:+	chr1
2.11E-22	2.82E-19	6.924	1.052	-2.719	0.001	0.074	-0.073	CKAP2	chr13:53029762-53030637:+	chr13
2.78E-07	5.77E-05	4.776	1.666	-1.519	0.008	0.081	-0.072	RASA1	chr5:86665718-86667916:+	chr5
4.42E-12	1.95E-09	5.655	1.687	-1.745	0.007	0.080	-0.072	TTK	chr6:80750421-80751814:+	chr6
9.46E-07	0.00018	6.352	3.971	-0.677	0.041	0.114	-0.072	EDEM2	chr20:33703762-33706400:-	chr20
1.91E-07	4.12E-05	4.226	1.757	-1.266	0.016	0.087	-0.071	FBXL19	chr16:30958270-30958352:+	chr16
1.70E-09	5.36E-07	4.797	1.716	-1.483	0.006	0.077	-0.071	DDIT3	chr12:57911243-57911488:-	chr12
1.48E-07	3.27E-05	4.688	2.014	-1.219	0.015	0.085	-0.070	CHTF8	chr16:69155088-69155338:-	chr16
8.05E-11	3.12E-08	4.588	0.978	-2.230	0.002	0.072	-0.070	NCAPG	chr4:17824747-17825253:+	chr4
7.21E-16	4.89E-13	5.362	0.646	-3.053	0.000	0.068	-0.068	CLEC3B	chr3:45043101-45046767:+	chr3
1.94E-13	1.03E-10	5.349	1.454	-1.879	0.005	0.073	-0.068	MINK1	chr17:4796064-4796240:+	chr17
1.13E-08	3.15E-06	6.207	2.252	-1.463	0.011	0.078	-0.068	DHX38	chr16:72139524-72139882:+	chr16
6.39E-06	0.00095	4.232	2.013	-1.072	0.014	0.081	-0.067	TRRAP	chr7:98579584-98580862:+	chr7
1.35E-19	1.36E-16	6.915	1.565	-2.144	0.004	0.071	-0.067	KTN1	chr14:56100060-56101230:+	chr14
2.60E-06	0.00043	9.416	5.975	-0.656	0.033	0.100	-0.066	NAGK	chr2:71299882-71300592:+	chr2

3.31E-05	0.00375	5.125	3.171	-0.693	0.044	0.110	-0.066	ASUN	chr12:27070393-27070576:-	chr12
1.41E-06	0.00025	4.010	1.280	-1.647	0.006	0.072	-0.066	MTOR	chr1:11272544-11272852:-	chr1
9.26E-06	0.0013	3.857	1.648	-1.227	0.016	0.082	-0.066	ANKZF1	chr2:220100035-220100182:+	chr2
5.04E-05	0.00529	5.052	3.106	-0.702	0.036	0.101	-0.065	KCTD9	chr8:25290170-25290845:-	chr8
3.00E-32	7.97E-29	19.137	3.962	-2.272	0.002	0.066	-0.064	ANXA3	chr4:79475643-79494320:+	chr4
2.85E-12	1.28E-09	4.449	1.003	-2.150	0.003	0.067	-0.064	ATPAF2	chr17:17925187-17927937:-	chr17
1.29E-16	9.55E-14	4.963	0.523	-3.246	0.000	0.064	-0.064	PTPN11	chr12:112915535-112915638:+	chr12
1.22E-12	5.72E-10	6.393	2.498	-1.356	0.010	0.073	-0.063	SUZ12	chr17:30315517-30320247:+	chr17
7.66E-07	0.00014	3.888	1.463	-1.410	0.007	0.070	-0.063	CTNNAL1	chr9:111741781-111745424:-	chr9
1.40E-35	4.38E-32	7.096	0.785	-3.175	0.001	0.063	-0.063	ACAA2	chr18:47311743-47313660:-	chr18
3.42E-27	6.25E-24	6.670	0.564	-3.563	0.001	0.063	-0.062	ATF6B	chr6:32095540-32095893:-	chr6
3.42E-13	1.76E-10	7.685	1.803	-2.092	0.004	0.066	-0.062	MRPS18C	chr4:84378112-84379477:+	chr4
9.58E-33	2.71E-29	8.486	0.557	-3.929	0.000	0.062	-0.061	AKAP8L	chr19:15491445-15507960:-	chr19
4.91E-08	1.20E-05	4.901	0.952	-2.365	0.002	0.064	-0.061	WDR34	chr9:131398064-131398559:-	chr9
2.34E-09	7.23E-07	4.757	1.529	-1.638	0.007	0.068	-0.061	ANAPC2	chr9:140069968-140070159:-	chr9
6.88E-37	2.58E-33	13.475	2.350	-2.520	0.002	0.062	-0.061	GUK1	chr1:228335401-228336058:+	chr1
7.15E-05	0.00703	4.877	1.892	-1.366	0.013	0.073	-0.061	NAT10	chr11:34161043-34161927:+	chr11
0.00073	0.04079	5.071	0.862	-2.557	0.002	0.062	-0.060	BUB1	chr2:111417629-111419158:-	chr2
3.52E-13	1.80E-10	4.659	1.059	-2.138	0.004	0.064	-0.060	ZC3H7A	chr16:11862969-11864638:-	chr16
1.69E-10	6.24E-08	6.381	2.012	-1.665	0.006	0.066	-0.060	DYNC1I2	chr2:172584929-172585212:+	chr2
6.57E-06	0.00097	4.269	1.196	-1.835	0.003	0.062	-0.060	MYO19	chr17:34854422-34854918:-	chr17
4.99E-14	2.79E-11	5.297	0.074	-6.168	0.000	0.060	-0.060	ATPAF1	chr1:47108989-47110832:-	chr1
2.41E-128	1.84E-123	62.469	#####	-0.352	0.031	0.090	-0.059	S100A8	chr1:153363051-153363516:-	chr1
8.02E-22	1.01E-18	13.876	2.357	-2.557	0.001	0.061	-0.059	ITGAM	chr16:31338257-31339437:+	chr16
7.99E-15	4.81E-12	5.845	1.413	-2.049	0.004	0.063	-0.059	NUP98	chr11:3697620-3697738:-	chr11
4.08E-08	1.02E-05	4.522	1.752	-1.368	0.012	0.071	-0.059	KIAA0319L	chr1:35917393-35919157:-	chr1
2.40E-22	3.16E-19	6.261	0.089	-6.135	0.000	0.058	-0.058	MRPS9	chr2:105713783-105716106:+	chr2
2.68E-39	1.25E-35	7.769	1.160	-2.744	0.001	0.059	-0.057	SF3A2	chr19:2247022-2247564:+	chr19
1.29E-06	0.00023	5.287	1.361	-1.958	0.006	0.063	-0.057	TTC3	chr21:38570327-38572514:+	chr21
2.95E-20	3.12E-17	6.709	1.935	-1.794	0.005	0.062	-0.057	TPR	chr1:186300729-186301326:-	chr1
1.06E-21	1.31E-18	6.666	0.069	-6.598	0.000	0.056	-0.056	TBC1D15	chr12:72315235-72316743:+	chr12
1.69E-31	4.35E-28	6.150	0.080	-6.259	0.000	0.056	-0.056	DOCK8	chr9:317129-325647:+	chr9
2.44E-10	8.76E-08	4.307	0.107	-5.337	0.000	0.055	-0.055	DENND4A	chr15:65962545-65964129:-	chr15
1.48E-13	7.98E-11	5.803	1.636	-1.826	0.004	0.059	-0.055	PTPRJ	chr11:48171551-48171633:+	chr11
5.23E-45	3.63E-41	8.456	1.239	-2.770	0.001	0.055	-0.054	REXO2	chr11:114316810-114318499:+	chr11
0.0001	0.0094	10.726	6.167	-0.799	0.025	0.079	-0.054	TRABD	chr22:50635781-50635865:+	chr22
1.35E-26	2.33E-23	6.026	0.067	-6.488	0.000	0.053	-0.053	TP53I11	chr11:44957238-44958353:-	chr11
0.00083	0.04478	5.195	3.015	-0.785	0.026	0.079	-0.053	PPP6R2	chr22:50832565-50845095:+	chr22
1.38E-18	1.24E-15	5.084	0.772	-2.720	0.001	0.054	-0.053	ATP6V1A	chr3:113497683-113499879:+	chr3
5.94E-13	2.96E-10	4.663	1.030	-2.179	0.003	0.056	-0.053	PPP3CB	chr10:75231388-75234676:-	chr10
5.29E-06	0.0008	7.989	3.456	-1.209	0.011	0.064	-0.052	CPSF1	chr8:145624053-145624168:-	chr8
1.53E-41	8.35E-38	10.453	1.425	-2.875	0.001	0.053	-0.052	SRSF1	chr17:56082979-56083161:-	chr17
1.62E-10	6.03E-08	8.494	3.640	-1.223	0.011	0.063	-0.052	RASAL3	chr19:15565390-15565467:-	chr19
9.38E-12	4.00E-09	7.564	1.870	-2.016	0.003	0.054	-0.052	STK17B	chr2:197004545-197005972:-	chr2
2.72E-12	1.23E-09	6.146	2.527	-1.282	0.010	0.061	-0.051	NFE2L2	chr2:178096759-178097119:-	chr2
7.33E-11	2.87E-08	4.075	0.607	-2.747	0.001	0.052	-0.050	PIP5K1B	chr9:71433462-71437514:+	chr9
1.85E-10	6.76E-08	4.023	0.590	-2.769	0.001	0.051	-0.050	FAM65C	chr20:49225085-49225149:-	chr20
2.52E-08	6.56E-06	4.545	0.751	-2.598	0.002	0.052	-0.050	SCFD1	chr14:31169465-31171484:+	chr14
4.00E-07	8.03E-05	5.138	1.854	-1.471	0.007	0.057	-0.050	AKAP10	chr17:19812609-19813238:-	chr17
4.84E-10	1.67E-07	7.127	3.431	-1.055	0.014	0.064	-0.050	EIF3B	chr7:2419147-2419815:+	chr7
7.08E-11	2.78E-08	7.985	1.836	-2.121	0.003	0.053	-0.049	DGKZ	chr11:46389298-46389527:+	chr11
2.71E-05	0.00318	4.193	2.192	-0.936	0.018	0.067	-0.049	SCLT1	chr4:129867320-129869650:-	chr4
1.47E-31	3.81E-28	7.147	1.180	-2.598	0.001	0.050	-0.048	BTK	chrX:100630322-100641049:-	chrX
4.71E-05	0.00501	5.233	1.728	-1.599	0.006	0.054	-0.048	KIF5B	chr10:32328377-32329311:-	chr10
9.79E-09	2.76E-06	4.308	1.156	-1.898	0.005	0.052	-0.048	HECTD3	chr1:45474012-45474207:-	chr1
6.59E-17	5.22E-14	6.227	0.804	-2.954	0.001	0.049	-0.048	CUL4A	chr13:113915074-113917776:+	chr13

1.33E-32	3.61E-29	7.642	1.348	-2.503	0.002	0.049	-0.048	NRD1	chr1:52293559-52299688:-	chr1
1.30E-21	1.56E-18	5.888	1.148	-2.359	0.003	0.050	-0.047	CDC27	chr17:45216273-45219218:-	chr17
2.40E-08	6.28E-06	4.137	1.189	-1.798	0.004	0.052	-0.047	AP5Z1	chr7:4827408-4827743:+	chr7
7.36E-10	2.46E-07	5.562	2.429	-1.195	0.010	0.057	-0.047	ZMYM2	chr13:20656271-20656905:+	chr13
6.37E-07	0.00012	5.118	1.231	-2.056	0.004	0.051	-0.047	KDM3A	chr2:86705389-86705705:+	chr2
1.85E-05	0.0023	5.062	2.967	-0.771	0.033	0.080	-0.047	UCKL1	chr20:62577342-62577513:-	chr20
1.30E-07	2.90E-05	4.177	1.239	-1.753	0.004	0.050	-0.047	MAVS	chr20:3845436-3846309:+	chr20
5.01E-08	1.22E-05	4.117	1.539	-1.420	0.006	0.052	-0.046	HCFC1	chrX:153229751-153230028:-	chrX
1.74E-36	6.31E-33	7.535	1.226	-2.620	0.001	0.047	-0.046	PAK1	chr11:77090455-77090938:-	chr11
1.34E-12	6.25E-10	4.650	0.098	-5.563	0.000	0.045	-0.045	SVIL	chr10:29756819-29759204:-	chr10
1.12E-12	5.31E-10	4.429	0.749	-2.564	0.002	0.047	-0.045	ZMIZ2	chr7:44795899-44796008:+	chr7
3.93E-08	9.84E-06	3.938	1.245	-1.661	0.005	0.048	-0.044	PDXDC1	chr16:15129411-15129852:+	chr16
7.59E-15	4.58E-12	5.799	1.941	-1.579	0.005	0.048	-0.043	GAK	chr4:844890-845537:-	chr4
0.00039	0.02613	4.158	1.650	-1.334	0.008	0.051	-0.043	CREB1	chr2:208425097-208432169:+	chr2
3.74E-22	4.80E-19	6.618	1.127	-2.554	0.001	0.044	-0.043	GPS1	chr17:80013702-80013861:+	chr17
1.01E-58	1.53E-54	26.081	9.022	-1.532	0.004	0.047	-0.043	LRRC75A-AS	chr17:16344445-16344670:+	chr17
1.75E-26	2.99E-23	6.339	0.785	-3.014	0.001	0.043	-0.043	CLASRP	chr19:45572507-45573243:+	chr19
2.32E-36	8.15E-33	9.092	1.233	-2.882	0.001	0.043	-0.042	PSTPIP1	chr15:77317660-77317818:+	chr15
8.10E-13	3.97E-10	4.833	1.330	-1.861	0.004	0.046	-0.042	SLC11A1	chr2:219257854-219258817:+	chr2
2.32E-10	8.37E-08	6.241	1.346	-2.213	0.002	0.044	-0.042	CRLF3	chr17:29124438-29130918:-	chr17
7.06E-36	2.34E-32	8.401	2.218	-1.922	0.008	0.050	-0.041	FBXW5	chr9:139837450-139837800:-	chr9
2.26E-10	8.18E-08	6.743	3.714	-0.860	0.019	0.061	-0.041	NADSYN1	chr11:71174532-71175078:+	chr11
4.63E-09	1.37E-06	4.794	1.553	-1.626	0.005	0.045	-0.041	CUL1	chr7:148451243-148454059:+	chr7
1.54E-48	1.41E-44	11.070	1.792	-2.627	0.001	0.041	-0.040	NONO	chrX:70516898-70517210:+	chrX
1.45E-10	5.43E-08	4.204	1.126	-1.900	0.003	0.042	-0.040	ZRANB1	chr10:126660688-126662195:+	chr10
1.06E-20	1.16E-17	6.533	0.445	-3.877	0.000	0.040	-0.039	DOCK8	chr9:432325-433857:+	chr9
6.61E-11	2.61E-08	4.545	1.469	-1.630	0.004	0.043	-0.039	NCOR1	chr17:15967517-15968183:-	chr17
0.00015	0.0125	4.051	1.927	-1.072	0.009	0.047	-0.038	FEZ2	chr2:36780340-36782825:-	chr2
8.54E-11	3.29E-08	4.686	1.292	-1.859	0.003	0.042	-0.038	TBPL1	chr6:134301399-134303688:+	chr6
0.00013	0.0116	4.747	2.708	-0.810	0.017	0.055	-0.038	PHYKPL	chr5:177649600-177649852:-	chr5
3.79E-42	2.12E-38	11.494	2.260	-2.346	0.002	0.040	-0.038	ITGAM	chr16:31284840-31286849:+	chr16
1.61E-16	1.18E-13	5.085	0.961	-2.403	0.002	0.040	-0.038	MAN1A1	chr6:119511061-119514941:-	chr6
2.08E-19	2.00E-16	25.464	3.529	-2.851	0.001	0.039	-0.038	RPL24	chr3:101401354-101401614:-	chr3
2.13E-06	0.00036	4.255	1.736	-1.293	0.007	0.045	-0.038	PPP1R12A	chr12:80200133-80201005:-	chr12
1.81E-19	1.76E-16	6.944	1.411	-2.299	0.001	0.039	-0.037	NHP2	chr5:177576860-177577888:-	chr5
2.17E-28	4.35E-25	9.633	2.498	-1.947	0.003	0.040	-0.037	HADHA	chr2:26437446-26437921:-	chr2
1.38E-10	5.19E-08	4.437	1.316	-1.753	0.003	0.040	-0.037	GTF2F2	chr13:45841512-45857556:+	chr13
5.77E-31	1.39E-27	8.525	2.917	-1.547	0.004	0.041	-0.036	OS9	chr12:58109977-58110164:+	chr12
9.94E-21	1.10E-17	6.545	2.100	-1.640	0.004	0.040	-0.036	MCM3AP	chr21:47655361-47656742:-	chr21
4.15E-06	0.00065	4.109	1.811	-1.182	0.009	0.045	-0.036	CDC27	chr17:45234507-45234595:-	chr17
5.68E-19	5.28E-16	5.610	1.014	-2.468	0.001	0.037	-0.036	LRPPRC	chr2:44145291-44145394:-	chr2
3.90E-11	1.58E-08	4.397	0.773	-2.508	0.001	0.036	-0.035	TRAPPC10	chr21:45457809-45472142:+	chr21
4.21E-08	1.04E-05	5.376	2.604	-1.046	0.010	0.045	-0.035	CYLD	chr16:50813956-50815142:+	chr16
1.80E-05	0.00225	6.188	3.528	-0.811	0.017	0.052	-0.035	FAM76B	chr11:95513113-95516228:-	chr11
4.91E-18	4.24E-15	5.785	0.936	-2.627	0.001	0.036	-0.035	PNPLA6	chr19:7625651-7625886:+	chr19
1.15E-07	2.60E-05	5.049	0.737	-2.776	0.001	0.035	-0.035	NT5C3A	chr7:33055500-33057050:-	chr7
2.24E-10	8.14E-08	3.997	0.854	-2.226	0.001	0.036	-0.035	MRPS27	chr5:71524211-71528269:-	chr5
5.56E-08	1.34E-05	6.767	3.451	-0.972	0.015	0.050	-0.035	MBOAT2	chr2:9004381-9008575:-	chr2
2.81E-05	0.00328	4.902	2.317	-1.081	0.010	0.044	-0.034	MMS19	chr10:99219517-99219802:-	chr10
2.30E-21	2.67E-18	6.589	1.063	-2.631	0.001	0.034	-0.033	LRRC75A-AS	chr17:16343568-16344670:+	chr17
3.93E-13	1.98E-10	4.391	0.590	-2.897	0.001	0.033	-0.032	TCERG1	chr5:145883103-145883371:+	chr5
4.60E-05	0.00492	8.614	5.780	-0.576	0.022	0.053	-0.032	USP15	chr12:62783480-62783562:+	chr12
3.32E-13	1.72E-10	5.857	2.268	-1.369	0.005	0.037	-0.032	MYB	chr6:135507159-135508950:+	chr6
8.88E-28	1.71E-24	7.008	1.518	-2.207	0.002	0.033	-0.031	NBEAL2	chr3:47042670-47042740:+	chr3
7.08E-17	5.56E-14	6.850	0.912	-2.908	0.000	0.032	-0.031	GSDMD	chr8:144643999-144644083:+	chr8
0.00026	0.01907	9.459	0.794	-3.574	0.000	0.031	-0.031	SF3B1	chr2:198267784-198268308:-	chr2

1.09E-14	6.46E-12	5.231	0.984	-2.411	0.001	0.032	-0.031	SAP30BP	chr17:73689563-73695838:+	chr17
5.08E-05	0.00533	3.750	1.709	-1.134	0.008	0.039	-0.030	ANAPC2	chr9:140074996-140075239:-	chr9
2.67E-13	1.40E-10	5.042	0.721	-2.806	0.001	0.031	-0.030	UBXN11	chr1:26609461-26610632:-	chr1
3.61E-36	1.23E-32	10.070	1.326	-2.925	0.001	0.031	-0.030	CD36	chr7:80301357-80302070:+	chr7
2.44E-17	2.03E-14	7.606	2.609	-1.544	0.004	0.034	-0.030	HIF1A	chr14:62207907-62211405:+	chr14
5.01E-07	9.77E-05	4.249	1.610	-1.400	0.006	0.036	-0.030	CAPRIN2	chr12:30888157-30893953:-	chr12
6.51E-30	1.42E-26	11.055	2.499	-2.145	0.001	0.030	-0.029	GPX1	chr3:49395200-49395459:-	chr3
6.61E-06	0.00097	4.412	1.571	-1.489	0.006	0.035	-0.029	KIAA0100	chr17:26969116-26969292:-	chr17
0.00046	0.02943	5.136	3.216	-0.675	0.015	0.044	-0.029	RBCK1	chr20:409234-409571:+	chr20
2.27E-07	4.79E-05	6.741	4.221	-0.675	0.021	0.050	-0.029	RGL2	chr6:33261105-33261189:-	chr6
0.00038	0.02554	4.188	2.522	-0.732	0.014	0.042	-0.029	KDM7A	chr7:139796876-139797344:-	chr7
3.02E-07	6.21E-05	5.707	2.537	-1.169	0.007	0.036	-0.028	DCK	chr4:71888278-71889263:+	chr4
1.01E-23	1.47E-20	5.846	0.767	-2.930	0.000	0.029	-0.028	HIGD2A	chr5:175815975-175816311:+	chr5
5.38E-05	0.00559	12.907	9.106	-0.503	0.030	0.058	-0.028	AP2S1	chr19:47342878-47349249:-	chr19
5.91E-06	0.00088	5.352	2.932	-0.868	0.008	0.036	-0.028	STK38	chr6:36466281-36467649:-	chr6
2.90E-13	1.51E-10	5.870	1.179	-2.315	0.001	0.029	-0.028	IARS	chr9:95007368-95009658:-	chr9
0.00036	0.02444	4.250	1.480	-1.522	0.005	0.032	-0.027	MITD1	chr2:99788124-99790377:-	chr2
0.00089	0.04753	20.160	#####	-0.515	0.633	0.660	-0.027	LYST	chr1:235992340-235993525:-	chr1
1.28E-15	8.38E-13	4.669	0.575	-3.021	0.000	0.027	-0.027	MBD4	chr3:129156809-129158572:-	chr3
4.43E-06	0.00069	3.878	1.713	-1.179	0.005	0.032	-0.027	MRPL40	chr22:19422418-19423149:+	chr22
1.84E-18	1.64E-15	5.600	1.345	-2.057	0.001	0.028	-0.027	ARAP1	chr11:72404529-72404736:-	chr11
3.99E-05	0.00439	3.760	1.719	-1.129	0.006	0.033	-0.027	GNPTG	chr16:1402308-1411695:+	chr16
4.06E-07	8.13E-05	10.604	7.114	-0.576	0.016	0.043	-0.026	FMNL1	chr17:43322784-43322985:+	chr17
0.00011	0.00966	4.651	0.103	-5.492	0.000	0.026	-0.026	MRPL3	chr3:131181738-131186934:-	chr3
7.12E-10	2.39E-07	5.365	2.139	-1.327	0.004	0.031	-0.026	SMARCD2	chr17:61910804-61910946:-	chr17
0.00043	0.02767	3.796	1.784	-1.090	0.015	0.041	-0.026	PBRM1	chr3:52692359-52696148:-	chr3
4.88E-05	0.00515	4.288	1.785	-1.264	0.005	0.031	-0.026	CUL4A	chr13:113864403-113873243:+	chr13
1.23E-15	8.07E-13	5.460	1.044	-2.387	0.001	0.026	-0.026	MBOAT2	chr2:9048865-9083315:-	chr2
1.67E-06	0.00029	4.001	1.515	-1.401	0.003	0.029	-0.025	EIF4G3	chr1:21137396-21139650:-	chr1
1.05E-07	2.40E-05	4.248	1.315	-1.692	0.002	0.027	-0.025	CA1	chr8:86250389-86250480:-	chr8
1.96E-07	4.20E-05	4.662	1.024	-2.187	0.002	0.026	-0.024	CDK2	chr12:56361954-56362539:+	chr12
1.29E-16	9.55E-14	6.464	1.674	-1.949	0.002	0.025	-0.023	ITGA4	chr2:182395377-182396362:+	chr2
5.87E-05	0.006	4.300	1.181	-1.864	0.002	0.025	-0.023	STARD3	chr17:37816527-37816662:+	chr17
0.00024	0.01794	3.645	1.635	-1.156	0.005	0.028	-0.023	BRIX1	chr5:34922393-34922624:+	chr5
1.97E-06	0.00034	6.839	4.068	-0.750	0.010	0.033	-0.023	MYO1G	chr7:45003777-45004013:-	chr7
4.76E-15	2.93E-12	6.635	1.381	-2.264	0.001	0.024	-0.023	PFDN5	chr12:53689424-53691607:+	chr12
1.71E-19	1.68E-16	5.217	0.559	-3.223	0.000	0.023	-0.022	NOP58	chr2:203160561-203162080:+	chr2
6.46E-11	2.56E-08	4.563	1.370	-1.736	0.002	0.024	-0.022	TIMM17B	chrX:48751115-48751182:-	chrX
0.00022	0.01665	4.294	2.085	-1.042	0.006	0.028	-0.022	SEC63	chr6:108225945-108227651:-	chr6
4.41E-06	0.00069	5.864	3.656	-0.682	0.014	0.035	-0.021	AKT2	chr19:40746029-40747844:-	chr19
9.00E-11	3.45E-08	8.371	2.457	-1.768	0.001	0.022	-0.021	CHI3L1	chr1:203154527-203155443:-	chr1
1.35E-13	7.31E-11	4.035	0.094	-5.427	0.000	0.021	-0.021	PCNP	chr3:101293124-101298615:+	chr3
3.42E-10	1.19E-07	4.296	0.833	-2.366	0.001	0.021	-0.020	CD163	chr12:7648016-7649408:-	chr12
2.45E-07	5.13E-05	4.551	1.512	-1.590	0.002	0.022	-0.020	HSPA4	chr5:132439719-132439902:+	chr5
1.46E-20	1.59E-17	6.200	1.400	-2.147	0.001	0.021	-0.020	UBA1	chrX:47065513-47065623:+	chrX
1.49E-15	9.66E-13	5.946	1.352	-2.137	0.001	0.021	-0.020	SYF2	chr1:25554745-25555488:-	chr1
9.40E-16	6.27E-13	4.976	1.079	-2.205	0.001	0.021	-0.020	NUDT3	chr6:34256733-34261227:-	chr6
7.46E-06	0.00108	4.377	1.749	-1.324	0.004	0.024	-0.020	HACD4	chr9:21026765-21029293:-	chr9
0.00035	0.02366	3.995	1.735	-1.203	0.005	0.025	-0.020	MYCBP2	chr13:77640242-77641715:-	chr13
0.00021	0.01637	4.428	1.214	-1.866	0.001	0.021	-0.020	PRPF3	chr1:150318968-150321619:+	chr1
2.37E-10	8.53E-08	5.848	2.083	-1.489	0.002	0.022	-0.019	ABTB1	chr3:127395425-127395783:+	chr3
0.00014	0.01214	4.644	1.903	-1.287	0.004	0.023	-0.019	CCNA2	chr4:122740084-122740526:-	chr4
7.70E-12	3.31E-09	9.486	5.003	-0.923	0.008	0.027	-0.019	FERMT3	chr11:63979220-63986701:+	chr11
1.23E-09	3.97E-07	3.975	0.108	-5.207	0.000	0.019	-0.019	TMEM57	chr1:25815785-25817874:+	chr1
7.98E-13	3.93E-10	6.006	1.554	-1.950	0.001	0.020	-0.019	MGST3	chr1:165619202-165620230:+	chr1
0.00037	0.02499	4.107	2.436	-0.754	0.008	0.027	-0.018	ARL2BP	chr16:57283765-57284303:+	chr16

8.76E-24	1.29E-20	17.901	4.508	-1.989	0.001	0.020	-0.018	MNDA	chr1:158815794-158817490:+	chr1
2.96E-05	0.00342	4.076	1.395	-1.547	0.003	0.021	-0.018	SUPT16H	chr14:21825540-21826085:-	chr14
6.68E-16	4.57E-13	4.764	0.070	-6.081	0.000	0.018	-0.018	PTK2B	chr8:27279901-27287574:+	chr8
7.16E-10	2.40E-07	9.034	4.291	-1.074	0.005	0.023	-0.018	PTP4A2	chr1:32377443-32381495:-	chr1
0.00013	0.01095	4.403	1.752	-1.330	0.003	0.020	-0.018	XPO1	chr2:61721245-61722589:-	chr2
4.77E-05	0.00506	5.032	1.534	-1.714	0.001	0.019	-0.017	MYO1G	chr7:45004146-45004543:-	chr7
0.00036	0.02448	4.987	2.319	-1.104	0.005	0.022	-0.017	SEC22B	chr1:145109685-145112354:+	chr1
3.40E-10	1.19E-07	4.828	0.069	-6.139	0.000	0.017	-0.017	ZNF207	chr17:30692507-30694775:+	chr17
2.81E-12	1.27E-09	4.799	0.070	-6.099	0.000	0.017	-0.017	ADD1	chr4:2877838-2883603:+	chr4
0.0003	0.0214	3.855	1.939	-0.991	0.011	0.028	-0.016	IMMT	chr2:86398460-86400772:-	chr2
3.18E-20	3.33E-17	9.656	2.015	-2.261	0.000	0.017	-0.016	TFRC	chr3:195782191-195785154:-	chr3
4.89E-08	1.19E-05	4.389	1.610	-1.447	0.002	0.018	-0.016	TMEM63A	chr1:226043662-226044352:-	chr1
0.00014	0.01223	5.043	2.201	-1.196	0.004	0.020	-0.016	CLINT1	chr5:157240265-157241192:-	chr5
1.87E-25	3.04E-22	8.175	0.063	-7.022	0.000	0.014	-0.014	TFRC	chr3:195799040-195800800:-	chr3
5.23E-05	0.00546	5.226	3.060	-0.772	0.007	0.021	-0.014	MAF1	chr8:145161867-145161963:+	chr8
2.78E-07	5.77E-05	5.448	0.545	-3.322	0.000	0.014	-0.013	SPG21	chr15:65262578-65266939:-	chr15
4.60E-05	0.00492	10.180	8.340	-0.288	0.025	0.039	-0.013	CD36	chr7:80290527-80292288:+	chr7
1.76E-19	1.73E-16	5.787	1.054	-2.457	0.001	0.013	-0.013	CCT2	chr12:69992202-69993621:+	chr12
1.75E-05	0.00219	4.090	1.730	-1.241	0.002	0.013	-0.011	FDPS	chr1:155282187-155287710:+	chr1
8.52E-06	0.00121	4.488	1.194	-1.911	0.001	0.012	-0.011	UFC1	chr1:161127108-161127388:+	chr1
1.34E-10	5.05E-08	4.312	1.165	-1.888	0.001	0.012	-0.011	SLTM	chr15:59185284-59185477:-	chr15
0.00034	0.02317	3.832	1.709	-1.165	0.003	0.013	-0.011	TM9SF3	chr10:98303980-98307651:-	chr10
7.27E-08	1.70E-05	4.842	2.093	-1.210	0.002	0.013	-0.011	DEK	chr6:18256699-18258183:-	chr6
1.73E-09	5.43E-07	4.184	0.075	-5.808	0.000	0.010	-0.010	PTTG1	chr5:159849411-159849702:+	chr5
6.27E-10	2.12E-07	4.396	1.141	-1.946	0.001	0.011	-0.010	CNPY3	chr6:42902337-42903274:+	chr6
6.55E-12	2.86E-09	5.790	0.593	-3.288	0.000	0.010	-0.009	SERBP1	chr1:67891987-67895670:-	chr1
1.00E-10	3.83E-08	4.943	1.720	-1.523	0.001	0.010	-0.009	ATP5C1	chr10:7841158-7841707:+	chr10
4.59E-07	9.05E-05	4.217	1.430	-1.560	0.002	0.011	-0.009	CDC20	chr1:43826917-43827852:+	chr1
6.42E-19	5.89E-16	5.834	0.781	-2.901	0.000	0.009	-0.009	PSMA7	chr20:60712019-60712419:-	chr20
6.54E-08	1.55E-05	5.467	2.432	-1.169	0.002	0.011	-0.008	CCT5	chr5:10263427-10264749:+	chr5
1.57E-09	4.99E-07	4.478	0.543	-3.044	0.000	0.008	-0.008	ATP6V1G1	chr9:117350201-117354812:+	chr9
2.90E-20	3.09E-17	8.545	2.317	-1.883	0.001	0.009	-0.008	HNRNPK	chr9:86593214-86593287:-	chr9
2.13E-11	8.86E-09	7.141	2.304	-1.632	0.001	0.008	-0.008	PGD	chr1:10477175-10477412:+	chr1
2.15E-38	8.80E-35	24.571	5.144	-2.256	0.000	0.008	-0.008	TPT1	chr13:45911539-45912794:-	chr13
7.23E-06	0.00105	5.120	2.692	-0.928	0.003	0.011	-0.008	EIF4A2	chr3:186505672-186506080:+	chr3
1.57E-28	3.23E-25	6.913	1.488	-2.216	0.000	0.008	-0.007	TXN	chr9:113013761-113018691:-	chr9
2.22E-06	0.00038	4.601	1.012	-2.184	0.001	0.008	-0.007	CAPG	chr2:85622106-85622660:-	chr2
2.34E-22	3.09E-19	7.435	2.018	-1.882	0.000	0.008	-0.007	LSP1	chr11:1905255-1905482:+	chr11
1.55E-35	4.78E-32	16.126	3.283	-2.296	0.000	0.007	-0.007	RPL27A	chr11:8704813-8705536:+	chr11
1.94E-07	4.16E-05	4.128	1.059	-1.963	0.000	0.007	-0.007	CCT6A	chr7:56129543-56130358:+	chr7
0.00082	0.04444	3.736	1.791	-1.061	0.002	0.009	-0.007	RAB1A	chr2:65316225-65318116:-	chr2
8.45E-05	0.00807	7.786	5.618	-0.471	0.005	0.012	-0.007	PADI4	chr1:17682623-17682836:+	chr1
2.33E-12	1.06E-09	7.650	1.703	-2.167	0.000	0.007	-0.007	HNRNPA2B1	chr7:26233331-26235466:-	chr7
9.72E-12	4.14E-09	6.327	2.054	-1.623	0.002	0.008	-0.007	TSPO	chr22:43547611-43555197:+	chr22
1.52E-09	4.85E-07	5.942	2.640	-1.170	0.002	0.008	-0.007	EIF4B	chr12:53421973-53427574:+	chr12
5.45E-08	1.31E-05	5.074	2.505	-1.018	0.002	0.009	-0.006	PSMB1	chr6:170844510-170846321:-	chr6
6.25E-06	0.00093	3.962	1.482	-1.418	0.001	0.007	-0.006	TAF15	chr17:34147442-34149625:+	chr17
1.67E-38	7.09E-35	16.528	5.743	-1.525	0.001	0.006	-0.006	RPS27A	chr2:55462099-55462545:+	chr2
4.39E-09	1.30E-06	6.198	1.571	-1.980	0.000	0.006	-0.005	PADI4	chr1:17657645-17660419:+	chr1
1.53E-07	3.38E-05	7.660	5.072	-0.595	0.005	0.011	-0.005	RPL15	chr3:23958665-23959327:+	chr3
5.91E-08	1.41E-05	4.221	1.164	-1.858	0.000	0.006	-0.005	PA2G4	chr12:56503078-56503622:+	chr12
0.00055	0.03344	3.767	1.835	-1.037	0.002	0.007	-0.005	NASP	chr1:46082376-46083113:+	chr1
1.56E-09	4.96E-07	4.032	1.133	-1.831	0.000	0.006	-0.005	ALOX5	chr10:45924213-45935847:+	chr10
0.00038	0.02543	4.241	1.118	-1.924	0.001	0.005	-0.005	ERP29	chr12:112451414-112457543:+	chr12
4.78E-05	0.00507	4.342	1.915	-1.181	0.001	0.006	-0.005	GSTK1	chr7:142961770-142962038:+	chr7
0.00075	0.04172	3.923	1.855	-1.081	0.001	0.005	-0.004	SEC11A	chr15:85214031-85223943:-	chr15

4.62E-09	1.37E-06	4.545	0.817	-2.476	0.000	0.004	-0.004	CANX	chr5:179151785-179153660:+	chr5
4.11E-13	2.07E-10	4.400	0.806	-2.450	0.000	0.004	-0.004	EIF3H	chr8:117661187-117668094:-	chr8
5.74E-27	1.01E-23	14.147	5.804	-1.286	0.001	0.005	-0.004	RPS27A	chr2:55462099-55462548:+	chr2
1.72E-07	3.75E-05	13.470	9.282	-0.537	0.003	0.006	-0.003	CAMP	chr3:48266165-48266752:+	chr3
2.31E-05	0.00279	3.902	1.879	-1.054	0.001	0.004	-0.003	UBE2D3	chr4:103720678-103722610:-	chr4
3.97E-06	0.00063	7.326	1.543	-2.247	0.000	0.003	-0.003	RPL9	chr4:39455867-39456152:-	chr4
7.17E-28	1.40E-24	10.133	2.693	-1.912	0.000	0.003	-0.002	PFN1	chr17:4849320-4849922:-	chr17
1.21E-07	2.73E-05	4.179	1.549	-1.431	0.000	0.003	-0.002	CYBB	chrX:37660602-37663109:+	chrX
3.78E-11	1.54E-08	13.833	3.369	-2.038	0.000	0.002	-0.002	TPT1	chr13:45912933-45913631:-	chr13
2.49E-09	7.68E-07	4.054	0.592	-2.777	0.000	0.002	-0.002	P4HB	chr17:79804961-79805118:-	chr17
1.33E-15	8.71E-13	8.291	4.325	-0.939	0.001	0.002	-0.002	RPS10	chr6:34392633-34392848:-	chr6
5.22E-45	3.63E-41	14.277	2.734	-2.385	0.000	0.002	-0.001	LYZ	chr12:69744053-69745971:+	chr12
2.89E-07	5.99E-05	7.818	3.778	-1.049	0.000	0.002	-0.001	RPL27A	chr11:8705629-8706243:+	chr11
1.98E-23	2.87E-20	7.778	2.692	-1.531	0.000	0.001	-0.001	RPL19	chr17:37359363-37360302:+	chr17
1.84E-29	3.94E-26	19.834	4.695	-2.079	0.000	0.001	-0.001	S100A9	chr1:153330358-153330714:+	chr1
7.66E-27	1.34E-23	6.699	0.071	-6.555	0.000	0.001	-0.001	RPL4	chr15:66792532-66792630:-	chr15
0.0004	0.02644	4.108	2.163	-0.926	0.000	0.001	-0.001	PSAP	chr10:73588859-73590882:-	chr10
3.56E-07	7.24E-05	4.346	0.986	-2.140	0.000	0.001	-0.001	RPL8	chr8:146015874-146016661:-	chr8
3.43E-09	1.04E-06	5.113	2.168	-1.238	0.000	0.001	-0.001	RPL41	chr12:56510444-56510537:+	chr12
2.87E-06	0.00047	4.721	2.209	-1.095	0.000	0.001	-0.001	RPS11	chr19:49999729-50000429:+	chr19
1.80E-06	0.00031	4.434	1.433	-1.630	0.000	0.001	0.000	FTH1	chr11:61733002-61734783:-	chr11
2.85E-10	1.01E-07	5.054	1.510	-1.742	0.000	0.001	0.000	RPL21	chr13:27829492-27830302:+	chr13
0.00028	0.01992	3.865	1.914	-1.014	0.000	0.001	0.000	RPS10	chr6:34392636-34392848:-	chr6
1.53E-11	6.39E-09	13.276	6.480	-1.035	0.000	0.000	0.000	S100A9	chr1:153330910-153333099:+	chr1
0.00025	0.01845	7.780	5.614	-0.471	0.000	0.000	0.000	LYZ	chr12:69742325-69743877:+	chr12
5.17E-06	0.00079	8.532	6.303	-0.437	0.553	0.548	0.005	DNAJA4	chr15:78566767-78567942:+	chr15
0.00093	0.04869	4.789	2.940	-0.704	0.758	0.700	0.058		chr12:78940-87255:+	chr12
2.27E-08	6.01E-06	9.145	4.577	-0.998	0.461	0.284	0.176	RPS15A	chr16:18799478-18800302:-	chr16
2.14E-11	8.86E-09	5.261	0.690	-2.932	NA	0.592	NA	BCL6	chr3:187449671-187451320:-	chr3
8.50E-56	9.72E-52	11.105	2.203	-2.334	NA	0.895	NA	CHTF18	chr16:843275-844033:+	chr16
1.87E-05	0.00232	3.780	1.712	-1.143	NA	0.549	NA	TAB3	chrX:30864209-30864667:-	chrX
6.19E-18	5.29E-15	4.839	0.519	-3.221	NA	0.723	NA	YIF1A	chr11:66053069-66053171:-	chr11
4.89E-22	6.18E-19	8.371	2.170	-1.948	NA	0.050	NA	ORM1	chr9:117085528-117085924:+	chr9
7.00E-05	0.00692	3.409	1.525	-1.161	NA	0.743	NA		chr17:41316848-41318996:-	chr17

n				WT_PSI									MUT		
start	end	strand	distance to canonical site	AA306	AA307	AA308	AA309	RA006	RA007	RA008	RA010	RA011	RA015	AA301	AA302
35646515	35647729	+	17	0.000	0.000	0.000	0.000	0.000	0.250	0.500	0.000	0.375	1.000	0.833	1.000
89519558	89527429	-	13	0.429	0.000	0.000	0.429	0.000	0.000	0.000	0.000	0.143	0.756	0.850	0.765
23545542	23556543	-	14	0.000	0.019	0.056	0.050	0.000	0.000	0.029	0.061	0.067	0.750	0.697	0.683
102074109	102076648	+	23	0.024	0.009	0.044	0.000	0.000	0.042	0.000	0.000	0.032	0.763	0.631	0.664
53689726	53691607	+	26	0.125	0.056	0.111	0.000	0.067	0.118	0.000	0.000	0.000	0.674	0.670	0.695
64119859	64120198	+	17	0.005	0.012	0.023	0.012	0.033	0.015	0.009	0.011	0.021	0.668	0.629	0.431
89778631	89779081	+	15	0.050	0.091	0.200	0.000	0.000	0.000	0.250	0.000	0.000	0.636	0.537	0.465
91269954	91271340	-	20	0.060	0.157	0.148	0.106	0.115	0.092	0.143	0.130	0.052	0.744	0.724	0.507
42835782	42845927	-	14	0.000	0.000	1.000	0.143	0.000	0.000	0.000	0.000	0.000	0.667	0.710	0.667
138725126	138725368	-	16	0.130	0.133	0.250	0.167	0.136	0.125	0.152	0.167	0.000	0.500	0.692	0.591
109102365	109102954	+	12	0.023	0.011	0.100	0.000	0.000	0.016	0.000	0.000	0.016	0.600	0.661	0.424
9133521	9136361	-	12	0.000	0.000	0.182	0.000	0.000	0.000	0.200	0.000	0.000	0.400	0.938	0.429
85848703	85850728	+	20	0.000	0.000	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.263	0.556	0.630
65716854	65718145	-	18	0.038	0.000	0.079	0.000	0.032	0.019	0.024	0.111	0.000	0.238	0.545	0.656
25158620	25160574	-	23	0.000	0.033	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.500	0.391	0.375
109767079	109767338	-	13	0.020	0.028	0.033	0.019	0.019	0.024	0.025	0.027	0.015	0.622	0.514	0.404
47315814	47326808	-	16	0.423	0.148	0.333	0.200	0.200	0.538	0.150	0.188	0.313	1.000	0.769	0.667
52283339	52283671	+	14	0.000	0.045	0.104	0.000	0.000	0.250	0.000	0.050	0.118	0.759	0.431	0.383
97285514	97297048	-	14	0.000	0.000	0.048	0.000	0.024	0.000	0.000	0.034	0.023	0.563	0.543	0.345
9960294	9962150	+	24	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.000	0.609	0.341	0.379
58115775	58117036	+	17	0.000	0.000	0.053	0.000	0.000	0.000	0.000	0.000	0.250	0.500	0.348	0.250
212515623	212519131	+	13	0.041	0.053	0.069	0.034	0.078	0.032	0.044	0.044	0.068	0.762	0.472	0.400
23237381	23238985	+	14	0.022	0.046	0.061	0.019	0.041	0.032	0.063	0.065	0.032	0.655	0.433	0.335
94157563	94162500	+	16	0.017	0.031	0.111	0.026	0.037	0.027	0.065	0.022	0.015	0.619	0.375	0.310
57908543	57909780	+	17	0.024	0.000	0.071	0.033	0.000	0.000	0.026	0.000	0.000	0.160	0.625	0.387
225670232	225670842	-	12	0.000	0.073	0.300	0.000	0.240	0.167	0.069	0.196	0.063	1.000	0.385	0.417
156532467	156532925	-	9	0.000	0.000	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.527	0.457	0.284
184566984	184567705	+	18	0.030	0.031	0.000	0.017	0.000	0.000	0.014	0.013	0.031	0.647	0.237	0.222
56552496	56553390	+	16	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.412	0.421	0.429
45300424	45300861	+	13	0.000	0.016	0.055	0.015	0.028	0.006	0.006	0.021	0.000	0.433	0.443	0.243
220044486	220044888	+	31	0.000	0.056	0.108	0.042	0.000	0.000	0.000	0.025	0.050	0.478	0.518	0.404
102276735	102286155	-	17	0.000	0.024	0.000	0.000	0.025	0.000	0.000	0.000	0.000	0.542	0.412	0.450
47970658	47971529	+	17	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.360	0.304	0.284
140508222	140508388	+	44	0.250	0.000	0.083	0.000	0.333	0.091	0.000	0.000	0.700	0.688	0.417	0.350
30811173	30818033	+	14	0.043	0.000	0.000	0.000	0.059	0.111	0.000	0.000	0.000	0.357	0.468	0.267
156721227	156723466	+	27	0.000	0.000	0.000	0.029	0.000	0.000	0.000	0.000	0.000	0.538	0.216	0.200
56874549	56875878	+	22	0.000	0.000	0.000	0.000	0.000	0.000	0.028	0.000	0.000	0.429	0.405	0.152
96305665	96306117	+	16	0.038	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.333	0.414	0.407
35813154	35813262	-	11	0.075	0.028	0.086	0.042	0.045	0.022	0.007	0.047	0.050	0.487	0.375	0.329
23283431	23285704	-	14	0.000	0.000	0.000	0.017	0.000	0.000	0.021	0.111	0.000	0.667	0.250	0.263
89358208	89371613	-	22	0.188	0.300	0.533	0.462	0.333	0.300	0.231	0.385	0.750	0.778	0.738	0.615
76943821	76950041	-	14	0.042	0.035	0.053	0.035	0.011	0.036	0.047	0.045	0.050	0.493	0.474	0.301
995352	995438	+	28	0.091	0.082	0.000	0.060	0.158	0.026	0.182	0.023	0.096	0.478	0.278	0.214
184577128	184580081	-	13	0.013	0.019	0.118	0.000	0.000	0.000	0.044	0.057	0.026	0.475	0.298	0.260
708345	708509	+	15	0.022	0.033	0.071	0.014	0.023	0.064	0.000	0.091	0.182	0.559	0.327	0.316
56649301	56649931	+	18	0.049	0.063	0.171	0.224	0.082	0.033	0.080	0.063	0.000	0.583	0.294	0.340
57148330	57153007	-	21	0.000	0.000	0.042	0.000	0.000	0.000	0.000	0.000	0.000	0.345	0.267	0.149
124495800	124496355	+	13	0.000	0.013	0.000	0.000	0.000	0.000	0.014	0.000	0.008	0.483	0.278	0.173
33319712	33321272	+	22	0.000	0.021	0.013	0.032	0.000	0.000	0.000	0.020	0.000	0.529	0.245	0.100

101458311	101460665	-	14	0.000	0.000	0.026	0.000	0.000	0.000	0.000	0.000	0.000	0.357	0.266	0.186
196792336	196792578	-	16	0.045	0.048	0.068	0.029	0.025	0.063	0.102	0.048	0.061	0.409	0.365	0.220
7393537	7395239	+	14	0.074	0.077	0.059	0.077	0.038	0.040	0.000	0.143	0.056	0.750	0.286	0.368
177684584	177686721	-	15	0.000	0.000	0.023	0.000	0.000	0.000	0.030	0.000	0.000	0.333	0.262	0.250
68602750	68603777	-	20	0.007	0.000	0.007	0.000	0.000	0.011	0.000	0.009	0.000	0.836	0.131	0.261
41040824	41046743	+	24	0.000	0.000	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.320	0.325	0.253
62376299	62376433	-	21	0.000	0.000	0.010	0.000	0.005	0.000	0.000	0.000	0.004	0.541	0.198	0.113
67936274	67937041	+	12	0.311	0.200	0.429	0.317	0.429	0.265	0.261	0.407	0.150	0.655	0.656	0.471
26970492	26971275	+	14	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.259	0.200	0.143
41164295	41164946	+	12	0.333	0.104	0.034	0.000	0.318	0.030	0.063	0.121	0.167	0.478	0.526	0.364
24177167	24179250	-	47	0.190	0.000	0.056	0.241	0.279	0.148	0.000	0.333	0.000	0.625	0.536	0.394
33080642	33083060	+	15	0.039	0.020	0.037	0.000	0.000	0.000	0.024	0.020	0.045	0.375	0.390	0.125
50966162	50966940	-	15	0.000	0.000	0.007	0.008	0.001	0.004	0.000	0.000	0.002	0.347	0.161	0.171
27107890	27113871	+	12	0.000	0.017	0.069	0.000	0.083	0.034	0.052	0.036	0.000	0.389	0.250	0.175
239070358	239071364	+	12	0.014	0.000	0.000	0.004	0.029	0.000	0.000	0.000	0.000	0.237	0.329	0.227
3142384	3144471	+	21	0.000	0.000	0.000	0.000	0.029	0.000	0.010	0.000	0.000	0.186	0.380	0.241
65388438	65389694	+	21	0.029	0.068	0.095	0.109	0.184	0.182	0.085	0.088	0.064	0.475	0.396	0.280
36631196	36634598	-	17	0.037	0.090	0.125	0.032	0.050	0.176	0.087	0.231	0.120	0.300	0.481	0.179
35871070	35873587	+	21	0.000	0.013	0.000	0.000	0.000	0.000	0.012	0.000	0.006	0.306	0.229	0.157
103297360	103298629	+	14	0.000	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.319	0.182	0.127
127624271	127624818	-	21	0.000	0.000	0.036	0.000	0.000	0.000	0.000	0.000	0.018	0.231	0.250	0.258
43459193	43460039	-	13	0.000	0.000	0.053	0.028	0.024	0.000	0.017	0.000	0.083	0.366	0.179	0.085
19498664	19499145	-	21	0.000	0.000	0.167	0.007	0.051	0.000	0.020	0.026	0.000	0.351	0.095	0.145
62574713	62576906	-	18	0.014	0.013	0.078	0.000	0.000	0.020	0.000	0.012	0.000	0.250	0.260	0.107
74131271	74133179	+	18	0.000	0.000	0.000	0.000	0.000	0.019	0.022	0.000	0.000	0.159	0.150	0.185
24788662	24788947	-	19	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.321	0.040	0.200
172479474	172480187	+	18	0.000	0.000	0.019	0.000	0.000	0.000	0.000	0.000	0.000	0.170	0.155	0.118
68274469	68290089	-	17	0.000	0.000	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.436	0.146	0.104
99502922	99504468	+	17	0.000	0.000	0.000	0.000	0.000	0.000	0.026	0.000	0.000	0.283	0.259	0.172
89633169	89643287	+	14	0.000	0.000	0.076	0.000	0.019	0.000	0.000	0.000	0.000	0.316	0.136	0.154
5595522	5598803	-	13	0.005	0.008	0.014	0.003	0.003	0.011	0.000	0.000	0.000	0.214	0.363	0.166
185056773	185060696	+	14	0.027	0.068	0.063	0.059	0.033	0.027	0.038	0.017	0.020	0.279	0.260	0.210
126051219	126052036	-	17	0.016	0.005	0.020	0.021	0.013	0.044	0.022	0.042	0.061	0.419	0.200	0.143
179835005	179846373	-	15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.022	0.108	0.200	0.154
170388019	170393736	-	18	0.000	0.000	0.008	0.000	0.000	0.006	0.000	0.000	0.000	0.237	0.213	0.212
61741366	61742868	+	12	0.000	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.213	0.304	0.067
995352	995433	+	33	0.038	0.056	0.071	0.000	0.030	0.026	0.069	0.044	0.057	0.333	0.188	0.154
109181708	109183328	+	29	0.022	0.000	0.043	0.000	0.000	0.011	0.000	0.000	0.014	0.224	0.229	0.195
205240384	205240923	+	17	0.071	0.026	0.250	0.073	0.021	0.000	0.012	0.007	0.063	0.225	0.285	0.073
19480449	19481411	-	15	0.072	0.049	0.000	0.039	0.125	0.196	0.060	0.052	0.299	0.359	0.359	0.224
96377507	96409878	+	19	0.007	0.011	0.000	0.000	0.029	0.013	0.009	0.010	0.000	0.156	0.370	0.100
30884737	30884871	+	10	0.000	0.000	0.013	0.024	0.000	0.000	0.000	0.000	0.000	0.120	0.141	0.115
4104213	4104471	+	21	0.004	0.009	0.038	0.000	0.000	0.006	0.017	0.008	0.025	0.199	0.191	0.205
39064138	39066874	+	14	0.000	0.000	0.094	0.000	0.000	0.000	0.000	0.000	0.000	0.286	0.275	0.117
110085186	110086201	+	14	0.007	0.006	0.020	0.000	0.000	0.008	0.005	0.009	0.000	0.294	0.154	0.108
91966506	91967193	+	17	0.042	0.000	0.087	0.041	0.056	0.050	0.125	0.000	0.091	0.250	0.320	0.121
36351217	36352738	-	20	0.000	0.000	0.091	0.006	0.027	0.000	0.000	0.000	0.008	0.101	0.343	0.154
23242938	23243141	-	12	0.000	0.000	0.037	0.000	0.011	0.000	0.001	0.000	0.005	0.152	0.167	0.162
24207702	24222524	+	17	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.209	0.192	0.190
184587317	184588487	+	16	0.015	0.015	0.022	0.014	0.038	0.034	0.000	0.056	0.046	0.185	0.219	0.098
129886490	129891532	-	16	0.000	0.027	0.008	0.000	0.000	0.000	0.000	0.000	0.010	0.234	0.171	0.156
176916843	176917870	-	9	0.010	0.012	0.029	0.000	0.008	0.018	0.022	0.000	0.000	0.280	0.194	0.137
70955022	70956733	+	14	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.326	0.106	0.064
43917703	43917875	-	18	0.023	0.000	0.008	0.028	0.029	0.030	0.000	0.042	0.000	0.403	0.172	0.167
62555000	62556481	+	13	0.000	0.000	0.047	0.008	0.013	0.000	0.000	0.000	0.000	0.240	0.112	0.118
129284873	129285369	-	12	0.009	0.000	0.017	0.000	0.009	0.007	0.003	0.006	0.010	0.113	0.187	0.178

21627930	21628401	-	16	0.020	0.045	0.021	0.015	0.025	0.014	0.009	0.037	0.033	0.347	0.135	0.133
25224487	25225688	+	19	0.000	0.011	0.000	0.000	0.000	0.019	0.007	0.000	0.009	0.050	0.269	0.279
52880320	52880412	+	21	0.022	0.025	0.028	0.010	0.014	0.000	0.020	0.026	0.029	0.231	0.232	0.193
113346630	113348840	+	15	0.005	0.005	0.019	0.013	0.014	0.000	0.010	0.000	0.005	0.294	0.234	0.106
43917718	43917875	-	33	0.014	0.000	0.017	0.006	0.022	0.000	0.000	0.000	0.000	0.258	0.252	0.132
49416665	49419178	-	24	0.008	0.000	0.000	0.000	0.000	0.007	0.000	0.011	0.000	0.178	0.196	0.097
110128653	110128830	-	14	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.136	0.273	0.131
41084119	41084353	+	14	0.010	0.011	0.020	0.007	0.018	0.007	0.013	0.015	0.014	0.239	0.173	0.128
125759641	125760854	+	21	0.014	0.000	0.000	0.018	0.000	0.000	0.020	0.017	0.041	0.258	0.289	0.125
61415872	61416044	-	27	0.600	0.647	0.333	1.000	0.667	0.600	0.857	0.833	0.714	0.882	0.944	0.944
30124850	30125145	-	18	0.040	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.247	0.113	0.043
53666642	53668573	+	27	0.000	0.077	0.000	0.000	0.059	0.000	0.000	0.000	0.000	0.357	0.192	0.074
29450134	29460566	+	24	0.000	0.000	0.013	0.000	0.000	0.000	0.000	0.006	0.000	0.154	0.218	0.104
37416268	37417879	-	13	0.060	0.132	0.000	0.032	0.000	0.039	0.071	0.000	0.029	0.300	0.178	0.196
37635000	37638902	+	20	0.101	0.045	0.051	0.027	0.091	0.065	0.094	0.107	0.094	0.474	0.250	0.071
11546528	11546892	+	14	0.333	1.000	1.000	0.500	0.000	0.667	0.000	0.000	0.600	0.375	0.360	1.000
110437590	110449795	+	14	0.059	0.008	0.032	0.009	0.019	0.018	0.006	0.013	0.007	0.237	0.152	0.197
35282127	35284762	-	22	0.000	0.000	0.029	0.000	0.000	0.000	0.000	0.000	0.000	0.143	0.220	0.186
118972032	118972329	-	17	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.292	0.122	0.095
156785905	156786466	-	18	0.040	0.056	0.000	0.100	0.059	0.000	0.064	0.063	0.065	0.185	0.227	0.267
128645231	128655032	-	17	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.149	0.172	0.095
14031736	14034130	+	15	0.000	0.000	0.018	0.000	0.000	0.000	0.000	0.036	0.000	0.061	0.119	0.174
5497082	5498027	+	22	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.067	0.181	0.155
40493182	40494590	+	15	0.077	0.075	0.038	0.068	0.097	0.032	0.072	0.024	0.133	0.074	0.241	0.258
64494851	64496334	-	15	0.102	0.065	0.072	0.079	0.114	0.159	0.037	0.043	0.091	0.231	0.273	0.222
99752805	99752884	-	17	0.000	0.024	0.011	0.046	0.024	0.008	0.028	0.000	0.022	0.200	0.197	0.146
28824687	28824838	+	9	0.045	0.064	0.111	0.000	0.106	0.087	0.081	0.000	0.031	0.343	0.273	0.089
49848903	49849302	-	14	0.032	0.045	0.051	0.026	0.058	0.033	0.043	0.024	0.038	0.181	0.270	0.118
94192765	94194101	-	17	0.000	0.000	0.008	0.000	0.007	0.004	0.000	0.000	0.000	0.227	0.017	0.061
109235490	109236193	+	18	0.023	0.000	0.067	0.000	0.000	0.000	0.000	0.000	0.000	0.102	0.159	0.167
24538115	24550920	-	21	0.025	0.000	0.000	0.016	0.000	0.000	0.000	0.027	0.000	0.074	0.143	0.149
203157627	203162080	+	21	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.062	0.184	0.091
68363687	68367788	+	20	0.000	0.002	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.163	0.087	0.089
33724998	33725896	+	14	0.016	0.009	0.015	0.014	0.026	0.022	0.011	0.000	0.014	0.250	0.111	0.088
122152653	122156016	-	17	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.188	0.110	0.085
39285969	39294768	-	23	0.000	0.000	0.053	0.000	0.000	0.000	0.000	0.000	0.000	0.155	0.124	0.127
100477090	100480840	+	17	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.133	0.067	0.127
19044700	19050714	-	24	0.007	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.006	0.051	0.142	0.123
208607067	208611755	+	15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.230	0.068	0.035
41762591	41763349	+	20	0.004	0.000	0.000	0.000	0.005	0.006	0.000	0.011	0.000	0.125	0.101	0.123
103422451	103426031	-	14	0.000	0.056	0.000	0.034	0.053	0.000	0.000	0.000	0.000	0.000	0.241	0.102
49044681	49048099	-	14	0.010	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.279	0.163	0.038
75566590	75566865	-	20	0.017	0.069	0.000	0.051	0.040	0.032	0.011	0.054	0.100	0.174	0.065	0.124
53381039	53385575	-	18	0.000	0.007	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.089	0.111	0.104
179318078	179319411	+	19	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.182	0.103	0.140
8923170	8932072	-	26	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.222	0.013	0.000
74978548	74979611	-	25	0.008	0.013	0.038	0.000	0.000	0.000	0.012	0.012	0.053	0.100	0.221	0.000
49420971	49421673	-	13	0.000	0.000	0.012	0.004	0.003	0.000	0.000	0.007	0.000	0.054	0.078	0.061
39605783	39608267	-	14	0.017	0.008	0.000	0.000	0.016	0.009	0.000	0.032	0.000	0.130	0.065	0.152
64900741	64900940	-	17	0.000	0.000	0.010	0.000	0.000	0.007	0.000	0.012	0.021	0.140	0.125	0.068
62648920	62649352	+	12	0.007	0.013	0.019	0.002	0.010	0.005	0.018	0.015	0.000	0.129	0.098	0.104
35140133	35144342	+	22	0.030	0.035	0.095	0.025	0.000	0.022	0.000	0.000	0.000	0.167	0.093	0.079
99788124	99789876	-	14	0.032	0.042	0.059	0.067	0.017	0.021	0.018	0.041	0.012	0.000	0.222	0.205
47347748	47399698	-	13	0.000	0.000	0.000	0.017	0.020	0.018	0.013	0.019	0.000	0.114	0.111	0.125
41579226	41582593	-	27	0.016	0.031	0.000	0.064	0.013	0.018	0.077	0.031	0.036	0.102	0.071	0.173
74740929	74741526	-	29	0.046	0.041	0.061	0.063	0.054	0.051	0.039	0.055	0.088	0.309	0.081	0.093

53690336	53691607	+	26	0.000	0.000	0.000	0.000	0.000	0.035	0.013	0.000	0.000	0.084	0.106	0.096
118883973	118885685	+	18	0.000	0.000	0.025	0.000	0.010	0.008	0.000	0.009	0.000	0.105	0.042	0.087
348842	350802	+	19	0.000	0.000	0.000	0.022	0.000	0.000	0.000	0.000	0.000	0.203	0.073	0.031
155630725	155631097	-	20	0.007	0.007	0.000	0.004	0.013	0.000	0.005	0.000	0.000	0.138	0.068	0.053
202122979	202123313	-	15	0.038	0.033	0.049	0.035	0.067	0.031	0.034	0.031	0.052	0.131	0.156	0.125
15479151	15480956	-	17	0.000	0.010	0.006	0.000	0.000	0.000	0.000	0.008	0.000	0.153	0.041	0.032
186324918	186325417	-	17	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.006	0.117	0.146	0.069
103771555	103772589	-	14	0.026	0.011	0.000	0.019	0.000	0.017	0.014	0.015	0.024	0.029	0.116	0.040
235914679	235915304	-	16	0.112	0.096	0.058	0.073	0.079	0.095	0.120	0.056	0.146	0.165	0.276	0.135
142651631	142654913	-	16	0.135	0.182	0.054	0.113	0.104	0.039	0.091	0.212	0.000	0.202	0.232	0.216
100606071	100606400	+	7	0.017	0.031	0.033	0.029	0.040	0.077	0.000	0.150	0.176	0.056	0.192	0.125
51174022	51189680	+	11	0.051	0.063	0.038	0.046	0.094	0.023	0.032	0.025	0.027	0.118	0.210	0.111
54566334	54566405	-	18	0.010	0.029	0.046	0.000	0.030	0.048	0.000	0.000	0.018	0.128	0.051	0.061
155546181	155547476	-	14	0.000	0.008	0.015	0.006	0.000	0.013	0.000	0.000	0.009	0.205	0.027	0.035
73486840	73487110	+	19	0.000	0.007	0.000	0.000	0.000	0.019	0.000	0.010	0.000	0.188	0.043	0.105
38947708	38948761	+	16	0.010	0.000	0.014	0.014	0.000	0.018	0.016	0.014	0.034	0.248	0.032	0.014
67692736	67692830	-	16	0.023	0.010	0.011	0.022	0.031	0.008	0.039	0.035	0.045	0.143	0.103	0.082
33261713	33261810	-	19	0.160	0.130	0.151	0.114	0.111	0.096	0.146	0.114	0.092	0.176	0.206	0.265
89870311	89870397	-	16	0.018	0.042	0.055	0.005	0.000	0.026	0.043	0.023	0.038	0.131	0.125	0.074
150411956	150413168	-	11	0.012	0.014	0.004	0.027	0.027	0.012	0.008	0.017	0.014	0.100	0.096	0.090
40849590	40854970	-	18	0.010	0.000	0.018	0.010	0.000	0.008	0.000	0.000	0.000	0.131	0.094	0.056
39911977	39915230	-	18	0.004	0.004	0.000	0.013	0.009	0.000	0.000	0.006	0.005	0.146	0.088	0.039
75131105	75131350	-	18	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.010	0.164	0.050	0.031
64877396	64877934	+	19	0.003	0.005	0.008	0.005	0.004	0.002	0.003	0.004	0.000	0.091	0.078	0.075
31288371	31289273	+	14	0.007	0.012	0.009	0.004	0.017	0.015	0.013	0.004	0.008	0.092	0.121	0.055
79556146	79563141	-	15	0.017	0.004	0.021	0.017	0.000	0.023	0.021	0.013	0.006	0.093	0.129	0.034
48651705	48652184	+	15	0.021	0.046	0.050	0.033	0.037	0.015	0.043	0.018	0.043	0.119	0.095	0.082
38899637	38911982	+	17	0.000	0.009	0.007	0.000	0.000	0.012	0.008	0.000	0.026	0.132	0.042	0.000
160253916	160255339	-	15	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.071	0.028	0.101
35236222	35236271	+	21	0.082	0.070	0.069	0.192	0.130	0.151	0.128	0.053	0.111	0.147	0.217	0.208
7404789	7405128	+	22	0.000	0.014	0.015	0.000	0.000	0.000	0.000	0.000	0.000	0.062	0.103	0.035
78203439	78205120	-	20	0.007	0.008	0.000	0.000	0.000	0.000	0.004	0.011	0.005	0.098	0.063	0.060
64494863	64496334	-	27	0.000	0.000	0.015	0.079	0.046	0.014	0.071	0.015	0.000	0.143	0.059	0.075
34953032	34969039	+	13	0.000	0.000	0.000	0.000	0.031	0.013	0.000	0.013	0.037	0.125	0.069	0.087
20194635	20195113	-	18	0.005	0.014	0.000	0.016	0.000	0.011	0.014	0.011	0.054	0.119	0.116	0.072
99025904	99052328	-	21	0.042	0.024	0.000	0.000	0.000	0.025	0.033	0.050	0.035	0.090	0.045	0.101
115934003	115935732	-	16	0.000	0.009	0.010	0.000	0.008	0.000	0.000	0.008	0.001	0.052	0.140	0.104
90342810	90344341	-	19	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.121	0.049	0.039
229407118	229422214	+	18	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.130	0.042	0.129
55579730	55583167	+	21	0.003	0.012	0.000	0.000	0.000	0.000	0.003	0.000	0.005	0.031	0.100	0.123
99127257	99127503	-	24	0.002	0.002	0.008	0.002	0.000	0.006	0.003	0.000	0.003	0.086	0.031	0.019
153751362	153751571	+	18	0.007	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.143	0.045	0.038
53029762	53030637	+	20	0.007	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.045	0.065	0.086
86665718	86667916	+	18	0.016	0.000	0.000	0.000	0.017	0.009	0.000	0.000	0.032	0.096	0.072	0.050
80750421	80751814	+	21	0.004	0.000	0.000	0.013	0.009	0.004	0.000	0.000	0.034	0.067	0.068	0.074
33703762	33706400	-	25	0.045	0.064	0.058	0.042	0.032	0.033	0.007	0.043	0.049	0.099	0.139	0.111
30958270	30958352	+	20	0.017	0.009	0.000	0.028	0.015	0.014	0.011	0.033	0.017	0.106	0.118	0.099
57911243	57911488	-	21	0.000	0.020	0.000	0.004	0.023	0.000	0.000	0.009	0.000	0.082	0.074	0.087
69155088	69155338	-	14	0.016	0.020	0.045	0.010	0.023	0.000	0.020	0.000	0.000	0.040	0.108	0.099
17824747	17825253	+	16	0.006	0.000	0.000	0.006	0.009	0.000	0.000	0.000	0.000	0.034	0.120	0.057
45043101	45046767	+	15	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.076	0.075	0.063
4796064	4796240	+	33	0.000	0.009	0.009	0.006	0.008	0.000	0.000	0.008	0.007	0.101	0.071	0.045
72139524	72139882	+	21	0.009	0.000	0.025	0.010	0.014	0.000	0.025	0.007	0.006	0.175	0.049	0.081
98579584	98580862	+	24	0.043	0.025	0.000	0.012	0.019	0.014	0.000	0.000	0.015	0.058	0.056	0.064
56100060	56101230	+	13	0.003	0.009	0.000	0.000	0.000	0.005	0.004	0.014	0.000	0.060	0.071	0.071
71299882	71300592	+	19	0.018	0.036	0.026	0.021	0.040	0.043	0.022	0.019	0.077	0.120	0.143	0.085

27070393	27070576	-	18	0.063	0.042	0.068	0.040	0.035	0.023	0.039	0.048	0.039	0.086	0.054	0.142
11272544	11272852	-	12	0.000	0.020	0.000	0.000	0.025	0.000	0.011	0.000	0.000	0.037	0.041	0.059
220100035	220100182	+	13	0.011	0.028	0.000	0.011	0.000	0.014	0.036	0.000	0.046	0.091	0.057	0.077
25290170	25290845	-	16	0.036	0.042	0.042	0.009	0.029	0.000	0.059	0.096	0.011	0.145	0.087	0.116
79475643	79494320	+	13	0.002	0.001	0.005	0.004	0.002	0.003	0.002	0.001	0.000	0.080	0.043	0.038
17925187	17927937	-	15	0.000	0.000	0.000	0.019	0.000	0.008	0.000	0.000	0.000	0.033	0.051	0.073
112915535	112915638	+	22	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.113	0.028	0.033
30315517	30320247	+	13	0.013	0.005	0.006	0.012	0.000	0.005	0.022	0.016	0.014	0.079	0.104	0.096
111741781	111745424	-	19	0.010	0.018	0.034	0.006	0.000	0.000	0.000	0.000	0.000	0.088	0.049	0.063
47311743	47313660	-	21	0.000	0.000	0.004	0.002	0.000	0.000	0.000	0.000	0.000	0.071	0.066	0.056
32095540	32095893	-	12	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.098	0.040	0.041
84378112	84379477	+	21	0.000	0.000	0.010	0.003	0.000	0.003	0.000	0.005	0.014	0.092	0.043	0.024
15491445	15507960	-	21	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.049	0.039
131398064	131398559	-	17	0.009	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.081	0.029
140069968	140070159	-	43	0.006	0.000	0.014	0.007	0.015	0.009	0.000	0.000	0.014	0.114	0.067	0.024
228335401	228336058	+	13	0.002	0.004	0.004	0.001	0.001	0.001	0.000	0.002	0.000	0.048	0.088	0.041
34161043	34161927	+	19	0.000	0.000	0.000	0.000	0.008	0.032	0.000	0.000	0.073	0.098	0.094	0.039
111417629	111419158	-	15	0.000	0.015	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.145	0.006	0.016
11862969	11864638	-	17	0.000	0.000	0.000	0.000	0.000	0.009	0.016	0.000	0.007	0.019	0.071	0.060
172584929	172585212	+	14	0.005	0.000	0.003	0.003	0.011	0.004	0.010	0.005	0.012	0.144	0.084	0.030
34854422	34854918	-	18	0.000	0.000	0.000	0.000	0.008	0.015	0.000	0.000	0.000	0.080	0.028	0.056
47108989	47110832	-	15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.083	0.044	0.017
153363051	153363516	-	17	0.031	0.031	0.035	0.031	0.034	0.028	0.031	0.032	0.025	0.092	0.089	0.082
31338257	31339437	+	30	0.002	0.001	0.004	0.000	0.001	0.000	0.002	0.001	0.001	0.063	0.030	0.024
3697620	3697738	-	13	0.003	0.005	0.000	0.004	0.000	0.000	0.000	0.020	0.000	0.037	0.072	0.064
35917393	35919157	-	15	0.008	0.000	0.009	0.036	0.022	0.017	0.008	0.000	0.011	0.073	0.037	0.113
105713783	105716106	+	21	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.080	0.048	0.042
2247022	2247564	+	28	0.000	0.003	0.003	0.000	0.002	0.000	0.003	0.000	0.000	0.066	0.056	0.051
38570327	38572514	+	18	0.000	0.005	0.038	0.000	0.000	0.000	0.000	0.000	0.008	0.090	0.025	0.018
186300729	186301326	-	15	0.000	0.000	0.003	0.006	0.013	0.005	0.003	0.007	0.005	0.055	0.075	0.060
72315235	72316743	+	19	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.035	0.069	0.059
317129	325647	+	23	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.056	0.057	0.038
65962545	65964129	-	18	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.043	0.013
48171551	48171633	+	14	0.000	0.003	0.009	0.000	0.000	0.000	0.014	0.008	0.004	0.061	0.048	0.066
114316810	114318499	+	48	0.002	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.058	0.052	0.049
50635781	50635865	+	12	0.022	0.013	0.041	0.036	0.016	0.017	0.017	0.010	0.057	0.098	0.101	0.074
44957238	44958353	-	24	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.043	0.063
50832565	50845095	+	22	0.044	0.005	0.031	0.008	0.016	0.009	0.077	0.000	0.040	0.099	0.078	0.046
113497683	113499879	+	17	0.005	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.037	0.066	0.052
75231388	75234676	-	16	0.005	0.000	0.000	0.000	0.000	0.007	0.006	0.007	0.000	0.080	0.069	0.043
145624053	145624168	-	24	0.011	0.013	0.019	0.002	0.025	0.000	0.024	0.009	0.000	0.061	0.021	0.035
56082979	56083161	-	17	0.000	0.001	0.001	0.001	0.000	0.002	0.001	0.000	0.000	0.064	0.061	0.041
15565390	15565467	-	16	0.015	0.008	0.014	0.013	0.014	0.009	0.007	0.010	0.011	0.081	0.047	0.026
197004545	197005972	-	21	0.002	0.002	0.018	0.000	0.000	0.000	0.002	0.000	0.001	0.037	0.043	0.056
178096759	178097119	-	22	0.014	0.007	0.014	0.006	0.004	0.009	0.023	0.009	0.007	0.097	0.047	0.061
71433462	71437514	+	16	0.000	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.000	0.045	0.060	0.041
49225085	49225149	-	13	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.032	0.056	0.072
31169465	31171484	+	17	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.011	0.047	0.016
19812609	19813238	-	19	0.000	0.000	0.000	0.008	0.000	0.020	0.009	0.005	0.017	0.027	0.088	0.038
2419147	2419815	+	23	0.028	0.019	0.015	0.018	0.009	0.007	0.027	0.000	0.005	0.070	0.080	0.044
46389298	46389527	+	24	0.002	0.001	0.009	0.000	0.016	0.000	0.000	0.000	0.000	0.074	0.028	0.021
129867320	129869650	-	12	0.021	0.000	0.014	0.020	0.037	0.017	0.018	0.014	0.021	0.047	0.096	0.060
100630322	100641049	-	19	0.002	0.004	0.000	0.003	0.000	0.000	0.000	0.000	0.002	0.051	0.033	0.069
32328377	32329311	-	17	0.000	0.018	0.038	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.035	0.034
45474012	45474207	-	18	0.000	0.008	0.000	0.007	0.017	0.010	0.000	0.000	0.000	0.069	0.087	0.061
113915074	113917776	+	24	0.000	0.000	0.004	0.000	0.000	0.003	0.000	0.000	0.000	0.075	0.081	0.039

52293559	52299688	-	17	0.000	0.000	0.006	0.006	0.000	0.000	0.000	0.000	0.003	0.051	0.040	0.037
45216273	45219218	-	15	0.000	0.000	0.005	0.000	0.005	0.000	0.000	0.000	0.012	0.049	0.054	0.042
4827408	4827743	+	41	0.000	0.005	0.000	0.007	0.008	0.010	0.000	0.000	0.010	0.117	0.057	0.024
20656271	20656905	+	15	0.020	0.009	0.013	0.009	0.006	0.012	0.004	0.004	0.011	0.049	0.067	0.022
86705389	86705705	+	25	0.000	0.000	0.000	0.000	0.000	0.013	0.013	0.000	0.006	0.121	0.043	0.013
62577342	62577513	-	13	0.017	0.044	0.013	0.031	0.011	0.020	0.036	0.082	0.045	0.086	0.042	0.092
3845436	3846309	+	20	0.007	0.004	0.000	0.000	0.000	0.008	0.016	0.000	0.000	0.050	0.014	0.033
153229751	153230028	-	15	0.011	0.000	0.000	0.005	0.016	0.000	0.008	0.000	0.015	0.057	0.051	0.042
77090455	77090938	-	21	0.000	0.000	0.002	0.005	0.003	0.001	0.000	0.000	0.002	0.037	0.067	0.058
29756819	29759204	-	14	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.024	0.091	0.037
44795899	44796008	+	15	0.000	0.000	0.015	0.000	0.000	0.006	0.000	0.000	0.000	0.038	0.087	0.031
15129411	15129852	+	20	0.000	0.006	0.008	0.000	0.000	0.000	0.000	0.018	0.011	0.091	0.041	0.037
844890	845537	-	17	0.000	0.012	0.007	0.003	0.004	0.000	0.000	0.009	0.008	0.043	0.032	0.036
208425097	208432169	+	17	0.021	0.017	0.023	0.009	0.000	0.000	0.000	0.000	0.000	0.038	0.043	0.026
80013702	80013861	+	15	0.002	0.000	0.003	0.000	0.003	0.003	0.000	0.000	0.000	0.039	0.047	0.032
16344445	16344670	+	11	0.003	0.004	0.007	0.003	0.004	0.004	0.004	0.003	0.003	0.031	0.056	0.053
45572507	45573243	+	36	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.032	0.042	0.039
77317660	77317818	+	20	0.000	0.001	0.002	0.000	0.000	0.000	0.000	0.000	0.003	0.064	0.035	0.025
219257854	219258817	+	25	0.013	0.004	0.000	0.012	0.000	0.000	0.003	0.003	0.001	0.065	0.064	0.042
29124438	29130918	-	21	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.006	0.000	0.023	0.064	0.052
139837450	139837800	-	24	0.002	0.006	0.056	0.002	0.003	0.000	0.003	0.003	0.000	0.054	0.027	0.040
71174532	71175078	+	20	0.021	0.019	0.015	0.018	0.038	0.021	0.012	0.021	0.010	0.077	0.036	0.062
148451243	148454059	+	15	0.003	0.000	0.000	0.000	0.011	0.005	0.010	0.006	0.007	0.034	0.037	0.017
70516898	70517210	+	16	0.000	0.002	0.002	0.000	0.002	0.001	0.002	0.000	0.002	0.051	0.043	0.026
126660688	126662195	+	18	0.000	0.006	0.000	0.006	0.000	0.000	0.000	0.013	0.000	0.033	0.035	0.046
432325	433857	+	17	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.081	0.019	0.023
15967517	15968183	-	15	0.004	0.004	0.000	0.000	0.017	0.003	0.000	0.010	0.003	0.049	0.031	0.038
36780340	36782825	-	17	0.000	0.000	0.024	0.000	0.026	0.013	0.000	0.009	0.007	0.024	0.037	0.072
134301399	134303688	+	17	0.010	0.011	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.034	0.040
177649600	177649852	-	18	0.004	0.030	0.041	0.010	0.007	0.013	0.010	0.025	0.010	0.044	0.094	0.020
31284840	31286849	+	20	0.003	0.002	0.001	0.004	0.001	0.001	0.002	0.001	0.000	0.030	0.034	0.025
119511061	119514941	-	12	0.000	0.000	0.015	0.000	0.000	0.000	0.000	0.004	0.000	0.032	0.033	0.045
101401354	101401614	-	17	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.038	0.041	0.038
80200133	80201005	-	19	0.009	0.000	0.000	0.000	0.035	0.005	0.000	0.000	0.011	0.058	0.043	0.051
177576860	177577888	-	20	0.000	0.003	0.002	0.000	0.006	0.000	0.000	0.000	0.000	0.061	0.024	0.029
26437446	26437921	-	15	0.004	0.002	0.005	0.002	0.005	0.001	0.001	0.002	0.001	0.055	0.039	0.021
45841512	45857556	+	20	0.008	0.000	0.012	0.000	0.000	0.005	0.000	0.000	0.000	0.061	0.036	0.035
58109977	58110164	+	30	0.001	0.006	0.009	0.003	0.007	0.007	0.000	0.002	0.006	0.035	0.048	0.030
47655361	47656742	-	20	0.000	0.007	0.002	0.000	0.005	0.005	0.010	0.006	0.000	0.027	0.043	0.035
45234507	45234595	-	16	0.005	0.016	0.000	0.010	0.025	0.011	0.000	0.013	0.000	0.080	0.045	0.023
44145291	44145394	-	18	0.000	0.000	0.004	0.002	0.000	0.000	0.000	0.006	0.000	0.031	0.057	0.027
45457809	45472142	+	18	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.021	0.053	0.019
50813956	50815142	+	14	0.019	0.014	0.006	0.017	0.009	0.000	0.008	0.007	0.009	0.033	0.044	0.042
95513113	95516228	-	22	0.020	0.016	0.013	0.014	0.012	0.031	0.012	0.021	0.012	0.071	0.043	0.045
7625651	7625886	+	13	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.004	0.000	0.067	0.036	0.029
33055500	33057050	-	17	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.002	0.055	0.015	0.005
71524211	71528269	-	15	0.000	0.000	0.000	0.000	0.000	0.005	0.007	0.000	0.000	0.023	0.042	0.037
9004381	9008575	-	16	0.002	0.015	0.013	0.009	0.010	0.014	0.023	0.025	0.027	0.050	0.049	0.028
99219517	99219802	-	18	0.007	0.010	0.021	0.009	0.000	0.008	0.005	0.016	0.013	0.033	0.072	0.043
16343568	16344670	+	11	0.000	0.000	0.002	0.004	0.000	0.000	0.002	0.000	0.000	0.026	0.037	0.046
145883103	145883371	+	15	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.039	0.029	0.031
62783480	62783562	+	14	0.012	0.034	0.012	0.017	0.021	0.018	0.026	0.020	0.034	0.068	0.069	0.058
135507159	135508950	+	21	0.009	0.005	0.006	0.009	0.010	0.005	0.003	0.000	0.000	0.032	0.035	0.025
47042670	47042740	+	28	0.000	0.001	0.002	0.000	0.002	0.000	0.004	0.001	0.006	0.026	0.045	0.026
144643999	144644083	+	45	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.038	0.015	0.022
198267784	198268308	-	24	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.072	0.034	0.004

73689563	73695838	+	24	0.000	0.000	0.008	0.003	0.000	0.000	0.000	0.000	0.000	0.021	0.036	0.048
140074996	140075239	-	16	0.011	0.000	0.021	0.006	0.007	0.000	0.011	0.020	0.000	0.073	0.032	0.020
26609461	26610632	-	32	0.000	0.000	0.004	0.000	0.000	0.003	0.000	0.000	0.000	0.014	0.044	0.015
80301357	80302070	+	15	0.000	0.002	0.000	0.001	0.001	0.000	0.000	0.002	0.000	0.029	0.036	0.024
62207907	62211405	+	17	0.005	0.005	0.004	0.008	0.003	0.006	0.002	0.002	0.003	0.049	0.043	0.031
30888157	30893953	-	16	0.000	0.017	0.000	0.000	0.000	0.011	0.000	0.011	0.018	0.043	0.039	0.040
49395200	49395459	-	19	0.000	0.001	0.001	0.001	0.001	0.000	0.002	0.002	0.000	0.028	0.013	0.029
26969116	26969292	-	19	0.004	0.000	0.017	0.000	0.000	0.011	0.004	0.010	0.003	0.073	0.014	0.009
409234	409571	+	23	0.004	0.014	0.016	0.009	0.034	0.018	0.013	0.031	0.000	0.066	0.032	0.032
33261105	33261189	-	21	0.010	0.019	0.016	0.032	0.021	0.021	0.018	0.021	0.033	0.038	0.054	0.061
139796876	139797344	-	28	0.000	0.020	0.008	0.034	0.025	0.012	0.000	0.000	0.025	0.064	0.040	0.044
71888278	71889263	+	12	0.004	0.005	0.007	0.004	0.028	0.009	0.003	0.003	0.003	0.070	0.021	0.016
175815975	175816311	+	20	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.021	0.026
47342878	47349249	-	42	0.028	0.027	0.030	0.027	0.028	0.022	0.030	0.022	0.058	0.041	0.057	0.068
36466281	36467649	-	17	0.015	0.019	0.003	0.000	0.008	0.003	0.009	0.004	0.014	0.034	0.037	0.044
95007368	95009658	-	14	0.002	0.000	0.000	0.001	0.000	0.000	0.000	0.010	0.000	0.044	0.034	0.010
99788124	99790377	-	14	0.000	0.000	0.008	0.010	0.010	0.000	0.000	0.016	0.000	0.012	0.014	0.022
235992340	235993525	-	3	0.692	0.773	0.574	0.776	0.634	0.362	0.698	0.677	0.507	0.647	0.668	0.646
129156809	129158572	-	15	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.023	0.030	0.045
19422418	19423149	+	11	0.004	0.000	0.000	0.018	0.004	0.011	0.005	0.000	0.000	0.049	0.021	0.033
72404529	72404736	-	13	0.000	0.002	0.002	0.000	0.003	0.000	0.000	0.002	0.003	0.027	0.022	0.046
1402308	1411695	+	48	0.005	0.000	0.005	0.020	0.000	0.006	0.008	0.000	0.009	0.009	0.044	0.025
43322784	43322985	+	13	0.011	0.018	0.013	0.014	0.015	0.026	0.013	0.017	0.019	0.050	0.039	0.033
131181738	131186934	-	18	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.035	0.003	0.000
61910804	61910946	-	23	0.010	0.005	0.004	0.002	0.005	0.000	0.003	0.000	0.011	0.027	0.014	0.019
52692359	52696148	-	27	0.024	0.000	0.047	0.000	0.034	0.000	0.024	0.000	0.006	0.029	0.050	0.041
113864403	113873243	+	15	0.008	0.008	0.000	0.011	0.000	0.006	0.000	0.012	0.000	0.007	0.026	0.037
9048865	9083315	-	18	0.000	0.000	0.003	0.003	0.000	0.000	0.000	0.000	0.000	0.040	0.024	0.015
21137396	21139650	-	18	0.003	0.000	0.004	0.000	0.009	0.003	0.008	0.000	0.003	0.047	0.037	0.027
86250389	86250480	-	20	0.000	0.010	0.000	0.006	0.003	0.000	0.000	0.000	0.000	0.013	0.041	0.027
56361954	56362539	+	22	0.000	0.006	0.000	0.000	0.004	0.000	0.005	0.000	0.000	0.011	0.028	0.007
182395377	182396362	+	21	0.005	0.002	0.000	0.003	0.000	0.002	0.000	0.003	0.000	0.024	0.015	0.023
37816527	37816662	+	21	0.000	0.000	0.003	0.000	0.007	0.002	0.000	0.000	0.003	0.044	0.008	0.008
34922393	34922624	+	19	0.000	0.020	0.000	0.013	0.000	0.012	0.000	0.000	0.000	0.032	0.016	0.019
45003777	45004013	-	15	0.008	0.008	0.015	0.002	0.007	0.017	0.006	0.019	0.008	0.047	0.022	0.032
53689424	53691607	+	26	0.000	0.000	0.003	0.002	0.002	0.000	0.000	0.004	0.000	0.006	0.029	0.028
203160561	203162080	+	21	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.021	0.018	0.025
48751115	48751182	-	14	0.003	0.000	0.006	0.000	0.005	0.000	0.005	0.000	0.000	0.021	0.034	0.016
108225945	108227651	-	19	0.012	0.009	0.012	0.000	0.008	0.000	0.000	0.012	0.000	0.030	0.032	0.024
40746029	40747844	-	11	0.010	0.014	0.020	0.008	0.017	0.009	0.023	0.020	0.004	0.031	0.034	0.036
203154527	203155443	-	13	0.000	0.001	0.002	0.000	0.000	0.000	0.004	0.002	0.000	0.005	0.021	0.028
101293124	101298615	+	18	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.012	0.023
7648016	7649408	-	18	0.005	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.016	0.025	0.025
132439719	132439902	+	22	0.003	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.024	0.020	0.022
47065513	47065623	+	23	0.001	0.001	0.000	0.004	0.000	0.000	0.002	0.002	0.000	0.038	0.014	0.016
25554745	25555488	-	18	0.001	0.002	0.003	0.000	0.001	0.000	0.002	0.000	0.000	0.018	0.021	0.015
34256733	34261227	-	24	0.002	0.000	0.004	0.000	0.000	0.002	0.000	0.000	0.000	0.023	0.011	0.022
21026765	21029293	-	42	0.000	0.000	0.005	0.000	0.004	0.008	0.000	0.000	0.018	0.049	0.023	0.020
77640242	77641715	-	18	0.008	0.011	0.019	0.000	0.007	0.000	0.000	0.003	0.000	0.007	0.016	0.045
150318968	150321619	+	13	0.000	0.000	0.005	0.005	0.000	0.000	0.000	0.003	0.000	0.033	0.000	0.011
127395425	127395783	+	26	0.000	0.002	0.004	0.007	0.004	0.003	0.000	0.003	0.000	0.020	0.024	0.038
122740084	122740526	-	15	0.005	0.000	0.003	0.004	0.003	0.003	0.000	0.015	0.000	0.033	0.020	0.009
63979220	63986701	+	21	0.005	0.005	0.013	0.005	0.009	0.005	0.009	0.005	0.017	0.030	0.019	0.031
25815785	25817874	+	26	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016	0.040	0.013
165619202	165620230	+	20	0.000	0.000	0.000	0.002	0.003	0.001	0.000	0.000	0.003	0.038	0.023	0.012
57283765	57284303	+	19	0.011	0.009	0.000	0.011	0.000	0.011	0.004	0.016	0.013	0.047	0.027	0.019

158815794	158817490	+	27	0.001	0.001	0.002	0.002	0.002	0.000	0.000	0.001	0.001	0.032	0.016	0.009
21825540	21826085	-	14	0.000	0.000	0.004	0.000	0.006	0.000	0.000	0.000	0.017	0.049	0.026	0.011
27279901	27287574	+	35	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.037	0.011
32377443	32381495	-	15	0.005	0.004	0.006	0.003	0.006	0.001	0.007	0.007	0.007	0.033	0.016	0.014
61721245	61722589	-	18	0.003	0.003	0.000	0.003	0.000	0.000	0.006	0.003	0.008	0.047	0.036	0.017
45004146	45004543	-	27	0.002	0.000	0.003	0.002	0.000	0.000	0.002	0.000	0.004	0.000	0.045	0.019
145109685	145112354	+	18	0.002	0.003	0.000	0.007	0.004	0.000	0.008	0.003	0.018	0.012	0.011	0.020
30692507	30694775	+	15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.021	0.007	0.004
2877838	2883603	+	21	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.009	0.007
86398460	86400772	-	24	0.015	0.011	0.027	0.000	0.007	0.009	0.000	0.016	0.018	0.023	0.031	0.034
195782191	195785154	-	18	0.000	0.000	0.000	0.001	0.000	0.001	0.000	0.002	0.000	0.009	0.011	0.016
226043662	226044352	-	20	0.000	0.003	0.000	0.000	0.009	0.004	0.000	0.002	0.004	0.004	0.029	0.029
157240265	157241192	-	29	0.002	0.000	0.010	0.000	0.000	0.006	0.000	0.017	0.000	0.027	0.019	0.010
195799040	195800800	-	16	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.023	0.010	0.010
145161867	145161963	+	27	0.009	0.009	0.007	0.001	0.009	0.004	0.008	0.011	0.003	0.028	0.017	0.011
65262578	65266939	-	17	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.027	0.007	0.000
80290527	80292288	+	17	0.027	0.024	0.024	0.029	0.016	0.024	0.026	0.026	0.033	0.033	0.045	0.035
69992202	69993621	+	21	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.000	0.003	0.013	0.012	0.008
155282187	155287710	+	21	0.002	0.000	0.004	0.004	0.000	0.004	0.003	0.004	0.000	0.013	0.015	0.003
161127108	161127388	+	18	0.004	0.002	0.000	0.002	0.001	0.000	0.000	0.000	0.000	0.011	0.005	0.005
59185284	59185477	-	24	0.000	0.003	0.000	0.002	0.000	0.003	0.000	0.000	0.000	0.011	0.015	0.013
98303980	98307651	-	16	0.000	0.000	0.004	0.000	0.004	0.000	0.003	0.000	0.014	0.012	0.020	0.012
18256699	18258183	-	12	0.003	0.002	0.004	0.001	0.004	0.003	0.000	0.003	0.000	0.015	0.006	0.013
159849411	159849702	+	13	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.018	0.005
42902337	42903274	+	37	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.001	0.017	0.009	0.005
67891987	67895670	-	18	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.006	0.004
7841158	7841707	+	27	0.002	0.000	0.000	0.001	0.003	0.001	0.002	0.000	0.000	0.011	0.006	0.011
43826917	43827852	+	13	0.001	0.013	0.002	0.000	0.000	0.001	0.000	0.000	0.000	0.014	0.010	0.006
60712019	60712419	-	13	0.000	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.007	0.010
10263427	10264749	+	18	0.001	0.006	0.001	0.001	0.001	0.002	0.002	0.004	0.004	0.014	0.014	0.010
117350201	117354812	+	19	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.007	0.011	0.005
86593214	86593287	-	19	0.001	0.001	0.001	0.002	0.001	0.000	0.001	0.000	0.001	0.010	0.005	0.006
10477175	10477412	+	20	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.000	0.002	0.012	0.004	0.005
45911539	45912794	-	15	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.007	0.005
186505672	186506080	+	18	0.002	0.005	0.000	0.004	0.001	0.008	0.004	0.008	0.000	0.004	0.013	0.011
113013761	113018691	-	18	0.000	0.000	0.001	0.000	0.000	0.001	0.001	0.001	0.000	0.008	0.008	0.009
85622106	85622660	-	24	0.000	0.002	0.000	0.003	0.001	0.001	0.000	0.000	0.000	0.016	0.005	0.002
1905255	1905482	+	27	0.000	0.001	0.001	0.000	0.000	0.000	0.001	0.001	0.000	0.011	0.009	0.009
8704813	8705536	+	16	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.005	0.006
56129543	56130358	+	17	0.001	0.000	0.001	0.000	0.000	0.001	0.000	0.000	0.000	0.008	0.003	0.004
65316225	65318116	-	20	0.000	0.002	0.001	0.000	0.007	0.004	0.000	0.002	0.001	0.016	0.004	0.002
17682623	17682836	+	15	0.004	0.003	0.006	0.007	0.007	0.002	0.008	0.006	0.000	0.011	0.009	0.010
26233331	26235466	-	16	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.001	0.000	0.005	0.003	0.003
43547611	43555197	+	18	0.000	0.001	0.001	0.001	0.000	0.000	0.000	0.001	0.009	0.014	0.004	0.008
53421973	53427574	+	15	0.002	0.001	0.001	0.003	0.002	0.001	0.001	0.003	0.001	0.013	0.004	0.005
170844510	170846321	-	16	0.002	0.000	0.002	0.001	0.004	0.004	0.003	0.002	0.002	0.009	0.008	0.009
34147442	34149625	+	18	0.000	0.006	0.000	0.001	0.000	0.000	0.002	0.000	0.002	0.008	0.007	0.009
55462099	55462545	+	18	0.000	0.000	0.002	0.000	0.001	0.000	0.001	0.001	0.001	0.007	0.006	0.005
17657645	17660419	+	18	0.001	0.001	0.001	0.000	0.001	0.000	0.000	0.000	0.000	0.011	0.004	0.001
23958665	23959327	+	13	0.004	0.004	0.006	0.006	0.006	0.003	0.004	0.010	0.006	0.009	0.012	0.015
56503078	56503622	+	18	0.000	0.000	0.001	0.001	0.000	0.001	0.000	0.000	0.000	0.011	0.005	0.003
46082376	46083113	+	21	0.001	0.002	0.002	0.001	0.001	0.000	0.005	0.000	0.002	0.006	0.003	0.006
45924213	45935847	+	30	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.002	0.005	0.008	0.007
112451414	112457543	+	16	0.000	0.001	0.000	0.000	0.001	0.000	0.002	0.000	0.000	0.004	0.001	0.009
142961770	142962038	+	46	0.003	0.003	0.000	0.000	0.001	0.000	0.006	0.000	0.000	0.006	0.006	0.003
85214031	85223943	-	17	0.001	0.003	0.002	0.000	0.002	0.001	0.001	0.000	0.001	0.005	0.005	0.004

179151785	179153660	+	20	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.004	0.003	0.001
117661187	117668094	-	21	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.001	0.005	0.004	0.004
55462099	55462548	+	15	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.000	0.001	0.004	0.005	0.004
48266165	48266752	+	30	0.003	0.003	0.002	0.001	0.003	0.003	0.004	0.004	0.000	0.004	0.005	0.006
103720678	103722610	-	20	0.001	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.001	0.002	0.003	0.005
39455867	39456152	-	21	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.002	0.001
4849320	4849922	-	27	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.002	0.002
37660602	37663109	+	20	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.001	0.001	0.004	0.003	0.001
45912933	45913631	-	21	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.001	0.001
79804961	79805118	-	12	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.001	0.001
34392633	34392848	-	15	0.001	0.000	0.000	0.001	0.001	0.001	0.001	0.000	0.001	0.003	0.002	0.002
69744053	69745971	+	28	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.001	0.001
8705629	8706243	+	21	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.004	0.001	0.001
37359363	37360302	+	27	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.001	0.001
153330358	153330714	+	30	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.001	0.001
66792532	66792630	-	17	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.001
73588859	73590882	-	24	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.001	0.001	0.003	0.001	0.001
146015874	146016661	-	18	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000
56510444	56510537	+	21	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.000
49999729	50000429	+	21	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.001	0.001
61733002	61734783	-	14	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.001
27829492	27830302	+	18	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000
34392636	34392848	-	18	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000
153330910	153333099	+	20	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
69742325	69743877	+	10	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
78566767	78567942	+	10	0.649	0.389	0.650	0.638	0.400	0.429	0.636	0.563	0.625	0.419	0.515	0.635
78940	87255	+	10	0.667	0.750	0.600	0.889	0.750	0.667	1.000	0.500	1.000	0.333	0.875	0.889
18799478	18800302	-	50	0.333	0.231	0.500	0.444	0.455	0.739	0.444	0.500	0.500	0.248	0.269	0.314
187449671	187451320	-	14	0.500	0.000	0.000	NA	0.000	0.500	0.000	0.000	0.000	0.636	0.600	0.500
843275	844033	+	6	NA	0.750	0.857	0.600	0.250	1.000	NA	0.000	NA	0.872	0.914	0.871
30864209	30864667	-	20	0.333	0.250	0.000	0.250	0.500	NA	0.143	0.400	0.000	0.636	0.538	0.833
66053069	66053171	-	25	0.000	0.000	0.000	0.250	0.000	0.000	NA	0.000	0.000	0.833	0.882	0.750
117085528	117085924	+	18	0.004	0.000	0.008	0.000	0.003	0.001	0.003	0.002	NA	0.057	0.042	0.043
41316848	41318996	-	18	1.000	0.500	1.000	NA	0.000	NA	0.000	0.500	0.000	0.500	0.833	1.000

_PSI			WT_reads_counts									MUT_reads_counts					
AA303	AA304	AA305	countData.AA306	countData.AA307	countData.AA308	countData.AA309	countData.RA006	countData.RA007	countData.RA008	countData.RA010	countData.RA011	countData.RA015	countData.AA301	countData.AA302	countData.AA303	countData.AA304	countData.AA305
1.000	0.857	0.647	0	0	0	0	0	1	1	0	3	5	5	8	15	12	11
0.905	0.760	0.952	3	0	0	3	0	0	0	0	1	31	17	13	19	19	20
0.716	0.742	0.733	0	1	1	1	0	0	1	2	2	24	23	28	48	23	44
0.647	0.598	0.527	3	1	5	0	0	3	0	0	1	74	53	87	77	58	59
0.533	0.592	0.747	2	2	3	0	1	2	0	0	0	31	65	41	24	58	65
0.552	0.703	0.497	4	11	31	7	18	11	4	5	9	346	239	162	435	365	188
0.700	0.652	0.727	2	1	1	0	0	0	2	0	0	7	22	20	7	30	16
0.779	0.632	0.600	8	20	9	10	10	10	12	13	4	29	76	37	53	36	39
0.500	0.750	0.765	0	0	3	2	0	0	0	0	0	8	22	16	7	15	13
0.800	0.750	0.706	3	2	1	1	3	3	5	1	0	2	9	13	8	15	12
0.729	0.587	0.302	2	1	2	0	0	1	0	0	1	12	41	25	43	27	13
0.900	0.368	0.357	0	0	2	0	0	0	1	0	0	2	15	3	9	7	5
0.591	0.594	0.525	0	0	1	0	0	0	0	0	0	5	15	17	13	38	21
0.548	0.520	0.786	1	0	3	0	1	1	1	1	0	5	12	42	17	13	22
0.400	0.571	0.857	0	1	0	1	0	0	0	0	0	3	9	6	8	8	6
0.589	0.535	0.481	12	21	35	6	10	23	13	14	6	304	148	97	348	191	143
0.833	0.750	0.630	11	4	2	2	2	7	3	3	5	5	10	8	15	12	17
0.724	0.600	0.419	0	1	5	0	0	3	0	1	2	41	25	18	55	33	26
0.692	0.479	0.362	0	0	1	0	1	0	0	2	1	18	19	19	27	34	25
0.412	0.444	0.552	0	0	4	0	0	0	0	0	0	14	15	22	7	20	16
0.545	0.609	0.625	0	0	1	0	0	0	0	0	1	6	8	7	6	14	5
0.600	0.383	0.352	22	34	44	9	34	13	15	24	27	176	60	84	153	101	87
0.619	0.452	0.418	10	17	26	7	19	20	30	17	20	400	235	191	470	331	231
0.622	0.632	0.327	1	3	3	1	1	1	3	1	1	13	9	13	23	24	16
0.286	0.716	0.563	1	0	1	1	0	0	1	0	0	4	40	12	8	48	27
0.522	0.545	0.444	0	3	3	0	6	3	2	9	4	10	5	5	12	18	12
0.444	0.451	0.424	0	0	1	0	0	0	0	0	0	39	32	23	12	23	25
0.739	0.467	0.259	2	4	0	1	0	0	1	1	2	11	9	8	17	14	7
0.628	0.190	0.381	0	0	0	0	0	0	0	0	0	14	8	3	27	4	8
0.468	0.497	0.423	0	2	14	9	14	1	1	2	0	52	435	147	103	249	82
0.365	0.417	0.410	0	2	4	1	0	0	0	1	1	22	44	19	27	25	16
0.389	0.357	0.233	0	1	0	0	1	0	0	0	0	13	7	9	7	10	7
0.576	0.419	0.398	0	0	0	0	0	0	0	0	0	32	21	23	87	44	45
0.563	0.556	0.737	1	0	1	0	3	1	0	0	7	11	5	7	9	10	14
0.250	0.486	0.643	1	0	0	0	1	1	0	0	0	5	22	8	2	17	9
0.538	0.564	0.280	0	0	0	2	0	0	0	0	0	7	8	12	7	22	7
0.469	0.444	0.412	0	0	0	0	0	0	2	0	0	12	17	5	15	28	21
0.455	0.348	0.333	1	0	0	0	0	0	0	0	0	4	12	11	5	8	6
0.441	0.508	0.355	18	3	19	21	13	6	1	4	7	110	171	119	97	199	81
0.414	0.517	0.182	0	0	0	1	0	0	1	4	0	6	4	5	12	15	4
0.793	0.778	0.758	3	9	8	6	3	3	3	5	6	21	62	24	23	21	25
0.414	0.273	0.400	6	8	7	4	2	4	6	9	13	35	27	25	36	18	28
0.542	0.634	0.429	5	6	0	3	6	2	6	1	7	11	5	9	13	26	12
0.427	0.489	0.302	1	1	9	0	0	0	2	2	1	28	25	26	32	44	29
0.615	0.250	0.311	1	1	2	1	1	3	0	1	2	19	16	25	16	17	14
0.609	0.531	0.167	3	3	6	11	4	4	2	3	0	14	10	17	28	17	7
0.500	0.427	0.338	0	0	1	0	0	0	0	0	0	10	12	13	16	32	24
0.452	0.406	0.206	0	1	0	0	0	0	1	0	1	29	10	9	33	26	7
0.654	0.211	0.289	0	2	1	3	0	0	0	1	0	18	12	5	34	8	13

0.391	0.416	0.281	0	0	3	0	0	0	0	0	0	20	17	19	25	32	25
0.457	0.470	0.268	8	6	5	4	3	8	11	5	11	18	27	20	32	54	22
0.375	0.186	0.217	2	1	1	1	1	1	0	1	1	9	6	7	3	8	5
0.356	0.333	0.300	0	0	2	0	0	0	1	0	0	11	11	15	16	24	6
0.304	0.107	0.145	1	0	1	0	0	2	0	1	0	46	13	18	73	12	19
0.244	0.378	0.222	0	0	1	0	0	0	0	0	0	16	26	24	21	31	16
0.535	0.196	0.117	0	0	2	0	1	0	0	0	1	59	23	12	69	22	17
0.705	0.433	0.581	14	8	3	13	9	9	12	11	6	19	21	24	31	13	18
0.500	0.205	0.342	0	0	0	0	0	0	0	0	0	7	7	6	10	8	13
0.429	0.105	0.450	5	5	1	0	7	1	2	4	5	11	10	8	21	2	9
0.308	0.225	0.300	4	0	1	7	12	9	0	1	0	5	15	13	4	9	6
0.300	0.219	0.256	2	1	1	0	0	0	1	1	3	9	16	5	9	7	11
0.386	0.281	0.200	0	0	4	2	1	2	0	0	10	52	66	61	329	129	108
0.314	0.358	0.224	0	2	2	0	2	1	3	2	0	7	12	7	16	19	15
0.242	0.158	0.347	1	0	0	1	2	0	0	0	0	9	82	29	16	34	17
0.196	0.241	0.274	0	0	0	0	1	0	1	0	0	8	19	14	9	13	17
0.481	0.205	0.231	2	5	2	6	7	4	4	5	3	19	19	14	26	8	9
0.429	0.417	0.286	4	7	6	2	2	13	4	9	3	6	25	15	15	20	14
0.388	0.200	0.170	0	1	0	0	0	0	1	0	2	11	11	11	26	18	15
0.417	0.286	0.116	0	3	0	0	0	0	0	0	1	15	8	10	15	16	5
0.359	0.171	0.172	0	0	1	0	0	0	0	0	1	9	6	8	14	6	5
0.317	0.308	0.257	0	0	1	2	1	0	1	0	4	15	12	5	13	12	9
0.398	0.500	0.065	0	0	4	1	3	0	2	2	0	34	54	11	94	61	2
0.459	0.204	0.175	1	1	4	0	0	1	0	1	0	11	13	6	17	11	10
0.311	0.367	0.218	0	0	0	0	0	1	2	0	0	10	17	22	28	36	19
0.257	0.267	0.290	0	0	0	0	0	0	0	1	0	9	1	5	9	8	9
0.164	0.473	0.286	0	0	1	0	0	0	0	0	0	9	18	10	12	53	18
0.322	0.244	0.105	0	0	1	0	0	0	0	0	0	44	25	13	46	40	14
0.240	0.087	0.319	0	0	0	0	0	0	2	0	0	15	21	11	12	4	15
0.341	0.280	0.173	0	0	5	0	1	0	0	0	0	31	8	8	44	35	13
0.206	0.180	0.202	2	4	4	1	1	4	0	0	0	42	99	45	62	50	57
0.337	0.190	0.246	3	7	5	7	2	2	4	1	2	24	39	26	28	23	29
0.373	0.145	0.159	3	1	3	4	2	10	3	6	19	18	12	13	25	11	11
0.218	0.268	0.352	0	0	0	0	0	0	0	1	1	8	13	10	12	19	19
0.370	0.188	0.063	0	0	1	0	0	1	0	0	0	9	13	18	20	12	4
0.271	0.175	0.261	0	2	0	0	0	0	0	0	0	16	7	2	13	11	12
0.267	0.375	0.200	2	4	2	0	1	2	2	2	4	6	3	6	4	9	4
0.211	0.265	0.172	3	0	3	0	0	1	0	0	2	11	24	22	8	26	15
0.280	0.387	0.333	8	6	3	6	2	0	6	1	1	16	466	9	116	41	7
0.236	0.337	0.306	6	9	0	5	7	10	10	6	38	42	51	32	25	34	33
0.193	0.316	0.133	1	2	0	0	3	1	1	1	0	15	20	9	16	24	13
0.179	0.404	0.273	0	0	1	3	0	0	0	0	0	3	10	9	7	23	12
0.230	0.262	0.171	1	3	6	0	0	1	4	2	5	33	42	50	48	74	38
0.229	0.188	0.154	0	0	3	0	0	0	0	0	0	8	14	9	8	6	6
0.441	0.137	0.077	1	1	3	0	0	1	1	1	0	10	8	7	15	7	4
0.200	0.333	0.273	1	0	2	2	1	1	2	0	1	3	8	4	4	11	3
0.196	0.215	0.246	0	0	7	1	2	0	0	0	1	8	37	19	20	31	29
0.161	0.243	0.308	0	0	7	0	2	0	1	0	6	5	19	32	39	50	69
0.184	0.264	0.127	0	0	0	0	0	0	1	0	0	9	19	15	7	14	7
0.229	0.444	0.133	1	2	1	1	3	2	0	5	4	5	7	4	8	16	6
0.365	0.071	0.175	0	2	1	0	0	0	0	0	1	11	7	10	19	5	7
0.170	0.236	0.188	2	3	7	0	1	2	3	0	0	37	38	32	34	45	26
0.244	0.314	0.096	0	0	0	0	0	0	0	1	0	14	9	6	11	22	7
0.161	0.134	0.200	5	0	1	9	4	5	0	2	0	31	16	21	9	13	11
0.172	0.370	0.158	0	0	5	1	1	0	0	0	0	18	15	14	21	60	19
0.214	0.322	0.141	2	0	2	0	2	2	1	1	5	9	31	36	22	64	18

0.366	0.179	0.075	5	13	3	3	5	2	2	8	8	17	19	21	26	14	10
0.096	0.237	0.185	0	2	0	0	0	2	1	0	2	2	7	19	7	9	5
0.147	0.159	0.231	7	6	7	3	3	0	4	4	4	42	82	66	32	44	58
0.175	0.133	0.167	1	1	1	1	2	0	2	0	4	5	15	7	22	11	10
0.217	0.134	0.102	3	0	2	2	3	0	0	0	0	16	26	16	13	13	5
0.229	0.128	0.244	1	0	0	0	0	1	0	1	0	8	21	10	19	12	11
0.167	0.226	0.133	1	0	0	0	0	0	0	0	1	3	21	11	6	12	4
0.238	0.230	0.116	7	9	13	3	7	3	8	8	9	77	70	57	90	79	46
0.163	0.190	0.089	1	0	0	1	0	0	1	1	3	8	11	6	7	12	5
0.759	0.935	0.727	3	11	3	4	8	3	12	5	5	15	17	17	22	29	16
0.248	0.324	0.079	3	0	0	1	0	0	0	0	0	20	59	10	51	97	7
0.174	0.190	0.111	0	1	0	0	1	0	0	0	0	5	14	5	4	8	5
0.153	0.196	0.176	0	0	5	0	0	0	0	1	0	36	43	23	79	49	63
0.167	0.164	0.225	4	7	0	2	0	2	3	0	1	9	8	10	4	9	9
0.268	0.158	0.200	8	2	2	1	2	3	3	3	3	9	10	3	11	6	5
0.857	0.444	0.667	1	3	1	4	0	2	0	0	3	3	9	13	6	4	6
0.221	0.127	0.136	10	2	3	1	2	2	1	2	1	28	19	23	32	17	19
0.028	0.103	0.280	0	0	1	0	0	0	0	0	0	6	11	8	1	4	14
0.261	0.070	0.085	0	0	0	0	0	0	1	0	0	14	10	10	18	7	6
0.000	0.231	0.302	2	8	0	3	2	0	6	6	4	5	5	8	0	3	13
0.204	0.197	0.098	0	0	0	0	0	0	0	1	0	18	20	14	29	26	12
0.109	0.267	0.203	0	0	1	0	0	0	0	2	0	2	10	15	5	28	12
0.092	0.162	0.237	1	0	0	0	0	0	0	0	0	10	54	52	6	45	41
0.147	0.309	0.273	15	3	5	11	14	6	5	1	2	10	48	47	17	71	44
0.263	0.275	0.130	5	5	5	3	8	13	2	3	4	9	12	14	15	19	7
0.203	0.131	0.111	0	4	2	5	4	1	2	0	2	24	24	19	29	13	8
0.035	0.372	0.109	3	5	2	0	5	2	5	0	2	23	15	5	2	29	7
0.173	0.227	0.138	9	12	6	4	11	7	14	4	10	15	17	12	23	22	15
0.271	0.266	0.031	0	0	1	0	1	2	0	0	0	15	2	11	26	34	4
0.158	0.189	0.107	1	0	1	0	0	0	0	0	0	6	14	9	6	7	3
0.186	0.172	0.127	2	0	0	1	0	0	0	2	0	4	10	14	16	15	16
0.050	0.216	0.194	0	0	0	0	0	0	0	0	0	4	14	4	2	27	14
0.193	0.174	0.094	0	1	0	0	0	0	0	1	0	28	22	20	29	36	18
0.203	0.056	0.169	3	1	1	2	3	3	2	0	2	8	7	9	16	5	12
0.165	0.123	0.123	0	0	0	0	0	0	0	0	0	12	17	11	17	14	13
0.238	0.088	0.096	0	0	1	0	0	0	0	0	0	11	11	15	19	6	10
0.217	0.191	0.040	0	0	0	0	0	0	0	0	0	10	5	10	15	17	4
0.097	0.200	0.165	1	0	1	0	0	0	0	0	1	5	18	18	14	24	17
0.212	0.153	0.061	0	0	0	0	0	0	0	0	0	14	5	3	18	11	5
0.183	0.188	0.046	1	0	0	0	1	1	0	2	0	12	14	19	17	19	5
0.100	0.200	0.200	0	1	0	1	1	0	0	0	0	0	14	5	4	7	7
0.175	0.063	0.041	1	0	0	1	0	0	0	0	0	17	14	3	7	5	2
0.310	0.205	0.112	2	14	0	4	5	2	1	7	9	12	7	13	40	17	10
0.142	0.242	0.045	0	1	1	0	0	0	0	0	0	11	66	21	27	56	6
0.078	0.128	0.083	0	0	0	0	0	0	0	0	0	8	6	12	5	10	6
0.261	0.173	0.034	0	0	0	0	0	0	0	0	0	12	1	0	18	14	2
0.163	0.213	0.078	1	2	3	0	0	0	1	1	7	4	51	0	22	27	6
0.136	0.268	0.083	0	0	2	1	1	0	0	1	0	13	21	15	29	84	21
0.154	0.122	0.089	2	1	0	0	1	1	0	3	0	10	6	16	16	15	11
0.114	0.157	0.085	0	0	1	0	0	1	0	2	3	18	20	15	19	25	13
0.145	0.143	0.089	3	4	5	1	3	2	3	3	0	31	78	43	36	95	26
0.189	0.034	0.222	1	2	2	2	0	1	0	0	0	3	11	7	10	1	6
0.154	0.176	0.087	1	3	2	1	1	5	1	2	2	0	4	8	8	3	4
0.129	0.111	0.101	0	0	0	3	3	3	2	3	0	4	10	14	8	9	10
0.222	0.056	0.200	1	2	0	5	1	1	5	1	1	6	3	9	10	4	10
0.262	0.132	0.084	14	8	20	14	12	13	9	9	12	51	29	24	51	35	17

0.115	0.152	0.104	0	0	0	0	0	2	1	0	0	8	17	9	10	21	7
0.190	0.138	0.095	0	0	2	0	2	1	0	1	0	9	5	8	20	13	10
0.171	0.122	0.036	0	0	0	1	0	0	0	0	0	12	6	2	14	10	3
0.219	0.096	0.072	2	2	0	1	3	0	1	0	0	24	20	11	50	28	13
0.154	0.174	0.126	20	16	19	20	38	15	13	10	10	48	38	42	50	67	40
0.192	0.162	0.054	0	2	1	0	0	0	0	1	0	32	10	7	25	49	11
0.127	0.102	0.065	0	0	0	0	1	0	0	0	1	7	12	9	10	13	8
0.133	0.152	0.224	2	1	0	1	0	1	1	1	2	1	5	2	8	10	13
0.180	0.171	0.229	24	35	9	8	13	15	21	11	37	22	29	18	22	37	30
0.135	0.209	0.218	17	6	5	45	21	8	6	7	0	19	108	57	13	48	19
0.194	0.111	0.282	1	1	1	1	1	2	0	3	3	1	5	5	7	4	11
0.122	0.140	0.145	8	8	5	6	11	3	4	3	3	8	25	14	18	18	17
0.211	0.090	0.160	1	2	3	0	3	4	0	0	1	5	6	6	15	8	12
0.108	0.132	0.084	0	1	2	1	0	2	0	0	1	9	1	4	11	14	8
0.033	0.141	0.059	0	1	0	0	0	1	0	1	0	12	3	10	2	14	6
0.129	0.150	0.043	1	0	2	1	0	8	2	2	17	30	4	1	15	17	3
0.091	0.164	0.098	3	1	1	3	4	1	4	3	3	3	9	9	3	10	6
0.208	0.190	0.223	48	59	44	15	26	27	41	38	17	28	37	57	66	28	35
0.226	0.069	0.065	4	11	7	1	0	5	7	4	7	8	15	14	28	10	8
0.101	0.129	0.083	2	3	1	3	8	3	3	3	3	16	25	13	23	24	13
0.080	0.113	0.060	1	0	1	1	0	1	0	0	0	11	15	9	7	12	7
0.090	0.069	0.098	1	1	0	3	1	0	0	1	1	14	18	9	13	16	18
0.080	0.115	0.068	1	0	0	0	0	0	0	1	1	11	11	4	9	17	10
0.091	0.115	0.065	1	2	4	2	2	1	1	1	0	22	35	27	29	52	24
0.095	0.097	0.087	8	20	13	2	21	21	12	4	8	137	77	40	211	91	73
0.073	0.160	0.080	5	1	3	4	0	4	4	2	1	16	48	11	17	41	16
0.079	0.179	0.138	15	12	14	55	22	11	12	4	2	57	156	85	34	188	67
0.200	0.086	0.066	0	2	1	0	0	5	1	0	14	9	5	0	20	6	5
0.182	0.065	0.049	0	2	0	0	0	0	0	0	3	5	2	8	14	7	3
0.202	0.198	0.170	7	9	7	5	7	8	14	4	2	27	25	22	21	16	18
0.103	0.105	0.093	0	1	2	0	0	0	0	0	0	4	12	5	7	16	12
0.094	0.084	0.105	2	2	0	0	0	0	1	2	1	13	16	14	15	17	16
0.106	0.123	0.130	0	0	1	3	3	1	4	1	0	5	2	4	5	7	7
0.060	0.066	0.126	0	0	0	0	2	1	0	1	3	6	6	9	3	5	11
0.113	0.060	0.075	1	5	0	2	0	1	3	2	13	7	13	11	11	6	13
0.198	0.119	0.056	5	2	0	0	0	2	2	3	2	7	6	12	16	16	7
0.086	0.029	0.079	0	3	2	0	2	0	0	2	1	5	21	23	20	6	11
0.102	0.118	0.035	0	0	0	0	0	0	0	0	0	50	13	19	11	49	13
0.011	0.078	0.074	0	0	0	0	0	0	0	0	0	7	4	13	1	8	8
0.072	0.050	0.095	1	5	0	0	0	0	1	0	1	11	15	26	26	14	29
0.137	0.086	0.107	1	1	2	1	0	2	1	0	1	28	22	8	55	35	43
0.075	0.068	0.082	1	0	1	0	0	0	0	0	0	11	3	4	9	7	10
0.047	0.083	0.120	2	0	0	0	0	1	0	0	0	9	31	30	9	26	29
0.139	0.104	0.024	3	0	0	0	2	1	0	0	3	9	8	5	14	13	2
0.120	0.109	0.040	1	0	0	3	2	1	0	0	1	12	13	13	16	25	5
0.135	0.159	0.038	9	11	11	4	3	6	1	5	4	10	16	16	21	21	4
0.053	0.097	0.048	2	1	0	2	1	1	1	2	1	5	6	8	4	9	5
0.072	0.028	0.118	0	3	0	1	3	0	0	1	0	12	26	6	11	3	4
0.065	0.053	0.147	2	3	4	1	1	0	2	0	0	2	11	12	6	6	14
0.105	0.036	0.079	1	0	0	1	1	0	0	0	0	2	19	9	8	4	8
0.031	0.064	0.101	0	0	0	1	0	0	0	0	0	10	22	15	5	14	21
0.087	0.100	0.035	0	2	1	1	1	0	0	1	1	9	14	9	9	19	4
0.071	0.041	0.053	2	0	4	2	3	0	4	1	1	24	10	19	11	9	8
0.071	0.085	0.154	5	3	0	1	1	2	0	0	3	3	4	6	4	7	12
0.036	0.089	0.097	1	3	0	0	0	1	1	3	0	7	17	22	6	21	26
0.063	0.090	0.098	10	19	11	7	9	17	12	7	73	14	44	29	22	15	21

0.172	0.094	0.114	7	4	5	5	3	2	3	3	3	7	5	15	10	10	9
0.141	0.112	0.043	0	2	0	0	2	0	1	0	0	2	4	6	11	12	4
0.088	0.133	0.045	1	2	0	1	0	1	2	0	3	2	4	6	6	10	2
0.077	0.093	0.089	4	6	3	1	2	0	6	9	1	8	15	10	6	9	9
0.082	0.118	0.038	4	3	20	4	4	6	2	2	0	204	74	60	302	251	78
0.084	0.069	0.092	0	0	0	2	0	1	0	0	0	3	8	9	9	12	8
0.078	0.054	0.080	1	0	0	0	0	0	0	0	0	9	4	7	10	8	11
0.068	0.052	0.041	4	1	1	3	0	1	4	3	2	15	25	27	13	12	8
0.063	0.115	0.044	1	1	4	1	0	0	0	0	0	5	6	7	4	9	3
0.048	0.079	0.059	0	0	1	1	0	0	0	0	0	16	26	24	12	25	13
0.089	0.062	0.047	0	0	1	0	0	0	0	0	0	22	14	13	20	20	14
0.087	0.093	0.057	0	0	4	1	0	1	0	1	3	25	13	10	30	35	23
0.074	0.115	0.049	0	0	1	0	0	0	0	0	0	15	40	17	28	52	13
0.132	0.106	0.009	2	1	0	0	0	0	0	0	0	2	25	8	7	13	1
0.063	0.086	0.055	1	0	2	1	2	1	0	0	1	10	9	3	7	14	5
0.039	0.095	0.062	2	5	4	2	1	1	0	2	0	35	216	44	35	104	42
0.100	0.088	0.021	0	0	0	0	1	5	0	0	6	5	13	8	9	14	3
0.175	0.027	0.004	0	1	1	0	0	0	0	0	0	17	2	5	30	8	1
0.080	0.087	0.065	0	0	0	0	0	1	2	0	1	2	8	6	10	12	7
0.050	0.038	0.048	2	0	1	1	3	1	3	1	4	16	23	7	9	8	11
0.136	0.041	0.033	0	0	0	0	1	3	0	0	0	8	4	10	16	5	3
0.115	0.067	0.032	0	0	0	0	0	0	0	0	0	11	12	4	18	19	6
0.092	0.089	0.098	1328	1079	3617	453	2255	2105	744	961	319	8973	4086	3432	#####	3147	5692
0.074	0.128	0.046	2	2	9	0	1	0	2	1	1	91	18	19	147	117	31
0.037	0.075	0.091	1	1	0	1	0	0	0	3	0	5	20	15	6	24	16
0.049	0.075	0.080	1	0	1	3	2	2	1	0	1	7	3	12	5	8	7
0.085	0.067	0.026	0	0	0	0	0	0	0	0	0	15	19	15	19	30	8
0.057	0.048	0.073	0	1	1	0	1	0	1	0	0	19	31	28	16	26	32
0.149	0.042	0.052	0	1	3	0	0	0	0	0	2	12	4	4	20	9	10
0.070	0.032	0.077	0	0	1	2	5	2	1	2	2	10	16	17	15	8	17
0.032	0.105	0.038	0	0	0	0	0	0	0	0	0	9	28	14	8	40	9
0.075	0.069	0.041	0	0	0	0	0	0	0	0	0	7	7	6	14	12	9
0.097	0.114	0.033	0	0	0	0	0	0	0	0	0	4	12	2	11	16	4
0.058	0.098	0.024	0	1	2	0	0	0	3	2	1	11	6	12	21	18	5
0.066	0.056	0.051	1	0	0	0	0	3	0	0	0	25	47	41	25	44	25
0.017	0.088	0.098	10	8	32	14	10	8	8	4	20	52	58	44	11	56	58
0.054	0.036	0.086	0	0	0	0	0	0	0	0	0	10	9	16	24	6	17
0.124	0.081	0.043	6	1	3	1	2	1	11	0	4	11	13	7	13	11	6
0.050	0.064	0.056	1	0	0	0	0	1	0	0	0	4	13	10	9	11	9
0.070	0.018	0.054	1	0	0	0	0	1	1	1	0	7	9	6	11	2	7
0.066	0.144	0.055	5	8	4	1	10	0	10	4	0	21	7	12	17	55	23
0.061	0.025	0.066	0	1	1	1	0	2	1	0	0	29	61	50	47	24	69
0.074	0.111	0.039	8	7	6	5	6	7	3	7	6	29	11	8	32	36	10
0.066	0.088	0.037	1	1	7	0	0	0	1	0	1	20	20	24	21	30	16
0.054	0.080	0.027	4	2	2	2	1	2	5	2	3	10	13	14	13	21	7
0.094	0.037	0.033	0	0	0	0	0	1	0	0	0	3	16	6	11	6	3
0.018	0.102	0.025	0	0	0	1	0	0	0	0	0	2	13	12	1	13	1
0.090	0.079	0.068	0	0	0	0	0	0	2	0	0	1	8	2	13	11	7
0.091	0.032	0.063	0	0	0	1	0	4	2	1	4	3	15	6	18	5	8
0.096	0.048	0.045	8	4	5	9	3	3	3	0	2	14	39	15	20	17	16
0.095	0.063	0.033	1	1	4	0	6	0	0	0	0	20	11	9	45	25	14
0.074	0.065	0.059	3	0	2	2	4	2	2	1	4	5	7	4	6	6	3
0.038	0.065	0.043	1	2	0	1	0	0	0	0	1	10	11	29	15	25	17
0.029	0.152	0.044	0	5	5	0	0	0	0	0	0	4	6	7	6	28	11
0.026	0.041	0.031	0	1	0	1	1	1	0	0	0	6	21	9	2	5	3
0.030	0.022	0.045	0	0	1	0	0	1	0	0	0	14	38	12	9	6	13

0.040	0.070	0.059	0	0	2	3	0	0	0	0	1	19	20	18	16	34	25
0.042	0.072	0.041	0	0	1	0	1	0	0	0	2	7	25	14	10	20	9
0.036	0.055	0.021	0	1	0	1	1	1	0	0	1	9	9	3	5	7	2
0.079	0.064	0.061	5	2	2	2	2	3	1	1	4	9	11	3	16	13	9
0.060	0.028	0.039	0	0	0	0	0	2	2	0	1	24	8	2	8	6	5
0.073	0.098	0.090	2	5	1	6	1	1	5	6	3	5	6	14	6	13	12
0.098	0.056	0.051	1	1	0	0	0	1	2	0	0	4	2	5	14	8	6
0.072	0.065	0.027	2	0	0	1	1	0	1	0	2	6	8	7	7	10	4
0.035	0.039	0.049	0	0	1	2	1	1	0	0	1	14	25	19	17	14	17
0.074	0.025	0.019	0	0	0	0	0	0	0	0	0	4	11	5	19	5	3
0.041	0.028	0.060	0	0	1	0	0	1	0	0	0	5	11	4	6	4	10
0.053	0.023	0.044	0	1	1	0	0	0	0	2	1	7	5	6	7	4	6
0.065	0.058	0.055	0	4	3	1	1	0	0	2	2	7	8	10	18	16	13
0.039	0.128	0.030	3	3	2	1	0	0	0	0	0	3	5	3	4	21	4
0.020	0.057	0.070	1	0	1	0	1	1	0	0	0	9	22	15	5	26	27
0.032	0.054	0.056	14	8	68	9	38	38	25	5	8	216	353	439	267	708	462
0.028	0.048	0.069	0	0	2	0	0	0	0	0	0	9	19	13	9	22	20
0.059	0.037	0.035	0	1	2	0	0	0	0	0	3	39	15	14	45	18	19
0.025	0.049	0.031	2	2	0	1	0	0	2	1	1	4	8	7	6	5	4
0.036	0.017	0.071	0	0	4	0	0	0	0	2	0	4	26	15	14	5	22
0.058	0.062	0.057	1	3	7	1	1	0	2	1	0	18	30	23	27	40	25
0.056	0.063	0.070	6	6	4	3	11	6	4	5	2	21	9	16	17	16	20
0.085	0.031	0.067	1	0	0	0	2	1	1	1	3	3	7	4	12	6	13
0.058	0.042	0.028	0	2	2	0	2	1	2	0	2	41	51	34	51	61	32
0.044	0.054	0.043	0	1	0	1	0	0	0	2	0	4	9	6	6	11	5
0.036	0.061	0.017	0	0	1	0	0	0	0	0	0	13	4	7	13	19	5
0.048	0.052	0.039	1	1	0	0	2	1	0	2	1	6	6	7	8	8	6
0.054	0.022	0.074	0	0	5	0	3	3	0	1	1	2	5	10	7	3	7
0.038	0.052	0.072	2	2	1	0	0	0	0	0	0	2	14	8	6	13	12
0.057	0.064	0.050	1	6	8	1	2	2	2	4	2	5	10	3	11	7	7
0.032	0.068	0.050	3	3	2	2	2	1	2	2	0	53	23	22	80	71	46
0.028	0.045	0.059	0	0	2	0	0	0	0	1	0	4	16	11	4	12	12
0.036	0.044	0.034	1	1	27	0	0	2	1	0	1	261	300	319	261	486	330
0.042	0.058	0.017	2	0	0	0	4	2	0	0	4	8	4	6	6	7	2
0.054	0.039	0.024	0	1	1	0	4	0	0	0	0	22	14	21	20	26	14
0.041	0.054	0.028	4	1	4	2	4	1	1	1	1	35	43	25	40	59	26
0.042	0.028	0.036	2	0	2	0	0	1	0	0	0	10	7	9	8	8	8
0.038	0.052	0.044	1	4	7	2	5	5	0	1	4	23	34	21	24	35	23
0.042	0.045	0.048	0	3	1	0	3	2	4	2	0	8	24	14	14	19	15
0.027	0.066	0.028	1	2	0	2	2	2	0	1	0	6	12	5	3	12	3
0.040	0.036	0.032	0	0	1	1	0	0	0	1	0	8	21	11	12	16	12
0.065	0.030	0.028	0	1	0	0	0	0	0	0	1	4	10	3	13	6	6
0.087	0.030	0.035	6	8	1	3	2	0	2	2	3	4	8	8	16	7	11
0.087	0.057	0.008	6	6	3	4	3	6	4	6	3	17	17	11	22	16	2
0.038	0.019	0.028	0	0	0	0	0	0	2	1	0	13	25	10	11	6	6
0.099	0.022	0.017	0	0	0	1	0	0	0	0	1	8	6	1	22	7	4
0.038	0.025	0.051	0	0	0	0	0	1	1	0	0	3	8	9	6	7	10
0.041	0.089	0.043	1	4	4	5	2	6	4	5	2	21	26	12	16	34	13
0.005	0.069	0.038	2	2	4	2	0	2	1	2	2	5	16	11	1	17	7
0.016	0.040	0.037	0	0	1	1	0	0	1	0	0	12	18	28	10	30	25
0.052	0.023	0.024	0	0	0	1	0	0	0	0	0	7	7	10	12	7	6
0.056	0.050	0.020	6	18	5	9	11	10	16	9	29	26	47	29	28	28	7
0.056	0.047	0.026	4	1	2	4	3	2	1	0	0	9	9	12	17	21	9
0.027	0.049	0.024	0	1	1	0	1	0	2	1	3	14	14	12	21	22	10
0.050	0.046	0.018	0	0	3	0	0	0	0	0	0	16	5	14	27	22	9
0.000	0.075	0.003	0	0	0	0	0	0	0	2	0	68	35	4	0	82	3

0.016	0.048	0.025	0	0	2	1	0	0	0	0	0	5	15	16	5	18	7
0.027	0.056	0.025	2	0	3	1	1	0	1	2	0	6	5	3	3	10	3
0.022	0.055	0.036	0	0	1	0	0	1	0	0	0	2	8	4	7	18	10
0.047	0.015	0.034	0	2	0	2	1	0	0	1	0	17	80	42	36	26	28
0.032	0.019	0.032	3	3	3	3	2	2	1	1	1	51	33	16	18	12	19
0.000	0.035	0.061	0	2	0	0	0	2	0	1	1	8	15	13	0	12	10
0.023	0.047	0.043	1	2	2	2	2	0	5	4	0	26	38	52	36	114	65
0.045	0.035	0.033	1	0	1	0	0	2	1	2	1	12	2	2	10	7	9
0.056	0.042	0.036	1	4	5	3	9	5	3	6	0	9	8	8	14	10	6
0.066	0.047	0.030	4	13	8	8	8	8	6	8	9	7	14	18	26	12	7
0.021	0.047	0.038	0	4	1	3	3	1	0	0	8	8	10	7	4	6	6
0.039	0.041	0.026	2	2	2	2	6	2	1	1	1	15	17	9	14	16	9
0.038	0.030	0.018	0	0	2	0	0	0	0	0	0	9	9	12	15	20	9
0.035	0.100	0.048	33	19	35	54	25	25	24	9	35	28	116	96	31	124	43
0.024	0.033	0.045	6	12	1	0	2	2	3	2	13	4	6	10	9	5	11
0.044	0.020	0.024	1	0	0	1	0	0	0	2	0	13	30	6	15	13	10
0.086	0.009	0.051	0	0	2	2	2	0	0	3	0	1	2	4	13	2	9
0.667	0.650	0.682	63	92	113	59	116	71	134	63	69	189	211	122	118	130	103
0.024	0.022	0.020	0	0	0	0	1	0	0	0	0	7	11	15	7	8	5
0.025	0.033	0.030	1	0	0	3	1	3	1	0	0	7	4	8	4	7	6
0.027	0.025	0.023	0	2	1	0	1	0	0	1	2	7	8	16	13	9	7
0.028	0.048	0.042	1	0	1	4	0	1	1	0	2	1	8	4	4	8	6
0.029	0.073	0.031	14	33	17	9	16	33	16	21	42	48	28	25	31	58	24
0.068	0.049	0.002	0	0	0	0	0	0	0	0	0	8	1	0	17	23	1
0.041	0.037	0.044	5	2	2	1	2	0	1	0	4	8	5	7	13	12	12
0.037	0.074	0.016	3	0	2	0	2	0	3	0	1	2	7	6	4	10	2
0.006	0.056	0.055	2	2	0	3	0	1	0	2	0	1	10	9	1	13	11
0.043	0.023	0.013	0	0	1	2	0	0	0	0	0	16	17	8	19	13	5
0.036	0.000	0.025	1	0	1	0	2	1	2	0	1	8	6	5	9	0	5
0.030	0.022	0.029	0	1	0	2	1	0	0	0	0	3	31	7	5	8	4
0.023	0.059	0.027	0	1	0	0	1	0	1	0	0	3	12	3	5	26	8
0.017	0.043	0.027	3	2	0	2	0	1	0	2	0	7	8	16	7	33	18
0.061	0.025	0.004	0	0	1	0	2	1	0	0	1	9	2	2	14	7	1
0.031	0.051	0.021	0	2	0	3	0	3	0	0	0	4	4	4	4	12	5
0.025	0.029	0.042	5	8	12	1	4	8	4	14	8	17	7	13	16	16	19
0.021	0.017	0.041	0	0	2	1	2	0	0	1	0	4	24	17	12	16	32
0.036	0.022	0.014	0	1	0	0	0	0	0	0	0	6	10	15	13	12	7
0.025	0.029	0.021	1	0	2	0	2	0	1	0	0	5	14	5	7	11	6
0.039	0.038	0.004	4	2	4	0	2	0	0	2	0	5	8	6	10	12	1
0.050	0.036	0.024	4	7	5	4	6	3	8	7	1	7	18	13	16	14	8
0.013	0.032	0.031	0	4	2	0	0	0	9	5	0	9	20	58	18	32	27
0.018	0.018	0.021	0	0	0	0	0	0	0	0	0	6	5	8	5	8	8
0.000	0.033	0.030	1	0	0	0	0	0	1	0	0	1	29	9	0	6	3
0.011	0.019	0.035	1	0	5	0	0	0	0	0	0	8	9	11	4	10	15
0.024	0.020	0.016	1	1	0	3	0	0	1	1	0	17	10	13	13	14	12
0.019	0.038	0.014	1	1	2	0	1	0	1	0	0	10	14	8	11	30	7
0.026	0.023	0.021	1	0	2	0	0	1	0	0	0	8	4	11	11	10	9
0.016	0.024	0.010	0	0	2	0	1	2	0	0	5	14	4	5	8	7	3
0.033	0.031	0.020	2	4	3	0	2	0	0	1	0	1	2	8	7	8	4
0.049	0.025	0.008	0	0	2	2	0	0	0	1	0	10	0	4	14	9	2
0.012	0.033	0.005	0	2	4	2	3	2	0	2	0	10	21	17	10	13	2
0.027	0.045	0.003	3	0	1	2	1	1	0	1	0	11	18	5	7	22	1
0.036	0.031	0.017	11	8	16	6	8	5	10	6	16	25	24	39	47	42	19
0.011	0.026	0.006	0	0	0	0	0	0	0	0	0	4	22	4	3	10	1
0.020	0.020	0.006	0	0	0	2	3	1	0	0	1	13	40	11	11	14	3
0.022	0.026	0.021	3	2	0	4	0	2	1	3	3	8	9	8	4	7	5

0.025	0.023	0.012	7	7	25	4	14	2	3	6	5	113	56	39	269	120	60
0.016	0.012	0.013	0	0	1	0	2	0	0	0	3	10	10	5	4	5	4
0.013	0.011	0.012	0	0	0	0	0	0	0	0	0	10	13	4	7	5	5
0.042	0.022	0.011	8	6	7	5	8	1	7	8	9	35	25	21	50	38	16
0.010	0.007	0.004	2	1	0	1	0	0	2	1	3	11	14	9	4	3	2
0.005	0.012	0.033	1	0	2	1	0	0	1	0	4	0	15	8	3	7	17
0.050	0.015	0.025	1	1	0	3	1	0	3	1	7	3	5	10	22	6	11
0.029	0.030	0.011	0	0	0	0	0	0	0	0	0	7	4	2	14	24	7
0.033	0.011	0.011	0	0	0	0	0	0	0	0	0	12	7	4	16	7	6
0.000	0.041	0.039	3	1	2	0	1	1	0	1	2	2	9	7	0	11	9
0.011	0.026	0.027	0	0	0	4	0	2	0	1	0	22	94	79	37	118	76
0.020	0.012	0.016	0	2	0	0	3	2	0	1	1	1	7	10	13	4	6
0.018	0.035	0.009	1	0	5	0	0	3	0	5	0	13	8	5	12	19	4
0.016	0.020	0.008	0	0	0	0	0	0	0	0	0	42	68	41	42	76	21
0.018	0.035	0.016	4	5	3	1	6	2	4	4	1	11	15	5	6	19	7
0.031	0.008	0.008	0	1	0	0	0	0	0	0	0	17	4	0	26	5	5
0.048	0.035	0.035	39	19	11	57	15	20	27	15	40	14	72	47	27	51	22
0.020	0.014	0.014	0	0	0	0	0	2	0	0	1	9	17	10	15	25	16
0.009	0.017	0.024	1	0	2	2	0	2	1	1	0	4	9	2	3	11	12
0.030	0.018	0.003	2	1	0	1	1	0	0	0	0	5	3	3	15	14	2
0.018	0.008	0.008	0	2	0	1	0	2	0	0	0	4	7	7	10	5	4
0.007	0.012	0.017	0	0	1	0	1	0	1	0	6	3	11	6	2	6	7
0.022	0.014	0.009	3	1	3	1	2	2	0	1	0	9	6	12	12	12	7
0.018	0.005	0.005	0	0	0	0	0	0	0	0	0	6	25	5	8	4	3
0.014	0.011	0.009	0	0	4	0	0	0	0	0	1	8	4	3	9	7	5
0.018	0.019	0.005	0	0	1	0	0	0	0	0	0	5	11	7	20	37	8
0.017	0.008	0.009	2	0	0	1	3	1	2	0	0	8	6	11	15	9	10
0.009	0.018	0.009	1	2	1	0	0	1	0	0	0	8	12	7	3	18	6
0.014	0.012	0.007	0	1	1	0	0	0	0	0	0	4	12	14	21	17	8
0.012	0.004	0.013	2	4	1	1	1	3	2	2	3	12	16	7	12	5	16
0.001	0.018	0.006	0	0	0	0	0	0	0	1	0	5	10	4	1	18	6
0.013	0.013	0.006	2	2	2	4	3	1	3	1	2	20	17	18	30	42	19
0.010	0.015	0.005	3	2	6	1	0	2	1	0	3	30	6	9	25	27	9
0.010	0.007	0.006	7	5	32	6	7	3	7	6	5	367	238	141	409	298	215
0.015	0.007	0.015	2	4	0	3	1	6	3	5	0	3	11	9	12	11	13
0.010	0.006	0.008	0	0	2	0	0	2	2	1	0	18	19	20	22	16	17
0.016	0.004	0.006	0	1	0	1	1	1	0	0	0	11	2	1	18	2	3
0.006	0.003	0.008	0	5	2	0	0	1	3	3	1	29	19	17	20	6	18
0.009	0.009	0.006	2	1	15	1	3	2	4	3	3	100	62	86	115	185	84
0.014	0.011	0.004	1	0	1	0	0	1	0	0	0	4	4	7	11	16	5
0.008	0.013	0.010	0	1	1	0	4	3	0	1	1	8	2	1	4	9	5
0.012	0.011	0.017	12	6	26	5	30	8	7	8	0	22	18	13	49	14	21
0.016	0.011	0.005	2	1	2	1	0	0	1	2	0	9	14	13	45	43	16
0.010	0.004	0.010	1	1	6	2	0	0	0	1	2	21	6	13	26	8	18
0.010	0.008	0.010	3	1	2	3	3	2	1	3	1	17	6	11	17	24	20
0.007	0.009	0.009	2	0	2	1	5	4	3	1	1	7	12	13	7	13	11
0.004	0.013	0.004	0	4	0	1	0	0	1	0	1	5	7	9	2	11	3
0.007	0.008	0.005	4	4	27	6	24	10	9	5	10	98	97	92	113	202	115
0.009	0.008	0.003	2	1	2	0	2	1	0	0	0	23	8	1	34	11	4
0.009	0.009	0.011	7	5	11	12	13	7	6	7	9	13	25	33	18	30	29
0.003	0.008	0.004	0	0	1	1	0	2	0	0	0	10	9	5	2	13	5
0.018	0.005	0.001	1	1	2	2	2	0	3	0	1	4	3	7	8	6	1
0.004	0.005	0.006	0	0	2	0	0	0	0	0	2	8	7	6	8	4	5
0.014	0.001	0.004	0	1	0	0	1	0	2	0	0	4	1	12	17	1	5
0.005	0.007	0.010	3	4	0	0	1	0	4	0	0	5	7	4	5	9	13
0.007	0.011	0.000	1	2	3	0	2	1	1	0	1	5	3	4	9	14	0

0.010	0.004	0.003	0	0	1	0	0	0	0	1	0	5	6	3	18	10	7
0.003	0.003	0.005	0	0	0	1	0	0	0	0	1	8	7	8	6	7	10
0.004	0.007	0.003	8	7	10	9	25	23	5	4	12	55	78	74	63	180	72
0.007	0.007	0.006	29	11	18	2	51	39	33	13	0	21	47	86	257	115	104
0.006	0.002	0.005	2	1	2	1	1	0	1	1	2	2	7	7	9	4	7
0.004	0.008	0.000	0	0	4	0	0	1	1	0	1	19	8	4	25	69	4
0.003	0.004	0.002	1	4	3	4	4	5	2	1	0	41	22	19	57	58	32
0.003	0.002	0.003	0	0	0	0	0	3	0	1	4	7	5	2	14	4	6
0.003	0.004	0.001	0	1	10	0	2	8	3	0	9	71	40	25	114	188	38
0.004	0.001	0.002	0	0	0	0	1	0	0	0	0	7	4	6	14	4	6
0.002	0.003	0.002	6	2	4	13	13	7	6	2	4	26	26	23	23	48	24
0.002	0.002	0.001	0	3	8	0	2	5	0	2	5	93	57	34	93	103	76
0.002	0.002	0.001	4	4	8	6	8	6	7	0	3	37	10	12	28	32	15
0.002	0.002	0.001	1	2	3	2	6	5	1	3	0	25	21	21	22	37	16
0.002	0.000	0.001	6	5	28	0	8	6	1	7	1	327	78	72	350	46	126
0.001	0.002	0.001	0	0	0	0	0	0	0	0	0	12	11	16	15	42	14
0.002	0.001	0.001	0	1	3	2	1	1	1	2	5	10	4	4	9	3	5
0.001	0.001	0.000	1	0	1	1	0	0	0	0	0	7	5	1	11	15	5
0.001	0.000	0.001	3	1	0	1	3	4	1	0	2	13	10	7	12	8	10
0.001	0.001	0.001	0	2	0	0	2	2	4	0	6	8	8	10	6	10	8
0.000	0.000	0.001	0	0	1	2	0	0	0	2	1	9	6	14	2	6	12
0.001	0.001	0.001	0	0	4	1	0	0	2	0	0	4	10	6	14	16	11
0.001	0.001	0.000	1	0	4	0	3	2	1	0	0	5	3	4	10	11	3
0.000	0.000	0.000	9	26	24	0	23	11	4	20	5	101	63	43	134	59	41
0.000	0.000	0.000	6	17	10	7	15	13	18	7	14	17	16	25	21	31	24
0.419	0.667	0.632	24	7	13	30	10	9	7	9	5	13	50	47	13	48	24
0.800	0.455	0.846	4	6	3	8	3	6	1	4	2	1	7	8	8	5	11
0.242	0.412	0.221	2	3	13	4	10	17	8	4	4	26	21	22	36	75	19
0.750	0.600	0.467	1	0	0	0	0	1	0	0	0	7	18	11	3	3	7
0.921	0.893	0.896	0	3	6	3	1	1	0	0	0	41	64	54	35	92	43
0.538	0.286	0.462	2	2	0	1	1	0	1	2	0	7	7	5	7	2	6
0.625	0.750	0.500	0	0	0	1	0	0	0	0	0	5	15	9	5	9	3
0.040	0.081	0.037	2	0	8	0	1	1	1	1	0	20	24	9	60	42	16
0.778	0.615	0.733	2	1	1	0	0	0	0	1	0	2	5	7	7	8	11

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