The histone lysine methyltransferase KMT2D sustains a gene expression program that represses B cell lymphoma development

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Supplementary Information:

Supplementary Figures

Supplementary Figure Legends

Supplementary Tables

Suppl Figure 1

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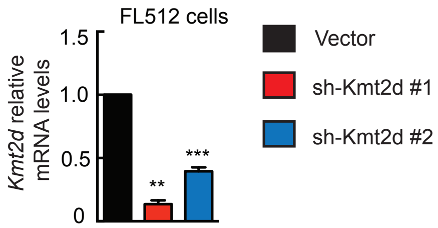

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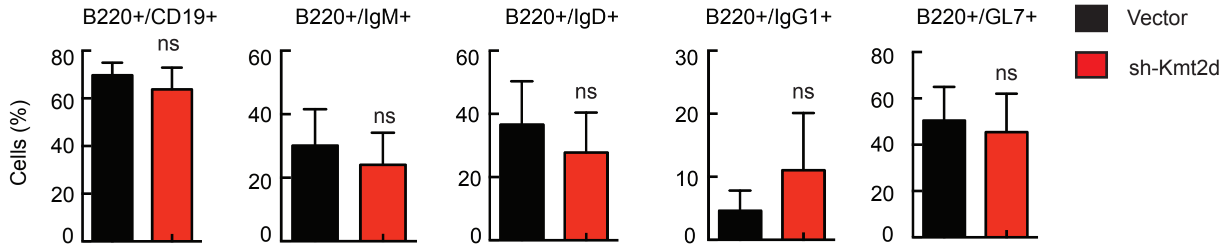

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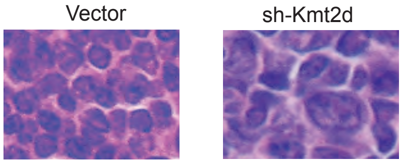

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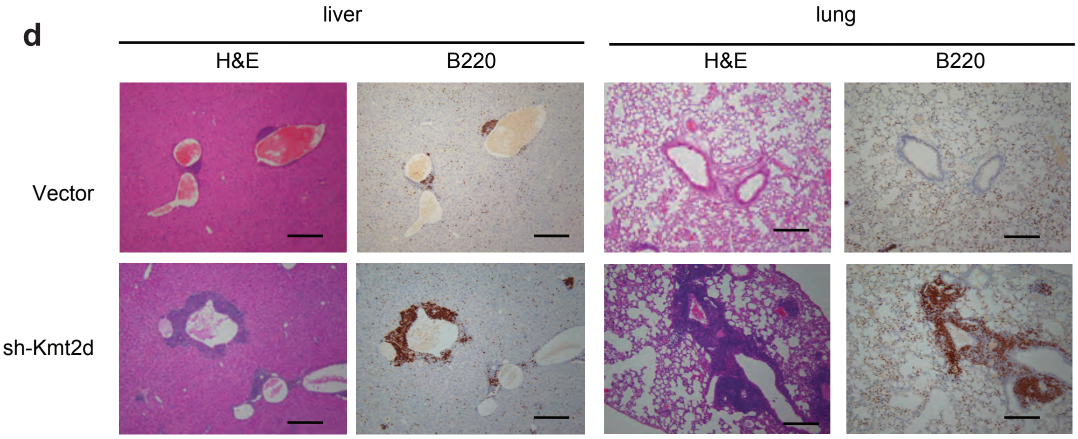

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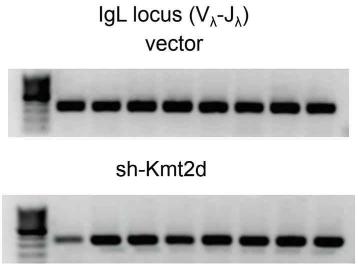

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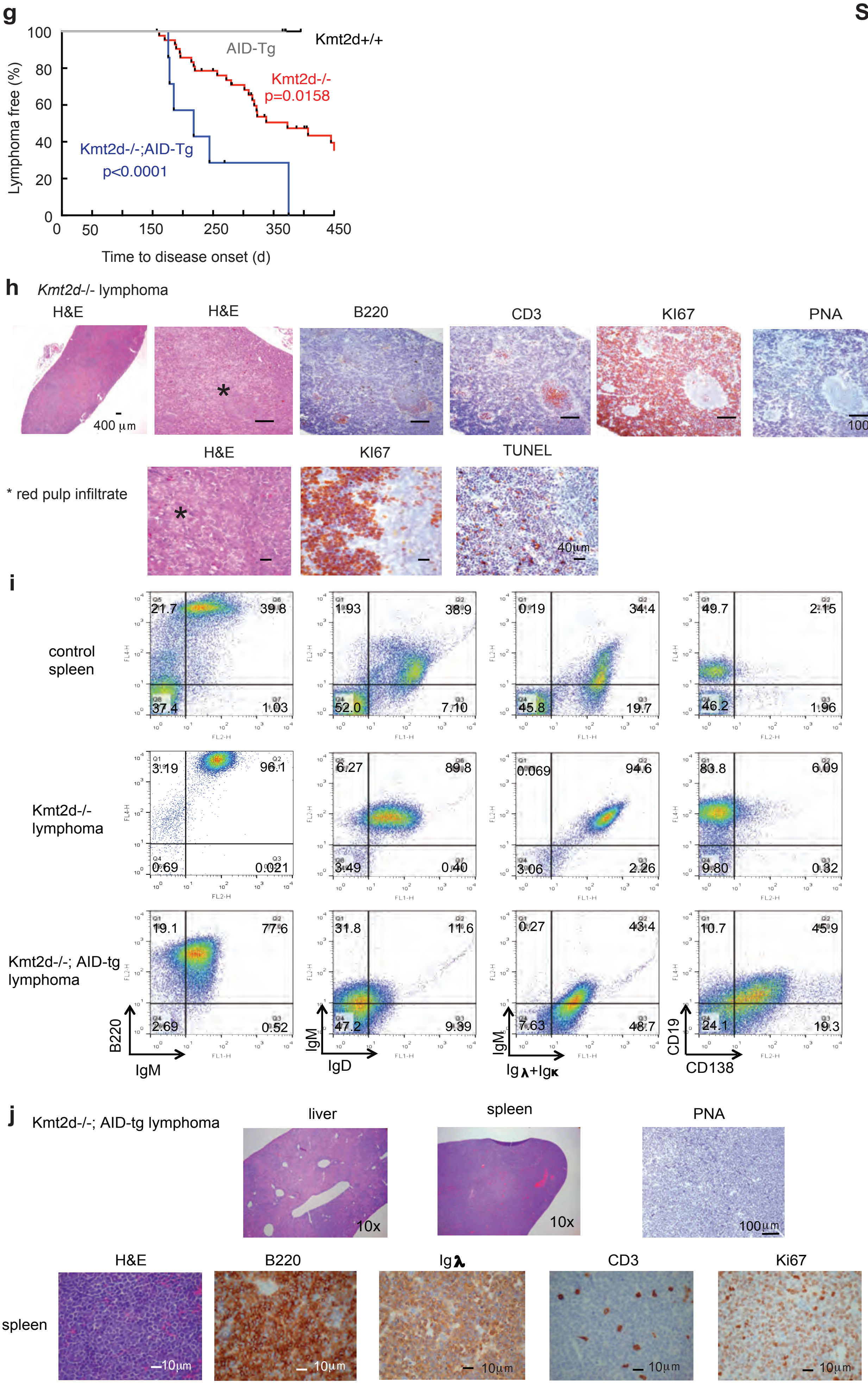
B220+ cDNA from	VH primer	JH primer	region sequenced	# bp analyzed	# mismatches	%
vector #1	VHA-F	JH4-RV1	VDJH4	255	41	16.08
vector #2	VHA-F	JH4-RV1	VDJH4	308	9	2.92
vector #3	VHA-F	JH4-RV1	VDJH4	307	15	4.89
sh-Kmt2d #1	VHA-F	JH4-RV1	VDJH4	312	17	5.45
sh-Kmt2d #2	VHA-F	JH4-RV1	VDJH4	327	10	3.06
sh-Kmt2d #3	VHA-F	JH4-RV1	VDJH4	304	32	10.53

Suppl Figure 1 (continued)



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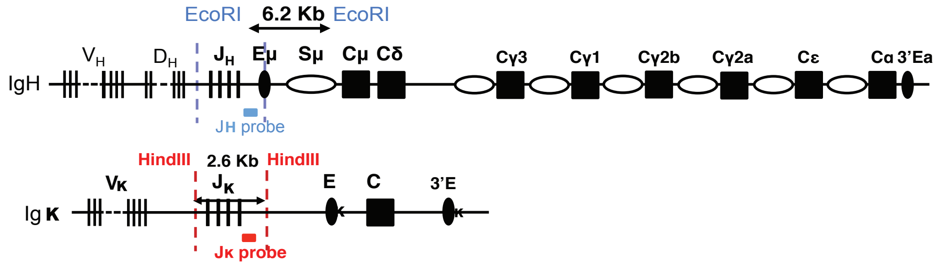

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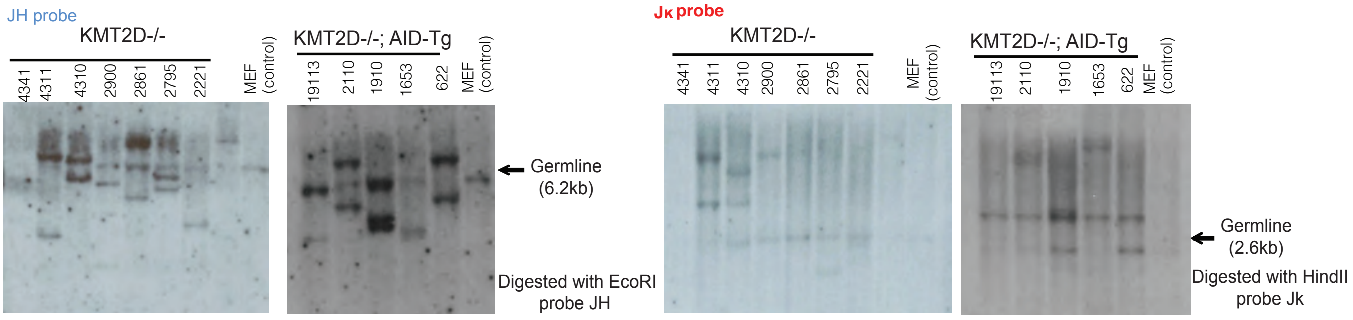

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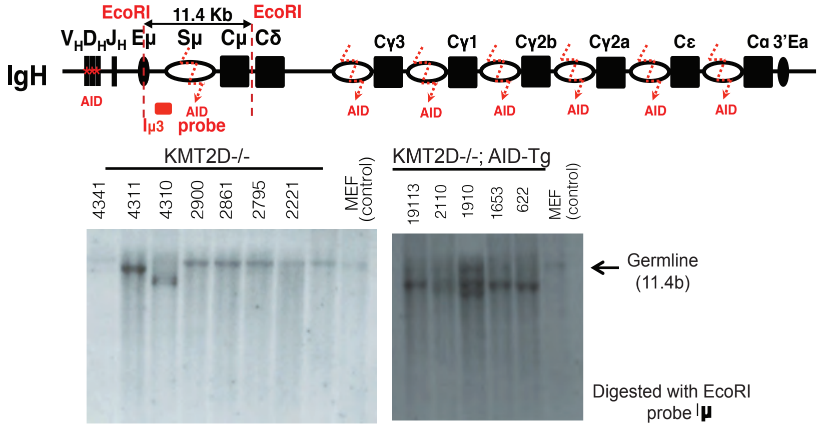

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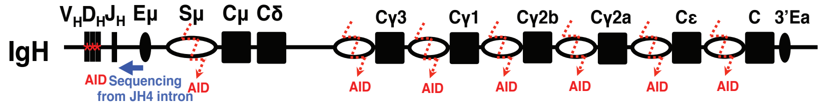


Genotype	Tumor	VDJ (bp)	mutations (bp)
Kmt2d-/-	1900	288	0
Kmt2d-/-	4310	280	1
Kmt2d-/-	4311	280	0
Kmt2d-/-	2861	332	0
Kmt2d-/-	2900	323	0
Kmt2d-/-	4341	316	0

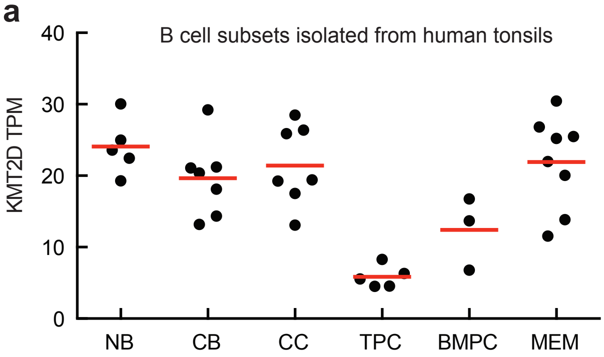
Genotype	tumor	VDJ (bp)	mutations (bp)
Kmt2d-/-;AID-tg+	622	308	5
Kmt2d-/-;AID-tg+	1650	308	3
Kmt2d-/-;AID-tg+	2100	292	3
Kmt2d-/-;AID-tg+	1653	290	3
Kmt2d-/-;AID-tg+	1816	290	5

Supplementary Figure 1. ***Kmt2d*** **deficiency accelerates B cell lymphoma development in mice.**

(**a**). Relative *Kmt2d* mRNA levels by qRT-PCR in FL512 mouse lymphoma cells transduced with vector or different shRNAs against KMT2D (#1 and #2). Bars represent mean of 2 biological replicates, error bars indicate standard deviation; **$p<0.01$, ***$p<0.001$ by two-tailed t-test. (**b**). Quantification of flow cytometry data showed in **Fig. 1f**. Values represent mean ± SD (n=4 mice per genotype). Bars represent mean ± SD (n=4 tumors per genotype). Two-tailed Student's t-test was used to determine statistical significance. No statistical significance was found. (**c**). High power image (100x) of H&E stained VavPBcl2-vector and VavPBcl2-shKmt2d lymphoma cells. (**d**). Representative histologic sections stained with H&E and immunohistochemical detection of B220+ lymphoma cells in the liver (left) and lung (right) of diseased mice with control (vector) and *Kmt2d* shRNA. Scale bars are 100 µm. (**e**). Tumor clonality analysis on VavPBcl2/vector and VavPBcl2/sh-Kmt2d tumors, each lane corresponds to one tumor. PCR analysis of Vλ1-Jλ light chain rearrangements was performed on cDNA of B220+ lymphoma cells. (**f**). Table summarizing the results of the analysis of SHM in DNA from VavPBcl2/vector and VavPBcl2/sh-Kmt2d lymphomas. (**g**). Kaplan-Meier analysis of disease free survival of Kmt2d$^{+/+}$ (*Kmt2d*$^{+/+}$ CD19-Cre^{-}=8, 3 females and 5 males), Kmt2d$^{-/-}$ (*Kmt2d*$^{f/f}$ CD19-Cre^{+}, n=43, 22 females and 21 males) (p value Kmt2d$^{+/+}$ vs Kmt2d$^{-/-}$ = 0.0158); AID-Tg (*Kmt2d*$^{+/+}$;*IgκAID*-Tg n=14, 6 females and 8 males) and Kmt2d$^{-/-}$; AID-Tg (*Kmt2d*$^{f/f}$; CD19-Cre^{+}; AID-Tg n=7, 2 females and 5 males) cohorts. (p value AID-Tg *vs Kmt2d*$^{-/-}$*; AID*-Tg < 0.0001). (**h**). Representative histologic sections stained with H&E and immunohistochemical detection of B220, CD3, Ki67, PNA and TUNEL of Kmt2d$^{-/-}$ tumors. Asterisk represents red pulp infiltration by monotonous atypical B lymphocytes. (**i**). Representative FCM analysis of Kmt2d$^{-/-}$ and Kmt2d$^{-/-}$;AID-Tg tumors, using antibodies against B220, IgM, IgD, IgL (Igκ + Igλ), CD19 and CD138 as indicated (see also **Supplementary. Table 2**). (**j**). Representative histologic sections stained with H&E and immunohistochemical detection of PNA, B220, Igλ, CD3, and Ki67, in Kmt2d$^{-/-;}$AID-Tg tumors**.** (**k**). Schema of the IgH and Igκ loci showing restriction sites and probes used. (**l**). Southern blots showing clonal rearrangements in the JH (left) and Jκ (right) loci for the indicated tumors. (**m**). Southern blot analysis for detection of rearrangements in the Sμ region of DNA from indicated tumors, probes and restriction enzyme used are indicated at the bottom right of each panel. Position of the germ-line bands is shown. DNA from MEFS was used as control. Dotted lines represent the AID-induced DNA damage in switch regions during CSR. (**n**). Table summarizing the results of the analysis of SHM in DNA from Kmt2d$^{-/-}$ and Kmt2d$^{-/-}$;AID-Tg tumors. The diagram on the top shows the region of the IgH locus used for PCR amplification and sequencing. Asterisks represent the mutations caused by AID in VDJ region during SHM.

Suppl Figure 2

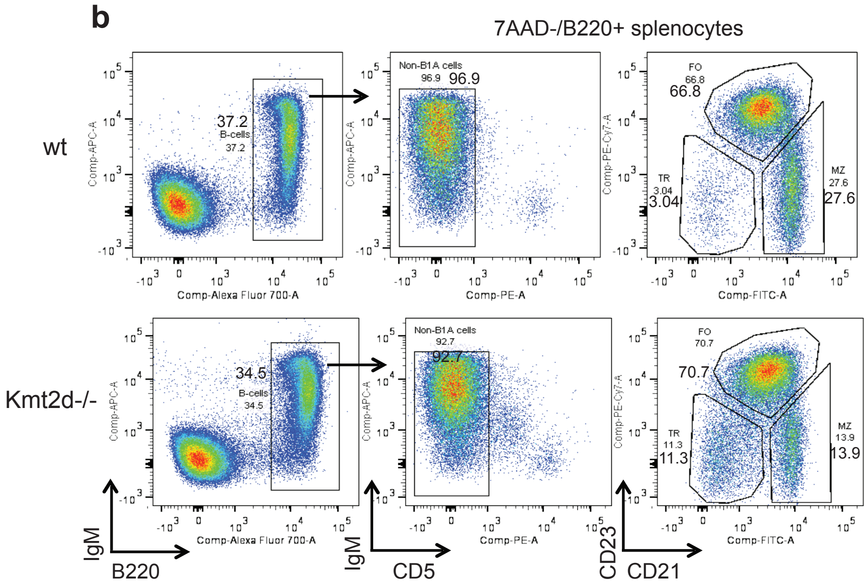
a



TPM= transcripts per million

NB=Naive B Cells
CB= Centroblasts
CC= Centrocytes
TPC= Tonsil Plasma Cells
BMPC=Bone Marrow Plasma Cellls
MEM= Memory Cells

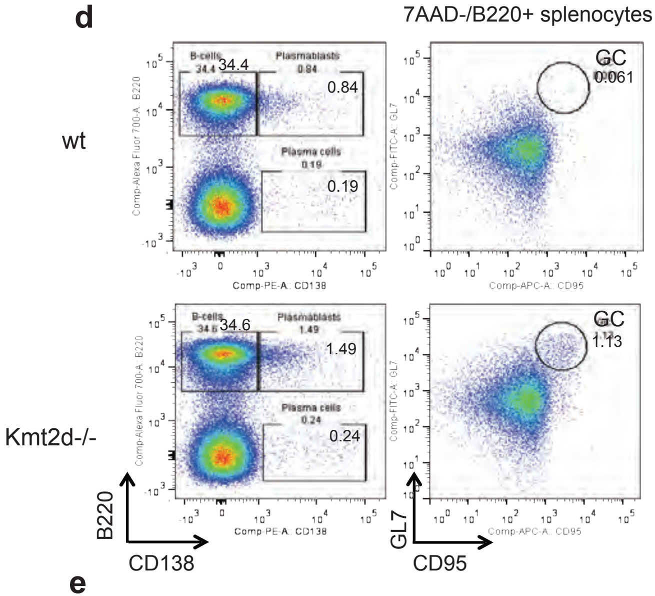
b



c

		B cells	non-B1A	Transitional	Follicular	Marginal Zone
wt	%		97.18 ± 0.39	4.46 ±1.98	68.18 ± 3.8	21.11 ± 4.91
	number of cells	2.76E+07 ± 5.59E+06	2.68E+07 ± 5.54E+07	1.24E+06 ± 5.59E+05	1.90E+07 ±4.87E+08	5.68E+06 ± 7.20E+05
Kmt2d-/-	%		94.36 ± 1.08	9.78 ± 2.02	58.48 ± 10.0	17.94± 5.24
	number of cells	2.34E+07 ± 6.43E+06	2.21E+07 ± 6.03E+07	2.36E+06 ± 9.95E+05	1.41E+07 ±5.72E+08	3.99E+06 ± 5.65E+05
ttest			*0.01*	*0.02*	*0.18*	*0.45*

d



e

		B cells	Germinal center	IPC/Plasmablasts	Plasma cells
wt	%		0.046 ± 0.01	3.48±2.81	0.21 ±0.05
	number of cells	2.62E+07 ± 4.71E+06	1.238E+04 ± 3.41E+03	9.23E+05 ± 7.87E+05	1.29E+05 ±1.83E+04
Kmt2d-/-	%		0.45 ± 0.36	3.97± 0.12	0.52 ± 0.32
	number of cells	2.28E+07 ±3.44E+06	1.09E+05 ± 9.90E+04	9.04E+05 ± 1.20E+05	3.33E+05 ±1.68E+05
ttest			*0.11*	*0.73*	*0.16*

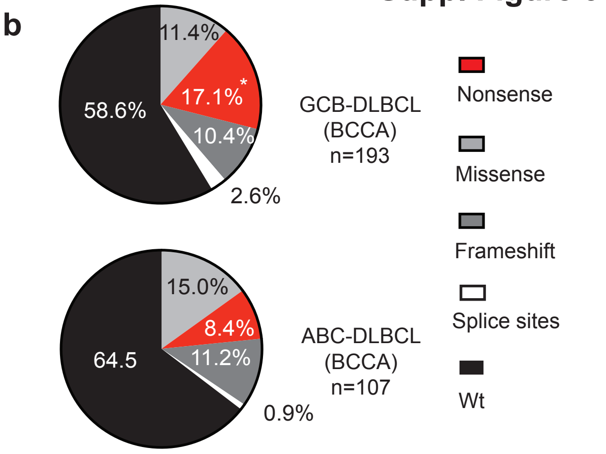
Supplementary Figure 2. KMT2D deficiency affects physiological B cell behavior

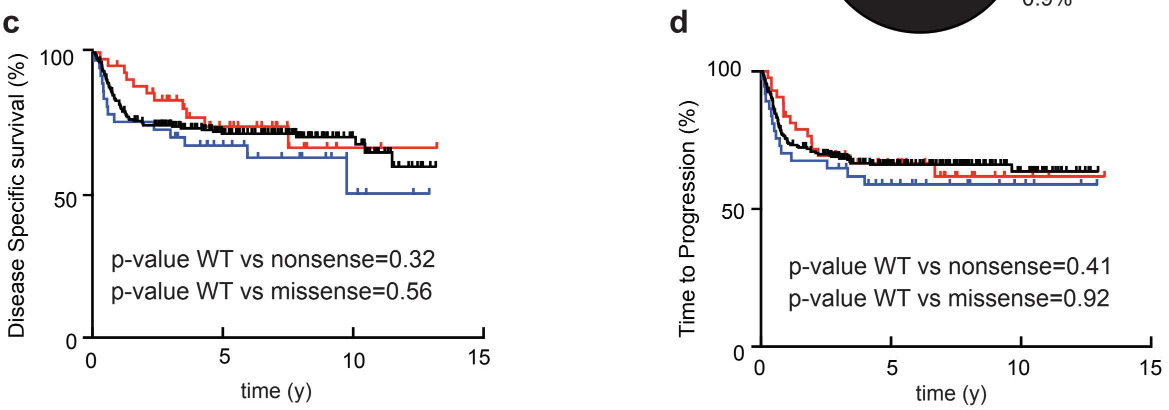
(**a**). RNAseq analysis of *KMT2D* gene expression in different mature B cell populations from human tonsils. Each red dot represents a separate human tonsil and the mean expression is represented in TPM (transcripts per million). NB= Naïve B cells, CB= centroblasts, CC= centrocytes, TPC= Tonsil Plasma Cells, BMPC= Bone Marrow Plasma Cells, MEM= Memory cells. (**b**). Characterization of B cell populations in Kmt2d$^{-/-}$ mice. Representative FCM analysis on wt and Kmt2d$^{-/-}$ spleens to determine different B cell populations using antibodies against B220, IgM, CD5, CD23 and CD21as indicated. TR: transitional, FO: follicular, MZ: marginal zone. (**c**). Table summarizing the total number of B cells and percentages for each B cell population relative to total number of live B220+ cells (7ADD-, B220+) in wt and Kmt2d$^{-/-}$ spleens. (**d**). Characterization of B cell populations in Kmt2d$^{-/-}$ mice. Representative FCM analysis on wt and Kmt2d$^{-/-}$ spleens (same mice as in **c,d**) to determine different B cell populations using antibodies against B220, IgM, CD138, CD95 and GL7 as indicated, GC: Germinal center cells. (**e**). Table summarizing the total number of B cells and percentages for each B cell population relative to total number of live B220+ cells (7ADD-, B220+, except plasma cells) in wt and Kmt2d$^{-/-}$ spleens. The percentage of plasma cells was calculated relative to total number of live cells (7ADD-). Values in (**c**) and (**e**) represent mean ± SD (3 wt (2 females and 1 male) and 4 females Kmt2d$^{-/-}$ were used;, 4-5.5 months old). Two-tailed Student's t-test was used to determine statistical significance and was calculated using each population percentage

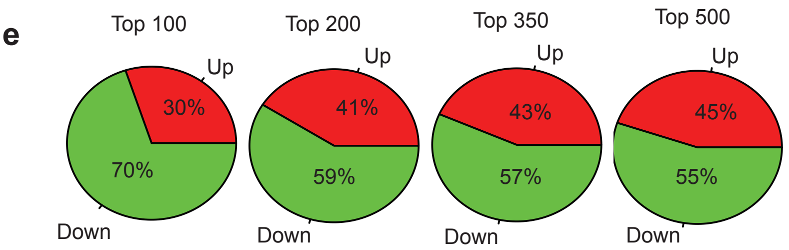
Suppl Figure 3

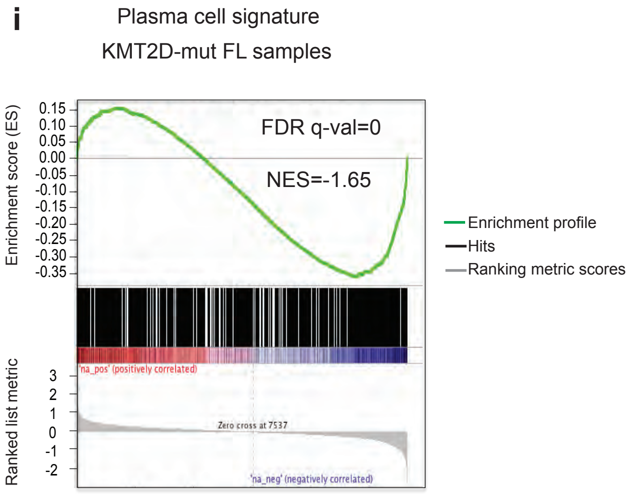
a

KMT2D mutation	Grade				p-value		
	I	II	III	total	I vs II	I vs III	II vs III
wt	16	29	17	62			
nonsense	5	16	8	29	0.15	0.22	0.20
missense	5	0	1	6	0.01	0.11	0.38
frameshift	1	0	0	1	0.37	0.50	1.00
total	11	16	9	36	**0.18**	**0.20**	**0.20**



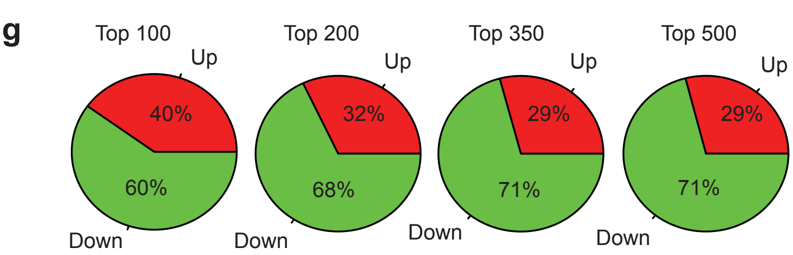


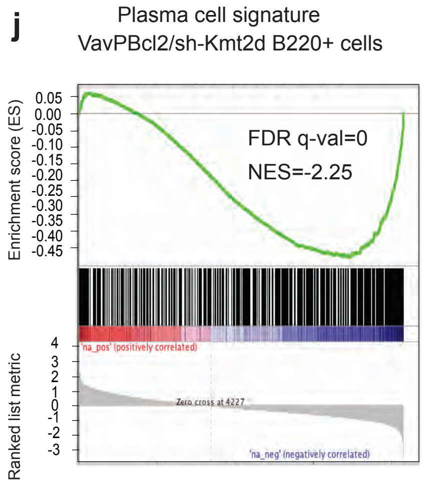




f

#of Top Transcripts	Up regulated	Down regulated	P-val cutoff
100	30 (30%)	70 (70%)	0.00162
200	82 (41%)	118 (59%)	0.00431
350	152 (43%)	198 (57%)	0.0106
500	224 (45%)	276 (55%)	0.0172
1073	528 (49%)	545 (51%)	0.05





h

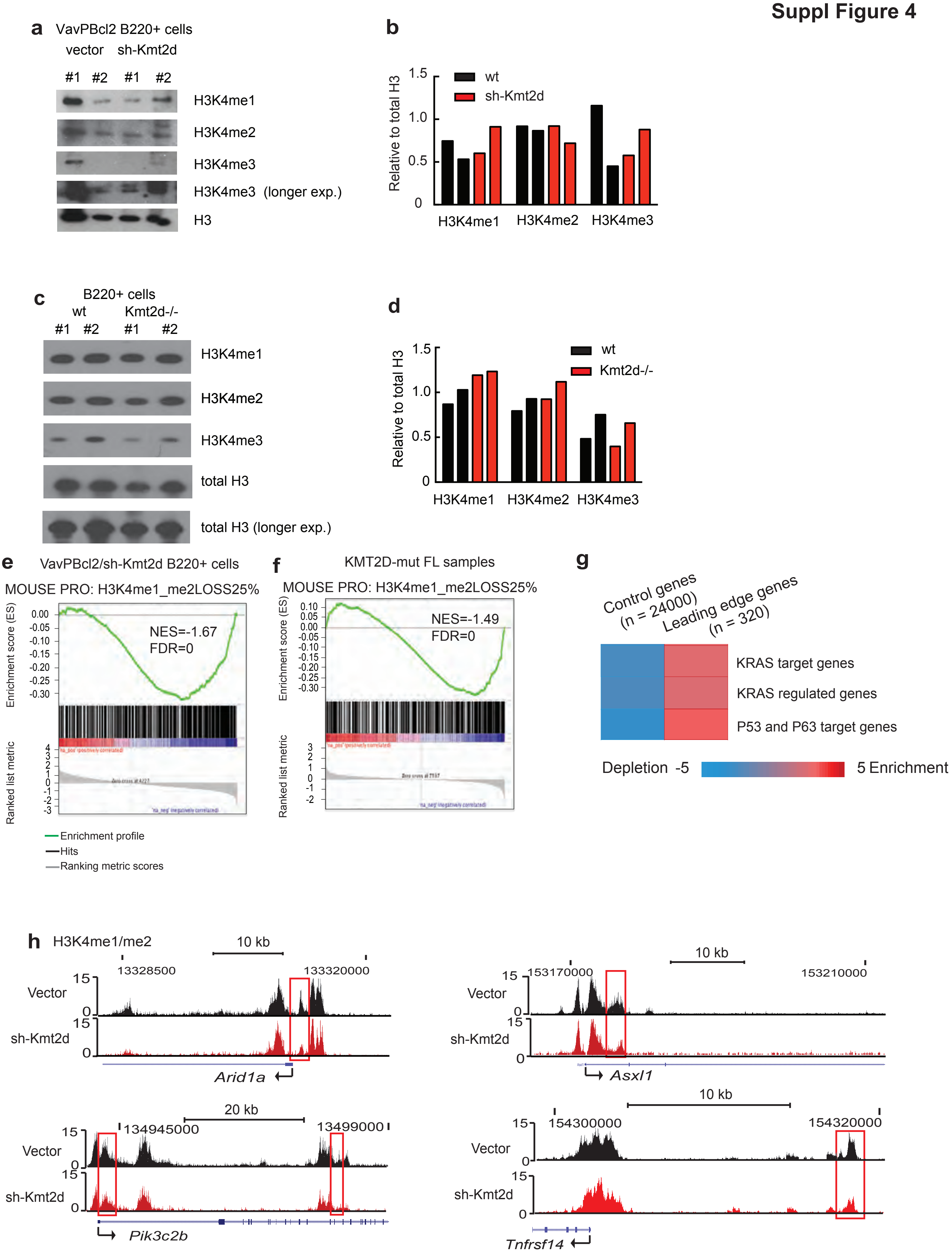
#of Top Transcripts	Up regulated	Down regulated	P-val cutoff
100	40 (40%)	60 (60%)	5.1e-5
200	64 (32%)	136 (68%)	2.31e-4
350	102 (29%)	248 (71%)	6.54e-4
500	145 (29%)	355 (71%)	1.29e-3
3210	1730 (54%)	1480 (46%)	0.022

Supplementary Figure 3. Consequences of KMT2D mutations in human FL and DLBCL.

(**a**). Table summarizing *KMT2D* mutations found in FL patients and the grade of the disease. Fisher's exact tests were performed in order to determine correlation between mutation type and grade. Overall, no significant correlation was found. (**b**). Percentage of cases with DLBCL carrying *KMT2D* mutations by type of mutation and DLBCL subtype (ABC: activated B cell; n=107; GCB: germinal center B cell; n=193). P value for nonsense mutations in GC versus ABC type =0.038 (*) by Fisher Exact test. (**c**) **and** (**d**) Kaplan-Meier curves representing disease specific survival (DSS) (**c**), and time to progression (TTP) (**d**) in years from DLBCL cases for three groups according to *KMT2D* mutation status (wt, n=215; nonsense mutation, n=37; missense mutation, n=43). Significance was estimated with the log-rank test. (**e**). Percentage of up or down-regulated genes in the top 100/200/350/500 differentially expressed genes in KMT2D^{mut} FL patients vs. KMT2D^{wt} FL patients (ranked by p-val). (**f**). Percentage in top 100/200/350/500/1073 differentially expressed genes and corresponding minimum p-val in KMT2D^{mut} FL patients vs. KMT2D^{wt} FL patients (ranked by p-val). (**g**). Percentage of up or down-regulated genes in top 100/200/350/500 differentially expressed genes in VavPBcl2-shKmt2d vs. VavPBcl2-vector B220^{+} lymphoma B cells (ranked by p-val). (**h**). Percentage of up or down-regulated genes in top 100/200/350/500/3210 differentially expressed genes and corresponding minimum p-val in VavPBcl2-shKmt2d vs. VavPBcl2-vector B220^{+} lymphoma B cells. (**i**). GSEA of differentially expressed genes ranked by log2 fold change in KMT2D^{mut} FL samples versus KMT2D^{wt} FL samples compared to Plasma cell differentiation signature gene set. (**j**). GSEA of differentially expressed genes ranked by log2 fold change in VavPBcl2/sh-Kmt2d vs.

VavPBcl2/vector B220$^+$ lymphoma B cells compared to Plasma cell differentiation signature gene set. NES, normalized enrichment score. FDR, false discovery rate.

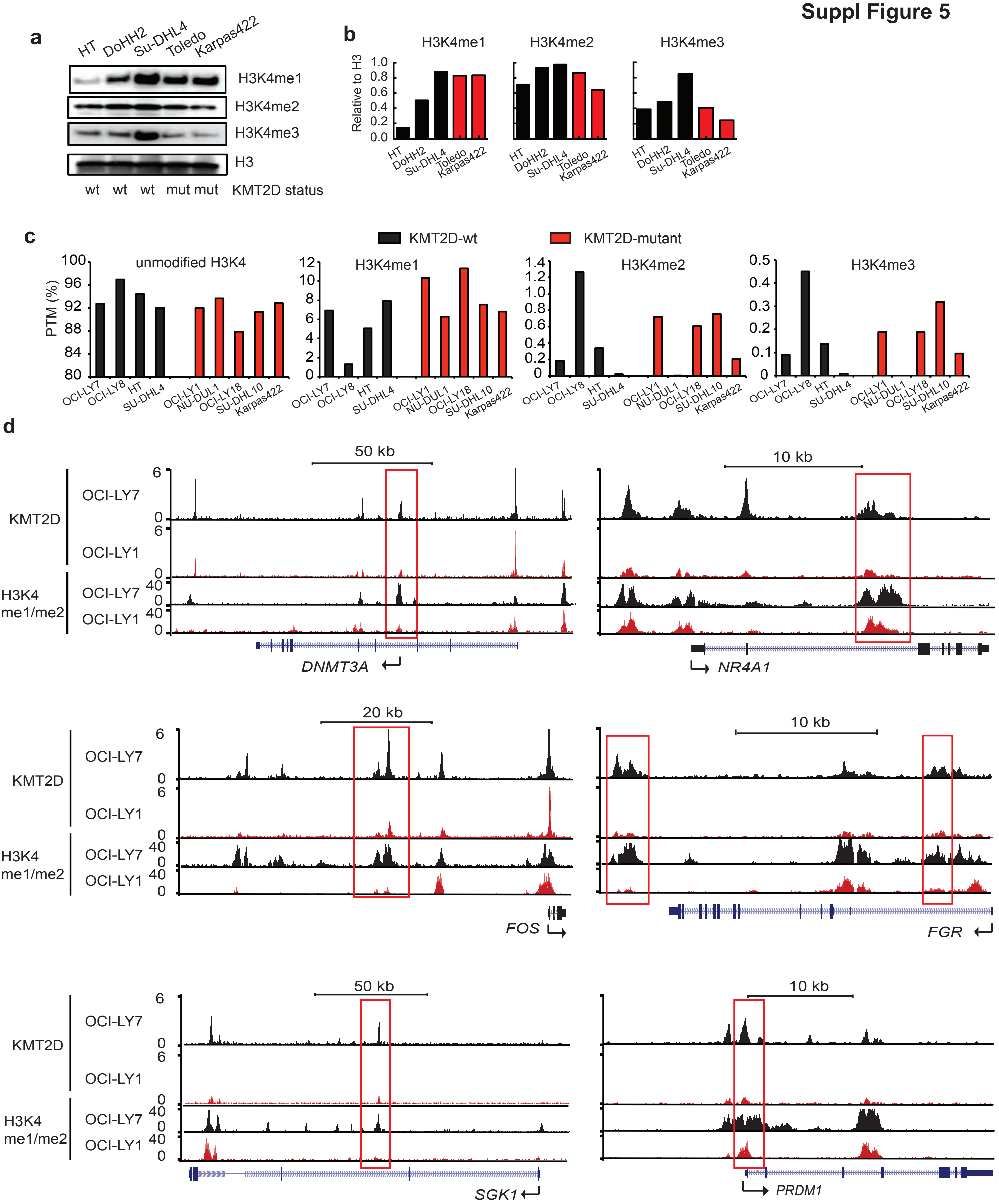
Suppl Figure 4



Supplementary Figure 4. **Epigenetic effects of KMT2D on target genes in mouse lymphomas.**

(**a**). Immunoblot of total lysates of B220+ lymphoma cells isolated from VavPbcl2-vector and VavPbcl2-shKmt2d tumors. (**b**) Quantification of global H3K4^{me1}, H3K4^{me2} and H3K4^{me3} by ImageJ software. (**c**). Immunoblot of histone lysates of B220+ cells isolated from wild type and Kmt2d$^{-/-}$ mice. (**d**) Quantification of global H3K4^{me1}, H3K4^{me2} and H3K4^{me3} by ImageJ software. (**e) and (f).** GSEA analysis of genes with a $\geq$25% reduction in H3K4me1/2 read density at promoters (p-value<0.05) in *Kmt2d* knockdown tumors compared to ranked log2 fold change levels identified by RNA-seq in *Kmt2d* B220 knockdown tumors or KMT2D^{mut} FL patients. NES, normalized enrichment score. FDR, false discovery rate. (**g**). Pathway analysis of down-regulated genes with a $\geq$25% reduction in H3K4 $^{me1/me2}$ read density at promoters (p<0.05) identified by GSEA leading edge analysis (n=321) in sh-*Kmt2d* B220+ tumors and KMT2D^{mut} FL patients compared to lymphoid signature database from the Staudt Lab (http://lymphochip.nih.gov/signaturedb/) and MysigDB. The background included around 24,000 genes from Refseq gene annotation. Statistical signficance was determined by hypergeometric tests and shown in the color key. The red color indicates (in $\log_{10}$) the over-represented *p*-values and the blue shows under-representation (**h**). Normalized UCSC read density tracks of H3K4$^{me1/me2}$ ChIP-seq peaks from MACS-sorted B220 positive lymphoma B cells in VavPBcl2-vector (vector) and VavPBcl2-shKmt2d (sh-Kmt2d) lymphomas for the indicated genes.

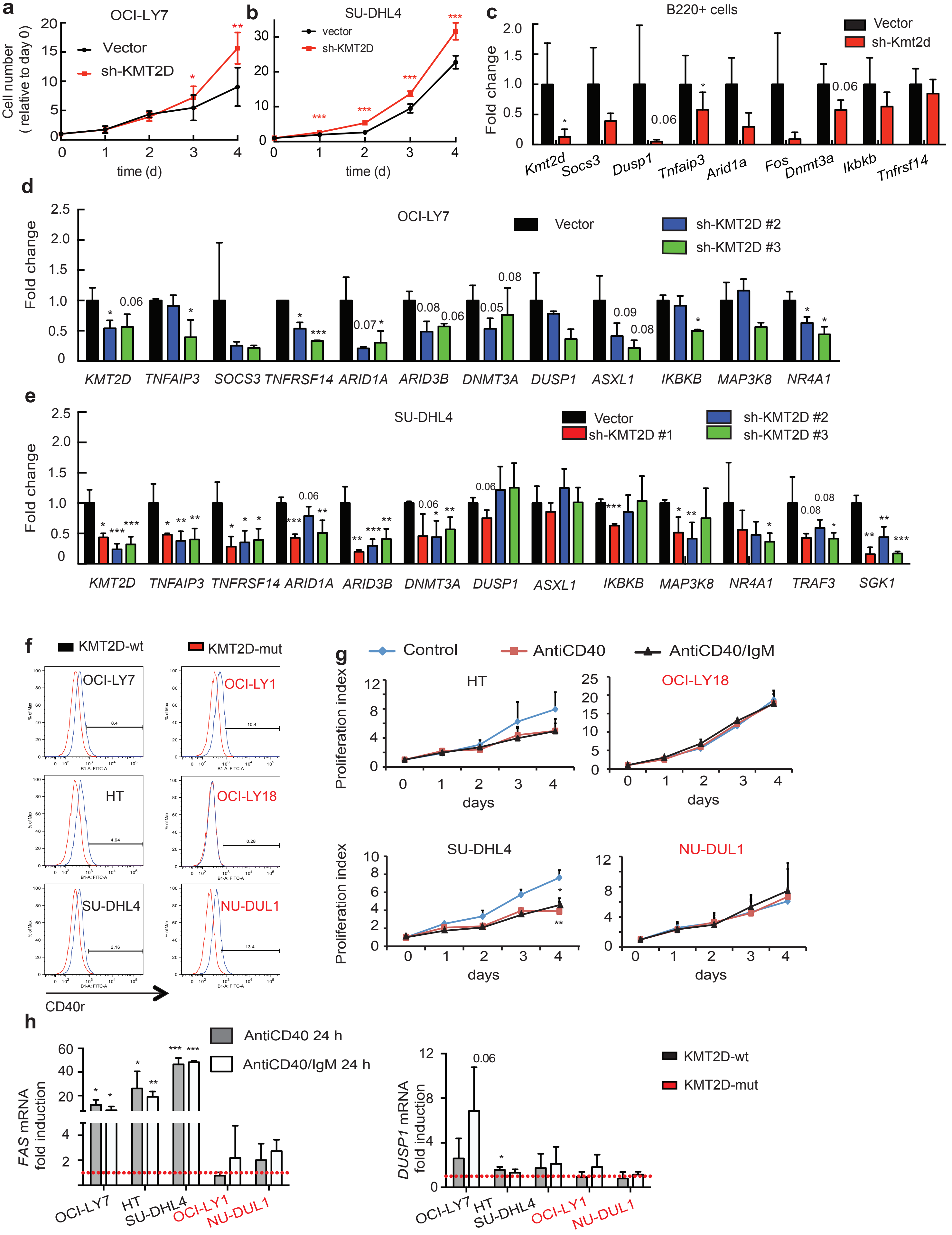
Suppl Figure 5



Supplementary Figure 5. **Identification of KMT2D target genes in human lymphoma cells.**

(**a**). Immunoblot of histone lysates from *KMT2D* wild type (HT, DOHH2, SU-DHL4) and *KMT2D* mutant (Toledo, Karpas422) DLBCL cell lines. (**b**). Quantification of global H3K4me1, H3K4me2 and H3K4me3 by ImageJ software. (**c**). Quantitative Mass spectrometry analysis of mono-, di-, tri-methylated histone H3K4. Represented as the percentage of global H3K4 post-translational modification (%PTM) in KMT2D wt (black) and KMT2D nonsense mutant (red) DLBCL cell lines (average of two biological replicates). (**d**). Normalized UCSC read density tracks of KMT2D ChIP-seq peaks in OCI-LY7 (black) and OCI-LY1 (red) and H3K4me1/2 ChIP-seq peaks in OCI-LY7 (black) and OCI-LY1 (red) for indicated genes.

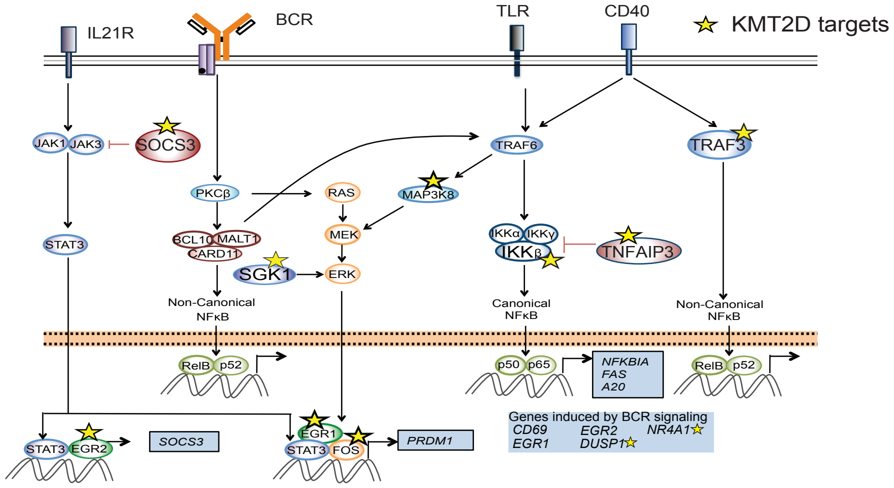
Suppl Figure 6



Supplementary Figure 6. **KMT2D inactivation affects growth and survival pathways in lymphoma cells**

(**a**) **and** (**b**). Proliferation of isogenic OCI-LY7 (**a**) and SU-DHL4 (**b**) lymphoma cells transduced with vector control or an shRNA against KMT2D. Values represent mean of 3 replicates, error bars indicate standard deviation; *p<0.05, **p<0.01, ***p<0.001 by two-tailed t-test. (**c**)**.** Relative mRNA levels by qRT-PCR of *KMT2D* targets in MACS-sorted B220$^+$ lymphoma B cells from VavPBcl2-vector (vector) and VavPBcl2-shKmt2d (sh-Kmt2d) lymphomas. Bars represent mean of 4-5 biological replicates ± s.d; Two-tailed Student's t-test was used to determine statistical significance: *p<0.05, **p<0.01, or number indicating p-value. (**d**) **and** (**e**)**.** Relative mRNA levels by qRT-PCR of *KMT2D* targets in isogenic OCI-LY7 (**d**) and SU-DHL4 (**e**) lymphoma cells transduced with vector or different shRNAs against KMT2D. Bars represent mean of 3-6 biological replicates, error bars indicate standard deviation; *p<0.05, **p<0.01, ***p<0.001 by two-tailed t-test. (**f**)**.** Flow cytometry analysis of CD40 receptor expression (CD40r) in the indicated KMT2D wild type and mutant cell lines. Red line represents isotype control, blue line represents anti-CD40r. (**g**). Growth curves for indicated cell lines treated with anti-CD40 or anti-CD40/anti-IgM for 4 days. Data correspond to one representative assay from a total of 3 independent assays. (**h**). Gene expression analysis in *KMT2D* wild type or mutant lymphoma cell lines upon anti-CD40 or anti-CD40/IgM treatment for 24h. Bars represent mean of 3 biological replicates (2 biological replicates for NU-DUL1 anti-CD40+IgM) ± s.d. Two-tailed Student's t-test was used to determine statistical significance *p<0.05, **p<0.01, ***p<0.001 or number indicating p-value**.** Red labels represent KMT2D^{mut} cell lines and black labels represent KMT2D^{wt} cell lines.

Suppl Figure 7



Supplementary Figure 7. Schematic diagram indicating KMT2D target genes in relation to the affected signaling pathways.

KMT2D targets indentified by direct ChIP binding and verified by knockdown are marked by a star. These targets are both positive and negative regulators of IL21, BCR, and CD40 signaling pathways.

Supplemental Tables.

Supplementary Table 1. Surface marker analysis in murine lymphomas

Supplementary Table 2. FL and DLBCL subject features and KMT2D mutation

Supplementary Table 3. Downregulated genes in FL subjects with KMT2D mutations and B220$^+$ lymphoma cells from vav-BCL2 tumors

Supplementary Table 4. Leading edge genes from GSEA and genes associated with pathways

Supplementary Table 5. ChIP peaks with occupancy loss in vavPBcl2/sh-Kmt2d vs vavPBcl2/vector B220$^+$ lymphoma cells and OCI-LY1 (KMT2D^{mut}) vs OCI-LY7 (KMT2D^{wt}) cell lines

Supplementary Table 6. Genes with 50% H3K4me2 loss and KMT2D binding in OCI-LY1 vs OCI-LY7 used for GSEA

Supplementary Table 1

Surface marker analysis of murine vavP-Bcl2 lymphomas

	B220+								
	CD19+	IgM+	IgD+	IgG1+	GL7+	Thy1+	CD4+	CD8+	Sca-1
VavPBcl2-v1	72.6	19.8	28.9	8.59	53.2	16.3	15.1	4.03	87.3
VavPBcl2-v2	70.4	20.9	21.5	2.55	62.8	26.2	16.2	6.19	90.3
VavPBcl2-v3	62	41.7	50.7	1.51	29.5	31.9	14.9	13.5	83.4
VavPBcl2-v4	73.8	38.2	45.4	5.76	56.2	19.1	10.9	7.44	85.4
VavPBcl2-shKmt2d-1	56.6	24.4	39.2	3.43	33.3	20.4	14.8	7.86	69.9
VavPBcl2-shKmt2d-2	62.5	19.9	36.4	8.18	32	17.9	15.1	7.51	70.3
VavPBcl2-shKmt2d-3	77	16.4	11.7	24.2	67.6	12.9	17.7	2.59	91.5
VavPBcl2-shKmt2d-4	58.9	20	23.8	8.35	48.8	15.8	16.4	4.47	74.1

Surface markers analysis in Kmt2d-/- lymphomas

		IgM	IgD	IgL	CD19	B220	CD138	HSA	CD43	CD11b	CD4	CD8	CD3
Kmt2d-/-	1558	-	-	-	+	-	+/-	+	int	nd	-	-	-
Kmt2d-/-	2221	+	-	+	+	low	low	+	low	nd	-	-	-
Kmt2d-/-	4311	low	low	+	low	low	+/-	+	+	nd	-	-	-
Kmt2d-/-	2861	low	-	low	+	+	+	+	+	nd	-	-	-
Kmt2d-/-	2900	low	-	-	low	-	+/-	+	+	nd	-	-	-
Kmt2d-/-	4341	+	low	+	low	+	+/-	+	low	nd	-	-	-
Kmt2d-/-	2119	+	-	+	low	low	-	+	low	nd	-	-	-
Kmt2d-/-	4390	+	-	+	+	low	+	+	int	-	-	-	-
Kmt2d-/-	4383	low	-	+	+	low	+/-	+	int	-	-	-	-
Kmt2d-/-	1643	low	low	+	+	+	-	+	low int	-	-	-	-
Kmt2d-/-	4812	+	+	+	-	+	low	+	int	-	-	-	-
Kmt2d-/-	1651	-	-	-	low	-	+/-	+	int	-	-	-	-
Kmt2d-/-	4380	+	+	+	+	+	-	+	+	-	-	-	-
Kmt2d-/-	4982	low	-	+	-	+	+	+	int	-	-	-	-
Kmt2d-/-	5020	-	-	-	low	+	-	+	low	-	-	-	-
Kmt2d-/-	4737	low	-	low	+	+	+/-	-	+	-	-	-	-
Kmt2d-/-	1673	-	nd	-	+	low	-	+	low	-	-	-	-
Kmt2d-/-	4378	+	+	+	+	+	-	+	low	-	-	-	-
Kmt2d-/-	2795	low	-	+	+	low	-	+	int	nd	-	-	-
Kmt2d-/-	4384	+	low	+	+	+	-	+	low	-	-	-	-
Kmt2d-/-	1719	-	-	-	+	-	-	+	int	-	-	-	-
Kmt2d-/-;AID-tg	1816	low	-	low	low	+	+	+	low	nd	-	-	-
Kmt2d-/-;AID-tg	622	-	-	-	-	+	+	+	+	nd	-	-	-
Kmt2d-/-;AID-tg	1910	+	-	+	+	+	+/-	+	int	nd	-	-	-
Kmt2d-/-;AID-tg	2110	+	low	+	low	+	+	+	low	nd	-	-	-
Kmt2d-/-;AID-tg	19113	-	-	-	+	+	low	+	+	nd	-	-	-

-, negative
+, positive
low, low positive
int, intermedia
nd, not determined

Suppl Table 2. FL and DLBCL patient features and KMT2D mutations

FL patient features

Sample ID	Gender	Age at Biopsy	Grade	KMT2D Mutations
1	M	46	1	Missense
2	M	28	2 (50%) and 3B (50%)	
3	F	55	2 (90%), DLBCL (10%)	Nonsense
4	F	86	3A	Nonsense
5	F	57	1	FS
6	M	59	1	
8	M	56	2	
9	F	53	1	
10	F	48	2	Nonsense
12	F	39	1	Nonsense
13	F	60	1	
14	M	83	3A, 3B, focal DLBCL	Nonsense
15	F	58	2	
17	M	82	3A (20%), DLBCL (80%)	
18	F	76	1	
19	F	70	2 (50%), 3A (50%)	
3128	F	38	2	Nonsense
3467	M	41	1 to 2 (or 3)	Nonsense
3663	M	52	N.A.	Nonsense
3704	F	76	1	
3900	F	47	1 to 2	Nonsense
3986	M	79	2, 3	
3989	M	56	1 to 2	
4077	M	76	N.A.	
4079	M	45	1 to 2	
4129	M	60	1 to 2	Nonsense
4263	M	86	3	Nonsense
4277	F	54	1	Missense
4293	F	63	DLBCL(60%), 3B (40%)	
4466	F	48	2	Nonsense
4535	F	64	3A (40%), 3B (60%)	
4537	F	60	1 to 2	

20	M	41	3A	
21	M	77	1	
22	F	73	2	
23	M	59	2	
24	M	37	1	
25	F	48	1	
26	F	85	1 (80%), 3B (20%)	
27	M	78	2	Nonsense
28	M	80	1	Nonsense
29	M	52	1	Missense
1483	M	54	N.A.	
1985	M	45	N.A.	Nonsense
1988	F	77	1	Missense
2042	F	77	1	
2159	F	53	1, focal 2	
2211	F	47	1	
2228	F	75	2, 3	
2286	M	75	3	
2375	M	62	1, 2, with transformation to 3	
2507	M	55	3	Nonsense
2621	M	45	1	
2665	F	55	1, 2	Nonsense
2678	F	52	1	Nonsense

4568	F	66	1 to 2 (50%), 3A (50%)	Nonsense
4570	F	86	1 to 2	
4582	M	54	3A	
4585	M	41	1 to 2	Nonsense
4596	F	4	N.A.	
4609	M	65	2	
4625	M	27	N.A.	
4730	F	67	1 to 2	Nonsense
4747	F	49	1	Nonsense
4760	F	63	2	
4763	M	60	2	Nonsense
4774	M	49	1	Missense
4792	F	38	1 to 2 (95%), 3B (5%)	Nonsense
4849	F	47	2	
4948	F	72	3B	
4955	F	70	2 (99%), 3A (1%)	
4973	M	83	3A	Nonsense
4981	M	57	1 to 2	
5057	F	59	3	
5187	F	70	2	
5227	M	77	1	
5249	F	61	2	
5327	F	72	2	

2702	F	49	2	
2703	F	54	2	
2769	F	61	2	
2800	M	35	1	
2806	M	36	2, 3	Missense
2868	F	73	2, focal 3	
2870	M	45	2	
2966	F	82	1	Nonsense
2984	F	43	2	Nonsense
2985	M	61	2	
2990	F	73	1	
2998	M	78	1 to 2	
3012	M	47	1	

5402	M	69	1 to 2	
5403	M	69	1 to 2	
5405	M	60	3A	
5620	F	58	1 to 2	
5644	M	51	2	Nonsense
5836	M	65	2	
6013	F	78	2	
6095	F	48	1 to 2	Nonsense
6136	F	65	1	
6223	F	69	1 to 2 (30%), 3A (60%), 3B (10%)	Nonsense
6291	F	89	1 to 2	
6292	M	59	1 to 2	Nonsense
6307	M	58	2	

Supplementary Table 2 (cont). FL and DLBCL patient features and KMT2D mutations

KMT2D mutation specifics in FL subjects

Sample ID	CHROM	POS	REF	ALT	VAF(%)	MUTATION TYPE	EFF....CODON.QN	AA CHANGE	Platform
3	12	49445095	G	A	56.45	NONSENSE	Cag/Tag	Q791*	Exome
1	12	49440147	A	T	44.2	MISSENSE	aaT/aaA	N1493K	Exome
14	12	49437746	C	A	100	NONSENSE	Gag/Tag	E1742*	Exome
3	12	49434532	G	A	35.48	NONSENSE	Cag/Tag	Q2341*	Exome
12	12	49433626	C	A	46.88	NONSENSE	Gaa/Taa	E2643*	Exome
27	12	49431004	G	A	42.86	NONSENSE	Cag/Tag	Q3379*	Exome
28	12	49427330	G	A	50	NONSENSE	Cag/Tag	Q3720*	Exome
10	12	49426355	G	A	52.24	NONSENSE	Cag/Tag	Q4045*	Exome
4	12	49426151	C	A	29.31	NONSENSE	Gga/Tga	G4113*	Exome
29	12	49420466	A	T	48.92	MISSENSE	Tgc/Agc	C5095S	Exome
2678	12	49448188	C	A	25.92	NONSENSE	tGg/tTg	W141*	Targeted
2984	12	49443617	G	A	32.57	NONSENSE	Cga/Tga	R1252*	Targeted
4466	12	49443617	G	A	32.96	NONSENSE	Cga/Tga	R1252*	Targeted
4747	12	49443617	G	A	49.68	NONSENSE	Cga/Tga	R1252*	Targeted
6905	12	49443617	G	A	48.27	NONSENSE	Cga/Tga	R1252*	Targeted
2806	12	49440428	A	T	28.99	MISSENSE	cTg/cAg	L1461R	Targeted
1988	12	49440428	A	G	25.51	MISSENSE	cTg/cCg	L1461R	Targeted
1988	12	49440429	G	T	25.01	MISSENSE	Ctg/Atg	L1461M	Targeted
3467	12	49440444	A	T	34.98	MISSENSE	Tgc/Agc	C1456S	Targeted
2665	12	49438067	G	A	47.78	NONSENSE	Cga/Tga	R1702*	Targeted
3990	12	49438067	G	A	46.25	NONSENSE	Cga/Tga	R1702*	Targeted
4792	12	49438022	G	A	51.93	NONSENSE	Cag/Tag	Q1717*	Targeted
2966	12	49436062	C	T	28.03	NONSENSE	tgG/tgA	W1973*	Targeted
4277	12	49435872	C	T	39.57	MISSENSE	Ggt/Agt	G2037S	Targeted
2507	12	49433394	G	A	32.9	NONSENSE	Cga/Tga	R2685*	Targeted
5644	12	49433220	G	A	91.34	NONSENSE	Cag/Tag	Q2743*	Targeted
3663	12	49432396	G	A	49.61	NONSENSE	Cga/Tga	R2915*	Targeted
4973	12	49432345	G	A	33.95	NONSENSE	Cag/Tag	Q2932*	Targeted
4129	12	49431667	G	A	62.98	NONSENSE	Cag/Tag	Q3158*	Targeted
3128	12	49431358	G	A	41.71	NONSENSE	Cag/Tag	Q3261*	Targeted
6292	12	49430956	G	A	63.86	NONSENSE	Caa/Taa	Q3395*	Targeted
4730	12	49427687	G	A	43.02	NONSENSE	Caa/Taa	Q3610*	Targeted
6095	12	49427294	G	A	45.39	NONSENSE	Cag/Tag	Q3732*	Targeted
1985	12	49427027	G	A	50.44	NONSENSE	Cag/Tag	Q3821*	Targeted
2665	12	49426961	G	A	46.57	NONSENSE	Cag/Tag	Q3843*	Targeted
6223	12	49426700	G	A	29.75	NONSENSE	Cag/Tag	Q3930*	Targeted
4568	12	49425962	C	A	47.77	NONSENSE	Gga/Tga	G4176*	Targeted
4263	12	49425710	G	A	42.8	NONSENSE	Caa/Taa	Q4260*	Targeted
4763	12	49425644	G	A	49.55	NONSENSE	Cga/Tga	R4282*	Targeted
2716	12	49425448	T	G	26.76	MISSENSE	cAg/cGg	Q4347R	Targeted
4774	12	49420847	G	C	55.56	MISSENSE	Cct/Gct	P4968A	Targeted
3467	12	49420796	C	T	49.7	MISSENSE	Gtg/Atg	V4985M	Targeted
3467	12	49420789	C	T	49.65	NONSENSE	tGg/tAg	W4987*	Targeted
3467	12	49420788	C	T	49.6	NONSENSE	tgG/tgA	W4987*	Targeted
4792	12	49420108	C	A	29.13	MISSENSE	cGc/cTc	R5214L	Targeted
6223	12	49420071	G	C	31.62	MISSENSE	tgC/tgG	C5226W	Targeted
4585	12	49420059	A	T	41.89	NONSENSE	tgT/tgA	C5230*	Targeted
6223	12	49418439	G	C	40.89	MISSENSE	cCc/cGc	P5325R	Targeted
6223	12	49418391	G	C	41.21	NONSENSE	tCa/tGa	S5341*	Targeted

Supplementary Table 2 (cont). FL and DLBCL patient features and KMT2D mutations

DLBCL patient features

		KMT2D nonsense mutation (n=37) n (%)	*KMT2D* misssense mutation (n=43) n (%)	KMT2D wild type (n=215) n (%)	*p*-value*	*p*-value**
Age	Median (range) - years	65 (35-89)	65 (19-84)	62 (16-92)		
	≤60 years	13 (35)	19 (44)	90 (42)	0.44	0.41
	>60 years	24 (65)	24 (56)	125 (58)		
Gender	Male	23 (67)	28 (65)	134 (62)	0.78	0.94
	Female	14 (33)	15 (35)	81 (38)		
Stage	Limited	16 (44)	21 (49)	98 (46)		0.8
	Advanced	20 (56)	22 (51)	114 (54)	0.84	
	N/A	1	0	3		
LDH	Normal	14 (44)	20 (52)	95 (47)		0.66
	>ULN	18 (56)	19 (48)	106 (53)	0.61	
	N/A	5	4	14		
ECOG PS	0-1	19 (53)	31 (72)	144 (68)		0.059
	2 or more	17 (47)	12 (28)	68 (32)	0.077	
	N/A	1	0	3		
Extranodal sites	0-1	29 (81)	37 (86)	172 (81)		0.83
	2 or more	7 (19)	6 (14)	40 (19)	0.93	
	N/A	1	0	3		
IPI score	Low (0-1)	10 (30)	15 (38)	71 (34)	0.18	0.14
	Intermediate (2-3)	12 (37)	20 (48)	96 (46)		
	High (4-5)	11 (33)	6 (14)	40 (20)		
	N/A	4	2	8		
Survival	Median (range) - years	4.5 (0.1-12.9)	5.1 (0.3-13.2)	4.8 (0.1-13.1)		
	Death	17 (39)	15 (35)	82 (38)	0.37	0.33
	Alive	20 (61)	28 (65)	133 (62)		

* nonsense mutation vs WT
** nonsense mutation vs WT+misssense mutation

Supplementary Table 2 (cont). FL and DLBCL patient features and KMT2D mutations

KMT2D mutation specificis in DLBCL subjects

SAMPLE	CHROM	POS	REF	ALT	VAF (%)	MUTATION TYPE	EFF....CODON.QN	AA CHANGE	COO
DLC003	chr12	49427072	G	T	6.5	MISSENSE	Cag/Aag	p.Gln3806Lys/c.11416C>A	GCB
DLC004	chr12	49447313	GCAGT	G	7.73	FRAME SHIFT	actgcc/	p.260Thr_262Argfs/c.781_783delGTCA	GCB
DLC004	chr12	49443646	A	T	9.89	NONSENSE	tTg/tAg	p.Leu1242*/c.3725T>A	GCB
DLC010	chr12	49426577	G	A	37.62	NONSENSE	Caa/Taa	p.Gln3971*/c.11911C>T	GCB
DLC019	chr12	49440199	G	C	57.14	MISSENSE	tCc/tGc	p.Ser1476Cys/c.4427C>G	GCB
DLC019	chr12	49444081	G	A	54.08	MISSENSE	cCa/cTa	p.Pro1097Leu/c.3290C>T	GCB
DLC023	chr12	49447085	T	TA	41.8	FRAME SHIFT	tct/tctT	p.285Ser_286Lysfs/c.858_859insT	ABC
DLC025	chr12	49434415	G	A	25.35	NONSENSE	Cag/Tag	p.Gln2380*/c.7138C>T	UNC
DLC027	chr12	49440199	G	C	27.57	MISSENSE	tCc/tGc	p.Ser1476Cys/c.4427C>G	GCB
DLC027	chr12	49444081	G	A	30.6	MISSENSE	cCa/cTa	p.Pro1097Leu/c.3290C>T	GCB
DLC027	chr12	49447416	G	C	24.24	MISSENSE	Cgc/Ggc	p.Arg228Gly/c.682C>G	GCB
DLC031	chr12	49443799	G	A	54.97	MISSENSE	cCg/cTg	p.Pro1191Leu/c.3572C>T	GCB
DLC035	chr12	49443799	G	A	60.55	MISSENSE	cCg/cTg	p.Pro1191Leu/c.3572C>T	ABC
DLC042	chr12	49434145	G	A	9.59	MISSENSE	Ccc/Tcc	p.Pro2470Ser/c.7408C>T	GCB
DLC043	chr12	49444497	CT	C	17.91	FRAME SHIFT	gag/	p.957Glu_958Tyrfs/c.2873_2874delA	ABC
DLC043	chr12	49415855	AGAT	A	44.47	FRAME SHIFT	atc/	p.5496Ile_5497Serdel/c.16489_16490delCTA	ABC
DLC044	chr12	49431873	AC	A	83.72	FRAME SHIFT	gtg/	p.3088Val_3089Glufs/c.9265_9266delG	GCB
DLC044	chr12	49416625	C	G	30.67	MISSENSE	aaG/aaC	p.Lys5362Asn/c.16086G>C	GCB
DLC046	chr12	49444034	CCAGGGCTGGGG	C	43.86	FRAME SHIFT	gccccagccctg/	p.1108Ala_1112Aspfs/c.3326_3330delGTCCCGACCCC	ABC
DLC048	chr12	49416062	C	T	50.94	SPLICE SITE			ABC
DLC050	chr12	49420213	C	A	12.72	MISSENSE	cGt/cTt	p.Arg5179Leu/c.15536G>T	GCB
DLC054	chr12	49434973	G	A	16.25	MISSENSE	Ccc/Tcc	p.Pro2194Ser/c.6580C>T	ABC
DLC054	chr12	49435002	G	A	12.5	MISSENSE	cCc/cTc	p.Pro2184Leu/c.6551C>T	ABC
DLC055	chr12	49425043	CCCTCGGA	C	38.32	FRAME SHIFT	tccgagggg/	p.4479Ser_4482Leufs/c.13438_13441delGGAGCCT	GCB
DLC057	chr12	49434162	G	A	8.17	MISSENSE	gCc/gTc	p.Ala2464Val/c.7391C>T	GCB
DLC059	chr12	49442461	T	C	31.12	MISSENSE	gAc/gGc	p.Asp1371Gly/c.4112A>G	ABC
DLC063	chr12	49435964	C	T	96.89	NONSENSE	tGg/tAg	p.Trp2006*/c.6017G>A	NA
DLC064	chr12	49442458	TTGTC	T	40.38	FRAME SHIFT	gacaaa/	p.1370Asp_1372Phefs/c.4111_4113delACAG	ABC
DLC064	chr12	49427364	G	C	53.56	MISSENSE	agC/agG	p.Ser3708Arg/c.11124C>G	ABC
DLC065	chr12	49427189	G	T	44.55	MISSENSE	Caa/Aaa	p.Gln3767Lys/c.11299C>A	GCB
DLC065	chr12	49445334	G	A	52.63	MISSENSE	cCg/cTg	p.Pro711Leu/c.2132C>T	GCB
DLC067	chr12	49420109	G	A	21.4	MISSENSE	Cgc/Tgc	p.Arg5214Cys/c.15640C>T	NA
DLC069	chr12	49424114	C	A	51.6	NONSENSE	Gag/Tag	p.Glu4650*/c.13948G>T	ABC
DLC070	chr12	49424741	G	A	43.12	NONSENSE	Cga/Tga	p.Arg4536*/c.13606C>T	ABC
DLC080	chr12	49427112	AG	A	8.22	FRAME SHIFT	cct/	p.3791Pro_3792Glnfs/c.11375_11376delC	GCB
DLC080	chr12	49431178	G	A	6.29	NONSENSE	Cga/Tga	p.Arg3321*/c.9961C>T	GCB
DLC081	chr12	49424398	G	A	31.81	NONSENSE	Cag/Tag	p.Gln4609*/c.13825C>T	GCB
DLC081	chr12	49432578	A	T	41.28	NONSENSE	tTg/tAg	p.Leu2854*/c.8561T>A	GCB
DLC082	chr12	49441750	T	A	92.35	NONSENSE	Aag/Tag	p.Lys1412*/c.4234A>T	GCB
DLC084	chr12	49427947	G	A	37.23	MISSENSE	aCt/aTt	p.Thr3548Ile/c.10643C>T	UNC
DLC085	chr12	49421078	G	A	46.46	NONSENSE	Cag/Tag	p.Gln4891*/c.14671C>T	GCB
DLC087	chr12	49446425	CT	C	51.48	FRAME SHIFT	caa/	p.392Gln_393Glyfs/c.1179_1180delA	GCB
DLC088	chr12	49436114	C	T	34.62	SPLICE SITE			GCB
DLC091	chr12	49420493	G	A	19.87	NONSENSE	Cga/Tga	p.Arg5086*/c.15256C>T	UNC
DLC096	chr12	49424741	G	A	37.88	NONSENSE	Cga/Tga	p.Arg4536*/c.13606C>T	GCB
DLC100	chr12	49448751	TG	T	31.82	FRAME SHIFT	cca/	p.35Pro_36Hisfs/c.107_108delC	GCB
DLC100	chr12	49446377	C	T	28.4	MISSENSE	Ggg/Agg	p.Gly410Arg/c.1228G>A	GCB
DLC100	chr12	49446797	T	C	35.82	MISSENSE	gAg/gGg	p.Glu338Gly/c.1013A>G	GCB
DLC111	chr12	49438042	G	T	14.24	MISSENSE	aCg/aAg	p.Thr1710Lys/c.5129C>A	ABC
DLC115	chr12	49446154	TCTC	T	28.42	FRAME SHIFT	gag/	p.436Glu_437Metdel/c.1309_1310delGAG	GCB
DLC115	chr12	49434600	C	T	49.52	MISSENSE	gGc/gAc	p.Gly2318Asp/c.6953G>A	GCB
DLC119	chr12	49436624	GA	G	31.47	FRAME SHIFT	ctc/	p.1893Leu_1894Phefs/c.5681_5682delT	UNC
DLC121	chr12	49447426	T	G	25.62	SPLICE SITE			GCB
DLC121	chr12	49427848	A	T	53.2	SPLICE SITE			GCB
DLC123	chr12	49444133	C	G	42.59	MISSENSE	Gaa/Caa	p.Glu1080Gln/c.3238G>C	NA
DLC126	chr12	49444464	AG	A	26.56	FRAME SHIFT	cct/	p.968Pro_969Glufs/c.2906_2907delC	GCB
DLC128	chr12	49420654	C	T	17.99	MISSENSE	tGc/tAc	p.Cys5032Tyr/c.15095G>A	ABC
DLC128	chr12	49436062	C	T	27.27	NONSENSE	tgG/tgA	p.Trp1973*/c.5919G>A	ABC
DLC129	chr12	49446773	CAG	C	5.46	FRAME SHIFT	ctctgt/	p.344Leu_346Hisfs/c.1035_1037delTC	GCB
DLC129	chr12	49431947	A	T	9.84	MISSENSE	gaT/gaA	p.Asp3064Glu/c.9192T>A	GCB
DLC129	chr12	49431983	A	T	9.38	NONSENSE	taT/taA	p.Tyr3052*/c.9156T>A	GCB
DLC135	chr12	49425446	CCT	C	9	FRAME SHIFT	cag/	p.4346Gln_4347Glyfs/c.13040_13041delGA	GCB
DLC136	chr12	49420397	C	CA	28.41	FRAME SHIFT	tgt/tgtT	p.5116Cys_5117Alafs/c.15351_15352insT	ABC
DLC137	chr12	49442443	T	A	36.36	MISSENSE	cAg/cTg	p.Gln1377Leu/c.4130A>T	ABC
DLC140	chr12	49425132	TGCCAGCAG	T	9.15	FRAME SHIFT	ctgctggca/	p.4449Leu_4452Glyfs/c.13348_13351delCGGTCGTC	GCB
DLC146	chr12	49438749	C	T	67.44	SPLICE SITE			GCB
DLC147	chr12	49422945	TC	T	21.73	FRAME SHIFT	gag/	p.4716Glu_4717Glufs/c.14149_14150delG	GCB
DLC148	chr12	49444034	CCAGGGCTGGGG	C	8.71	FRAME SHIFT	gccccagccctg/	p.1108Ala_1112Aspfs/c.3326_3330delGTCCCGACCCC	UNC
DLC148	chr12	49426993	G	A	6.21	MISSENSE	tCc/tTc	p.Ser3832Phe/c.11495C>T	UNC
DLC148	chr12	49419968	G	A	29.75	NONSENSE	Cag/Tag	p.Gln5261*/c.15781C>T	UNC
DLC149	chr12	49435457	C	T	5.29	MISSENSE	cGc/cAc	p.Arg2072His/c.6215G>A	ABC
DLC154	chr12	49425370	C	T	38.6	MISSENSE	gGt/gAt	p.Gly4373Asp/c.13118G>A	GCB
DLC157	chr12	49436001	C	T	52.52	MISSENSE	Gac/Aac	p.Asp1994Asn/c.5980G>A	GCB
DLC163	chr12	49427270	G	A	47.89	NONSENSE	Cag/Tag	p.Gln3740*/c.11218C>T	GCB
DLC167	chr12	49425124	C	T	52.2	MISSENSE	cGc/cAc	p.Arg4455His/c.13364G>A	GCB
DLC169	chr12	49420493	G	A	41.33	NONSENSE	Cga/Tga	p.Arg5086*/c.15256C>T	GCB

DLC171	chr12	49425847	A	C	35.65	NONSENSE	tTa/tGa	p.Leu4214*/c.12641T>G	GCB
DLC175	chr12	49425457	G	C	52.33	MISSENSE	cCc/cGc	p.Pro4344Arg/c.13031C>G	ABC
DLC178	chr12	49425446	CCT	C	14.34	FRAME SHIFT	cag/	p.4346Gln_4347Glyfs/c.13040_13041delGA	GCB
DLC178	chr12	49420190	C	G	32.33	MISSENSE	Gcc/Ccc	p.Ala5187Pro/c.15559G>C	GCB
DLC186	chr12	49433361	G	A	41.88	NONSENSE	Cag/Tag	p.Gln2696*/c.8086C>T	GCB
DLC194	chr12	49445812	AT	A	25.44	FRAME SHIFT	gaa/	p.550Glu_551Serfs/c.1653_1654delA	GCB
DLC194	chr12	49425188	C	A	20.19	NONSENSE	Gag/Tag	p.Glu4434*/c.13300G>T	GCB
DLC196	chr12	49416417	G	A	10.34	MISSENSE	Cgg/Tgg	p.Arg5432Trp/c.16294C>T	UNC
DLC196	chr12	49426997	G	A	24	NONSENSE	Cag/Tag	p.Gln3831*/c.11491C>T	UNC
DLC202	chr12	49420578	C	T	24.45	NONSENSE	tgG/tgA	p.Trp5057*/c.15171G>A	GCB
DLC203	chr12	49426396	GGGTCTACGGT	G	39.42	FRAME SHIFT	accgtagaccca/	p.4027Thr_4031Alafs/c.12082_12086delCCAGATGCCA	ABC
DLC203	chr12	49447782	T	C	41.13	MISSENSE	Agt/Ggt	p.Ser218Gly/c.652A>G	ABC
DLC204	chr12	49445632	G	GT	26.03	FRAME SHIFT	cca/ccaA	p.610Pro_611Profs/c.1833_1834insA	UNC
DLC205	chr12	49436019	TG	T	21.3	FRAME SHIFT	ccc/	p.1986Pro_1987Thrfs/c.5961_5962delC	GCB
DLC209	chr12	49420121	A	G	47.75	MISSENSE	Tac/Cac	p.Tyr5210His/c.15628T>C	ABC
DLC212	chr12	49420574	G	A	45	MISSENSE	Cac/Tac	p.His5059Tyr/c.15175C>T	GCB
DLC212	chr12	49427654	G	A	44.74	NONSENSE	Cag/Tag	p.Gln3612*/c.10834C>T	GCB
DLC213	chr12	49437566	C	T	26.85	SPLICE SITE			GCB
DLC214	chr12	49434487	G	A	19.42	NONSENSE	Cag/Tag	p.Gln2356*/c.7066C>T	GCB
DLC219	chr12	49437164	CCT	C	26.1	FRAME SHIFT	gag/	p.1837Glu_1838Glyfs/c.5513_5514delGA	ABC
DLC225	chr12	49436647	C	A	94.56	NONSENSE	Gaa/Taa	p.Glu1887*/c.5659G>T	GCB
DLC233	chr12	49440442	G	C	83.33	MISSENSE	tgC/tgG	p.Cys1456Trp/c.4368C>G	GCB
DLC235	chr12	49444748	TG	T	12.83	FRAME SHIFT	cca/	p.905Pro_906Profs/c.2717_2718delC	ABC
DLC240	chr12	49415628	C	A	35.94	NONSENSE	Gag/Tag	p.Glu5517*/c.16549G>T	GCB
DLC241	chr12	49420645	C	A	10.69	MISSENSE	tGt/tTt	p.Cys5035Phe/c.15104G>T	GCB
DLC245	chr12	49421654	G	A	11.43	NONSENSE	Cag/Tag	p.Gln4859*/c.14575C>T	GCB
DLC245	chr12	49445126	G	T	13.22	NONSENSE	tgC/tgA	p.Cys780*/c.2340C>A	GCB
DLC246	chr12	49424405	G	C	21.8	NONSENSE	taC/taG	p.Tyr4606*/c.13818C>G	GCB
DLC252	chr12	49424498	G	GA	58.57	FRAME SHIFT	ctc/ctTc	p.4574Leu_4575Phefs/c.13724_13725insT	GCB
DLC252	chr12	49427684	G	A	46.42	NONSENSE	Caa/Taa	p.Gln3602*/c.10804C>T	GCB
DLC254	chr12	49431981	GTA	G	22.28	FRAME SHIFT	tatact/	p.3051Tyr_3053Aspfs/c.9156_9158delAT	GCB
DLC254	chr12	49445890	ACT	A	21.05	FRAME SHIFT	gag/	p.524Glu_525Serfs/c.1574_1575delGA	GCB
DLC260	chr12	49421048	G	C	52.17	MISSENSE	Ctg/Gtg	p.Leu4901Val/c.14701C>G	ABC
DLC266	chr12	49425860	G	A	44.47	NONSENSE	Cag/Tag	p.Gln4210*/c.12628C>T	GCB
DLC269	chr12	49434325	G	A	42.02	NONSENSE	Cga/Tga	p.Arg2410*/c.7228C>T	GCB
DLC270	chr12	49435880	T	C	48.18	MISSENSE	gAc/gGc	p.Asp2034Gly/c.6101A>G	GCB
DLC272	chr12	49428376	CA	C	30.95	FRAME SHIFT	gct/	p.3475Ala_3476Glyfs/c.10428_10429delT	GCB
DLC279	chr12	49427318	G	A	5.43	NONSENSE	Cag/Tag	p.Gln3724*/c.11170C>T	ABC
DLC280	chr12	49421833	C	T	59.04	MISSENSE	cGg/cAg	p.Arg4825Gln/c.14474G>A	GCB
DLC281	chr12	49416067	C	T	38.5	MISSENSE	Gcc/Acc	p.Ala5470Thr/c.16408G>A	ABC
DLC282	chr12	49433388	G	A	53.78	NONSENSE	Cga/Tga	p.Arg2687*/c.8059C>T	GCB
DLC282	chr12	49448178	C	T	33.8	NONSENSE	tGg/tAg	p.Trp141*/c.422G>A	GCB
DLC286	chr12	49420631	C	T	37.32	MISSENSE	Gac/Aac	p.Asp5040Asn/c.15118G>A	GCB
DLC287	chr12	49433803	T	A	9.01	MISSENSE	Aca/Tca	p.Thr2584Ser/c.7750A>T	ABC
DLC291	chr12	49433050	C	T	68.29	MISSENSE	cGg/cAg	p.Arg2774Gln/c.8321G>A	ABC
DLC292	chr12	49444669	CT	C	47.92	FRAME SHIFT	cca/	p.931Pro_932Aspfs/c.2796_2797delA	GCB
DLC292	chr12	49431178	G	A	31.36	NONSENSE	Cga/Tga	p.Arg3321*/c.9961C>T	GCB
DLC294	chr12	49427123	GCTGGACC	G	21.43	FRAME SHIFT	ctggtccag/	p.3785Leu_3788Glnfs/c.11358_11361delGACCTGG	GCB
DLC295	chr12	49434957	TA	T	11.11	FRAME SHIFT	tat/	p.2198Tyr_2199Profs/c.6595_6596delT	GCB
DLC298	chr12	49443799	G	A	55.89	MISSENSE	cCg/cTg	p.Pro1191Leu/c.3572C>T	GCB
DLC299	chr12	49427017	T	C	24.66	MISSENSE	cAc/cGc	p.His3824Arg/c.11471A>G	GCB
DLC303	chr12	49434220	G	A	68.75	NONSENSE	Cag/Tag	p.Gln2445*/c.7333C>T	GCB
DLC304	chr12	49431990	A	G	49.36	MISSENSE	cTg/cCg	p.Leu3050Pro/c.9149T>C	GCB
DLC304	chr12	49438276	T	A	46.41	NONSENSE	Aaa/Taa	p.Lys1665*/c.4993A>T	GCB
DLC306	chr12	49420288	C	T	38.71	MISSENSE	cGg/cAg	p.Arg5154Gln/c.15461G>A	UNC
DLC308	chr12	49435048	C	T	9.17	MISSENSE	Gcc/Acc	p.Ala2169Thr/c.6505G>A	GCB
DLC309	chr12	49427365	CT	C	17.45	FRAME SHIFT	agc/	p.3707Ser_3708Leufs/c.11122_11123delA	GCB
DLC309	chr12	49433842	TG	T	10.44	FRAME SHIFT	ccc/	p.2569Pro_2570Thrfs/c.7710_7711delC	GCB
DLC313	chr12	49433837	C	CA	23.97	FRAME SHIFT	ttg/ttTg	p.2571Leu_2572Glyfs/c.7715_7716insT	GCB
DLC315	chr12	49437653	G	A	42.31	NONSENSE	Cag/Tag	p.Gln1773*/c.5317C>T	GCB
DLC317	chr12	49438050	GT	G	8.84	FRAME SHIFT	cac/	p.1706His_1707Thrfs/c.5120_5121delA	ABC
DLC318	chr12	49425446	CCT	C	7.14	FRAME SHIFT	cag/	p.4346Gln_4347Glyfs/c.13040_13041delGA	ABC
DLC319	chr12	49439706	GCT	G	40.6	FRAME SHIFT	gag/	p.1578Glu_1579Profs/c.4736_4737delGA	ABC
DLC332	chr12	49424455	G	A	53.57	NONSENSE	Cag/Tag	p.Gln4590*/c.13768C>T	ABC
DLC333	chr12	49431098	C	CA	27.62	FRAME SHIFT	atg/atTg	p.3346Met_3347Alafs/c.10040_10041insT	ABC
DLC335	chr12	49420475	A	G	10.54	MISSENSE	Tgc/Cgc	p.Cys5092Arg/c.15274T>C	NA
DLC337	chr12	49425348	T	TG	20.67	FRAME SHIFT	cca/ccCa	p.4379Pro_4380Aspfs/c.13139_13140insC	GCB
DLC339	chr12	49425655	C	A	45.91	MISSENSE	gGg/gTg	p.Gly4278Val/c.12833G>T	ABC
DLC344	chr12	49420060	C	A	46.32	MISSENSE	tGt/tTt	p.Cys5230Phe/c.15689G>T	GCB
DLC344	chr12	49427438	G	A	39.85	NONSENSE	Caa/Taa	p.Gln3684*/c.11050C>T	GCB
DLC351	chr12	49420669	C	T	31.54	MISSENSE	cGa/cAa	p.Arg5027Gln/c.15080G>A	GCB
DLC353	chr12	49432738	G	A	37.8	NONSENSE	Cga/Tga	p.Arg2801*/c.8401C>T	GCB
DLC354	chr12	49448505	CAG	C	59.05	FRAME SHIFT	ctctgt/	p.67Leu_69Asnfs/c.204_206delTC	GCB
DLC354	chr12	49434688	T	A	31.12	NONSENSE	Aag/Tag	p.Lys2289*/c.6865A>T	GCB
DLC355	chr12	49444073	C	G	42.13	MISSENSE	Gac/Cac	p.Asp1100His/c.3298G>C	GCB
DLC356	chr12	49448091	TG	T	17.91	FRAME SHIFT	cag/	p.169Gln_170Argfs/c.508_509delC	NA
DLC356	chr12	49444301	A	G	57.29	MISSENSE	Tgt/Cgt	p.Cys1024Arg/c.3070T>C	NA
DLC356	chr12	49426520	G	A	56.15	NONSENSE	Caa/Taa	p.Gln3990*/c.11968C>T	NA
DLC358	chr12	49443752	C	A	28.04	NONSENSE	Gag/Tag	p.Glu1207*/c.3619G>T	GCB
DLC360	chr12	49438243	G	C	48.25	MISSENSE	Cct/Gct	p.Pro1676Ala/c.5026C>G	NA

DLC360	chr12	49439908	G	A	25.3	NONSENSE	Cag/Tag	p.Gln1545*/c.4633C>T	NA
DLC364	chr12	49444986	T	TG	7.3	FRAME SHIFT	caa/cCaa	p.826Gln_827Profs/c.2479_2480insC	GCB
DLC368	chr12	49444192	T	A	8.88	MISSENSE	aAg/aTg	p.Lys1060Met/c.3179A>T	NA
DLC369	chr12	49448122	C	T	19.33	MISSENSE	Gtg/Atg	p.Val160Met/c.478G>A	ABC
DLC369	chr12	49437649	A	T	14.25	SPLICE SITE			ABC
DLC370	chr12	49445595	G	C	13.27	NONSENSE	tCa/tGa	p.Ser624*/c.1871C>G	ABC
DLC374	chr12	49425990	A	AT	15.81	FRAME SHIFT	aat/aaAt	p.4165Asn_4166Asnfs/c.12497_12498insA	GCB
DLC374	chr12	49445068	G	A	52.94	NONSENSE	Cag/Tag	p.Gln800*/c.2398C>T	GCB
DLC375	chr12	49428594	C	A	38.35	SPLICE SITE			GCB
DLC376	chr12	49420385	T	A	18.83	NONSENSE	Aag/Tag	p.Lys5122*/c.15364A>T	ABC
DLC379	chr12	49420683	AG	A	16.91	FRAME SHIFT	cct/	p.5021Pro_5022Aspfs/c.15065_15066delC	ABC
DLC379	chr12	49427900	G	A	19.38	MISSENSE	Ctc/Ttc	p.Leu3564Phe/c.10690C>T	ABC
DLC379	chr12	49419968	G	A	21.36	NONSENSE	Cag/Tag	p.Gln5261*/c.15781C>T	ABC
DLC381	chr12	49426266	TTG	T	13.6	FRAME SHIFT	caa/	p.4073Gln_4074Leufs/c.12220_12221delAC	NA
DLC382	chr12	49435874	G	A	5.29	MISSENSE	cCa/cTa	p.Pro2036Leu/c.6107C>T	GCB
DLC385	chr12	49435912	A	C	38.45	NONSENSE	taT/taG	p.Tyr2023*/c.6069T>G	ABC
DLC390	chr12	49442543	T	C	46.6	MISSENSE	Att/Gtt	p.Ile1344Val/c.4030A>G	ABC
DLC401	chr12	49440469	G	C	65.62	MISSENSE	gaC/gaG	p.Asp1447Glu/c.4341C>G	ABC
DLC405	chr12	49440185	C	CA	51.18	FRAME SHIFT	tgt/tgtT	p.1479Cys_1480Glyfs/c.4440_4441insT	GCB

Suppl Table 3. Downregulated genes in FL subjects with KMT2D mutations and B220+ lymphoma cells from vav-BCL2 mice with Kmt2d knockdown

Downreuglated genes in FL subjects with KMT2D mutations

hgnc_symbol	ensembl	pvalue	log2FoldChange	baseMean
HOOK1	ENSG00000134709	6.28E-08	-2.606026655	706.7347038
KLF11	ENSG00000172059	9.53E-07	-2.370164524	909.6064188
HSPA1A	ENSG00000204389	4.20E-06	-2.401910925	5976.573103
GATA3	ENSG00000107485	5.72E-06	-2.242672978	56.00309097
HSPA1B	ENSG00000204388	5.84E-06	-2.217373949	22492.80402
RARG	ENSG00000172819	1.18E-05	-1.311486444	271.3112
PMEPA1	ENSG00000124225	1.68E-05	-2.129472956	653.6239975
LDOC1L	ENSG00000188636	2.29E-05	-2.02552378	117.4697088
GAS7	ENSG00000007237	2.57E-05	-1.966175677	227.0592444
SLC12A7	ENSG00000113504	3.52E-05	-1.894448891	352.2864915
HSF5	ENSG00000176160	4.15E-05	-1.982160205	199.2051362
	ENSG00000244620	6.98E-05	-2.074107287	73.26705493
FBLN2	ENSG00000163520	7.03E-05	-1.938154167	152.8460752
DNAJB1	ENSG00000132002	7.44E-05	-1.725961423	84153.89323
FSCN1	ENSG00000075618	0.000139244	-1.492263287	648.6603338
LGMN	ENSG00000100600	0.000141125	-1.851330386	598.6973801
ZBTB32	ENSG00000011590	0.000160118	-1.653053877	191.3119358
CADM1	ENSG00000182985	0.000165012	-1.937632766	280.200564
INSR	ENSG00000171105	0.00016601	-1.775591642	122.2444057
TOX2	ENSG00000124191	0.000175472	-1.935813853	280.5918922
EPHA4	ENSG00000116106	0.000258582	-1.855175751	109.5839998
JUP	ENSG00000173801	0.000268424	-1.486993433	2295.612852
DIP2B	ENSG00000066084	0.000312881	-0.709884398	4475.311588
DFNB31	ENSG00000095397	0.000317896	-1.469110018	169.2763435
TNRC6C	ENSG00000078687	0.00031964	-1.485288921	931.1163257
KLF3	ENSG00000109787	0.000340936	-1.664604344	730.5146987
IGHV1-24	ENSG00000211950	0.000366089	-1.848397032	202.089348
CCR7	ENSG00000126353	0.000373795	-1.658934272	1849.86227
SELP	ENSG00000174175	0.000392464	-1.640301592	112.0636809
IGHV5-51	ENSG00000211966	0.000447991	-1.757680571	630.4949681
CSF1	ENSG00000184371	0.000487984	-1.732989273	92.5838862
C10orf128	ENSG00000204161	0.000489472	-1.599042647	684.3551232
CELF2-AS1	ENSG00000181800	0.000553244	-1.404190481	76.7017806
MB21D1	ENSG00000164430	0.000588397	-0.867517431	1248.833364
PLBD1	ENSG00000121316	0.000610453	-1.691797845	73.5238732
PRKAG2	ENSG00000106617	0.000614037	-1.542477676	370.9465921
BTBD19	ENSG00000222009	0.000614118	-1.281490271	238.8069845
MYO15B	ENSG00000266714	0.000629424	-1.581909602	5175.793929
SERPINB9	ENSG00000170542	0.000674352	-1.058396243	4643.215211
SELL	ENSG00000188404	0.000702888	-1.195693157	15709.3632
GGT7	ENSG00000131067	0.000715818	-1.605322203	409.1227928
PTGR1	ENSG00000106853	0.000718652	-1.717406138	38.73941355
HSPA6	ENSG00000173110	0.000733966	-1.781914772	5397.603654
CTSW	ENSG00000172543	0.000751669	-1.188254629	74.82128206
NRROS	ENSG00000174004	0.000756384	-1.55748082	423.7121647
KLHL29	ENSG00000119771	0.000756525	-1.418125515	406.3435128
PDCD1	ENSG00000188389	0.000766331	-1.622870799	61.43230126
LTBP3	ENSG00000168056	0.000767411	-1.231417808	1416.607314
SNX9	ENSG00000130340	0.000769685	-1.487982352	1176.107246
CLNK	ENSG00000109684	0.000802396	-1.7229022	1927.054381
HS3ST1	ENSG00000002587	0.000822461	-1.610432857	573.5306956
MVB12B	ENSG00000196814	0.000857942	-1.53314016	193.7879193
SDK2	ENSG00000069188	0.000915363	-1.660615152	881.4188107

HSPA7	ENSG00000225217	0.000920588	-1.696494557	586.6180212
IGHG3	ENSG00000211897	0.000951943	-1.494874772	2906.414024
NA	ENSG00000182909	0.00111216	-1.032777566	80.71002825
MED13L	ENSG00000123066	0.001188338	-0.658233094	6649.698973
ZC3HAV1	ENSG00000105939	0.001240794	-0.726893259	13880.41689
CDYL	ENSG00000153046	0.001283033	-0.683945294	1556.132604
ERRFI1	ENSG00000116285	0.001290286	-1.296969393	79.33536462
PREX1	ENSG00000124126	0.001342103	-1.588815424	2323.837504
SOCS3	ENSG00000184557	0.001353499	-1.341546299	2872.511726
COL9A3	ENSG00000092758	0.001360053	-1.629672474	382.5054064
IL7R	ENSG00000168685	0.001420076	-1.482575543	49.01257605
TNFRSF1B	ENSG00000028137	0.001452244	-1.49147337	961.3391172
NA	ENSG00000197701	0.001484156	-1.607546481	939.2321272
PLCH2	ENSG00000149527	0.001509958	-1.382678088	537.582655
SLC37A2	ENSG00000134955	0.001555573	-1.528370771	96.52147424
CALHM2	ENSG00000138172	0.0015569	-1.248271638	431.2546323
ARID3A	ENSG00000116017	0.001558929	-1.347961842	541.910903
NLRP7	ENSG00000167634	0.001562051	-1.600107604	104.7830301
DOK2	ENSG00000147443	0.001575767	-1.616930201	236.5509308
ZNF433	ENSG00000197647	0.001607769	-1.005493262	207.8991903
AHDC1	ENSG00000126705	0.001646654	-1.275105058	510.3285749
SNAI1	ENSG00000124216	0.001742307	-1.221692456	869.9016096
KLF4	ENSG00000136826	0.00174801	-1.478876785	2119.99914
IGHV3-11	ENSG00000211941	0.001783889	-1.594447265	170.8703115
LRRC56	ENSG00000161328	0.001798764	-1.057658253	359.108889
EGR3	ENSG00000179388	0.001804274	-1.43261652	5883.571467
	ENSG00000264781	0.001826948	-1.649283356	170.1717937
MTMR12	ENSG00000150712	0.001842663	-0.656343035	5496.286669
	ENSG00000212371	0.001954581	-1.379710068	178.3533953
IGKV1-9	ENSG00000241755	0.002107246	-1.539916047	62.00709916
HLX	ENSG00000136630	0.002123136	-1.522513001	125.2251883
GPR132	ENSG00000183484	0.002136375	-1.333499997	1024.258188
KAZALD1	ENSG00000107821	0.002335779	-1.30357649	59.17193049
IGKV3-11	ENSG00000241351	0.002343156	-1.477833276	306.3712762
PLK3	ENSG00000173846	0.002350355	-0.726482468	3365.839368
	ENSG00000233874	0.00237089	-0.555137641	91.38616381
IGKV1-16	ENSG00000240864	0.002430561	-1.569526749	104.1648362
AXIN2	ENSG00000168646	0.002485382	-1.567904975	156.6789534
ARRDC4	ENSG00000140450	0.002504073	-1.559261551	496.355505
IFITM2	ENSG00000185201	0.002665645	-0.93144556	1518.133196
ZMYND11	ENSG00000015171	0.002692508	-0.847938071	2071.931908
C1orf115	ENSG00000162817	0.0027265	-1.577717726	302.0243169
BAG3	ENSG00000151929	0.002741882	-1.331103564	3203.394329
LINC00963	ENSG00000204054	0.002761605	-1.425780833	81.76453826
NMT2	ENSG00000152465	0.00278311	-0.791688205	212.9669998
ARHGEF5	ENSG00000050327	0.00279243	-1.567143123	45.57794457
	ENSG00000268015	0.002927409	-0.958910746	48.45373821
CACNA1A	ENSG00000141837	0.002955696	-1.304419472	288.897533
CHORDC1	ENSG00000110172	0.002962833	-0.985695148	9769.159506
CD274	ENSG00000120217	0.003021799	-1.162072546	101.4330369
RN7SK	ENSG00000202198	0.003047549	-1.226467906	1893.629558
HMOX1	ENSG00000100292	0.003249469	-1.262052669	705.3677841
RAB34	ENSG00000109113	0.003362995	-1.456135048	372.0656921
IGHV3-49	ENSG00000211965	0.003409312	-1.499872487	154.1956644
	ENSG00000260077	0.003412572	-1.518147581	50.06376417
IL27RA	ENSG00000104998	0.003479438	-0.951994149	1270.998213
SQSTM1	ENSG00000161011	0.003515455	-0.52215924	5545.646248
CLCN7	ENSG00000103249	0.003584541	-0.672514959	6413.100849
JAM3	ENSG00000166086	0.00361224	-1.283885068	429.7201065

SYCE2	ENSG00000161860	0.003695917	-0.646980558	86.46650367
PARP14	ENSG00000173193	0.003720935	-0.896192383	15218.57649
PATL2	ENSG00000229474	0.003819702	-0.907410449	1715.947542
SIK3	ENSG00000160584	0.003872304	-0.531970885	5416.305576
PELI3	ENSG00000174516	0.003885214	-0.74178842	185.2758224
RNF130	ENSG00000113269	0.003918125	-1.331353855	341.1860825
SUFU	ENSG00000107882	0.004023752	-0.541831939	1059.354877
FBXW4	ENSG00000107829	0.004249071	-0.475495941	4387.838616
FAM43A	ENSG00000185112	0.004346381	-1.044728963	2305.832956
CAMKK1	ENSG00000004660	0.004375984	-1.052154902	293.0369706
SPG20	ENSG00000133104	0.004413395	-1.467249269	560.3494788
PRDM1	ENSG00000057657	0.004443008	-1.374809739	739.5559853
	ENSG00000203362	0.004568927	-0.843026285	46.85485639
SESTD1	ENSG00000187231	0.004633775	-0.820078329	2728.772328
IGHV1-2	ENSG00000211934	0.004641079	-1.43870881	298.5982172
FGR	ENSG00000000938	0.004657393	-1.390733538	1256.254801
SNORD3A	ENSG00000263934	0.004887424	-1.397721152	178.4536263
C11orf85	ENSG00000168070	0.004903994	-1.480483334	65.77374793
NABP1	ENSG00000173559	0.004978121	-0.976766388	2382.127912
	ENSG00000263606	0.004998783	-0.650360155	519.9027944
	ENSG00000267216	0.00500429	-0.678572327	51.57936185
PKD1	ENSG00000008710	0.005009649	-0.487782388	3879.783724
PLAUR	ENSG00000011422	0.005024536	-1.196117419	53.72817587
RYKP1	ENSG00000263219	0.005094108	-0.824682147	45.57856763
PIEZO1	ENSG00000103335	0.005101844	-1.364610047	1469.392301
RILPL2	ENSG00000150977	0.005106538	-0.76331206	1848.624506
GPX1	ENSG00000233276	0.005196913	-0.851218057	2568.928957
TCF7	ENSG00000081059	0.005236157	-1.067454918	406.4773948
SMG1P3	ENSG00000180747	0.00525927	-0.678554114	645.4986796
NAALAD2	ENSG00000077616	0.005356353	-0.821532871	269.397953
CD7	ENSG00000173762	0.005444962	-1.408884263	43.76833236
HPS1	ENSG00000107521	0.005557405	-0.387824182	10154.93153
LY6E	ENSG00000160932	0.005655379	-1.376047788	961.3049692
IGLV1-40	ENSG00000211653	0.005660673	-1.214471175	166.1517526
CDC42EP4	ENSG00000179604	0.005801027	-1.188779076	52.43855765
ACSS2	ENSG00000131069	0.005807684	-1.19132702	102.8866055
CD72	ENSG00000137101	0.005834777	-0.959280191	14157.69454
GDF11	ENSG00000135414	0.005876632	-0.898791037	275.7392487
ITGA5	ENSG00000161638	0.005912479	-1.388670037	91.36828002
XAB2	ENSG00000076924	0.005961575	-0.296193042	5034.424651
TNFRSF13B	ENSG00000240505	0.006175912	-1.388276609	1211.91348
	ENSG00000265517	0.00621176	-1.372646918	223.6550471
CCND1	ENSG00000110092	0.006298205	-0.994997881	231.3684014
GRK6P1	ENSG00000215571	0.006379697	-0.595153742	98.31827799
TLE1P1	ENSG00000228158	0.006431417	-1.398792453	137.465281
PTPRK	ENSG00000152894	0.006442566	-1.370200204	570.8393436
IGHV3-21	ENSG00000211947	0.006499833	-1.357188874	264.2493277
SERPINB6	ENSG00000124570	0.006546525	-1.313945181	603.0642676
RNF125	ENSG00000101695	0.006701709	-1.357384629	198.4843949
UST	ENSG00000111962	0.006816397	-1.299257377	360.1798649
ZNF492	ENSG00000229676	0.006833281	-1.428684519	47.4562949
TECR	ENSG00000099797	0.006833706	-0.828520855	2142.475421
ARID5A	ENSG00000196843	0.006839714	-0.783748744	3670.977783
RNF43	ENSG00000108375	0.006882135	-1.165735136	114.2890116
TBXAS1	ENSG00000059377	0.007065814	-1.316926216	157.1527074
GPAT2	ENSG00000186281	0.007110011	-1.38613601	49.83170129
DUSP6	ENSG00000139318	0.007126128	-0.887185222	4858.862542
TNFSF12	ENSG00000239697	0.007145773	-1.121247896	473.6690034
	ENSG00000237938	0.007215338	-0.850937628	69.13874639

SCML2	ENSG00000102098	0.007224749	-1.415022461	57.49995465
IL6	ENSG00000136244	0.007334792	-1.205049967	1759.424118
ARNTL	ENSG00000133794	0.007378966	-0.969262593	1525.822384
	ENSG00000245017	0.007407381	-0.853435557	44.25613498
NA	ENSG00000251606	0.007422564	-1.283536115	76.81784924
IRAK2	ENSG00000134070	0.007680771	-0.927445761	1868.408049
	ENSG00000263751	0.007703752	-1.404398383	171.9567079
ADAT3	ENSG00000213638	0.007712794	-0.614234878	40.82795355
NA	ENSG00000174194	0.007729464	-0.712977978	138.7163078
PARP15	ENSG00000173200	0.007811301	-1.174499508	9328.897754
THRA	ENSG00000126351	0.007897511	-0.865052788	296.1160371
ST6GALNAC3	ENSG00000184005	0.007909181	-1.358396716	42.35874597
HHEX	ENSG00000152804	0.007916049	-0.836242478	6494.896917
JUNB	ENSG00000171223	0.007985014	-0.749184467	62245.27361
ESAM	ENSG00000149564	0.008104033	-1.15466855	306.7436799
	ENSG00000230076	0.008137058	-0.629438838	442.5234279
NDRG2	ENSG00000165795	0.008173915	-1.236563446	98.69135497
	ENSG00000261207	0.008227809	-0.922712128	106.6976694
SLCO4A1	ENSG00000101187	0.008472558	-1.322724118	143.3655277
NAB2	ENSG00000166886	0.008502231	-0.766644034	1608.845189
MYRIP	ENSG00000170011	0.008800867	-1.38450835	40.53691189
MLF1	ENSG00000178053	0.009016763	-1.366785254	77.73280177
IGKV1-8	ENSG00000240671	0.009100048	-1.2828098	69.70373344
IL15RA	ENSG00000134470	0.009238207	-0.936494606	214.7324397
C10orf32	ENSG00000166275	0.009274214	-0.488659858	929.204537
HSPG2	ENSG00000142798	0.009498091	-1.307391609	67.64690145
	ENSG00000260521	0.009553421	-0.515066012	1924.570674
RPL19P21	ENSG00000230508	0.009626061	-0.858190511	205.8398479
KLF9	ENSG00000119138	0.009834837	-1.088107119	1673.680535
CSF1R	ENSG00000182578	0.009881442	-0.781550933	91.52630848
HES6	ENSG00000144485	0.00993007	-1.139381237	176.4842882
HSPE1	ENSG00000115541	0.010061733	-0.83502009	2773.999223
	ENSG00000217801	0.010142748	-1.201413301	162.9180178
KRT8P50	ENSG00000260799	0.010200039	-0.745914217	40.24249239
HSP90AA1	ENSG00000080824	0.010324636	-0.810978127	166583.0975
ZNF677	ENSG00000197928	0.010552071	-1.327290514	86.69821157
TCP1	ENSG00000120438	0.010648019	-0.585688181	11059.68746
HSP90AB2P	ENSG00000205940	0.010693579	-0.646087199	555.9836404
NOXA1	ENSG00000188747	0.010804546	-1.144873547	570.2339145
GDPGP1	ENSG00000183208	0.010844745	-0.481764667	130.1386326
IGLV7-43	ENSG00000211652	0.010853388	-1.164768667	41.44311137
MORN1	ENSG00000116151	0.010935368	-0.865462547	166.7716055
	ENSG00000266706	0.010954896	-1.34572516	133.5281503
IGLV2-14	ENSG00000211666	0.011049827	-1.159262864	147.920407
RNY1P16	ENSG00000199933	0.011113381	-0.993415692	53.30064432
MAN2A2	ENSG00000196547	0.011123908	-0.67989203	6355.79058
	ENSG00000234750	0.011200454	-0.966241286	41.04084603
FRAT1	ENSG00000165879	0.011370555	-0.501404353	1228.096356
CCDC113	ENSG00000103021	0.011493114	-1.051968416	80.64716993
CRAT	ENSG00000095321	0.011494857	-1.263462911	193.767124
PI4K2A	ENSG00000155252	0.011521642	-0.631058792	1899.479914
IGHV3-13	ENSG00000211942	0.011539003	-1.30098874	53.93412894
CHPT1	ENSG00000111666	0.011550456	-0.618869384	2254.916593
APOD	ENSG00000189058	0.011572134	-1.232696043	195.6866898
TRPM2	ENSG00000142185	0.011642077	-1.279229136	350.1801288
ATN1	ENSG00000111676	0.011763253	-0.959922214	4620.846114
CUBN	ENSG00000107611	0.011839579	-1.038946745	337.6392211
CLEC17A	ENSG00000187912	0.011850053	-1.065950296	4117.56126
	ENSG00000226915	0.011950717	-0.717010124	106.8592618

ANXA4	ENSG00000196975	0.012046453	-1.222438866	671.3293009
BCAS1	ENSG00000064787	0.012100929	-1.11821548	318.6914879
CRTC3	ENSG00000140577	0.012135728	-0.796529357	2857.465993
TLE1	ENSG00000196781	0.012156023	-1.315249851	951.6040937
SNORD64	ENSG00000270704	0.012340205	-0.976689672	46.5993745
MRPL18	ENSG00000112110	0.012391051	-0.531437021	2477.98452
CD5	ENSG00000110448	0.012428311	-1.207098153	114.9373747
HSPA2	ENSG00000126803	0.012555351	-1.184832125	573.2886948
SLC25A28	ENSG00000155287	0.012587065	-0.540945388	4196.766933
EFCAB12	ENSG00000172771	0.012696544	-0.944380622	874.7597314
ELL	ENSG00000105656	0.012718151	-0.47608329	1528.60021
	ENSG00000266408	0.012749697	-1.255563897	163.6684072
PDLIM1P1	ENSG00000270788	0.012768889	-1.111097815	40.22381041
SIRPB1	ENSG00000101307	0.012827767	-1.285673684	257.1286648
TMPPE	ENSG00000188167	0.01293819	-0.594812226	227.9648767
FSIP2	ENSG00000188738	0.013106601	-1.261574775	182.1930909
	ENSG00000259363	0.013293063	-1.089505882	73.1916989
NA	ENSG00000271738	0.013337744	-1.010575242	105.2468375
IGLV2-11	ENSG00000211668	0.013360593	-1.261924075	93.33711656
RPS6KL1	ENSG00000198208	0.013384424	-1.017349154	232.6989824
	ENSG00000260051	0.013395157	-0.856098969	173.7458631
C17orf51	ENSG00000212719	0.013501487	-1.033206873	117.9556452
FLNA	ENSG00000196924	0.013528771	-0.80118106	12729.56122
APCDD1	ENSG00000154856	0.013768831	-1.204136495	48.51628979
ZNF57	ENSG00000171970	0.013890307	-0.904575927	160.6008636
NFATC3	ENSG00000072736	0.013952989	-0.592538936	5030.012426
HSPD1	ENSG00000144381	0.014079291	-0.834656504	16542.34288
RGMB	ENSG00000174136	0.014121423	-0.969031231	816.7904819
	ENSG00000265612	0.01424417	-1.273655611	181.195624
HSP90AA2P	ENSG00000224411	0.014273528	-0.809563115	9517.453407
ANXA1	ENSG00000135046	0.014359378	-1.186019182	66.98079353
	ENSG00000231434	0.014402849	-0.820539972	703.996571
PDCD11	ENSG00000148843	0.014512013	-0.393152452	4084.309393
ERICH6-AS1	ENSG00000240137	0.014533272	-0.858461816	77.02174085
MAPK8IP3	ENSG00000138834	0.014598676	-0.678645373	21935.24166
CHL1	ENSG00000134121	0.014607331	-1.256049708	2873.305448
DOPEY2	ENSG00000142197	0.014615774	-0.812167024	3098.701088
DEDD2	ENSG00000160570	0.014620194	-0.755969098	8743.643667
RP9P	ENSG00000205763	0.014658921	-1.20680086	60.63961666
NA	ENSG00000248835	0.014718481	-0.462671362	319.4248328
SIPA1	ENSG00000213445	0.014762347	-0.533353162	15191.76327
UTRN	ENSG00000152818	0.014801752	-0.847065271	6079.33611
FHL1	ENSG00000022267	0.014896032	-1.097678174	65.31473023
LDOC1	ENSG00000182195	0.014902289	-1.284149894	182.101876
TMEM173	ENSG00000184584	0.015038176	-1.131433361	47.81961483
IGHV4-59	ENSG00000224373	0.015071556	-1.159388204	141.0175931
PDLIM7	ENSG00000196923	0.015131305	-0.732939801	1290.000033
ZKSCAN3	ENSG00000189298	0.015291931	-0.361461407	620.9615611
STARD5	ENSG00000172345	0.015316097	-0.619180438	1471.911204
EPHB1	ENSG00000154928	0.015562346	-1.261887238	1051.26415
PRR5	ENSG00000186654	0.015724868	-1.267072882	50.94493953
FBXO6	ENSG00000116663	0.015924967	-0.810615078	444.2864148
IGKV1-12	ENSG00000243290	0.015947631	-1.148121859	41.73155506
IFFO2	ENSG00000169991	0.016114377	-1.019836834	1365.794226
ZNF703	ENSG00000183779	0.016228734	-1.114062663	208.5500355
TBC1D27	ENSG00000128438	0.016513844	-1.22934711	1401.307749
TCTEX1D4	ENSG00000188396	0.016652488	-0.938040149	41.17765798
MSX1	ENSG00000163132	0.016718997	-1.251394405	156.5782407
NLRP6	ENSG00000174885	0.016726927	-1.098990167	54.41473605

IGHV1-46	ENSG00000211962	0.016729207	-1.188249692	92.1533394
CERS6	ENSG00000172292	0.016774947	-1.223816963	194.38565
TMEM8B	ENSG00000137103	0.017062675	-0.533310732	1237.689541
SNORA20	ENSG00000207392	0.017068628	-0.886575436	59.40897376
NA	ENSG00000174111	0.017122423	-0.638358286	321.2116424
TLR4	ENSG00000136869	0.017140445	-1.201233838	518.7400472
SCML1	ENSG00000047634	0.017243146	-1.250568353	435.2201969
AMOT	ENSG00000126016	0.017253164	-1.13474413	273.9477046
SH3RF3	ENSG00000172985	0.017309234	-1.185269628	54.67603133
CHN2	ENSG00000106069	0.017501618	-1.253695566	691.5220056
RRAGD	ENSG00000025039	0.017838901	-1.030968477	193.3427167
GNE	ENSG00000159921	0.017928242	-0.419064032	2274.374385
CD19	ENSG00000177455	0.018308888	-0.509899627	33891.93637
TNNT3	ENSG00000130595	0.01850668	-0.936756888	98.14925769
ITGB7	ENSG00000139626	0.018815613	-0.966572825	5215.626484
CIB1	ENSG00000185043	0.018830561	-0.479005766	6788.374752
	ENSG00000264469	0.018884791	-0.69481884	236.3138535
GPD1	ENSG00000167588	0.018936182	-0.643883077	98.13013357
GRAP2	ENSG00000100351	0.019209399	-1.194004512	71.49612787
SLC12A8	ENSG00000221955	0.019220746	-1.005503819	96.32113805
TOR4A	ENSG00000198113	0.01929589	-0.808531582	665.5792394
	ENSG00000228143	0.019532879	-0.853784472	41.80405943
IGKV1-27	ENSG00000244575	0.019621737	-1.165439195	85.18834223
MAP1A	ENSG00000166963	0.01975222	-1.022125996	423.4757321
IRF1	ENSG00000125347	0.020115773	-0.668801439	10626.68444
TGM2	ENSG00000198959	0.020407851	-1.133547932	258.9611168
DCBLD2	ENSG00000057019	0.020448429	-1.216961212	46.60052254
BANK1	ENSG00000153064	0.020618461	-0.511113901	35631.35192
TCFL5	ENSG00000101190	0.020743562	-0.636180545	742.9839979
PNMAL1	ENSG00000182013	0.020787187	-1.161353538	48.04038577
TYMP	ENSG00000025708	0.020939726	-0.811615728	1226.980696
	ENSG00000227176	0.02098221	-0.911402431	53.9165327
FAM90A1	ENSG00000171847	0.02099384	-0.983626669	56.16716739
CDH13	ENSG00000140945	0.021029805	-1.136767259	40.29529628
CARD9	ENSG00000187796	0.021117524	-0.995073783	217.5525363
	ENSG00000227359	0.021229996	-1.126016678	45.80711325
	ENSG00000215154	0.021424781	-0.682289565	85.62623181
MTND2P28	ENSG00000225630	0.021531275	-1.075526849	288.2213016
BTBD3	ENSG00000132640	0.021580741	-1.18368154	71.15113667
FAM46C	ENSG00000183508	0.021625756	-0.771754908	18720.49254
ARRDC5	ENSG00000205784	0.021800878	-1.016204994	72.36016585
SPATA6	ENSG00000132122	0.021823805	-1.214065055	62.45963769
ATP2B4	ENSG00000058668	0.022049182	-1.140421472	444.0579454
KIAA0125	ENSG00000226777	0.022107671	-1.15660731	661.657367
MYBPC2	ENSG00000086967	0.022111096	-0.967889346	393.5371292
C21orf140	ENSG00000222018	0.022148374	-0.828459219	47.59763205
SYNPO	ENSG00000171992	0.022195358	-1.090259999	813.8920424
CA11	ENSG00000063180	0.022222987	-0.873093888	272.5468224
CNKSR2	ENSG00000149970	0.022242361	-1.071050097	996.362537
NINJ1	ENSG00000131669	0.022262221	-1.014629363	922.4266601
PIK3R4	ENSG00000196455	0.022351509	-0.369837388	2652.545308
SNORD14E	ENSG00000200879	0.022388624	-0.759407038	462.5671564
PKN3	ENSG00000160447	0.022424372	-0.896253018	506.0252494
STK10	ENSG00000072786	0.02244301	-0.398798107	12049.32294
FAM213A	ENSG00000122378	0.022836876	-0.757713935	506.3941194
IKZF1	ENSG00000185811	0.022841952	-0.412822476	23021.15871
PDGFRB	ENSG00000113721	0.022870116	-1.065747545	61.41169631
GTPBP1	ENSG00000100226	0.022882485	-0.347002526	5962.246064
SCARNA21	ENSG00000252835	0.02301958	-0.979527529	54.59687538

BATF2	ENSG00000168062	0.023059478	-1.097151916	90.58658659
CD48	ENSG00000117091	0.023196459	-0.76188096	8329.524048
IGLV2-23	ENSG00000211660	0.023311434	-1.118587022	139.7149559
HSPB1	ENSG00000106211	0.023530229	-1.13167149	2233.454021
PODXL2	ENSG00000114631	0.023645662	-1.035746757	648.2074529
LDB1	ENSG00000198728	0.023656708	-0.434590018	7288.490979
SLC18B1	ENSG00000146409	0.023699892	-0.760350324	855.7405937
PLXND1	ENSG00000004399	0.023890109	-0.974891276	864.1082873
SDC4	ENSG00000124145	0.023935312	-1.155656524	484.0291519
TBX21	ENSG00000073861	0.023971334	-0.979969137	244.8584004
IGHV3-15	ENSG00000211943	0.024006111	-1.073020891	159.2467412
KCNG1	ENSG00000026559	0.024079196	-1.175195855	71.21895559
IFIT2	ENSG00000119922	0.024080414	-0.79047955	3508.199757
PLCB2	ENSG00000137841	0.024134149	-0.647318237	8241.957018
FAR2P2	ENSG00000178162	0.024243235	-1.083516578	332.3887502
KHDRBS2	ENSG00000112232	0.024245578	-1.183892663	120.1829082
METRN	ENSG00000103260	0.024364815	-0.700828677	226.6386241
DUSP3	ENSG00000108861	0.024505009	-0.714683152	964.0530077
DDAH2	ENSG00000213722	0.024520179	-0.72889651	1379.478662
RBM17P4	ENSG00000259585	0.024594336	-0.351613097	159.5923786
ZNF267	ENSG00000185947	0.024634397	-0.501381917	2596.404339
IGHV3-48	ENSG00000211964	0.024725303	-1.143943773	171.5860897
ZNF597	ENSG00000167981	0.02473649	-0.957524502	542.7136742
PHF20	ENSG00000025293	0.024809101	-0.252735525	4441.204806
KLHL25	ENSG00000183655	0.024899764	-0.541812203	173.0940416
MYOM1	ENSG00000101605	0.024935569	-0.743892948	659.6661694
RABEP2	ENSG00000177548	0.025051723	-0.466575911	8983.660561
NUMBL	ENSG00000105245	0.025063835	-0.512635726	695.6593648
DSE	ENSG00000111817	0.025097389	-0.91952286	625.4506096
IGHV2-26	ENSG00000211951	0.025118403	-0.98558931	50.00836084
NFRKB	ENSG00000170322	0.02514458	-0.285763143	3387.403527
PTCHD2	ENSG00000204624	0.025304818	-1.100355729	62.4863163
RILP	ENSG00000167705	0.025416055	-0.600578964	109.3833789
	ENSG00000269896	0.025440795	-0.877356158	177.7866638
ALOX15	ENSG00000161905	0.02552522	-1.102847588	122.0581344
DKK1	ENSG00000107984	0.025619909	-1.181142246	41.77606574
	ENSG00000233597	0.025835654	-0.750499917	144.0436501
KLF2	ENSG00000127528	0.025871361	-0.677178429	22016.7369
SIK1	ENSG00000142178	0.025945818	-0.906324575	68402.83126
NEIL2	ENSG00000154328	0.026041419	-0.678441789	701.1145322
	ENSG00000233028	0.026047896	-0.747664693	165.6573677
MYO1F	ENSG00000142347	0.026107467	-1.102330974	474.2062267
MYO5B	ENSG00000167306	0.02612698	-1.086714941	57.69740462
FAM129C	ENSG00000167483	0.026440782	-0.713921141	21002.88114
FAM69B	ENSG00000165716	0.026458923	-0.807096159	152.8128786
CPM	ENSG00000135678	0.026459213	-1.045619258	125.5256103
SKI	ENSG00000157933	0.026694256	-0.784390029	1493.096729
CLMN	ENSG00000165959	0.026778966	-1.022945471	763.1112578
	ENSG00000258733	0.026903358	-0.963759035	88.5244254
LGALS3BP	ENSG00000108679	0.026903661	-1.03448771	407.4829786
PLTP	ENSG00000100979	0.027089295	-0.86262273	160.7073169
ALDOC	ENSG00000109107	0.027407162	-0.705658636	1369.69727
WDR81	ENSG00000167716	0.027461234	-0.580517147	4867.117434
	ENSG00000244480	0.027508668	-0.619413673	108.922964
SYNGR1	ENSG00000100321	0.027565078	-0.919114562	1413.994046
NKG7	ENSG00000105374	0.02770669	-0.915811135	38.48480891
SH3BGR	ENSG00000185437	0.027900178	-0.625091	47.53933385
	ENSG00000270442	0.027942198	-0.558009866	58.26058264
CACFD1	ENSG00000160325	0.028100598	-0.611212486	943.356209

NEAT1	ENSG00000245532	0.028125571	-0.664301549	21998.08567
ZSCAN31	ENSG00000235109	0.02824106	-0.700936189	61.94573732
WDFY1	ENSG00000085449	0.028318021	-0.45272126	4749.323481
ARSD	ENSG00000006756	0.028371393	-1.078338413	79.69941964
LINC00884	ENSG00000233058	0.028655818	-0.779689819	41.77406133
CYB5RL	ENSG00000215883	0.028796359	-0.480385523	326.0419821
IFI30	ENSG00000216490	0.028889607	-0.861232978	586.8956869
RPS15AP40	ENSG00000233921	0.029184009	-0.657117578	71.10198154
NRARP	ENSG00000198435	0.029202336	-0.944582958	904.0486298
CD2	ENSG00000116824	0.02951878	-1.148674702	52.69369994
AFF1	ENSG00000172493	0.029522721	-0.820964101	2053.189617
CKAP4	ENSG00000136026	0.029890309	-0.998370867	482.1952569
CELSR3	ENSG00000008300	0.030320353	-0.943170934	567.8092691
CD69	ENSG00000110848	0.030352174	-0.824052158	125525.2147
KREMEN2	ENSG00000131650	0.03093099	-1.040851881	303.5627628
GLTSCR2	ENSG00000105373	0.031020656	-0.428803354	17703.00275
	ENSG00000182574	0.03106349	-0.760489093	48.42077363
WIPF2	ENSG00000171475	0.031219271	-0.345258424	5873.987233
ZFYVE27	ENSG00000155256	0.031224253	-0.322528945	5618.218826
IGHV1-3	ENSG00000211935	0.03132182	-1.050139337	84.73989246
DPP7	ENSG00000176978	0.031365163	-0.416176546	10119.77943
	ENSG00000265714	0.031388897	-1.110696926	178.2894238
CSGALNACT1	ENSG00000147408	0.031490456	-1.092553024	181.502698
FBXL15	ENSG00000107872	0.031877287	-0.427693864	660.2233671
ADAP2	ENSG00000184060	0.031942642	-0.670802085	777.6831187
CCDC144NL-AS1	ENSG00000233098	0.031965708	-1.131294411	104.9278031
VDR	ENSG00000111424	0.032062003	-1.116989092	764.438711
HSPH1	ENSG00000120694	0.032417519	-0.836036183	37131.89193
LAMP3	ENSG00000078081	0.03243215	-1.002698583	401.7316037
ADAM8	ENSG00000151651	0.032453368	-0.77466405	3725.033253
VWA7	ENSG00000204396	0.03251523	-0.933578055	48.74599777
PLEKHG4	ENSG00000196155	0.032659111	-0.924447286	86.042865
PGAP3	ENSG00000161395	0.032668618	-0.424053351	1319.056036
HSP90AB1	ENSG00000096384	0.032752592	-0.557921944	106947.8432
OAT	ENSG00000065154	0.03279342	-0.707895618	3547.950083
C10orf76	ENSG00000120029	0.032824503	-0.415153356	4550.945215
BPGM	ENSG00000172331	0.032955289	-0.683577542	1577.295769
NR4A2	ENSG00000153234	0.032985333	-0.931532486	31536.93308
PHTF1	ENSG00000116793	0.033376285	-0.483419061	1633.776673
SEMA3B	ENSG00000012171	0.033394342	-0.885056535	90.80456692
TRPV3	ENSG00000167723	0.033458754	-1.040270095	249.3318062
TGIF1	ENSG00000177426	0.033498727	-1.023714282	3928.642239
RAB20	ENSG00000139832	0.033651418	-1.111274053	50.53392861
	ENSG00000237989	0.034529095	-1.027494773	1108.405343
DNAJA1	ENSG00000086061	0.03462001	-0.653604105	48893.6446
SLC16A5	ENSG00000170190	0.03470936	-1.059949347	145.7113355
EEF1A1P13	ENSG00000250182	0.034785565	-0.491604877	6606.241509
SLA2	ENSG00000101082	0.034898423	-1.000028585	97.17387756
IGHV3-7	ENSG00000211938	0.034980627	-0.714466274	322.799965
AASS	ENSG00000008311	0.035134334	-1.054848039	191.4758339
MMP17	ENSG00000198598	0.035311394	-1.044396632	358.6460142
	ENSG00000260461	0.035351393	-0.591219971	125.5073405
POLL	ENSG00000166169	0.03571765	-0.309837119	1887.888278
CCDC102B	ENSG00000150636	0.035892782	-0.679114211	55.27593255
FBXO24	ENSG00000106336	0.035899011	-0.686220382	48.04625965
CD44	ENSG00000026508	0.035999501	-0.761054415	11474.22524
RAP2B	ENSG00000181467	0.036391863	-0.420652378	2221.716265
TJP3	ENSG00000105289	0.036449432	-0.803301813	63.07905413
CRB2	ENSG00000148204	0.03647401	-0.761576483	356.5059343

PAQR7	ENSG00000182749	0.036503249	-0.750270482	139.3848283
FAM150B	ENSG00000189292	0.036647813	-0.951977341	51.31512636
MIR25	ENSG00000207547	0.036676996	-0.662859949	82.3998348
RNF149	ENSG00000163162	0.036737914	-0.411117723	2220.106209
SLC25A30	ENSG00000174032	0.036770547	-0.571260187	1024.53341
TBKBP1	ENSG00000198933	0.036786213	-1.031552962	598.3495595
DNAJA1P3	ENSG00000215007	0.036797241	-0.667026797	821.4598011
HERC1	ENSG00000103657	0.037076957	-0.403058937	8732.618435
NTN1	ENSG00000065320	0.037085164	-0.924474319	85.40276875
SERPINE1	ENSG00000106366	0.037273577	-1.055427988	66.8821918
PLD4	ENSG00000166428	0.03729425	-1.019128192	1806.498631
TRGV4	ENSG00000211698	0.037313512	-0.776234876	104.3255648
FURIN	ENSG00000140564	0.037342723	-0.783918495	6054.720588
FAM65A	ENSG00000039523	0.037579158	-0.74582307	5572.927206
SPHK1	ENSG00000176170	0.037735568	-0.871859787	65.54749775
LDLRAP1	ENSG00000157978	0.038061603	-0.909970091	117.7267336
ZNF473	ENSG00000142528	0.038233551	-0.394956481	1187.617972
	ENSG00000225637	0.038349242	-1.017413232	88.46721738
IL17RA	ENSG00000177663	0.038952707	-0.480252097	2007.789839
PGF	ENSG00000119630	0.039060982	-0.803900141	70.27778726
FPGT-TNNI3K	ENSG00000259030	0.039095308	-0.934364666	78.14747369
IGHJ4	ENSG00000240041	0.039453436	-1.083658923	68.67369071
PAFAH2	ENSG00000158006	0.039631827	-0.336538914	840.1578067
RARA	ENSG00000131759	0.039874593	-0.723110759	1419.615028
TNFRSF12A	ENSG00000006327	0.039963907	-0.81536304	65.12605032
MTMR3	ENSG00000100330	0.040114051	-0.25893991	5906.828642
NAV2	ENSG00000166833	0.040197798	-1.030034484	73.78288523
COL5A2	ENSG00000204262	0.040249337	-0.7596624	140.940164
TMEM184A	ENSG00000164855	0.040323086	-0.776172325	38.78938458
ITPRIP	ENSG00000148841	0.040567224	-0.508058835	4532.6864
TELO2	ENSG00000100726	0.040730743	-0.404082659	3714.008493
KLRF1	ENSG00000150045	0.040747352	-1.066119307	97.28848873
	ENSG00000173727	0.040759747	-0.837550411	211.6706785
ABLIM2	ENSG00000163995	0.040992961	-1.035135847	67.87364371
FOXN3P1	ENSG00000176318	0.041038045	-0.606526518	62.8319276
ZNF442	ENSG00000198342	0.041067379	-0.703614518	310.356268
ADCY7	ENSG00000121281	0.041262726	-0.418980171	3909.215889
LFNG	ENSG00000106003	0.041577258	-0.753545533	974.983984
CTRC	ENSG00000162438	0.041988855	-0.780673286	37.71496075
PLAU	ENSG00000122861	0.042150006	-0.891823079	42.02881402
FMNL3	ENSG00000161791	0.042164533	-0.433624987	17082.6478
	ENSG00000257924	0.042506737	-1.061502409	83.47856494
RASA3	ENSG00000185989	0.042545385	-0.846872986	2470.783708
LINC00996	ENSG00000242258	0.042572771	-1.035550976	116.4294968
IGLV8-61	ENSG00000211638	0.042738443	-1.000732377	99.88302369
PRR5L	ENSG00000135362	0.042846835	-1.029804623	74.30085527
CHD7	ENSG00000171316	0.043039725	-0.382248282	10036.08605
RASD1	ENSG00000108551	0.043371868	-0.729662829	100.5060963
ALPL	ENSG00000162551	0.043546151	-1.045384778	746.2978616
ZNF14	ENSG00000105708	0.043628376	-0.548291616	938.46441
HERC3	ENSG00000138641	0.043709401	-0.55529592	5095.814568
ALPK2	ENSG00000198796	0.043727694	-1.032704778	43.62858665
C19orf71	ENSG00000183397	0.043838796	-0.46492666	237.8674143
SAFB2	ENSG00000130254	0.043868439	-0.234300485	7831.469912
SLC4A3	ENSG00000114923	0.044069583	-1.01434518	60.38008962
NOTCH1	ENSG00000148400	0.044083672	-0.644278717	4679.644712
HSP90AB3P	ENSG00000183199	0.044148842	-0.51016921	10744.85819
RAB24	ENSG00000169228	0.044247504	-0.540769751	306.0746047
IFNAR2	ENSG00000159110	0.044249509	-0.57905528	1277.573042

PHLDB3	ENSG00000176531	0.044278656	-0.525056477	580.3355019
RAB11FIP5	ENSG00000135631	0.044331533	-0.887300755	160.2423971
CD3E	ENSG00000198851	0.044355198	-0.98148352	81.81750275
NFKBIZ	ENSG00000144802	0.0444216	-0.612527615	15426.39283
CRY1	ENSG00000008405	0.044587701	-1.03683301	59.53112408
UACA	ENSG00000137831	0.044626096	-1.054907938	57.94598744
HSPA1L	ENSG00000204390	0.044830773	-0.97272724	100.8703761
NA	ENSG00000265150	0.044866356	-0.840325803	2852.430192
EPHB6	ENSG00000106123	0.044912739	-0.888922528	741.568143
VASH1	ENSG00000071246	0.044969159	-0.810827913	114.9492951
HEXIM1	ENSG00000186834	0.045075983	-0.709136234	12457.39581
DOK3	ENSG00000146094	0.045190441	-0.508914662	9843.265333
CYSLTR1	ENSG00000173198	0.045294395	-0.811705205	568.8399641
FAM132A	ENSG00000184163	0.045296189	-0.721194648	40.87301843
THEMIS2	ENSG00000130775	0.045303311	-0.830338957	1596.292919
APOL3	ENSG00000128284	0.045618869	-0.840043487	1123.986606
HSP90AA4P	ENSG00000205100	0.045767914	-0.674038632	124.3280168
COL8A2	ENSG00000171812	0.046004526	-0.791211594	43.2095101
C1R	ENSG00000159403	0.046079859	-0.727901518	58.15374921
NA	ENSG00000211939	0.04668379	-1.04207084	147.5792767
PARP9	ENSG00000138496	0.04699084	-0.57515454	2703.29381
	ENSG00000250155	0.04702265	-0.604993632	289.3496425
CD6	ENSG00000013725	0.047067069	-0.983694236	371.5244664
REPS1	ENSG00000135597	0.047139536	-0.430978364	4074.643438
RGS12	ENSG00000159788	0.047263148	-0.736972691	166.2071664
MFSD1P1	ENSG00000261868	0.047283726	-0.823923501	43.61282406
SIRT1	ENSG00000096717	0.047448513	-0.582715163	7653.279866
RENBP	ENSG00000102032	0.047486318	-0.860780685	485.363642
NA	ENSG00000198374	0.047529469	-0.837507141	121.7619742
TERF1	ENSG00000147601	0.047580439	-0.251681982	1050.44628
SLC12A6	ENSG00000140199	0.047726963	-0.762319861	1847.516403
SLC2A3P4	ENSG00000254088	0.047864413	-0.826336595	51.67196752
PITPNM3	ENSG00000091622	0.048024601	-0.753384842	51.49363126
WWP2	ENSG00000198373	0.048163726	-0.298834405	6857.522287
ABCD1	ENSG00000101986	0.048378578	-0.497404841	836.1464356
SIGIRR	ENSG00000185187	0.04838764	-0.68612648	666.7086672
RNASET2	ENSG00000026297	0.0485324	-0.570442924	5617.148898
	ENSG00000223821	0.04860157	-0.83215865	52.43949408
TPM2	ENSG00000198467	0.048744832	-0.961209154	499.096811
APOBR	ENSG00000184730	0.048874739	-0.780604669	231.9644076
MPP1	ENSG00000130830	0.04896819	-0.925063824	481.2364463
RIN3	ENSG00000100599	0.048970369	-0.981704754	913.562486
CDKN1A	ENSG00000124762	0.049076486	-0.766899361	21148.91718
CDIP1	ENSG00000089486	0.049319306	-0.818503091	456.1616353
FMNL2	ENSG00000157827	0.049491502	-0.91603724	554.9980333
ENO2	ENSG00000111674	0.049505784	-0.691625271	5171.433409
CDKN2D	ENSG00000129355	0.049522938	-0.528084154	2363.226701
EFHD2	ENSG00000142634	0.04968295	-0.472111822	7065.929214
	ENSG00000260279	0.049795021	-0.663479043	51.31535361
APOL1	ENSG00000100342	0.049815844	-0.870335664	764.5184107

Suppl Table 3 (cont.). Downregulated genes in FL subjects with KMT2D mutations and B220+ lymphoma cells from vav-BCL2 mice with Kmt2d knockdown

Genes downregulated in B220 positive lymphoma cells from VavPBcl2 sh-Kmt2d tumors vs VavPBcl2-vector tumors

gene symbol	ensembl	pvalue	padj	log2FoldChange	baseMean	hgnc_symbol
Lpl	ENSMUSG00000015568	2.06E-09	5.00E-06	-2.66849639	49.48262037	LPL
Rgs1	ENSMUSG00000026358	1.00E-08	1.46E-05	-2.816396672	1073.995217	RGS1
Adrbk2	ENSMUSG00000042249	2.55E-08	2.89E-05	-2.316244258	55.76356027	ADRBK2
Dusp1	ENSMUSG00000024190	2.58E-08	2.89E-05	-2.999263903	2217.251525	DUSP1
Klf4	ENSMUSG00000003032	3.02E-08	3.15E-05	-3.287908872	299.2336182	KLF4
Plk2	ENSMUSG00000021701	4.82E-08	4.39E-05	-2.74328799	217.2694707	PLK2
Rasgrp4	ENSMUSG00000030589	1.88E-07	0.000124988	-1.032147316	92.64153278	RASGRP4
Fosb	ENSMUSG00000003545	3.20E-07	0.000180082	-3.477771152	4934.293017	FOSB
Pbx1	ENSMUSG00000052534	3.21E-07	0.000180082	-1.610571041	165.32453	PBX1
Asph	ENSMUSG00000028207	5.71E-07	0.000297659	-1.477735757	27.67753747	ASPH
Wbscr17	ENSMUSG00000034040	1.07E-06	0.000490279	-1.769389326	48.282298	WBSCR17
Scn8a	ENSMUSG00000023033	1.38E-06	0.00059403	-1.909292146	204.8407371	SCN8A
Clu	ENSMUSG00000022037	1.95E-06	0.000749744	-2.124981508	28.97217448	CLU
Grin3a	ENSMUSG00000039579	2.74E-06	0.001001185	-3.456710374	4.798432678	GRIN3A
Marco	ENSMUSG00000026390	2.86E-06	0.001019084	-2.757499587	38.88665003	MARCO
Adcy6	ENSMUSG00000022994	2.97E-06	0.001032043	-3.225511666	7.175592488	ADCY6
Lilrb4	ENSMUSG00000062593	3.23E-06	0.001096783	-1.307407974	109.1638048	LILRB4
Egr1	ENSMUSG00000038418	3.87E-06	0.00120682	-2.660218304	4879.586708	EGR1
Ppp1r15a	ENSMUSG00000040435	3.89E-06	0.00120682	-2.439855766	3085.260647	PPP1R15A
Apobr	ENSMUSG00000042759	4.44E-06	0.001351529	-1.538778953	37.28736229	APOBR
Tns1	ENSMUSG00000055322	4.77E-06	0.001392569	-1.912291852	38.50870665	TNS1
Gramd1b	ENSMUSG00000040111	7.65E-06	0.002068562	-1.743407429	141.2322456	GRAMD1B
Vwf	ENSMUSG00000001930	1.03E-05	0.002633483	-2.382697447	6.738996347	VWF
Nod2	ENSMUSG00000055994	1.27E-05	0.003096494	-0.922291646	221.1208057	NOD2
Siglec1	ENSMUSG00000027322	1.32E-05	0.003136553	-2.726949868	15.52301448	SIGLEC1
Itga2b	ENSMUSG00000034664	1.39E-05	0.003145765	-1.456121576	28.09287216	ITGA2B
Psd2	ENSMUSG00000024347	1.54E-05	0.003304846	-2.125792023	16.96418361	PSD2
Ptp4a1	ENSMUSG00000026064	1.55E-05	0.003304846	-1.976484282	134.8184132	PTP4A1
Pld2	ENSMUSG00000020828	1.58E-05	0.003304846	-1.378714908	94.14783773	PLD2
Slc22a23	ENSMUSG00000038267	1.76E-05	0.003574348	-1.491328389	21.37201334	SLC22A23
Star	ENSMUSG00000031574	2.19E-05	0.004142547	-1.653300584	56.74425576	STAR
Dock5	ENSMUSG00000044447	2.47E-05	0.004561579	-1.896753351	17.43941047	DOCK5
Ptplad2	ENSMUSG00000028497	2.64E-05	0.004641388	-2.061147475	12.38206067	PTPLAD2
Psd3	ENSMUSG00000030465	3.42E-05	0.005605076	-2.04565605	78.56759814	PSD3
Bgn	ENSMUSG00000031375	4.13E-05	0.006613811	-2.297184737	10.41904097	BGN
Slc8a1	ENSMUSG00000054640	4.24E-05	0.006613811	-2.446393473	8.712193186	SLC8A1
Nlrp1b	ENSMUSG00000070390	4.43E-05	0.006739063	-1.371451662	45.31224194	NLRP1
Csf2rb2	ENSMUSG00000071714	4.71E-05	0.007089168	-1.805202078	44.47042122	CSF2RB
Cd69	ENSMUSG00000030156	4.83E-05	0.007114717	-1.697054756	1499.601504	CD69
Sspo	ENSMUSG00000029797	5.13E-05	0.007352169	-1.962387251	14.73690907	SSPO
Dock4	ENSMUSG00000035954	5.28E-05	0.007408941	-2.088623557	14.33005442	DOCK4
Atf3	ENSMUSG00000026628	5.99E-05	0.007872282	-2.272845585	57.89351011	ATF3
6430548M08Rik	ENSMUSG00000031824	6.00E-05	0.007872282	-1.689481524	34.80936177	KIAA0513
Fyco1	ENSMUSG00000025241	6.09E-05	0.007872282	-1.775754791	567.4333134	FYCO1
Gm684	ENSMUSG00000079559	6.22E-05	0.007958499	-2.629265541	30.80289861	COLCA2
Nlgn3	ENSMUSG00000031302	6.81E-05	0.008316188	-1.836724839	13.12952716	NLGN3
Lrp1	ENSMUSG00000040249	6.84E-05	0.008316188	-2.22911854	128.5806173	LRP1
Lrp4	ENSMUSG00000027253	6.90E-05	0.008316188	-2.099484255	8.345478819	LRP4
Havcr2	ENSMUSG00000020399	7.63E-05	0.008987505	-1.899705598	12.39990071	HAVCR2
Nfkbiz	ENSMUSG00000035356	7.81E-05	0.00910765	-1.506989112	638.1804961	NFKBIZ
Trim15	ENSMUSG00000050747	7.87E-05	0.00910765	-2.277779784	5.122292611	TRIM15
6330403A02Rik	ENSMUSG00000053963	8.46E-05	0.009642784	-1.471477346	13.86003662	C1orf95
Slc16a10	ENSMUSG00000019838	9.11E-05	0.010001108	-1.480688129	64.54262	SLC16A10
Padi2	ENSMUSG00000028927	9.58E-05	0.010353618	-1.068143616	260.4942761	PADI2
Frmd4a	ENSMUSG00000026657	0.00010485	0.011253612	-1.72228982	23.05872621	FRMD4A
Tead2	ENSMUSG00000030796	0.000110389	0.011761699	-1.268349705	46.63791248	TEAD2
Fam169a	ENSMUSG00000041817	0.000121609	0.012589575	-1.710241457	9.253708334	FAM169A
Vasn	ENSMUSG00000039646	0.000131586	0.013402871	-2.076497998	139.5475629	VASN
Gp49a	ENSMUSG00000089672	0.000133357	0.013402871	-1.615020534	23.39187201	LILRB4
Tbkbp1	ENSMUSG00000038517	0.000134056	0.013402871	-0.997421145	59.47426537	TBKBP1
Sort1	ENSMUSG00000068747	0.000153184	0.014116364	-1.619502059	39.84809268	SORT1
Itgb1bp2	ENSMUSG00000031312	0.000153449	0.014116364	-2.050345677	8.191181455	ITGB1BP2
Arhgap32	ENSMUSG00000041444	0.000154309	0.014116364	-1.900267823	11.00374662	ARHGAP32
Nrg4	ENSMUSG00000032311	0.000154588	0.014116364	-2.020306571	20.88599242	NRG4
Tspan9	ENSMUSG00000030352	0.000155496	0.014116364	-2.191326532	4.29913557	TSPAN9
Zbtb37	ENSMUSG00000043467	0.000158556	0.014116364	-1.446576548	258.6765671	ZBTB37
Zcchc14	ENSMUSG00000061410	0.000176414	0.015328068	-2.166427137	10.70475468	ZCCHC14
Pde4c	ENSMUSG00000031842	0.0001794	0.015413323	-1.302281586	138.4238558	PDE4C
Ttbk1	ENSMUSG00000015599	0.000183056	0.015413323	-1.390377996	66.39089031	TTBK1
Dnhd1	ENSMUSG00000030882	0.000183285	0.015413323	-0.926979245	204.6546441	DNHD1

Ankrd16	ENSMUSG00000047909	0.000185197	0.015413323	-0.998792317	857.1580809	ANKRD16
Ankrd61	ENSMUSG00000029607	0.000186213	0.015413323	-2.046083793	16.98421956	ANKRD61
Etohi1	ENSMUSG00000074519	0.000187954	0.015413323	-1.217110782	68.53278883	ZNF442
Zfp36	ENSMUSG00000044786	0.000190474	0.015532684	-1.456474181	8404.428092	ZFP36
Bbs2	ENSMUSG00000031755	0.000193814	0.01568575	-0.787575799	740.2933078	BBS2
Runx2	ENSMUSG00000039153	0.0001945	0.01568575	-1.904864387	26.56547154	RUNX2
Slc26a1	ENSMUSG00000046959	0.000199211	0.015900571	-1.561801487	11.30257131	SLC26A1
Elk4	ENSMUSG00000026436	0.000206469	0.016011688	-1.624547145	950.3110468	ELK4
Ptk6	ENSMUSG00000038751	0.00020723	0.016011688	-1.850532537	10.82785673	PTK6
Spred3	ENSMUSG00000037239	0.000208979	0.016011688	-1.416959185	31.21992833	SPRED3
Hpn	ENSMUSG00000001249	0.000210983	0.016011688	-2.171439542	6.446607001	HPN
Tbc1d8	ENSMUSG00000003134	0.000214106	0.016011688	-1.470253374	39.44898738	TBC1D8
Carns1	ENSMUSG00000075289	0.000219911	0.016294608	-1.41037029	590.4947326	CARNS1
Stard9	ENSMUSG00000033705	0.000237108	0.017219261	-1.822797935	115.7567616	STARD9
Gpr182	ENSMUSG00000058396	0.000242295	0.017422573	-1.713383849	10.58878259	GPR182
Mfsd2b	ENSMUSG00000037336	0.000252729	0.017829658	-2.138048658	14.80263876	MFSD2B
Fgd4	ENSMUSG00000022788	0.000254064	0.017829658	-2.159733108	4.616439369	FGD4
Dchs1	ENSMUSG00000036862	0.000261269	0.018028809	-1.621875815	17.92123837	DCHS1
Cd4	ENSMUSG00000023274	0.000262997	0.018028809	-1.295262339	134.1673578	CD4
Rims3	ENSMUSG00000032890	0.000270585	0.018029762	-1.950090439	22.81460888	RIMS3
Deptor	ENSMUSG00000022419	0.000274332	0.018029762	-1.772251398	10.1358429	DEPTOR
Zc3h6	ENSMUSG00000042851	0.000276376	0.018029762	-1.316978163	340.8142937	ZC3H6
Fbxl20	ENSMUSG00000020883	0.000276461	0.018029762	-1.400047212	822.1908281	FBXL20
Kcna2	ENSMUSG00000040724	0.000279612	0.018029762	-2.672876169	5.873194136	KCNA2
Chadl	ENSMUSG00000063765	0.000285076	0.018067559	-2.330056283	6.658916452	CHADL
Itgad	ENSMUSG00000070369	0.000285107	0.018067559	-1.501323109	137.956606	ITGAD
Pde1b	ENSMUSG00000022489	0.000285922	0.018067559	-1.27673416	390.0942618	PDE1B
Ceacam16	ENSMUSG00000014686	0.00029084	0.018226519	-1.682749383	227.6048411	CEACAM16
Zfp287	ENSMUSG00000005267	0.000296237	0.018255867	-0.965142445	281.7186824	ZNF287
Klf6	ENSMUSG00000000078	0.000298436	0.018255867	-1.821621138	3288.546144	KLF6
Egr2	ENSMUSG00000037868	0.000298907	0.018255867	-1.393708127	703.293856	EGR2
Gpr35	ENSMUSG00000026271	0.000302486	0.01832109	-1.521787015	16.29382022	GPR35
Clec9a	ENSMUSG00000046080	0.000319253	0.019162219	-1.723879784	13.51143487	CLEC9A
Rhob	ENSMUSG00000054364	0.000324982	0.019162219	-1.748356408	1486.356103	RHOB
Cacnb4	ENSMUSG00000017412	0.000325562	0.019162219	-1.041322794	32.76046261	CACNB4
Adam23	ENSMUSG00000025964	0.000330081	0.019350193	-2.224862791	15.68728041	ADAM23
Arl4c	ENSMUSG00000049866	0.000334635	0.019438666	-1.411187557	49.70635225	ARL4C
Npff	ENSMUSG00000023052	0.000336917	0.019438666	-1.286345909	19.73125903	NPFF
Pdzd4	ENSMUSG00000002006	0.000338417	0.019448302	-2.0564967	17.71933299	PDZD4
Tifab	ENSMUSG00000049625	0.000354388	0.02012841	-1.132022255	29.51786383	TIFAB
Dnajb9	ENSMUSG00000014905	0.000361291	0.020326045	-1.139495968	1169.569645	DNAJB9
Lrrc39	ENSMUSG00000027961	0.000364435	0.020326045	-1.545482427	23.0552134	LRRC39
Tnnt3	ENSMUSG00000061723	0.000386286	0.021118403	-0.987352253	43.77323144	TNNT3
Hspg2	ENSMUSG00000028763	0.000402718	0.021691792	-1.679153333	53.47278252	HSPG2
Zfyve9	ENSMUSG00000034557	0.000418847	0.021992476	-1.764697161	11.76562696	ZFYVE9
Nr4a1	ENSMUSG00000023034	0.000431055	0.022312433	-1.673712587	562.962306	NR4A1
Peli2	ENSMUSG00000021846	0.000435928	0.022402604	-2.422663668	3.880881547	PELI2
Erp27	ENSMUSG00000030219	0.000438927	0.022402604	-1.426292137	51.65998631	ERP27
Zscan30	ENSMUSG00000024274	0.000441607	0.022460416	-1.322286164	24.89340076	ZSCAN30
Fos	ENSMUSG00000021250	0.000464525	0.023301257	-2.357949096	13275.11206	FOS
Ccnd1	ENSMUSG00000070348	0.000466927	0.023341567	-1.17070802	31.02358047	CCND1
Ahnak	ENSMUSG00000069833	0.000470683	0.023358764	-2.062416424	1680.173855	AHNAK
Tet2	ENSMUSG00000040943	0.000474655	0.023358764	-1.897938543	284.6863129	TET2
Socs3	ENSMUSG00000053113	0.000482331	0.023456565	-0.778914185	381.5964304	SOCS3
Fam196b	ENSMUSG00000069911	0.000490387	0.023702587	-2.514870474	4.595410993	FAM196B
Zfp369	ENSMUSG00000021514	0.000494442	0.023748617	-1.665629112	159.9610263	ZNF274
Dgkh	ENSMUSG00000034731	0.000497279	0.023799292	-1.547762715	38.8310628	DGKH
Tgm2	ENSMUSG00000037820	0.000512176	0.024153243	-1.448477355	67.85696055	TGM2
Pde8b	ENSMUSG00000021684	0.000517871	0.024153243	-1.570338766	9.885745994	PDE8B
Ttc39b	ENSMUSG00000038172	0.000521879	0.024153243	-1.252097216	1288.028067	TTC39B
Sgpp2	ENSMUSG00000032908	0.000522421	0.024153243	-1.317481065	36.71535726	SGPP2
Usp35	ENSMUSG00000035713	0.000531228	0.024384685	-1.082047744	115.7539621	USP35
Parvb	ENSMUSG00000022438	0.000533758	0.024424045	-1.639534795	16.94850224	PARVB
Gpr152	ENSMUSG00000044724	0.000579798	0.025802775	-1.686187576	7.310734836	GPR152
Pear1	ENSMUSG00000028073	0.000588984	0.025914239	-0.962898932	752.752543	PEAR1
Ube2i	ENSMUSG00000015120	0.000596984	0.025981678	-1.295610489	954.5547059	UBE2I
Tmcc2	ENSMUSG00000042066	0.000598016	0.025981678	-2.279008363	52.12486744	TMCC2
Sez6l2	ENSMUSG00000030683	0.000607528	0.026082627	-1.174744011	45.06918512	SEZ6L2
Rab11fip2	ENSMUSG00000040022	0.000617794	0.026368242	-1.375870651	262.6668625	RAB11FIP2
Dpm1	ENSMUSG00000078919	0.000619853	0.026378988	-1.454695115	116.1047827	DPM1
Mecp2	ENSMUSG00000031393	0.000638248	0.026848711	-1.062638145	1280.061831	MECP2
Acp2	ENSMUSG00000002103	0.000653192	0.027218676	-1.111920414	157.0098306	ACP2
Samd8	ENSMUSG00000021770	0.000682225	0.027894796	-1.162239057	193.3696486	SAMD8
Iqce	ENSMUSG00000036555	0.000699693	0.028292003	-1.013854798	552.3055062	IQCE
Chrna2	ENSMUSG00000022041	0.000724236	0.028853706	-1.880406556	23.03180046	CHRNA2
Braf	ENSMUSG00000002413	0.000732744	0.029064841	-1.645744132	482.0690938	BRAF
Adam22	ENSMUSG00000040537	0.000736352	0.029128807	-1.467519536	21.67314744	ADAM22

Alpk3	ENSMUSG00000038763	0.000738987	0.029154048	-2.047155916	4.816961555	ALPK3
Zc3hav1l	ENSMUSG00000047749	0.000753422	0.029643379	-1.618197185	30.70909319	ZC3HAV1L
Clcn2	ENSMUSG00000022843	0.000763569	0.029877171	-1.191921359	43.40641403	CLCN2
Slc38a6	ENSMUSG00000044712	0.000776559	0.03008192	-1.048071927	142.5907025	SLC38A6
Tbc1d23	ENSMUSG00000022749	0.000777335	0.03008192	-0.999479142	424.229294	TBC1D23
Ptpdc1	ENSMUSG00000038042	0.000790761	0.030329028	-1.484380314	29.03252488	PTPDC1
Tctn1	ENSMUSG00000038593	0.000795347	0.030329028	-0.622094666	294.8930879	TCTN1
Itpripl2	ENSMUSG00000073859	0.000795977	0.030329028	-1.552002946	8.816377642	ITPRIPL2
Jun	ENSMUSG00000052684	0.000802027	0.030329028	-2.160247006	8020.746127	JUN
Metap1d	ENSMUSG00000041921	0.000802449	0.030329028	-0.609973578	606.0931886	METAP1D
Obscn	ENSMUSG00000061462	0.000803165	0.030329028	-2.183798912	24.35334393	OBSCN
Nr4a2	ENSMUSG00000026826	0.000803594	0.030329028	-1.989067864	25.0441257	NR4A2
Axl	ENSMUSG00000002602	0.000817943	0.03052382	-1.530728281	359.039184	AXL
Cln8	ENSMUSG00000026317	0.000819236	0.03052382	-1.34287642	46.28912776	CLN8
Klf7	ENSMUSG00000025959	0.000819712	0.03052382	-1.223255019	260.61713	KLF7
Ccnl1	ENSMUSG00000027829	0.000822814	0.030561357	-1.11646967	4010.711626	CCNL1
Plp1	ENSMUSG00000031425	0.000837012	0.030853205	-1.401889911	55.30656797	PLP1
Vamp2	ENSMUSG00000020894	0.000840388	0.030899599	-1.12310418	1037.633535	VAMP2
Zfyve28	ENSMUSG00000037224	0.0008486	0.031022264	-0.772489103	57.0132211	ZFYVE28
Lcp2	ENSMUSG00000002699	0.000875632	0.031327442	-0.862374515	510.7997865	LCP2
Gabbr1	ENSMUSG00000024462	0.000890466	0.031740688	-1.346141353	680.5141611	GABBR1
Zfp174	ENSMUSG00000054939	0.000898687	0.031840142	-0.967707083	28.98228042	ZNF174
Thbs3	ENSMUSG00000028047	0.000905663	0.032009602	-1.546344617	12.52096958	THBS3
Fgr	ENSMUSG00000028874	0.000912921	0.032188174	-0.614812973	556.771912	FGR
Ptprm	ENSMUSG00000033278	0.000923418	0.03235568	-2.176539279	10.76546163	PTPRM
Ccr2	ENSMUSG00000049103	0.000957734	0.033085629	-1.546823902	12.46833031	CCR2
Adam11	ENSMUSG00000020926	0.000960738	0.033085629	-2.090077764	35.19529734	ADAM11
Hip1	ENSMUSG00000039959	0.000966141	0.033085629	-1.330696206	182.2892978	HIP1
Sox5	ENSMUSG00000041540	0.000974751	0.03318395	-1.330513151	75.21368604	SOX5
Synpo	ENSMUSG00000043079	0.000990985	0.033407396	-1.438892605	15.99326057	SYNPO
Gm608	ENSMUSG00000068284	0.001001189	0.03367364	-1.739947459	1983.226642	KIAA2018
Pou2f1	ENSMUSG00000026565	0.001007623	0.033812121	-1.607513731	939.7315583	POU2F1
1700028K03Rik	ENSMUSG00000089798	0.001010216	0.033821385	-1.971705771	10.69377346	C1orf146
Nfat5	ENSMUSG00000003847	0.001018325	0.033871836	-1.821256847	1631.378438	NFAT5
Carf	ENSMUSG00000026017	0.001021005	0.033871836	-1.32669663	45.79511781	CARF
Gm614	ENSMUSG00000090141	0.001027951	0.034009558	-1.856503549	9.752766971	CXorf65
Gfra2	ENSMUSG00000022103	0.001037691	0.034009558	-1.972942717	30.54222793	GFRA2
Cttnbp2nl	ENSMUSG00000062127	0.001039136	0.034009558	-1.727450521	13.58433501	CTTNBP2NL
Rad9b	ENSMUSG00000038569	0.001045166	0.034076491	-1.12502387	67.51132281	RAD9B
Rab6b	ENSMUSG00000032549	0.001049312	0.034113143	-0.777837523	231.3277775	RAB6B
Mybpc2	ENSMUSG00000038670	0.001068908	0.034524263	-0.787990887	194.7536505	MYBPC2
Atxn1	ENSMUSG00000046876	0.00106988	0.034524263	-1.825378503	76.01911992	ATXN1
Pik3r6	ENSMUSG00000046207	0.001073783	0.034524263	-1.191103345	28.26961953	PIK3R6
Farp2	ENSMUSG00000034066	0.001109036	0.035225629	-0.971150366	75.08956959	FARP2
Itgam	ENSMUSG00000030786	0.00111149	0.035225629	-1.278158644	109.7427865	ITGAM
Fhdc1	ENSMUSG00000041842	0.001112406	0.035225629	-1.992900235	11.75848047	FHDC1
Gpr157	ENSMUSG00000047875	0.001117337	0.035225629	-1.186495937	51.21112294	GPR157
Sema5a	ENSMUSG00000022231	0.00111973	0.035225629	-1.594643342	57.4750412	SEMA5A
Tdo2	ENSMUSG00000028011	0.001138023	0.035647475	-1.479747742	12.53458474	TDO2
Iqgap2	ENSMUSG00000021676	0.001149215	0.035742861	-1.258050011	29.08656655	IQGAP2
Gda	ENSMUSG00000058624	0.001150863	0.035742861	-1.910003382	32.44621308	GDA
Dusp6	ENSMUSG00000019960	0.001155247	0.035802853	-1.191094253	906.6456664	DUSP6
Il1b	ENSMUSG00000027398	0.001169181	0.03615792	-1.89775988	47.08800643	IL1B
Wdfy1	ENSMUSG00000073643	0.001172593	0.036186753	-1.255042649	371.5815498	WDFY1
Itgax	ENSMUSG00000030789	0.001184169	0.036237565	-1.247330309	172.4690963	ITGAX
Zc3h12c	ENSMUSG00000035164	0.001186863	0.036244013	-1.999811212	145.8967019	ZC3H12C
Fut1	ENSMUSG00000008461	0.001196734	0.036359068	-1.215891369	22.88567235	FUT1
Sspn	ENSMUSG00000030255	0.001202941	0.036359068	-1.77726208	143.8983592	SSPN
Agap1	ENSMUSG00000055013	0.001205321	0.036359068	-1.827005908	9.997808786	AGAP1
Slc20a1	ENSMUSG00000027397	0.001205576	0.036359068	-0.99645932	915.8355255	SLC20A1
Cd5l	ENSMUSG00000015854	0.001211302	0.036383132	-1.673802969	305.6733454	CD5L
Slc38a5	ENSMUSG00000031170	0.001211359	0.036383132	-2.451657428	7.827237746	SLC38A5
Tulp2	ENSMUSG00000023467	0.001227043	0.036597733	-1.630866903	65.52661594	TULP2
Cd300ld	ENSMUSG00000034641	0.001228533	0.036597733	-1.633135674	17.06044102	CD300LD
Dse	ENSMUSG00000039497	0.001242309	0.036857689	-1.383628182	43.67319584	DSE
Man1c1	ENSMUSG00000037306	0.001247163	0.036926658	-1.018797877	43.36779018	MAN1C1
Slc38a9	ENSMUSG00000047789	0.001251777	0.036972668	-0.676897822	589.701862	SLC38A9
Armc9	ENSMUSG00000062590	0.001253783	0.036972668	-0.757768677	151.331344	ARMC9
Dgke	ENSMUSG00000000276	0.001281769	0.037565847	-1.04217362	382.7516859	DGKE
Tagln	ENSMUSG00000032085	0.001305948	0.037631548	-0.799451295	64.02575513	TAGLN
Impg2	ENSMUSG00000035270	0.001306141	0.037631548	-1.277898096	62.07141876	IMPG2
Cyp2u1	ENSMUSG00000027983	0.001307063	0.037631548	-1.625322473	10.96789881	CYP2U1
Per1	ENSMUSG00000020893	0.001329551	0.037848569	-1.493817053	1026.104012	PER1
Wdr78	ENSMUSG00000035126	0.001329929	0.037848569	-1.105139407	80.6910908	WDR78
Piwil2	ENSMUSG00000033644	0.00133989	0.037848569	-1.057180547	16.83165035	PIWIL2
Lcor	ENSMUSG00000025019	0.00134053	0.037848569	-1.802566928	257.9653543	LCOR
Fam126b	ENSMUSG00000038174	0.001346831	0.037879955	-1.514600603	207.8671293	FAM126B

Arl9	ENSMUSG00000063820	0.001361604	0.038010233	-2.007697083	3.970194176	ARL9
Mfsd4	ENSMUSG00000059149	0.001403555	0.038772731	-1.937948775	444.739803	MFSD4
Gem	ENSMUSG00000028214	0.001407793	0.038772731	-1.030813296	735.252472	GEM
Nrp1	ENSMUSG00000025810	0.0014233	0.039126003	-1.026079656	41.49195176	NRP1
Loxl3	ENSMUSG00000000693	0.001433139	0.039253589	-1.091331274	15.85034464	LOXL3
Ctnnd1	ENSMUSG00000034101	0.001433319	0.039253589	-1.456561402	48.63625709	CTNND1
Mtx3	ENSMUSG00000021704	0.001440455	0.03932394	-1.555572943	256.3570554	MTX3
Srgap3	ENSMUSG00000030257	0.00144281	0.03932394	-1.287860548	102.5694615	SRGAP3
Ppp1r3f	ENSMUSG00000039556	0.001456575	0.039593351	-0.748642694	101.5104631	PPP1R3F
Specc1	ENSMUSG00000042331	0.001491099	0.04005965	-1.522339041	38.14391744	SPECC1
Pak1	ENSMUSG00000030774	0.001504271	0.040127081	-1.324409193	15.64719258	PAK1
Tlr8	ENSMUSG00000040522	0.001507355	0.040127081	-1.98114572	13.91611408	TLR8
Aoc2	ENSMUSG00000078651	0.001509198	0.040127081	-1.189031157	87.54427606	AOC2
Ifih1	ENSMUSG00000026896	0.001530799	0.040392874	-0.853168096	77.83204665	IFIH1
Col20a1	ENSMUSG00000016356	0.001534908	0.040392874	-1.195109289	35.60469803	COL20A1
Zfand5	ENSMUSG00000024750	0.001550711	0.04063866	-0.587413401	1199.813172	ZFAND5
Dqx1	ENSMUSG00000009145	0.001567283	0.040865398	-0.944582107	96.17668182	DQX1
Impact	ENSMUSG00000024423	0.001582996	0.040897325	-1.262143225	352.4035286	IMPACT
Guf1	ENSMUSG00000029208	0.001612152	0.040959899	-0.785685742	529.2192097	GUF1
Lilra5	ENSMUSG00000070873	0.001616853	0.040959899	-1.856486125	13.04937651	LILRA5
St8sia1	ENSMUSG00000030283	0.001617552	0.040959899	-0.923887131	30.47780576	ST8SIA1
Evi5	ENSMUSG00000011831	0.00161909	0.040959899	-1.35473236	73.63568417	EVI5
Ptpre	ENSMUSG00000041836	0.001629267	0.041008996	-1.022144533	284.6119241	PTPRE
Vcam1	ENSMUSG00000027962	0.001654649	0.04135772	-1.512930989	463.4984908	VCAM1
Afap1	ENSMUSG00000029094	0.001676451	0.041687418	-1.511150161	26.15138084	AFAP1
Kcna3	ENSMUSG00000047959	0.001680231	0.041687418	-1.421594373	270.7066815	KCNA3
B4galnt2	ENSMUSG00000013418	0.001682119	0.041687418	-1.207778662	11.55931098	B4GALNT2
Mical3	ENSMUSG00000003178	0.001690196	0.041816605	-1.076535212	95.4659356	MICAL3
Sh3bp4	ENSMUSG00000036206	0.001719547	0.042185262	-1.680178506	25.78754028	SH3BP4
P2rx7	ENSMUSG00000029468	0.001728037	0.042322411	-1.011597402	43.62655299	P2RX7
Scai	ENSMUSG00000035236	0.001734236	0.042349233	-1.617574656	1233.894058	SCAI
Ubn2	ENSMUSG00000038538	0.001737836	0.042349233	-1.796709477	791.2081954	UBN2
Ino80d	ENSMUSG00000040865	0.001747516	0.042360628	-1.839055403	1154.013149	INO80D
Sox6	ENSMUSG00000051910	0.001749583	0.042360628	-2.37272878	7.592385073	SOX6
Daam2	ENSMUSG00000040260	0.001759771	0.042528781	-1.79754816	5.46460294	DAAM2
Adamdec1	ENSMUSG00000022057	0.001776703	0.042701049	-1.3876336	77.10787512	ADAMDEC1
Cd46	ENSMUSG00000016493	0.001794176	0.043004253	-1.007818003	41.30256018	CD46
Stx17	ENSMUSG00000061455	0.001798121	0.043028149	-1.118731586	435.4264888	STX17
Ppia	ENSMUSG00000071866	0.001813502	0.043134194	-0.83904338	194.8989037	PPIA
Trpm2	ENSMUSG00000009292	0.00182745	0.043192322	-1.699378652	112.6912182	TRPM2
Hipk2	ENSMUSG00000061436	0.001829821	0.043192322	-1.014916571	297.0900864	HIPK2
Slc14a1	ENSMUSG00000059336	0.001835899	0.043192322	-0.678347814	481.6850918	SLC14A1
Yod1	ENSMUSG00000046404	0.00183753	0.043192322	-1.406278097	173.53393	YOD1
Baz2b	ENSMUSG00000026987	0.001846712	0.043243687	-1.409386369	2296.598948	BAZ2B
Phlda1	ENSMUSG00000020205	0.001849472	0.043243687	-1.136949209	94.65351752	PHLDA1
Taok1	ENSMUSG00000017291	0.001856046	0.043243687	-1.602859887	1238.630797	TAOK1
Ccdc38	ENSMUSG00000036168	0.0018582	0.043243687	-1.410899128	32.88986262	CCDC38
Nrip2	ENSMUSG00000001520	0.001860453	0.043243687	-1.800337069	28.44699656	NRIP2
Ankrd23	ENSMUSG00000067653	0.001914453	0.043976315	-0.941425775	160.7948308	ANKRD23
Neb	ENSMUSG00000026950	0.001925784	0.044129772	-1.54919577	17.68960529	NEB
Guca1b	ENSMUSG00000023979	0.001937385	0.04423654	-1.088884026	42.83725195	GUCA1B
Plcb4	ENSMUSG00000039943	0.001941167	0.04423654	-1.375639815	19.44996019	PLCB4
Kctd18	ENSMUSG00000054770	0.001942565	0.04423654	-1.083525904	347.4675541	KCTD18
Kcnip4	ENSMUSG00000029088	0.001960055	0.044339257	-1.772663601	8.05695919	KCNIP4
Ptar1	ENSMUSG00000074925	0.001977223	0.044339257	-1.062707492	123.9886755	PTAR1
Gramd1a	ENSMUSG00000001248	0.001979745	0.044339257	-0.424852529	3045.373649	GRAMD1A
Ttn	ENSMUSG00000051747	0.001980412	0.044339257	-1.667179394	75.16634357	TTN
Phactr2	ENSMUSG00000062866	0.001983526	0.044339257	-1.025550939	27.5924515	PHACTR2
Rad54l2	ENSMUSG00000040661	0.001993949	0.044436148	-1.525655164	416.5510434	RAD54L2
Tsc22d1	ENSMUSG00000022010	0.00205227	0.045320697	-0.987807941	98.18193001	TSC22D1
Ubc	ENSMUSG00000008348	0.00206653	0.045566668	-0.97134897	2816.026898	UBC
Nav1	ENSMUSG00000009418	0.002092325	0.045858368	-1.905821597	18.05060464	NAV1
Myh10	ENSMUSG00000020900	0.002129334	0.046249219	-1.540387918	16.85034676	MYH10
Ache	ENSMUSG00000023328	0.002135986	0.046249219	-1.552066261	25.655598	ACHE
Tsnaxip1	ENSMUSG00000031893	0.002140448	0.046249219	-1.057077659	69.78482173	TSNAXIP1
Nfix	ENSMUSG00000001911	0.002147465	0.046249219	-0.97261198	51.35588561	NFIX
Alkbh1	ENSMUSG00000079036	0.002153497	0.046249219	-1.010881702	51.29066794	ALKBH1
Katnal1	ENSMUSG00000041298	0.002154394	0.046249219	-0.804276845	223.280228	KATNAL1
Bmp8a	ENSMUSG00000032726	0.002166725	0.046426588	-1.004131251	18.41173419	BMP8A
Lats1	ENSMUSG00000040021	0.002174684	0.046426588	-1.376277679	1162.252141	LATS1
Clec4n	ENSMUSG00000023349	0.002183619	0.046426588	-1.386549259	81.89343304	CLEC6A
Efcab5	ENSMUSG00000050944	0.002189126	0.046426588	-1.489437872	9.929930977	EFCAB5
Sparc	ENSMUSG00000018593	0.002192419	0.046426588	-1.975327488	9.129997659	SPARC
Cbl	ENSMUSG00000034342	0.00220791	0.046426588	-1.744766638	782.9917131	CBL
Klhl11	ENSMUSG00000048732	0.002213644	0.046426588	-1.343955816	146.3406721	KLHL11
Enpp4	ENSMUSG00000023961	0.002214191	0.046426588	-1.321217721	22.62334124	ENPP4
Plekhn1	ENSMUSG00000078485	0.00221426	0.046426588	-1.136355252	138.9971781	PLEKHN1

Ppp1r32	ENSMUSG00000035179	0.00221962	0.046426588	-1.523298784	9.419578344	PPP1R32
Mtss1l	ENSMUSG00000033763	0.002221923	0.046426588	-1.174775994	14.1449068	MTSS1L
Galnt3	ENSMUSG00000026994	0.002236168	0.046426588	-1.762087884	18.76526829	GALNT3
Il9r	ENSMUSG00000020279	0.002236372	0.046426588	-0.97765408	3809.992506	IL9R
Tbc1d2b	ENSMUSG00000037410	0.002267764	0.046696408	-0.999270003	85.55462826	TBC1D2B
Trip11	ENSMUSG00000021188	0.0022702	0.046696408	-1.535176925	800.9216782	TRIP11
Tmem86b	ENSMUSG00000045282	0.002286901	0.046884685	-1.047217658	63.04238682	TMEM86B
Syne1	ENSMUSG00000019769	0.0023038	0.047058371	-1.877779368	3279.656252	SYNE1
Gp1ba	ENSMUSG00000050675	0.002311492	0.047058371	-1.356583323	31.53577933	GP1BA
Pfkfb2	ENSMUSG00000026409	0.002322318	0.047212926	-1.497045407	294.8531523	PFKFB2
Cbx7	ENSMUSG00000053411	0.002328259	0.047267858	-0.715779175	3459.102659	CBX7
AI607873	ENSMUSG00000073490	0.00234156	0.047429523	-1.296738804	35.49601509	IFI16
Map3k12	ENSMUSG00000023050	0.002355717	0.047429523	-0.829678314	102.446822	MAP3K12
Zbtb20	ENSMUSG00000022708	0.002379116	0.04770324	-1.820714241	2455.246872	ZBTB20
Dennd2a	ENSMUSG00000038456	0.0024103	0.048185748	-1.350111632	15.06832752	DENND2A
Cd300e	ENSMUSG00000048498	0.002414153	0.048185748	-1.729362091	29.660255	CD300E
Mycbp2	ENSMUSG00000033004	0.002439526	0.048361253	-1.568007187	5286.770923	MYCBP2
Tnrc6b	ENSMUSG00000047888	0.002447265	0.048361253	-1.560737971	1599.751295	TNRC6B
Shank1	ENSMUSG00000038738	0.002448377	0.048361253	-1.643087277	209.4328718	SHANK1
Sntb2	ENSMUSG00000041308	0.002486274	0.048911235	-1.090574093	73.33470884	SNTB2
Dbndd2	ENSMUSG00000017734	0.002535013	0.049135724	-1.73560582	4.677556244	DBNDD2
Cd300lf	ENSMUSG00000047798	0.002553957	0.049144066	-1.322632383	273.8252648	CD300LF
Crb2	ENSMUSG00000035403	0.002555343	0.049144066	-0.947061108	29.09071441	CRB2
Krba1	ENSMUSG00000042810	0.002567868	0.049255149	-0.83320778	579.0831227	KRBA1
Kel	ENSMUSG00000029866	0.002579825	0.049307603	-2.261612038	11.44607619	KEL
Orai2	ENSMUSG00000039747	0.002580736	0.049307603	-0.822809874	729.947539	ORAI2
Rsad2	ENSMUSG00000020641	0.002600861	0.049562356	-1.537633979	50.73956779	RSAD2
Rpl9	ENSMUSG00000047215	0.002641511	0.050271371	-0.858074342	387.871764	RPL9
Map3k8	ENSMUSG00000024235	0.002670136	0.050679991	-0.975127519	333.0591158	MAP3K8
Ccdc15	ENSMUSG00000034303	0.002675095	0.050679991	-1.302502076	98.21644668	CCDC15
Leng8	ENSMUSG00000035545	0.002699137	0.050964335	-1.467377723	2103.885735	LENG8
Mdn1	ENSMUSG00000058006	0.002712939	0.050964335	-1.7505979	1735.486177	MDN1
Dclre1b	ENSMUSG00000027845	0.002724063	0.050964335	-0.57992325	219.655892	DCLRE1B
Sowaha	ENSMUSG00000044352	0.002733984	0.050964335	-2.238144676	3.917222135	SOWAHA
2410089E03Rik	ENSMUSG00000039801	0.002769457	0.051366919	-1.348311345	390.3736865	C5orf42
Rasgrf1	ENSMUSG00000032356	0.002787622	0.051507493	-2.052113626	4.694585864	RASGRF1
Sh2d4b	ENSMUSG00000037833	0.002802791	0.051670273	-1.537446362	9.694337764	SH2D4B
Zfp398	ENSMUSG00000062519	0.002803511	0.051670273	-0.915779997	299.5144412	ZNF398
Col27a1	ENSMUSG00000045672	0.0028163	0.051783881	-1.845653573	81.36372086	COL27A1
Myo5a	ENSMUSG00000034593	0.002822162	0.051792157	-1.396819539	2909.691163	MYO5A
Abl2	ENSMUSG00000026596	0.002838045	0.051848492	-1.628702314	1225.082798	ABL2
Krt80	ENSMUSG00000037185	0.002841812	0.051852421	-1.746138151	6.231696218	KRT80
Tnn	ENSMUSG00000026725	0.002875676	0.052209263	-1.959886816	5.971039031	TNN
Thbs1	ENSMUSG00000040152	0.002887544	0.052294633	-1.298747578	8.562818138	THBS1
1700094D03Rik	ENSMUSG00000078667	0.002929464	0.052651874	-0.732196825	209.5151333	C1orf189
Ash1l	ENSMUSG00000028053	0.002932519	0.052651874	-1.754682273	1970.209966	ASH1L
Tmc4	ENSMUSG00000019734	0.002960344	0.052858346	-1.004546281	54.44834478	TMC4
Hp	ENSMUSG00000031722	0.002960995	0.052858346	-1.83794817	8.653475049	HP
Nav2	ENSMUSG00000052512	0.002963538	0.052858346	-1.782120759	107.5243491	NAV2
Catsperg1	ENSMUSG00000049676	0.002968173	0.052858346	-1.508112659	12.13922305	CATSPERG
Sec61a2	ENSMUSG00000025816	0.002969651	0.052858346	-0.877853229	93.98347743	SEC61A2
Prdm9	ENSMUSG00000051977	0.002972988	0.052858346	-1.429579504	115.538749	PRDM9
Cd300a	ENSMUSG00000034652	0.002998384	0.053245034	-1.403402141	77.70668999	CD300A
Slc25a37	ENSMUSG00000034248	0.003008499	0.053294975	-1.134730368	1650.989541	SLC25A37
Tnfaip2	ENSMUSG00000021281	0.003039429	0.053612831	-1.775717837	45.89237934	TNFAIP2
Chd2	ENSMUSG00000078671	0.003041133	0.053612831	-1.591895817	2542.436522	CHD2
Ikzf2	ENSMUSG00000025997	0.003048044	0.053669846	-1.404534203	24.58346807	IKZF2
Fam43a	ENSMUSG00000046546	0.003078616	0.053934152	-1.417878054	907.7240983	FAM43A
Akap7	ENSMUSG00000039166	0.00309197	0.053934152	-0.655605359	145.4381737	AKAP7
Bhlhe40	ENSMUSG00000030103	0.003129818	0.05432337	-1.04247025	667.5769426	BHLHE40
Stac3	ENSMUSG00000040287	0.003133567	0.054323852	-1.266363504	20.95984489	STAC3
Dact1	ENSMUSG00000044548	0.003185813	0.054870363	-1.342059338	11.41799361	DACT1
Fyb	ENSMUSG00000022148	0.003191156	0.054870363	-1.610030752	122.6887965	FYB
Avil	ENSMUSG00000025432	0.003214187	0.054947866	-1.255659772	16.17126052	AVIL
Kcnd1	ENSMUSG00000009731	0.003247193	0.055250963	-1.599185958	6.01168036	KCND1
Csf3r	ENSMUSG00000028859	0.003255178	0.055250963	-1.642389834	33.57414213	CSF3R
Rmnd1	ENSMUSG00000019763	0.003321531	0.056009456	-0.48995226	276.3258512	RMND1
Setd1a	ENSMUSG00000042308	0.003327595	0.056009456	-1.041558973	418.5694017	SETD1A
Gan	ENSMUSG00000052557	0.003330562	0.056009456	-1.473204946	43.50547852	GAN
Zc3h12b	ENSMUSG00000035045	0.003337328	0.056058662	-1.896993441	7.052766727	ZC3H12B
Zbtb34	ENSMUSG00000068966	0.00334372	0.056101467	-1.427308398	133.0693166	ZBTB34
Cdh1	ENSMUSG00000000303	0.003348595	0.056118755	-1.881882209	7.820055577	CDH1
Ypel4	ENSMUSG00000034059	0.003358768	0.05612327	-2.11772407	7.526145089	YPEL4
Tubb4a	ENSMUSG00000062591	0.003361102	0.05612327	-0.786324181	49.46057703	TUBB4A
Ffar3	ENSMUSG00000019429	0.003375778	0.05612327	-1.202308212	17.75717605	FFAR3
B3gntl1	ENSMUSG00000046605	0.003386681	0.056162854	-0.771750202	178.7966126	B3GNTL1
Syngap1	ENSMUSG00000067629	0.003410452	0.056288681	-1.215855871	13.03974214	SYNGAP1

Nsd1	ENSMUSG00000021488	0.003413082	0.056288681	-1.375376804	2148.679253	NSD1
Brwd1	ENSMUSG00000022914	0.003416577	0.056288681	-1.336369197	2984.392424	BRWD1
Abcc10	ENSMUSG00000032842	0.003447156	0.056728455	-0.92578508	166.5399318	ABCC10
Sgk1	ENSMUSG00000019970	0.003472636	0.056928135	-1.217964374	242.1021591	SGK1
Sept8	ENSMUSG00000018398	0.003473557	0.056928135	-1.662776306	15.29154322	SEPT8
Il18rap	ENSMUSG00000026068	0.003478685	0.056928135	-1.294182699	18.67261236	IL18RAP
Pak6	ENSMUSG00000074923	0.003484399	0.056928135	-1.38425969	28.95921849	PAK6
Cxcr2	ENSMUSG00000026180	0.003496867	0.056928135	-1.643901634	6.206052059	CXCR2
Arrb1	ENSMUSG00000018909	0.00349829	0.056928135	-1.261598395	460.854442	ARRB1
Golgb1	ENSMUSG00000034243	0.003536364	0.057322531	-1.586091342	1426.180884	GOLGB1
Znrf3	ENSMUSG00000041961	0.003552849	0.057358555	-1.289816816	115.5558828	ZNRF3
Herc1	ENSMUSG00000038664	0.003553369	0.057358555	-1.600993273	2288.188266	HERC1
Rfx3	ENSMUSG00000040929	0.00364492	0.05799888	-1.44710635	277.553011	RFX3
Kcnc3	ENSMUSG00000062785	0.003666679	0.05799888	-1.108328538	54.16139083	KCNC3
Card9	ENSMUSG00000026928	0.003673456	0.05799888	-1.389264569	8.917365199	CARD9
Srcap	ENSMUSG00000090663	0.003676912	0.05799888	-1.153580425	748.3731953	SRCAP
Nova1	ENSMUSG00000021047	0.003680797	0.05799888	-1.007380636	59.97185208	NOVA1
Nid2	ENSMUSG00000021806	0.00369383	0.05799888	-1.610131061	4.342383157	NID2
Coro2b	ENSMUSG00000041729	0.003696141	0.05799888	-0.936981347	219.8276205	CORO2B
Ccdc88c	ENSMUSG00000021182	0.003699182	0.05799888	-1.40760636	2689.728726	CCDC88C
Rnasel	ENSMUSG00000066800	0.003716039	0.058030887	-1.222592056	150.2687524	RNASEL
Maml3	ENSMUSG00000061143	0.003767585	0.058640834	-1.36668595	50.91665869	MAML3
Rnf170	ENSMUSG00000013878	0.003769616	0.058640834	-0.820828806	111.3265901	RNF170
Pigm	ENSMUSG00000050229	0.003819737	0.058964109	-1.080536143	886.5961741	PIGM
Srcap	ENSMUSG00000053877	0.003827437	0.058964109	-1.52836921	708.9162389	SRCAP
Dennd1c	ENSMUSG00000002668	0.003846367	0.058964109	-0.471981213	1600.046754	DENND1C
Hebp1	ENSMUSG00000042770	0.003846644	0.058964109	-1.488000117	56.87657606	HEBP1
Tnfsf15	ENSMUSG00000050395	0.003858959	0.059045314	-1.441145642	7.753118656	TNFSF15
Abca1	ENSMUSG00000015243	0.003867151	0.059083883	-1.52438333	1690.872149	ABCA1
Arih2	ENSMUSG00000064145	0.003869712	0.059083883	-0.563328206	727.5401647	ARIH2
Wfikkn1	ENSMUSG00000071192	0.003885635	0.059083883	-1.257147849	12.30750834	WFIKKN1
Slc45a3	ENSMUSG00000026435	0.003888102	0.059083883	-1.434128841	17.82713476	SLC45A3
Trip6	ENSMUSG00000023348	0.003894598	0.059095054	-0.966567622	56.87380867	TRIP6
Dstyk	ENSMUSG00000042046	0.003906042	0.059185894	-1.553150494	129.1257716	DSTYK
Arhgap39	ENSMUSG00000033697	0.00392035	0.059185894	-0.928186181	161.7130493	ARHGAP39
Bmp2k	ENSMUSG00000034663	0.003927368	0.059185894	-1.120089834	2711.929603	BMP2K
Cep250	ENSMUSG00000038241	0.003934201	0.059185894	-1.460020135	1147.850975	CEP250
Far2	ENSMUSG00000030303	0.00397624	0.059346804	-1.622020245	48.45500845	FAR2
Sowahc	ENSMUSG00000071286	0.003990287	0.059392796	-1.093748254	268.1302328	SOWAHC
Spata1	ENSMUSG00000028188	0.003997948	0.059392796	-0.860112342	58.1100795	SPATA1
Arhgap29	ENSMUSG00000039831	0.00400681	0.059438427	-1.570536108	19.1194466	ARHGAP29
Mxd1	ENSMUSG00000001156	0.004018874	0.059515288	-0.856241302	320.1744354	MXD1
Aasdh	ENSMUSG00000055923	0.004028825	0.059539384	-0.759002725	331.7909899	AASDH
Tmem8b	ENSMUSG00000078716	0.004029932	0.059539384	-0.995315434	23.33478386	TMEM8B
Mdm4	ENSMUSG00000054387	0.004063883	0.059841595	-1.596188925	1628.120635	MDM4
Myo1h	ENSMUSG00000066952	0.004086459	0.059841595	-1.177975603	48.93474814	MYO1H
Mapk8ip3	ENSMUSG00000024163	0.004103724	0.059841595	-1.170440197	1821.199673	MAPK8IP3
Zbtb46	ENSMUSG00000027583	0.004124179	0.059841595	-1.126693849	33.20585388	ZBTB46
Szt2	ENSMUSG00000033253	0.004138726	0.059993027	-1.12068361	1435.76862	SZT2
Arhgap33	ENSMUSG00000036882	0.004205858	0.060304885	-1.015205327	132.308769	ARHGAP33
Adora3	ENSMUSG00000000562	0.00425102	0.060680686	-1.725183182	4.984216455	ADORA3
Tor1aip2	ENSMUSG00000050565	0.004283291	0.060938789	-1.338929927	560.3701064	TOR1AIP2
Etv6	ENSMUSG00000030199	0.004318738	0.061026738	-0.818437178	629.1260978	ETV6
Cpeb4	ENSMUSG00000020300	0.004334407	0.061070791	-1.467384446	502.19185	CPEB4
1810046K07Rik	ENSMUSG00000036027	0.004342074	0.061092939	-1.60859306	24.11001019	C11orf53
Phc3	ENSMUSG00000037652	0.00439176	0.061308249	-1.556736277	1067.209404	PHC3
Slco2a1	ENSMUSG00000032548	0.004433474	0.06162591	-1.054883975	71.23045085	SLCO2A1
Plekhm3	ENSMUSG00000051344	0.004439294	0.06162591	-1.255686597	1386.353413	PLEKHM3
4833420G17Rik	ENSMUSG00000062822	0.004468578	0.06171035	-0.536805313	1272.52028	C5orf34
Igfbp7	ENSMUSG00000036256	0.004485698	0.061728754	-1.739114272	11.93676987	IGFBP7
Ffar1	ENSMUSG00000044453	0.004486827	0.061728754	-1.423557065	294.0493983	FFAR1
Fbxo24	ENSMUSG00000089984	0.004535313	0.06191093	-1.163643833	15.0020521	FBXO24
Papss2	ENSMUSG00000024899	0.00453824	0.06191093	-1.517502056	8.874841112	PAPSS2
Pkd1l3	ENSMUSG00000048827	0.004546556	0.061966459	-1.21493691	38.22903908	PKD1L3
Hemgn	ENSMUSG00000028332	0.004579932	0.062117596	-1.325076701	182.0621619	HEMGN
Wwc2	ENSMUSG00000031563	0.004601686	0.062117596	-1.45414707	22.74419776	WWC2
Rnd3	ENSMUSG00000017144	0.004616673	0.062117596	-1.233769836	12.48476459	RND3
Snai1	ENSMUSG00000042821	0.004633021	0.062117596	-1.105681494	12.17247913	SNAI1
Sdc3	ENSMUSG00000025743	0.004667927	0.062340096	-1.293709622	349.3145776	SDC3
Ptprf	ENSMUSG00000033295	0.004715146	0.062573088	-2.05447342	9.076929938	PTPRF
Myo10	ENSMUSG00000022272	0.004716172	0.062573088	-1.168366523	63.26967784	MYO10
Tep1	ENSMUSG00000006281	0.004787927	0.063161972	-0.95245391	981.7871334	TEP1
Zfp112	ENSMUSG00000052675	0.004829136	0.063163419	-1.041550117	19.37446062	ZNF112
Zmym3	ENSMUSG00000031310	0.004843402	0.063194562	-0.541459127	745.7185446	ZMYM3
Csrnp1	ENSMUSG00000032515	0.004844469	0.063194562	-0.636381524	2137.416521	CSRNP1
Rnf213	ENSMUSG00000070327	0.004854846	0.063273376	-1.534003425	3460.74652	RNF213
Pik3c2b	ENSMUSG00000026447	0.004872695	0.063400617	-1.281902831	3027.686018	PIK3C2B

AW554918	ENSMUSG00000033632	0.004923976	0.063400617	-0.665426781	264.6898486	KIAA1328
Junb	ENSMUSG00000052837	0.004964373	0.063400617	-1.077389476	5217.437044	JUNB
Mgat4a	ENSMUSG00000026110	0.004972945	0.063400617	-1.18800224	987.5953597	MGAT4A
Cd302	ENSMUSG00000060703	0.004975971	0.063400617	-1.188706479	38.06684966	CD302
Tmcc3	ENSMUSG00000020023	0.004979606	0.063400617	-1.258450169	151.4550485	TMCC3
Kcng1	ENSMUSG00000074575	0.004989246	0.063400617	-1.206992014	51.83194036	KCNG1
Mtcp1	ENSMUSG00000031200	0.004997812	0.063400617	-1.27792211	138.7569717	CMC4
Amigo3	ENSMUSG00000032593	0.005013296	0.063400617	-1.231008729	98.18197283	AMIGO3
Map3k9	ENSMUSG00000042724	0.00502935	0.063400617	-1.29755695	800.0182799	MAP3K9
Insr	ENSMUSG00000005534	0.005031478	0.063400617	-1.401230214	410.6007626	INSR
Hfe	ENSMUSG00000006611	0.005034001	0.063400617	-1.420298017	41.01244102	HFE
Tnfaip3	ENSMUSG00000019850	0.005048695	0.063476148	-1.293504858	1834.228509	TNFAIP3
Tmem170b	ENSMUSG00000087370	0.005100505	0.06396329	-1.242339415	281.2235186	TMEM170B
St6galnac2	ENSMUSG00000057286	0.005162675	0.064301438	-1.296597821	13.47907473	ST6GALNAC2
Adamtsl4	ENSMUSG00000015850	0.00518308	0.064301438	-1.039438821	106.148533	ADAMTSL4
Plxnb3	ENSMUSG00000031385	0.005185852	0.064301438	-1.383598251	11.54105353	PLXNB3
1700029J07Rik	ENSMUSG00000071103	0.005189223	0.064301438	-1.006833881	124.0464484	C4orf47
Ghrl	ENSMUSG00000064177	0.005282908	0.064484775	-1.945347672	6.752720904	GHRL
Zfp831	ENSMUSG00000050600	0.005322418	0.064745525	-1.442124786	738.7168355	ZNF831
Ankrd11	ENSMUSG00000035569	0.005327079	0.064745525	-1.481449147	3727.235855	ANKRD11
Ikbke	ENSMUSG00000042349	0.005392208	0.065103445	-0.804442999	270.451603	IKBKE
Hspa1a	ENSMUSG00000091971	0.00540187	0.065107898	-2.01272039	1638.470421	HSPA1B
Hspa1a	ENSMUSG00000091971	0.00540187	0.065107898	-2.01272039	1638.470421	HSPA1A
Smg1	ENSMUSG00000030655	0.005414353	0.065107898	-1.620661319	5537.654304	SMG1
Paqr9	ENSMUSG00000064225	0.005415298	0.065107898	-1.43889666	11.23505493	PAQR9
Huwe1	ENSMUSG00000025261	0.005430988	0.065158666	-1.474874189	6709.960857	HUWE1
Atp8b4	ENSMUSG00000060131	0.005432493	0.065158666	-1.153326875	29.11909392	ATP8B4
Trim7	ENSMUSG00000040350	0.005460034	0.065221046	-0.749729901	2125.564446	TRIM7
Iffo1	ENSMUSG00000038271	0.005469791	0.065284165	-0.723614942	782.5437224	IFFO1
Lrrc16b	ENSMUSG00000022211	0.005517392	0.065322115	-0.916604133	48.51566458	LRRC16B
Zfp113	ENSMUSG00000037007	0.005517721	0.065322115	-1.073910455	182.7190222	ZNF3
Slc4a8	ENSMUSG00000023032	0.005534959	0.065394022	-1.021457519	698.6968473	SLC4A8
Kcnb1	ENSMUSG00000050556	0.005542382	0.065401897	-0.987740681	109.5872635	KCNB1
Wdr13	ENSMUSG00000031166	0.005596886	0.065779187	-1.161926916	368.6716062	WDR13
Mob1b	ENSMUSG00000006262	0.005616374	0.065955123	-0.977642742	507.2650533	MOB1B
Zcchc7	ENSMUSG00000035649	0.005624965	0.065991755	-1.033788412	1941.581156	ZCCHC7
Col7a1	ENSMUSG00000025650	0.005628536	0.065991755	-1.147532895	27.14193201	COL7A1
Mybpc3	ENSMUSG00000002100	0.005654101	0.066079188	-1.16002188	11.44074656	MYBPC3
Zzef1	ENSMUSG00000055670	0.005690898	0.066188857	-1.275593674	1810.175411	ZZEF1
Isl1	ENSMUSG00000042258	0.005724826	0.066188857	-1.037685718	45.06655869	ISL1
Slc9a9	ENSMUSG00000031129	0.005757394	0.066188857	-0.832841552	71.06300195	SLC9A9
Klf11	ENSMUSG00000020653	0.005771183	0.066188857	-1.355579779	165.3404477	KLF11
Ccl3	ENSMUSG00000000982	0.005780896	0.066188857	-1.443307871	25.28154734	CCL3L3
Fat1	ENSMUSG00000070047	0.005782589	0.066188857	-1.967272625	6.060135749	FAT1
Lrch4	ENSMUSG00000029720	0.005809925	0.066188857	-1.075722367	65.25377889	LRCH4
Herc2	ENSMUSG00000030451	0.005815333	0.066188857	-1.532534847	2148.837442	HERC2
Palm3	ENSMUSG00000047986	0.005820557	0.066188857	-1.191443456	19.84764565	PALM3
Dsel	ENSMUSG00000038702	0.005831258	0.066188857	-0.98287202	15.73048342	DSEL
Med1	ENSMUSG00000018160	0.005848133	0.06627733	-1.105994554	1269.517001	MED1
Rnf150	ENSMUSG00000047747	0.005902488	0.0665206	-1.54731947	4.722111847	RNF150
Ccnj	ENSMUSG00000025010	0.005906056	0.0665206	-1.151212748	200.6602739	CCNJ
Dbndd1	ENSMUSG00000031970	0.005929244	0.066627542	-1.670026792	8.639444548	DBNDD1
Plxdc1	ENSMUSG00000017417	0.005952523	0.066628684	-1.234409063	12.45504943	PLXDC1
Ppm1k	ENSMUSG00000037826	0.005953266	0.066628684	-1.286787958	503.49303	PPM1K
Hsd3b7	ENSMUSG00000042289	0.005963327	0.066628684	-0.66988067	47.16164	HSD3B7
Rxra	ENSMUSG00000015846	0.006014065	0.066693009	-1.275539069	62.88204094	RXRA
Snapc4	ENSMUSG00000036281	0.006027291	0.066693009	-0.977672401	567.576063	SNAPC4
Eng	ENSMUSG00000026814	0.00604389	0.066693009	-1.507521038	9.067408936	ENG
Mafg	ENSMUSG00000051510	0.006059564	0.066693009	-0.987908116	354.4876684	MAFG
Aak1	ENSMUSG00000057230	0.006125685	0.067058591	-1.28357627	209.4298147	AAK1
Hdgfrp3	ENSMUSG00000025104	0.006130934	0.067058591	-1.617522948	35.61538229	HDGFRP3
Ppl	ENSMUSG00000039457	0.006132988	0.067058591	-1.420542331	105.313222	PPL
F8	ENSMUSG00000031196	0.006140491	0.067064609	-0.949792321	28.91801433	F8
Sfxn5	ENSMUSG00000033720	0.006174661	0.067162096	-0.664024562	121.0857564	SFXN5
Zfp329	ENSMUSG00000057894	0.006205406	0.067267616	-1.098171615	350.5182412	ZNF329
Fan1	ENSMUSG00000033458	0.006207404	0.067267616	-1.28583474	73.11320238	FAN1
Slc38a9	ENSMUSG00000069056	0.006217953	0.067282035	-1.317676608	79.57055357	SLC38A9
Setbp1	ENSMUSG00000024548	0.006263451	0.067508043	-1.467343435	923.3840662	SETBP1
Fry	ENSMUSG00000056602	0.006273479	0.067508043	-1.438069053	454.1576082	FRY
Lrp5	ENSMUSG00000024913	0.006281916	0.067508043	-1.200802026	20.17448104	LRP5
Ampd3	ENSMUSG00000005686	0.006285088	0.067508043	-1.177240612	101.6812504	AMPD3
Heatr5b	ENSMUSG00000073113	0.006299001	0.067607739	-1.000644902	21.57806596	HEATR5B
Rbbp6	ENSMUSG00000030779	0.006352633	0.067912648	-1.111321921	2263.888205	RBBP6
Mfsd9	ENSMUSG00000041945	0.006376618	0.068040562	-1.268604805	11.31954383	MFSD9
Megf8	ENSMUSG00000045039	0.006424186	0.068296032	-1.535851825	17.50301396	MEGF8
Ccr3	ENSMUSG00000035448	0.006454714	0.068402961	-1.338024426	54.02627742	CCR3
Rbm15	ENSMUSG00000048109	0.006487665	0.068547606	-1.007967982	676.3291177	RBM15

Rab3il1	ENSMUSG00000024663	0.006500087	0.068547606	-1.417229715	36.77181948	RAB3IL1
Cep97	ENSMUSG00000022604	0.006571376	0.068860286	-0.799332426	327.8690795	CEP97
Sned1	ENSMUSG00000047793	0.006588593	0.068891979	-1.500202894	10.86745422	SNED1
Ephb2	ENSMUSG00000028664	0.006634926	0.068891979	-1.289117984	84.99084886	EPHB2
Capn3	ENSMUSG00000079110	0.006644226	0.068891979	-1.107875414	22.61978555	CAPN3
Prkdc	ENSMUSG00000022672	0.006676123	0.06891893	-1.322132873	932.1180528	PRKDC
Dcaf10	ENSMUSG00000035572	0.006684921	0.068960984	-0.58808453	444.4298506	DCAF10
Igsf6	ENSMUSG00000035004	0.006744162	0.06909071	-1.282504898	54.58029474	IGSF6
Dnmt3a	ENSMUSG00000020661	0.006794	0.069153049	-0.997039468	510.6695913	DNMT3A
Rapgef4	ENSMUSG00000049044	0.006797874	0.069153049	-0.776932861	325.4108559	RAPGEF4
Prkab2	ENSMUSG00000038205	0.006802918	0.069153049	-1.197868527	188.1813361	PRKAB2
Nfic	ENSMUSG00000055053	0.006819277	0.069221825	-0.96858722	255.2294523	NFIC
Pou6f1	ENSMUSG00000009739	0.006861902	0.069439372	-1.068296249	871.4861743	POU6F1
Dopey2	ENSMUSG00000022946	0.006887921	0.069464463	-1.061419275	373.3857369	DOPEY2
Pcf11	ENSMUSG00000041328	0.006917224	0.069484715	-1.222381213	1799.227623	PCF11
Trim36	ENSMUSG00000033949	0.006921338	0.069484715	-1.252366973	72.35444993	TRIM36
Klhdc10	ENSMUSG00000029775	0.006994734	0.069932964	-0.665516207	379.1279401	KLHDC10
Clcn1	ENSMUSG00000029862	0.007005496	0.069944749	-1.570622082	4.617537397	CLCN1
Ric8b	ENSMUSG00000035620	0.007029323	0.070065212	-0.631125899	295.3321598	RIC8B
Siglece	ENSMUSG00000030474	0.007046835	0.070108842	-1.470618851	41.54527022	SIGLEC9
Zfand1	ENSMUSG00000039795	0.007094405	0.070113266	-0.637343811	164.3488286	ZFAND1
Adam8	ENSMUSG00000025473	0.007099643	0.07011738	-1.036707183	24.71823835	ADAM8
Bod1l	ENSMUSG00000061755	0.007106209	0.070134776	-1.543825167	1261.686746	BOD1L1
8030462N17Rik	ENSMUSG00000047466	0.007145753	0.070287439	-0.922145578	338.3174376	C18orf25
Gtpbp2	ENSMUSG00000023952	0.007159196	0.070309167	-0.772834724	1803.078417	GTPBP2
Lair1	ENSMUSG00000055541	0.007249811	0.070348737	-1.037738249	105.3515399	LAIR1
P2rx1	ENSMUSG00000020787	0.007254594	0.070348737	-1.254284652	12.15216666	P2RX1
C4a	ENSMUSG00000015451	0.007287478	0.070348737	-1.01503145	16.26541338	C4B
C4a	ENSMUSG00000015451	0.007287478	0.070348737	-1.01503145	16.26541338	C4A
Hoxb4	ENSMUSG00000038692	0.007287846	0.070348737	-1.209095074	14.45189147	HOXB4
Gas7	ENSMUSG00000033066	0.007392635	0.070621924	-1.009367658	81.37762259	GAS7
Brca2	ENSMUSG00000041147	0.007484544	0.070998401	-1.191456499	238.2777251	BRCA2
Nbeal2	ENSMUSG00000056724	0.007531899	0.071206686	-1.126827729	808.7592777	NBEAL2
Kif19a	ENSMUSG00000010021	0.007622393	0.071736989	-0.734737348	91.5843586	KIF19
Ica1l	ENSMUSG00000026018	0.007690092	0.071775223	-1.443336665	7.367650444	ICA1L
Ttc23	ENSMUSG00000030555	0.007702962	0.071775223	-0.812200801	21.91071957	TTC23
Atxn7l1	ENSMUSG00000020564	0.007705129	0.071775223	-0.824102575	989.933163	ATXN7L1
Cul9	ENSMUSG00000040327	0.007788677	0.072118409	-0.864679679	308.5469277	CUL9
Plec	ENSMUSG00000022565	0.007804307	0.072165478	-1.54174215	1574.721059	PLEC
Kcnj16	ENSMUSG00000051497	0.007835819	0.072220199	-1.511399235	17.29287385	KCNJ16
Slc3a1	ENSMUSG00000024131	0.007848542	0.072220199	-1.383078768	7.33339704	SLC3A1
Eif4ebp3	ENSMUSG00000090264	0.007885379	0.072283221	-1.776557782	5.771300248	EIF4EBP3
Mks1	ENSMUSG00000034121	0.007891176	0.072283221	-0.550475874	233.977386	MKS1
Fblim1	ENSMUSG00000006219	0.007933775	0.072341363	-0.81082868	29.76432556	FBLIM1
Itga4	ENSMUSG00000027009	0.007967186	0.072341363	-1.413970532	1931.831585	ITGA4
Ikbkb	ENSMUSG00000031537	0.007968547	0.072341363	-0.89207925	2706.709153	IKBKB
Rc3h2	ENSMUSG00000075376	0.008032308	0.072378521	-1.364570284	932.1174907	RC3H2
Haus5	ENSMUSG00000078762	0.008062662	0.072438104	-0.283835278	679.5890562	HAUS5
Ptpn23	ENSMUSG00000036057	0.008064117	0.072438104	-0.994782459	739.6890278	PTPN23
Myl9	ENSMUSG00000067818	0.008082098	0.072510375	-1.549232468	5.941545471	MYL9
Glcci1	ENSMUSG00000029638	0.00810744	0.072555875	-1.6279329	50.39073291	GLCCI1
Kifc2	ENSMUSG00000004187	0.008121568	0.072596773	-0.774165418	71.08273593	KIFC2
Synj1	ENSMUSG00000022973	0.008164294	0.072836589	-1.161059001	317.353507	SYNJ1
Nlrc4	ENSMUSG00000039193	0.008185729	0.072836589	-0.735662725	598.0362046	NLRC4
Itpr1	ENSMUSG00000030102	0.008211332	0.072836589	-1.433819177	1622.512534	ITPR1
Pgap1	ENSMUSG00000073678	0.008212343	0.072836589	-1.295297968	243.338791	PGAP1
Ttc28	ENSMUSG00000033209	0.008245609	0.072969953	-1.297327488	106.70871	TTC28
Map4k2	ENSMUSG00000024948	0.00827772	0.072969953	-0.78559624	5121.273547	MAP4K2
Slc9a8	ENSMUSG00000039463	0.008297202	0.073048404	-0.652089377	1216.717822	SLC9A8
Map3k2	ENSMUSG00000024383	0.008348944	0.073238905	-1.350346656	682.1872842	MAP3K2
Tnfrsf19	ENSMUSG00000060548	0.008421582	0.073566153	-1.41626026	8.20855857	TNFRSF19
Plxna1	ENSMUSG00000030084	0.008431607	0.073566153	-1.2286356	94.76484065	PLXNA1
Wipi2	ENSMUSG00000029578	0.008456703	0.073653039	-0.487224804	1735.024181	WIPI2
Tcte1	ENSMUSG00000023949	0.008632849	0.074454297	-1.202709829	18.31170416	TCTE1
Tnik	ENSMUSG00000027692	0.008652909	0.074454297	-1.252380548	62.58573792	TNIK
B4galt6	ENSMUSG00000056124	0.00868173	0.074543057	-1.262365127	7.834040838	B4GALT6
Kcnc1	ENSMUSG00000058975	0.008684849	0.074543057	-0.915850033	30.18553447	KCNC1
4932438A13Rik	ENSMUSG00000037270	0.008686562	0.074543057	-1.437686908	2636.784272	KIAA1109
Plcxd2	ENSMUSG00000087141	0.00873337	0.074762504	-1.415657244	155.538752	PLCXD2
Cubn	ENSMUSG00000026726	0.008737753	0.074762504	-1.327862452	5.270437768	CUBN
Sfi1	ENSMUSG00000023764	0.008803498	0.075095961	-0.828576189	2164.403671	SFI1
Dusp18	ENSMUSG00000047205	0.008807583	0.075095961	-1.363665468	5.859329124	DUSP18
Tulp4	ENSMUSG00000034377	0.008910063	0.075366556	-1.029548616	374.1201536	TULP4
Zfp609	ENSMUSG00000040524	0.008929624	0.075452185	-1.397384853	292.4276051	ZNF609
Aire	ENSMUSG00000000731	0.008963416	0.075452185	-1.188740601	288.4261911	AIRE
Epb4.1l1	ENSMUSG00000027624	0.008989707	0.075452185	-1.504385872	7.357302465	EPB41L1
Slc24a5	ENSMUSG00000035183	0.009004574	0.075466731	-1.398389371	11.00741238	SLC24A5

Dmxl2	ENSMUSG00000041268	0.009006422	0.075466731	-1.38499073	102.8793973	DMXL2
Egf	ENSMUSG00000028017	0.009030382	0.075466731	-0.839725579	34.96998486	EGF
Itgb8	ENSMUSG00000025321	0.009035378	0.075466731	-1.424100187	29.70300082	ITGB8
Ttll3	ENSMUSG00000030276	0.009060147	0.075466731	-0.897196027	229.134985	TTLL3
Ulk3	ENSMUSG00000032308	0.009080264	0.075566723	-0.59051229	709.6822763	ULK3
Il18r1	ENSMUSG00000026070	0.009097507	0.075624321	-1.391598706	128.4917149	IL18R1
Prr22	ENSMUSG00000090273	0.009104819	0.075642027	-0.819095831	19.44019122	PRR22
Btbd11	ENSMUSG00000020042	0.009127177	0.075735185	-1.425794149	5.042056587	BTBD11
Zfp318	ENSMUSG00000015597	0.009176156	0.075735185	-1.395553179	1929.947983	ZNF318
Klf12	ENSMUSG00000072294	0.009189901	0.075735185	-1.374393318	52.04201957	KLF12
Timd4	ENSMUSG00000055546	0.009204937	0.07574096	-1.223804755	26.80434413	TIMD4
Atf7	ENSMUSG00000052414	0.009224568	0.075774346	-1.13733044	330.7587183	ATF7
Pggt1b	ENSMUSG00000024477	0.009273798	0.076135901	-0.794339849	438.3002968	PGGT1B
6330408A02Rik	ENSMUSG00000070814	0.009349864	0.076301544	-0.83965435	124.1229997	C19orf68
Slc7a8	ENSMUSG00000022180	0.009400941	0.076362011	-1.362461261	18.84625293	SLC7A8
Oaf	ENSMUSG00000032014	0.009474784	0.076482045	-1.338191086	5.323340694	OAF
Epb4.1l3	ENSMUSG00000024044	0.009497623	0.076510375	-1.390452016	35.21219197	EPB41L3
Cpd	ENSMUSG00000020841	0.009579655	0.076743728	-1.214763362	66.18727319	CPD
Zbtb43	ENSMUSG00000026788	0.009590203	0.076743728	-1.179724555	482.4853546	ZBTB43
Pf4	ENSMUSG00000029373	0.009606944	0.076762804	-1.282712847	7.78264168	PF4
Fbxl18	ENSMUSG00000066640	0.009632796	0.076794062	-0.932708501	208.3937876	FBXL18
Cd8a	ENSMUSG00000053977	0.009660648	0.076796357	-1.199732644	21.17237337	CD8A
Shb	ENSMUSG00000044813	0.009664651	0.076796357	-1.007689943	62.78622235	SHB
Mast1	ENSMUSG00000053693	0.009670486	0.076800919	-1.235703388	25.47046984	MAST1
Rccd1	ENSMUSG00000038930	0.009700371	0.076870965	-0.614437766	330.4262645	RCCD1
BC017158	ENSMUSG00000030780	0.009734412	0.077098865	-0.447126887	279.8311681	C16orf58
Bcl9l	ENSMUSG00000063382	0.009745742	0.07711483	-1.331878174	643.554208	BCL9L
Cd300lb	ENSMUSG00000063193	0.009751711	0.07711483	-1.516559706	8.868505377	CD300LB
Zfp867	ENSMUSG00000054519	0.009773899	0.077160413	-0.70745998	99.61684205	ZNF627
Eml5	ENSMUSG00000051166	0.009804541	0.077208873	-1.250789071	536.441661	EML5
Zcchc4	ENSMUSG00000029179	0.009823956	0.077221476	-0.653739629	367.9298302	ZCCHC4
Fam179a	ENSMUSG00000045761	0.009868742	0.077240875	-1.256245883	11.75812909	FAM179A
Apc	ENSMUSG00000005871	0.009971268	0.077461736	-1.512694223	1193.695641	APC
Zufsp	ENSMUSG00000039531	0.009979342	0.077467882	-0.571475058	872.6293115	ZUFSP
Mitf	ENSMUSG00000035158	0.010003561	0.077523519	-1.377312097	9.762648442	MITF
Cabin1	ENSMUSG00000020196	0.010014623	0.077550903	-0.705389929	1908.191728	CABIN1
Itpripl2	ENSMUSG00000073858	0.010034802	0.077638083	-1.549402052	7.266360753	ITPRIPL2
Atf7ip	ENSMUSG00000053935	0.010036519	0.077638083	-1.249684979	473.0102725	ATF7IP
Tnrc6c	ENSMUSG00000025571	0.010098179	0.077738507	-1.370300193	1068.118831	TNRC6C
Bace1	ENSMUSG00000032086	0.010100092	0.077738507	-1.581333569	107.0940562	BACE1
Arhgap31	ENSMUSG00000022799	0.010102722	0.077738507	-1.070499824	351.5413968	ARHGAP31
Camk2g	ENSMUSG00000021820	0.010114604	0.077738507	-0.69358034	359.6236645	CAMK2G
Abcc5	ENSMUSG00000022822	0.010148019	0.077738507	-1.037009776	283.9034448	ABCC5
Ankdd1b	ENSMUSG00000047117	0.010197876	0.077805875	-0.690139797	28.30465108	ANKDD1B
Rel	ENSMUSG00000020275	0.010217197	0.077805875	-1.24474685	751.2718915	REL
Coro7	ENSMUSG00000039637	0.01021946	0.077805875	-0.679054753	2271.570983	CORO7-PAM16
Coro7	ENSMUSG00000039637	0.01021946	0.077805875	-0.679054753	2271.570983	CORO7
Fam84b	ENSMUSG00000072568	0.010235383	0.077805875	-1.279368329	153.003237	FAM84B
Dock7	ENSMUSG00000028556	0.01026318	0.077824228	-1.325236649	13.18297993	DOCK7
Scn1b	ENSMUSG00000019194	0.010279127	0.077889678	-1.507647476	10.25864626	SCN1B
Coro2a	ENSMUSG00000028337	0.010282483	0.077889678	-0.766701661	1175.534362	CORO2A
Smarcad1	ENSMUSG00000029920	0.010298272	0.07790701	-0.512818993	650.0448339	SMARCAD1
Ep400	ENSMUSG00000029505	0.010310769	0.077942155	-1.227772446	3221.936449	EP400
Pcyt1a	ENSMUSG00000005615	0.010338473	0.077952492	-0.92222021	219.1119949	PCYT1A
Sytl2	ENSMUSG00000030616	0.010343618	0.077952492	-1.498680012	3.879270156	SYTL2
Pigl	ENSMUSG00000014245	0.010379841	0.077952492	-0.538816063	163.6964408	PIGL
Crybg3	ENSMUSG00000022723	0.010402189	0.077952492	-1.181733286	272.8233253	CRYBG3
Tgm1	ENSMUSG00000022218	0.010429239	0.078036842	-1.362663195	37.77807492	TGM1
Fanca	ENSMUSG00000032815	0.010436785	0.078045976	-0.530541536	402.1041096	FANCA
Tet1	ENSMUSG00000047146	0.010465681	0.078181957	-1.565179149	9.24043738	TET1
Rbak	ENSMUSG00000061898	0.010480995	0.078256307	-1.096973558	178.9377105	RBAK
Trp53inp2	ENSMUSG00000038375	0.010567025	0.078315781	-1.030868272	237.5116097	TP53INP2
Traf3	ENSMUSG00000021277	0.010581861	0.078315781	-0.981581757	1147.414028	TRAF3
Asxl2	ENSMUSG00000037486	0.010604351	0.078375553	-1.203026061	1459.529668	ASXL2
Tomt	ENSMUSG00000078630	0.010631728	0.078458711	-1.320509765	9.686753967	LRTOMT
Fzd7	ENSMUSG00000041075	0.010656151	0.078534581	-1.553523229	4.871059402	FZD7
Gm15800	ENSMUSG00000042744	0.010658149	0.078534581	-1.282111988	1435.465857	HECTD4
Dcdc2b	ENSMUSG00000078552	0.010711017	0.07878532	-0.847482737	19.73892051	DCDC2B
Vamp1	ENSMUSG00000030337	0.01075619	0.078842585	-1.118476656	590.3626967	VAMP1
Lpp	ENSMUSG00000033306	0.010770895	0.078842585	-1.35364225	1178.236921	LPP
Adamts10	ENSMUSG00000024299	0.01078637	0.078842585	-0.803103708	555.7565365	ADAMTS10
Arid3b	ENSMUSG00000004661	0.010833864	0.078976016	-0.883450121	1073.825873	ARID3B
Tnfrsf14	ENSMUSG00000042333	0.010856609	0.078976016	-0.764972942	211.1197315	TNFRSF14
Slc9a5	ENSMUSG00000014786	0.010920563	0.078998504	-0.920059587	86.75320744	SLC9A5
Armcx5	ENSMUSG00000072969	0.010925785	0.078998504	-0.848281897	211.1113973	ARMCX5
Pde7a	ENSMUSG00000069094	0.010961749	0.079068331	-0.777034393	3063.094707	PDE7A
Atp6v0a1	ENSMUSG00000019302	0.01097445	0.079068331	-0.681684194	1341.480343	ATP6V0A1

Nlrp3	ENSMUSG00000032691	0.011010566	0.079162474	-1.360081646	6.66949537	NLRP3
Parp4	ENSMUSG00000054509	0.011025369	0.079162474	-1.162848635	1349.639882	PARP4
Acvr2a	ENSMUSG00000052155	0.011078839	0.079429181	-1.410795042	39.41078536	ACVR2A
Klhl15	ENSMUSG00000043929	0.01110063	0.079546341	-0.722058534	130.8752231	KLHL15
H6pd	ENSMUSG00000028980	0.011139486	0.079629323	-0.945303747	159.2618312	H6PD
Ahnak2	ENSMUSG00000072812	0.011193122	0.07977832	-1.598257354	5.196868755	AHNAK2
Vps13d	ENSMUSG00000020220	0.011247414	0.079906123	-1.395797153	1714.340931	VPS13D
Pparg	ENSMUSG00000000440	0.011266344	0.079906123	-1.268339931	23.51793828	PPARG
Rdh5	ENSMUSG00000025350	0.011310794	0.079906123	-0.66050462	53.16966775	RDH5
Elac1	ENSMUSG00000036941	0.011319719	0.079906123	-0.99352373	254.0938282	ELAC1
Snx21	ENSMUSG00000050373	0.01132781	0.079906123	-0.99227817	56.81944821	SNX21
Atrx	ENSMUSG00000031229	0.011369959	0.080094606	-1.477889154	3213.381127	ATRX
Cflar	ENSMUSG00000026031	0.011382236	0.080094606	-0.840014556	932.5102315	CFLAR
Fpr2	ENSMUSG00000052270	0.011398353	0.080094606	-1.583510094	11.91190566	FPR2
Gatsl2	ENSMUSG00000015944	0.011413786	0.080094606	-1.011859696	45.13997458	GATSL2
Zfp182	ENSMUSG00000054737	0.011418571	0.080094606	-0.934727361	355.9913983	ZNF182
Vps13b	ENSMUSG00000037646	0.01152131	0.080416747	-1.219340813	1775.383479	VPS13B
Zfc3h1	ENSMUSG00000034163	0.011529173	0.080416747	-1.153676097	1066.170397	ZFC3H1
Scn11a	ENSMUSG00000034115	0.011568523	0.080448967	-1.399713114	25.44866353	SCN11A
Slc37a1	ENSMUSG00000024036	0.011589979	0.080448967	-0.4685812	419.8661639	SLC37A1
Klhl17	ENSMUSG00000078484	0.011607689	0.080452452	-0.724141288	487.3366677	KLHL17
Mink1	ENSMUSG00000020827	0.011612887	0.080452452	-1.080707027	962.9203679	MINK1
Fam160a2	ENSMUSG00000044465	0.011633901	0.080479239	-0.701047218	425.3063312	FAM160A2
Iqsec1	ENSMUSG00000034312	0.011687417	0.080554359	-1.093656066	1786.461153	IQSEC1
Dcaf17	ENSMUSG00000041966	0.011714786	0.080554359	-0.547531481	492.8370775	DCAF17
Fgfr1op	ENSMUSG00000069135	0.011722399	0.080561139	-0.763547185	905.6041286	FGFR1OP
Ccdc157	ENSMUSG00000051427	0.011789868	0.080777152	-1.029000742	183.4357355	CCDC157
Clip2	ENSMUSG00000063146	0.011826074	0.080777152	-1.122569614	1329.764484	CLIP2
Itsn1	ENSMUSG00000022957	0.01182741	0.080777152	-0.903866867	255.9923569	ITSN1
Asb1	ENSMUSG00000026311	0.011842372	0.080777152	-0.831421912	462.6032187	ASB1
Mlh3	ENSMUSG00000021245	0.011856197	0.080833677	-1.04460159	209.1006906	MLH3
Zfp799	ENSMUSG00000059000	0.011910005	0.080951538	-0.732542317	65.27742718	ZNF799
Zfp169	ENSMUSG00000050954	0.011926204	0.081003752	-1.294908135	167.1144371	ZNF169
Cbfa2t2	ENSMUSG00000038533	0.011962036	0.081070464	-0.908767566	371.3575282	CBFA2T2
Chd9	ENSMUSG00000056608	0.011994045	0.081166932	-1.100159791	1491.218452	CHD9
Irf2bp2	ENSMUSG00000051495	0.012021745	0.081235296	-0.76236622	756.3026508	IRF2BP2
Cds2	ENSMUSG00000058793	0.012049733	0.081235296	-1.025521462	2172.610644	CDS2
Fgfr1	ENSMUSG00000031565	0.012051033	0.081235296	-1.376954383	6.561949327	FGFR1
Kdm6b	ENSMUSG00000018476	0.012147736	0.081414373	-1.225070515	476.2268269	KDM6B
Eml6	ENSMUSG00000044072	0.012185013	0.081574279	-0.935140648	158.0163731	EML6
Zfp652	ENSMUSG00000075595	0.012191332	0.081574279	-1.149662359	838.1985096	ZNF652
Ern1	ENSMUSG00000020715	0.012193949	0.081574279	-1.144574032	333.6826332	ERN1
Pikfyve	ENSMUSG00000025949	0.012204559	0.081601543	-1.234326087	653.0891598	PIKFYVE
Arap2	ENSMUSG00000037999	0.012237526	0.081613544	-1.326495466	850.5387718	ARAP2
Notch2	ENSMUSG00000027878	0.012261467	0.081613544	-1.347836903	2849.787421	NOTCH2
Pilra	ENSMUSG00000046245	0.012305428	0.081677278	-1.264267285	54.74976696	PILRA
Ypel1	ENSMUSG00000022773	0.012380591	0.081884681	-1.274817096	20.16524856	YPEL1
Zfp619	ENSMUSG00000068959	0.012408281	0.081997141	-1.16471656	105.1300748	ZNF208
Mapkbp1	ENSMUSG00000033902	0.012434665	0.082041416	-1.318094576	171.109109	MAPKBP1
2310035C23Rik	ENSMUSG00000026319	0.012438058	0.082041416	-1.048083287	948.2303659	KIAA1468
Fam175a	ENSMUSG00000035234	0.012458381	0.082101576	-0.322958493	357.1688676	FAM175A
Rreb1	ENSMUSG00000039087	0.012473416	0.082106217	-1.258615152	566.2203327	RREB1
Vps13c	ENSMUSG00000035284	0.012502494	0.082132721	-1.449884329	636.8272029	VPS13C
Dicer1	ENSMUSG00000041415	0.012563814	0.082248674	-1.179366227	1209.609337	DICER1
Ypel2	ENSMUSG00000018427	0.012566472	0.082248674	-0.949394041	90.30261257	YPEL2
Glb1l	ENSMUSG00000026200	0.012600324	0.082248674	-0.594557335	103.5500513	GLB1L
Foxj1	ENSMUSG00000034227	0.012604363	0.082248674	-1.193647	7.897467497	FOXJ1
Mybpc1	ENSMUSG00000020061	0.012640075	0.082270966	-1.105863237	23.95869301	MYBPC1
Ccr5	ENSMUSG00000079227	0.01265449	0.082279553	-0.838907149	45.72863491	CCR5
Abca5	ENSMUSG00000018800	0.012711996	0.08247724	-1.137525942	54.20326943	ABCA5
Rpl5	ENSMUSG00000058558	0.01273057	0.082477951	-0.719350178	185.1102909	RPL5
Phlpp2	ENSMUSG00000031732	0.012742223	0.082477951	-1.296775998	529.3274256	PHLPP2
Gpr137c	ENSMUSG00000049092	0.012747347	0.082477951	-0.968774283	32.38544774	GPR137C
Agbl3	ENSMUSG00000038836	0.01281255	0.082552489	-0.712128	57.57861492	AGBL3
Rnft2	ENSMUSG00000032850	0.012878863	0.082639568	-1.138329132	13.45292751	RNFT2
Chd7	ENSMUSG00000041235	0.012879702	0.082639568	-1.344358345	1174.750646	CHD7
Snx30	ENSMUSG00000028385	0.012915274	0.082679318	-1.254863809	2511.189704	SNX30
Cry2	ENSMUSG00000068742	0.012933438	0.082693557	-0.780392708	237.0308156	CRY2
Bcl11a	ENSMUSG00000000861	0.013059492	0.08313169	-0.846871521	2381.390264	BCL11A
Zfp266	ENSMUSG00000060510	0.013064256	0.08313169	-0.836201437	421.7016832	ZNF266
Setd2	ENSMUSG00000044791	0.013076919	0.083153903	-1.233858658	3109.883982	SETD2
Golga4	ENSMUSG00000038708	0.013085396	0.08315521	-1.410611746	946.3615855	GOLGA4
Pkd1	ENSMUSG00000032855	0.013107031	0.083256453	-1.25706393	1450.558608	PKD1
Tom1l2	ENSMUSG00000000538	0.013160293	0.083473397	-0.872553987	354.9400208	TOM1L2
Olfr164	ENSMUSG00000050742	0.013169777	0.083473397	-1.769577951	4.603460573	OR2M3
Ylpm1	ENSMUSG00000021244	0.013238012	0.083666662	-1.269094094	1085.088728	YLPM1
Rnf144b	ENSMUSG00000038068	0.01324156	0.083666662	-1.409513394	16.36125811	RNF144B

Pygl	ENSMUSG00000021069	0.01324386	0.083666662	-1.263482657	30.1429258	PYGL
Zbtb10	ENSMUSG00000069114	0.013246181	0.083666662	-1.307274071	163.1503619	ZBTB10
Tnni3	ENSMUSG00000035458	0.013262794	0.083668691	-1.494042954	9.45094598	TNNI3
Slc16a6	ENSMUSG00000041920	0.01328088	0.083717371	-1.006810443	392.8612392	SLC16A6
Trim39	ENSMUSG00000045409	0.013354128	0.083895144	-1.074887341	1079.819369	TRIM39
Plekhg3	ENSMUSG00000052609	0.01338217	0.083903509	-1.296103299	162.5257675	PLEKHG3
Ccdc93	ENSMUSG00000026339	0.013414866	0.083933475	-0.965654671	690.6223703	CCDC93
Srsf6	ENSMUSG00000016921	0.013446932	0.083987327	-0.54523613	4162.449902	SRSF6
Srms	ENSMUSG00000027579	0.013467864	0.084043482	-0.728866239	107.6238678	SRMS
Ttll4	ENSMUSG00000033257	0.013496395	0.084072805	-1.124863854	699.3602601	TTLL4
Stx16	ENSMUSG00000027522	0.013507237	0.084072805	-1.128009415	1169.25115	STX16
Nnat	ENSMUSG00000067786	0.013531746	0.084072805	-1.725508992	5.25931015	NNAT
Fcamr	ENSMUSG00000026415	0.01355892	0.084072805	-1.362688019	54.51808086	FCAMR
Lrrk2	ENSMUSG00000036273	0.013590515	0.084072805	-1.296594474	3758.29599	LRRK2
Pik3r5	ENSMUSG00000020901	0.013594177	0.084072805	-0.891695424	285.3127537	PIK3R5
Chst10	ENSMUSG00000026080	0.01360608	0.084072805	-0.75860699	352.0285415	CHST10
Mest	ENSMUSG00000051855	0.013606933	0.084072805	-1.445806419	7.063098048	MEST
Sec31b	ENSMUSG00000051984	0.013611219	0.084072805	-0.845463405	52.73258518	SEC31B
Ppm1h	ENSMUSG00000034613	0.013615582	0.084072805	-0.908904339	90.97169596	PPM1H
Zfp319	ENSMUSG00000074140	0.013773578	0.084511524	-0.90977173	91.47128561	ZNF319
Rapgef6	ENSMUSG00000037533	0.013813357	0.084622765	-1.264839477	2122.483734	RAPGEF6
Ift172	ENSMUSG00000038564	0.013839401	0.084622765	-0.906813775	494.1281579	IFT172
Vwa3b	ENSMUSG00000026115	0.013850167	0.084622765	-0.895667969	42.76212315	VWA3B
Cacna1e	ENSMUSG00000004110	0.013858321	0.084622765	-1.556859069	1292.314025	CACNA1E
Aff1	ENSMUSG00000029313	0.013875677	0.084622765	-1.302883707	1175.504973	AFF1
Ermap	ENSMUSG00000028644	0.013892969	0.084622765	-1.450463901	46.88382186	ERMAP
Tmem184c	ENSMUSG00000031617	0.013930664	0.084622765	-0.525068253	989.7359675	TMEM184C
Rhbdf1	ENSMUSG00000020282	0.013938767	0.084622765	-0.516294435	838.4283363	RHBDF1
Soat2	ENSMUSG00000023045	0.013943717	0.084622765	-0.737847006	100.0823366	SOAT2
Gng7	ENSMUSG00000048240	0.01395281	0.084622765	-1.175175213	9.126091088	GNG7
Lmbrd2	ENSMUSG00000039704	0.013971423	0.084622765	-1.334315393	161.8316829	LMBRD2
Lpin1	ENSMUSG00000020593	0.014021343	0.08479343	-0.897112933	158.3380693	LPIN1
Slfn4	ENSMUSG00000000204	0.014055661	0.084909809	-1.37454427	8.686481829	SLFN12L
Ralgapa1	ENSMUSG00000021027	0.014059533	0.084909809	-1.035979226	1359.770867	RALGAPA1
Hbs1l	ENSMUSG00000019977	0.014137838	0.085171286	-0.383636946	594.4111461	HBS1L
Ubr4	ENSMUSG00000066036	0.014165681	0.08529108	-1.367407789	4783.041973	UBR4
Plcg1	ENSMUSG00000016933	0.014169409	0.08529108	-1.05144565	716.5135272	PLCG1
Hivep3	ENSMUSG00000028634	0.014221665	0.085500479	-1.366544196	437.8539865	HIVEP3
Fbxo33	ENSMUSG00000035329	0.014226749	0.085500479	-0.922857492	595.0925604	FBXO33
Atp7a	ENSMUSG00000033792	0.014235662	0.085500479	-1.338673753	139.417406	ATP7A
Gm5595	ENSMUSG00000069727	0.0142382	0.085500479	-0.773170744	25.05705696	ZNF14
Phyhd1	ENSMUSG00000079484	0.014249014	0.085515489	-1.22606884	8.545978464	PHYHD1
Pdzd3	ENSMUSG00000032105	0.014256958	0.085515489	-1.096249586	18.00905285	PDZD3
Hpgd	ENSMUSG00000031613	0.014263393	0.085515489	-1.168539353	58.67471523	HPGD
Camsap1	ENSMUSG00000026933	0.01426552	0.085515489	-1.034453308	295.3556777	CAMSAP1
Clk4	ENSMUSG00000020385	0.014292701	0.085577969	-0.746533133	2293.58935	CLK4
Zrsr2	ENSMUSG00000031370	0.014333022	0.085587696	-0.795569435	613.161291	ZRSR2
Tiam1	ENSMUSG00000002489	0.014335062	0.085587696	-1.161710618	18.69859792	TIAM1
Arsg	ENSMUSG00000020604	0.014362218	0.085587696	-0.611249494	66.61526984	ARSG
Col4a1	ENSMUSG00000031502	0.014362343	0.085587696	-1.736436393	4.319012166	COL4A1
Htt	ENSMUSG00000029104	0.014447773	0.085712485	-1.182975753	1374.807682	HTT
Nbeal1	ENSMUSG00000073664	0.014576816	0.086106778	-1.42251323	516.0124635	NBEAL1
Dntt	ENSMUSG00000025014	0.014586083	0.086106778	-1.485311762	10.27976592	DNTT
Mysm1	ENSMUSG00000062627	0.014625077	0.086118908	-1.309020275	899.5386502	MYSM1
Ier2	ENSMUSG00000053560	0.014631424	0.086118908	-1.061424662	1466.65366	IER2
Thsd7a	ENSMUSG00000032625	0.014651373	0.086187473	-1.51658018	130.2103467	THSD7A
Gabpb2	ENSMUSG00000038766	0.014654882	0.086187473	-1.368904628	2568.323307	GABPB2
Cx3cr1	ENSMUSG00000052336	0.014748951	0.086577436	-1.234893752	24.71223945	CX3CR1
Hmbox1	ENSMUSG00000021972	0.014790464	0.086590072	-1.100806882	411.2616329	HMBOX1
Tmem116	ENSMUSG00000029452	0.014794522	0.086590072	-0.829693167	27.65454245	TMEM116
Nktr	ENSMUSG00000032525	0.014816785	0.086685615	-1.276541199	2126.128977	NKTR
Son	ENSMUSG00000022961	0.014939539	0.086916083	-1.250812194	10173.49236	SON
Luc7l2	ENSMUSG00000029823	0.01501031	0.087035524	-1.216686276	3120.446062	LUC7L2
Mga	ENSMUSG00000033943	0.015021126	0.087035524	-1.422140515	1856.862273	MGA
Mtf1	ENSMUSG00000028890	0.015051469	0.087035524	-0.614696943	565.2191351	MTF1
Osgin1	ENSMUSG00000074063	0.015074657	0.087035524	-0.934577205	35.34599529	OSGIN1
Prrc2b	ENSMUSG00000039262	0.015085901	0.087035524	-1.315815004	3211.520645	PRRC2B
Atf7ip	ENSMUSG00000030213	0.015094996	0.087035524	-1.157296426	1295.961609	ATF7IP
Tubb1	ENSMUSG00000016255	0.015121462	0.087043584	-1.469723141	4.437466774	TUBB1
Bambi	ENSMUSG00000024232	0.015157437	0.087057911	-1.148265183	26.42514752	BAMBI
Bmpr2	ENSMUSG00000067336	0.015172738	0.087057911	-1.334507897	7.503170042	BMPR2
Gpr126	ENSMUSG00000039116	0.015173335	0.087057911	-1.803152709	4.140667144	GPR126
Pofut1	ENSMUSG00000046020	0.01517908	0.087057911	-0.733564734	681.5215003	POFUT1
Camk1	ENSMUSG00000030272	0.015187628	0.087057911	-0.884412759	33.3091197	CAMK1
Zscan18	ENSMUSG00000070822	0.015190072	0.087057911	-0.936068641	41.92761479	ZSCAN18
Cpt1b	ENSMUSG00000078937	0.015296491	0.087236616	-1.388248338	4.656045908	CPT1B
Clec4a1	ENSMUSG00000049037	0.015321287	0.087284863	-1.260313227	43.50034413	ZNF705A

Ankzf1	ENSMUSG00000026199	0.015360904	0.087284863	-0.627372186	644.9610673	ANKZF1
Tbc1d9	ENSMUSG00000031709	0.015366445	0.087284863	-1.229353144	120.5297296	TBC1D9
Akap13	ENSMUSG00000066406	0.015446813	0.087284863	-1.36765445	6065.538078	AKAP13
Large	ENSMUSG00000004383	0.015469655	0.087284863	-1.718597325	4.55211812	LARGE
Zfp451	ENSMUSG00000042197	0.015500985	0.087284863	-1.071814361	670.2461643	ZNF451
Snrnp48	ENSMUSG00000021431	0.015501114	0.087284863	-0.461869294	620.0762651	SNRNP48
Ccnt2	ENSMUSG00000026349	0.015517392	0.087284863	-1.128650326	1592.840299	CCNT2
Per3	ENSMUSG00000028957	0.015537494	0.087284863	-1.230573666	84.97264151	PER3
Zc3h12a	ENSMUSG00000042677	0.015622475	0.087554701	-0.746839415	635.7939315	ZC3H12A
Slc26a2	ENSMUSG00000034320	0.015638796	0.087554701	-1.165021166	396.2704163	SLC26A2
Bdp1	ENSMUSG00000049658	0.015639697	0.087554701	-1.40316165	977.7803975	BDP1
Nap1l5	ENSMUSG00000055430	0.015643123	0.087554701	-1.59336728	4.272282326	NAP1L5
Prpf40b	ENSMUSG00000023007	0.015662169	0.087611499	-0.863146261	181.1449725	PRPF40B
BC049715	ENSMUSG00000047515	0.015665274	0.087611499	-0.969711821	14.44523504	C12orf60
Hlcs	ENSMUSG00000040820	0.015685998	0.087660225	-0.599258484	657.5224388	HLCS
Phf20l1	ENSMUSG00000072501	0.015806079	0.087879521	-1.309698817	825.0755001	PHF20L1
Inpp4a	ENSMUSG00000026113	0.015954269	0.088257431	-1.137529888	422.0426148	INPP4A
Gspt2	ENSMUSG00000071723	0.016016795	0.088395311	-1.130172901	8.448835997	GSPT2
Lnpep	ENSMUSG00000023845	0.016056573	0.088395311	-1.423623155	2012.995619	LNPEP
Snca	ENSMUSG00000025889	0.016066477	0.088395311	-1.653914076	37.47042992	SNCA
BC030499	ENSMUSG00000037593	0.016066595	0.088395311	-1.318292994	6.051871419	SGK494
Adap2	ENSMUSG00000020709	0.016077509	0.088395311	-1.448725563	17.46968355	ADAP2
Trim40	ENSMUSG00000073399	0.016091193	0.088395311	-1.023776522	12.88183169	TRIM40
Sesn3	ENSMUSG00000032009	0.016091853	0.088395311	-0.784184409	1054.326844	SESN3
Cebpa	ENSMUSG00000034957	0.016140471	0.088456158	-0.981001607	26.20247198	CEBPA
Wdr11	ENSMUSG00000042055	0.016149472	0.088456158	-0.887442614	816.802302	WDR11
Usp48	ENSMUSG00000043411	0.016225097	0.08863688	-1.077064654	1800.697166	USP48
Znf512b	ENSMUSG00000000823	0.016235577	0.088658351	-1.183329772	740.0764865	ZNF512B
Disc1	ENSMUSG00000043051	0.016278169	0.088787979	-1.195411885	13.24347935	DISC1
Rai1	ENSMUSG00000062115	0.01629877	0.08883986	-1.003850007	559.4775749	RAI1
Crtc1	ENSMUSG00000003575	0.016331268	0.08898377	-0.657622848	378.3122648	CRTC1
Rgs2	ENSMUSG00000026360	0.016353982	0.089007859	-0.615116525	3983.63183	RGS2
Ino80	ENSMUSG00000034154	0.016449247	0.089260097	-1.068757463	1052.95832	INO80
Ndor1	ENSMUSG00000006471	0.016465402	0.089276715	-0.63707781	1204.967915	NDOR1
Rnf157	ENSMUSG00000052949	0.016476324	0.089276715	-0.417063462	1203.793529	RNF157
Ercc6	ENSMUSG00000054051	0.016488115	0.089276715	-1.248311611	630.521908	ERCC6
Zfp445	ENSMUSG00000047036	0.016497604	0.089276715	-1.374387942	794.9400438	ZNF445
Herc6	ENSMUSG00000029798	0.01651996	0.089278731	-0.479168344	499.7955735	HERC6
Kif21b	ENSMUSG00000041642	0.016550411	0.089335086	-1.313960897	3951.091126	KIF21B
Plcb2	ENSMUSG00000040061	0.016741841	0.089978148	-1.166546653	799.7453429	PLCB2
Mafb	ENSMUSG00000074622	0.016817768	0.090238122	-1.232904092	78.41605515	MAFB
Tet3	ENSMUSG00000034832	0.016843747	0.090244986	-1.412408945	950.5493543	TET3
Dak	ENSMUSG00000034371	0.016849619	0.090244986	-0.54048695	234.7445952	DAK
B3gnt5	ENSMUSG00000022686	0.016860797	0.090244986	-0.893470582	3041.540574	B3GNT5
Gpd1	ENSMUSG00000023019	0.016864678	0.090244986	-1.123377461	12.24390341	GPD1
Ipcef1	ENSMUSG00000064065	0.01693754	0.090563104	-1.197339847	223.1098492	IPCEF1
Cdk12	ENSMUSG00000003119	0.016948738	0.090583774	-1.114775744	1261.43648	CDK12
Fam46a	ENSMUSG00000032265	0.017075474	0.090867918	-1.241760066	178.0250189	FAM46A
Cep63	ENSMUSG00000032534	0.01709408	0.09089013	-0.643345706	721.3101443	CEP63
Brwd3	ENSMUSG00000063663	0.017104058	0.09089013	-1.288878033	414.7772581	BRWD3
Dnajc27	ENSMUSG00000020657	0.017132721	0.09089013	-0.916556136	365.4529266	DNAJC27
Megf11	ENSMUSG00000036466	0.017144438	0.090903508	-1.397054429	5.992120988	MEGF11
Sidt2	ENSMUSG00000034908	0.01717632	0.090973418	-0.30389852	3650.980474	SIDT2
Bptf	ENSMUSG00000040481	0.017219244	0.091068588	-1.255484699	5645.938968	BPTF
Scml4	ENSMUSG00000044770	0.017282247	0.091147173	-1.058845613	558.2429221	SCML4
Dync1h1	ENSMUSG00000018707	0.017314966	0.091244245	-1.31189975	4297.71315	DYNC1H1
Grap2	ENSMUSG00000042351	0.017337264	0.091326307	-0.966980345	688.6004098	GRAP2
Gpr68	ENSMUSG00000047415	0.017346335	0.091326307	-0.827817603	14.37827547	GPR68
Safb2	ENSMUSG00000042625	0.01736713	0.091326307	-1.081222905	2419.542369	SAFB2
Ubxn7	ENSMUSG00000053774	0.017377945	0.091337443	-1.161631386	1066.259893	UBXN7
Chd6	ENSMUSG00000057133	0.017400551	0.091337443	-1.275910886	1739.67433	CHD6
Unc13b	ENSMUSG00000028456	0.017403684	0.091337443	-1.123222103	20.84620494	UNC13B
Ccdc77	ENSMUSG00000030177	0.017441783	0.091450324	-0.711506154	294.3748403	CCDC77
Tub	ENSMUSG00000031028	0.01748396	0.091539944	-1.462061832	31.63584374	TUB
Cstf3	ENSMUSG00000027176	0.017507937	0.091569224	-0.331073953	737.3833886	CSTF3
Clk2	ENSMUSG00000068917	0.017577028	0.091569224	-0.5001039	1412.030818	CLK2
Ccnl2	ENSMUSG00000029068	0.017584162	0.091569224	-0.780939107	3762.265218	CCNL2
Dip2b	ENSMUSG00000023026	0.01763293	0.091655615	-1.133991122	1036.281289	DIP2B
Tbl1xr1	ENSMUSG00000027630	0.017654385	0.091688755	-0.965538897	1524.808036	TBL1XR1
Jup	ENSMUSG00000001552	0.017742308	0.09180532	-0.986127033	49.20842536	JUP
Asxl1	ENSMUSG00000042548	0.017747737	0.09180532	-1.040607547	1579.330115	ASXL1
Drp2	ENSMUSG00000000223	0.017792355	0.091869475	-0.983140086	8.632973327	DRP2
Mgat5	ENSMUSG00000036155	0.017882428	0.092106492	-1.144317333	152.6544653	MGAT5
Cdo1	ENSMUSG00000033022	0.017923746	0.092230527	-0.930566557	11.92817261	CDO1
Nup210l	ENSMUSG00000027939	0.01795143	0.092230527	-1.064090562	41.08688347	NUP210L
Nsun6	ENSMUSG00000026707	0.017983684	0.092230527	-0.525898694	208.924779	NSUN6
Acsl1	ENSMUSG00000018796	0.017991026	0.092230527	-0.755538669	337.0473674	ACSL1

Epha2	ENSMUSG00000006445	0.018014672	0.092230527	-1.430145009	8.540709877	EPHA2
Ddi2	ENSMUSG00000078515	0.018021228	0.092230527	-1.154007887	920.2798774	DDI2
Hoxb6	ENSMUSG00000000690	0.01803016	0.092230527	-1.408633271	4.529366864	HOXB6
Fbxo48	ENSMUSG00000044966	0.018033016	0.092230527	-0.740128736	46.60243776	FBXO48
Cdon	ENSMUSG00000038119	0.018037027	0.092230527	-0.882313552	240.5108328	CDON
Cd274	ENSMUSG00000016496	0.018056972	0.092230527	-1.07871155	562.3129892	CD274
Uevld	ENSMUSG00000043262	0.018087926	0.092230527	-0.817079183	66.60563383	UEVLD
Zfp612	ENSMUSG00000044676	0.018090738	0.092230527	-1.152059327	9.674349939	ZNF23
Klhl28	ENSMUSG00000020948	0.018123377	0.09224091	-0.91884418	288.5210522	KLHL28
Fam89a	ENSMUSG00000043068	0.018168698	0.092310644	-0.798230277	26.10340703	FAM89A
Zbtb49	ENSMUSG00000029127	0.018232097	0.092568319	-0.476637852	284.1677482	ZBTB49
Ttbk2	ENSMUSG00000090100	0.018295275	0.092695635	-1.391336151	87.55931245	TTBK2
Tgfbi	ENSMUSG00000035493	0.018379081	0.092830343	-1.072885574	115.2375347	TGFBI
Zfp26	ENSMUSG00000063108	0.018421429	0.092915547	-1.084262276	560.8614655	ZNF778
Lime1	ENSMUSG00000090077	0.018570164	0.09343974	-1.225126372	12.31650091	LIME1
Myo1f	ENSMUSG00000024300	0.018662534	0.093807512	-0.882847964	458.6474595	MYO1F
Prrc2c	ENSMUSG00000040225	0.018715482	0.093894237	-1.47120844	3170.162399	PRRC2C
Wdr60	ENSMUSG00000042050	0.018729727	0.093894237	-0.906283249	14.95670664	WDR60
Btbd8	ENSMUSG00000070632	0.018749861	0.093933419	-0.870852395	17.29502599	BTBD8
Ddx19b	ENSMUSG00000033658	0.018764804	0.093933419	-0.836449429	484.5248653	DDX19B
Gm13139	ENSMUSG00000067916	0.018790437	0.094029487	-1.086064455	10.94732811	ZNF616
Spen	ENSMUSG00000040761	0.018829033	0.094096986	-1.381698329	1027.433588	SPEN
Col11a2	ENSMUSG00000024330	0.018829367	0.094096986	-0.834142813	190.2070782	COL11A2
Zfp628	ENSMUSG00000074406	0.01883451	0.094096986	-0.542042243	397.8378315	ZNF628
Tas1r3	ENSMUSG00000029072	0.018884467	0.094096986	-0.568213464	51.20226003	TAS1R3
Cep350	ENSMUSG00000033671	0.018926406	0.094096986	-1.377044351	1466.110192	CEP350
Plk3	ENSMUSG00000028680	0.018987117	0.094198506	-0.70968689	229.0856183	PLK3
Serac1	ENSMUSG00000015659	0.019011358	0.094198506	-1.053993423	73.33354374	SERAC1
Hap1	ENSMUSG00000006930	0.019065758	0.094403443	-0.996510611	69.59838136	HAP1
Ccdc9	ENSMUSG00000041375	0.01908246	0.094403443	-0.702718121	1162.527853	CCDC9
Acot11	ENSMUSG00000034853	0.019145482	0.094542043	-1.135314984	30.51018249	ACOT11
Myo9a	ENSMUSG00000039585	0.019250347	0.094664867	-1.088410817	303.0822416	MYO9A
Aff4	ENSMUSG00000049470	0.019289776	0.094741879	-1.258925338	3470.402189	AFF4
Gpm6a	ENSMUSG00000031517	0.019373053	0.094801018	-1.162763364	247.9406564	GPM6A
Zmiz1	ENSMUSG00000007817	0.019376935	0.094801018	-1.3866755	931.2942481	ZMIZ1
Dnaic2	ENSMUSG00000034706	0.019413302	0.094832313	-0.986996817	13.02632144	DNAI2
Eme2	ENSMUSG00000073436	0.019415967	0.094832313	-0.729757875	282.211322	EME2
Rgp1	ENSMUSG00000028468	0.019460355	0.094941037	-1.028395859	844.9241291	RGP1
Zkscan1	ENSMUSG00000029729	0.019481088	0.094978437	-1.085946236	335.651014	ZKSCAN1
Ncor2	ENSMUSG00000029478	0.019530941	0.095189696	-1.184467949	1277.810028	NCOR2
Ranbp10	ENSMUSG00000037415	0.019629871	0.095462941	-0.869754355	767.6113446	RANBP10
Nin	ENSMUSG00000021068	0.019648724	0.095462941	-1.308382086	1346.623763	NIN
Pdp2	ENSMUSG00000048371	0.019723627	0.095703519	-0.849250329	140.40094	PDP2
Adam19	ENSMUSG00000011256	0.01976855	0.095715263	-1.126960649	634.7672398	ADAM19
Rnf214	ENSMUSG00000042790	0.019811125	0.095715263	-0.84177797	309.0177764	RNF214
Lpgat1	ENSMUSG00000026623	0.01981555	0.095715263	-0.879803263	2137.753401	LPGAT1
Acap3	ENSMUSG00000029033	0.019821331	0.095715263	-0.625280884	392.831564	ACAP3
Ppip5k1	ENSMUSG00000033526	0.019822628	0.095715263	-0.668430693	365.8628434	PPIP5K1
Zyg11b	ENSMUSG00000034636	0.019826354	0.095715263	-1.139551873	915.9211197	ZYG11B
Atad2b	ENSMUSG00000052812	0.019844406	0.095715263	-1.330003003	552.766295	ATAD2B
Mical3	ENSMUSG00000051586	0.019965345	0.095846214	-0.992577279	224.4029859	MICAL3
Clec4b1	ENSMUSG00000030147	0.019965902	0.095846214	-1.533481839	4.42757991	CLEC4C
Degs2	ENSMUSG00000021263	0.020009357	0.096014656	-1.045449322	249.6306372	DEGS2
Hif3a	ENSMUSG00000004328	0.020027935	0.096040658	-1.062633445	8.487928197	HIF3A
Gp9	ENSMUSG00000030054	0.020049221	0.09611116	-1.433603363	3.975682944	GP9
Med13	ENSMUSG00000034297	0.020097096	0.096182726	-1.253932367	3615.226429	MED13
Fcgr4	ENSMUSG00000059089	0.020143715	0.096255477	-1.160522854	84.67335768	FCGR3A
Fcgr4	ENSMUSG00000059089	0.020143715	0.096255477	-1.160522854	84.67335768	FCGR3B
Shisa3	ENSMUSG00000050010	0.020148657	0.096255477	-1.354883089	7.396057646	SHISA3
Card14	ENSMUSG00000013483	0.020151863	0.096255477	-1.488784593	4.134855448	CARD14
Pgam2	ENSMUSG00000020475	0.020208691	0.096453838	-0.874254092	42.29415437	PGAM2
Serping1	ENSMUSG00000023224	0.020257234	0.096600732	-1.46851951	4.460761253	SERPING1
Nipa1	ENSMUSG00000047037	0.020305754	0.096733808	-1.355631035	6.049910928	NIPA1
Acrbp	ENSMUSG00000072770	0.020379924	0.096995679	-0.665882973	127.5221364	ACRBP
Usp34	ENSMUSG00000056342	0.020394315	0.097000917	-1.245592918	2387.682289	USP34
Rictor	ENSMUSG00000050310	0.020473487	0.097282386	-1.340904671	1042.8486	RICTOR
Atxn1l	ENSMUSG00000069895	0.020532234	0.097316188	-1.167706306	824.1639304	ATXN1L
Kcnh7	ENSMUSG00000059742	0.020552572	0.097338954	-1.421541182	20.19665951	KCNH7
Tmem194b	ENSMUSG00000043015	0.020588529	0.097384643	-0.702580895	1251.883956	TMEM194B
Atxn7	ENSMUSG00000021738	0.02065255	0.097401325	-1.255286468	773.0175735	ATXN7
Pitpnm1	ENSMUSG00000024851	0.020670104	0.097401325	-0.685730815	1893.409241	PITPNM1
Abca7	ENSMUSG00000035722	0.020672008	0.097401325	-0.896529318	1678.793683	ABCA7
Chd8	ENSMUSG00000053754	0.02073566	0.097497474	-1.108100007	2582.749866	CHD8
Dcbld2	ENSMUSG00000035107	0.020739169	0.097497474	-0.896278859	41.47789801	DCBLD2
Atr	ENSMUSG00000032409	0.020773627	0.097619935	-1.045071667	730.5907763	ATR
Arc	ENSMUSG00000022602	0.020785282	0.097619935	-1.046036651	21.25006924	ARC
Tmem81	ENSMUSG00000048174	0.020817663	0.097662613	-1.066412805	101.5300744	TMEM81

Trim56	ENSMUSG00000043279	0.020833411	0.097662613	-1.347669212	1567.961398	TRIM56
Otud4	ENSMUSG00000036990	0.020887229	0.097846879	-1.312902713	1718.933544	OTUD4
Trerf1	ENSMUSG00000064043	0.020954295	0.098007493	-0.954539436	436.5849234	TRERF1
Rc3h1	ENSMUSG00000040423	0.0209618	0.098007493	-1.098873456	1021.721514	RC3H1
Pyroxd2	ENSMUSG00000060224	0.021008992	0.09813384	-1.101720545	12.90247692	PYROXD2
Fnbp4	ENSMUSG00000008200	0.021025321	0.098178699	-1.083836292	2906.519261	FNBP4
C8g	ENSMUSG00000015083	0.021093421	0.098276624	-0.710398943	42.09913467	C8G
A230050P20Rik	ENSMUSG00000038884	0.021163595	0.098310039	-0.735455602	413.8436488	C19orf66
A830010M20Rik	ENSMUSG00000044060	0.021166803	0.098310039	-1.062248038	169.4242824	KIAA1107
Arid1a	ENSMUSG00000007880	0.021174661	0.098310039	-1.267323856	3807.911199	ARID1A
Pigo	ENSMUSG00000028454	0.02117672	0.098310039	-0.574199906	731.2224965	PIGO
Tmem87b	ENSMUSG00000014353	0.021181412	0.098310039	-0.950106858	453.9553155	TMEM87B
Ralgapa2	ENSMUSG00000037110	0.021355006	0.098707733	-1.119998066	366.6264567	RALGAPA2
Atm	ENSMUSG00000034218	0.02140639	0.098766949	-1.356995482	1085.266522	ATM
Ccdc114	ENSMUSG00000040189	0.021437127	0.098868165	-0.749043204	49.0581057	CCDC114
Mphosph9	ENSMUSG00000038126	0.021455559	0.098921921	-0.986818653	509.2254015	MPHOSPH9
Rab12	ENSMUSG00000023460	0.021525336	0.099149677	-0.473015915	261.6254043	RAB12
Birc6	ENSMUSG00000024073	0.021554805	0.099191515	-1.30548857	4536.630806	BIRC6
Cdh5	ENSMUSG00000031871	0.021609473	0.099349126	-0.816789219	22.856724	CDH5
Lyst	ENSMUSG00000019726	0.021649841	0.099444322	-1.41308572	2164.991428	LYST
Ppargc1b	ENSMUSG00000033871	0.021758245	0.09962519	-1.002746533	110.3899446	PPARGC1B
Fem1c	ENSMUSG00000033319	0.021809067	0.099732756	-0.743798118	607.1405448	FEM1C
Upf3b	ENSMUSG00000036572	0.021853625	0.099805941	-0.985226886	762.2502718	UPF3B
Atp2a1	ENSMUSG00000030730	0.021854223	0.099805941	-1.213156411	22.42177377	ATP2A1
Slc4a7	ENSMUSG00000021733	0.021906324	0.099895848	-1.209137871	1840.303917	SLC4A7
Tsc1	ENSMUSG00000026812	0.021915951	0.099908536	-1.144463056	1042.615413	TSC1
Gfod1	ENSMUSG00000051335	0.021929835	0.099938159	-1.016421256	167.1676106	GFOD1
Proz	ENSMUSG00000031445	0.021970318	0.099938159	-1.073825063	42.30681128	PROZ

Supp Table 4. Leading edge genes from GSEA and genes associated with pathways

Leading edge genes from Figure 3g and 3h

400 leading edge genes determined by GSEA. Downregulated genes ranked by log2-fold change and determined by RNAseq were used for analysis
(B220 gene set q-value<0.1 and FL gene set p-value<0.05)

B220+ VavPBcl2-shKmt2d	KMT2D nonsense mutant FL
ACHE	ABCD1
ADAM8	ADAM8
ADAMTSL4	ADAP2
ADAP2	ADCY7
ADRBK2	AFF1
AFF1	AHDC1
AHNAK	ALPK2
AHNAK2	ALPL
APC	AMOT
APOBR	APOBR
ARAP2	ARID3A
ARHGAP31	ARID5A
ATP6V0A1	ARRDC4
BAMBI	ATN1
BCL9L	BANK1
BHLHE40	C10orf128
BOD1L1	C10orf76
CAPN3	C19orf71
CARD14	C1R
CARD9	CACNA1A
CARNS1	CADM1
CCDC9	CAMKK1
CCND1	CARD9
CCR2	CCND1
CD274	CD274
CD300A	CD44
CD4	CD69
CD69	CDC42EP4
CDH1	CDYL
CHD7	CHD7
CLIP2	CHN2
CLN8	CKAP4
CLU	CLCN7
CRB2	COL9A3
CSRNP1	CRB2
CUBN	CRTC3
CX3CR1	CUBN
DACT1	CYB5RL
DBNDD1	DCBLD2
DCBLD2	DFNB31
DEGS2	DIP2B
DIP2B	DNAJA1
DOPEY2	DNAJB1
DSE	DOK2
DUSP1	DOPEY2
DUSP6	DSE

EGR1
EGR2
EML5
ENG
EPHA2
FAM43A
FAM46A
FAN1
FAR2
FARP2
FBXL20
FBXO24
FFAR1
FGR
FOS
FOSB
FOXJ1
FRMD4A
FYB
GALNT3
GAS7
GHRL
GPD1
GPR157
GRAP2
HAVCR2
HEBP1
HERC1
HFE
HIPK2
HMBOX1
HSD3B7
HSPA1A
HSPA1B
HSPG2
HTT
IER2
IL18R1
IL1B
INSR
IQSEC1
ITGAM
JUNB
JUP
KCNG1
KDM6B
KIAA2018
KIF21B
KLF11
KLF4
LAIR1
LILRB4
LOXL3
LRCH4
LRP1

DUSP3
DUSP6
EGR3
ELL
EPHB6
ERRFI1
ESAM
FAM129C
FAM43A
FAM46C
FAM65A
FBXO24
FGR
FLNA
FMNL3
FSCN1
FURIN
GAS7
GATA3
GDF11
GPD1
GPR132
GRAP2
GTPBP1
HERC1
HERC3
HEXIM1
HHEX
HMOX1
HOOK1
HSP90AA1
HSPA1A
HSPA1B
HSPA1L
HSPG2
HSPH1
IFFO2
IFIT2
IFITM2
IKZF1
IL17RA
INSR
IRAK2
ITGA5
ITGB7
ITPRIP
JAM3
JUNB
JUP
KCNG1
KLF11
KLF2
KLF3
KLF4
KLF9

LRRC16B
MAPK8IP3
MDN1
MEGF8
MICAL3
MTSS1L
MYBPC2
MYBPC3
MYO1F
MYO5A
NAV2
NCOR2
NEB
NFKBIZ
NOTCH2
NR4A1
NR4A2
NRP1
NUP210L
OSGIN1
P2RX1
PAK1
PARVB
PDE4C
PELI2
PER1
PER3
PHACTR2
PIK3C2B
PIK3R5
PKD1
PLCB2
PLEC
PLEKHM3
PLK2
PLK3
PTK6
PTPDC1
PTPRE
PYROXD2
RAB6B
RAI1
RDH5
RNF213
RREB1
SCML4
SERPING1
SESN3
SGK1
SIDT2
SLFN12L
SNAI1
SOCS3
SPARC
SPECC1
LAMP3
LDLRAP1
LFNG
LRRC56
LTBP3
MAN2A2
MAPK8IP3
MED13L
MTMR12
MTMR3
MYBPC2
MYO1F
MYO5B
NAV2
NFATC3
NFKBIZ
NFRKB
NMT2
NOTCH1
NR4A2
NRARP
NTN1
PAFAH2
PARP14
PDCD11
PELI3
PHF20
PHLDB3
PHTF1
PI4K2A
PIK3R4
PKD1
PKN3
PLAUR
PLCB2
PLK3
PLXND1
PRDM1
PREX1
PRR5L
PTPRK
RAB11FIP5
RABEP2
RAP2B
RARA
RARG
RASA3
RGMB
RGS12
RIN3
RNF149
RNF43
SAFB2
SDC4
SELP

SPEN
SRGAP3
STAC3
STARD9
SYNGAP1
SYNPO
TAGLN
TBC1D8
TBC1D9
TBKBP1
TGFBI
TGM1
TGM2
TIAM1
TLR8
TMC4
TMEM8B
TNFRSF14
TNNT3
TNRC6B
TNRC6C
TRIM56
TRPM2
TSC1
TTC39B
TTN
VASN
VCAM1
VPS13C
VPS13D
WDFY1
ZBTB20
ZBTB43
ZC3H12A
ZC3H12B
ZFP36
ZMIZ1
ZNF14
ZNF208
ZNF23
ZNF3
ZNF398
ZNF442
ZNF628

SERPINE1
SIK3
SIRT1
SKI
SLC12A6
SLC12A7
SLC16A5
SLC25A30
SLC4A3
SNAI1
SNX9
SOCS3
SPATA6
ST6GALNAC3
STK10
SUFU
SYNPO
TBKBP1
TBXAS1
TELO2
TERF1
TGM2
THRA
TLR4
TMEM8B
TNFRSF1B
TNNT3
TNRC6C
TRPM2
UST
UTRN
WDFY1
WDR81
WIPF2
ZBTB32
ZC3HAV1
ZFYVE27
ZKSCAN3
ZMYND11
ZNF14
ZNF267
ZNF442
ZNF473
ZNF597

Supp Table 4 (cont.). Leading edge genes from GSEA and genes associated with pathways

Genes associated with significantly enriched pathways in Figure 3i

Lymphochip database pathways (http://lymphochip.nih.gov/signaturedb/index.html)						
Immediate Early genes=Immediate_early	EGR1	FOS	FOSB	ZFP36	JUNB	DUSP1
IL6 induced genes=IL6 LY10 Up all	EGR2	ZFP36	SGK1	JUNB	SOCS3	ZBTB20
IL10 induced genes=IL10_OCILy3 Up	CD274	BANK1	HMOX1	ZFP36	SGK1	SESN3
	SNX9	JUNB	IFITM2	BCL9L	SOCS3	PRDM1
	DUSP1					
HRAS target genes=HRAS_overexpression 2x up	NFKBIZ	EPHA2	EGR1	FOS	IL1B	ADAM8
	CD274	ZFP36	SDC4	IER2	JUNB	PLAUR
	PTPRE	DUSP6	DUSP1			
KRAS target genes=KRAS_Up.txt	TAGLN	ADCY7	HSPG2	NLRP1	SPARC	SNAI1
	SGK1	TGFBI	SERPINE1	JUNB	CADM1	
HRAS target genes=HRAS_overexpression_4x_up	EPHA2	EGR1	FOS	IL1B	ADAM8	ZFP36
	IER2	JUNB	PLAUR	DUSP6	DUSP1	
IL10 induced genes=IL10_OCILy3_Up	CD274	BANK1	HMOX1	ZFP36	SGK1	SESN3
	SNX9	JUNB	IFITM2	BCL9L	SOCS3	PRDM1
	DUSP1					
IL6 induced genes=IL6_Ly10_Up_all	EGR2	ZFP36	SGK1	JUNB	SOCS3	ZBTB20
Immediate Early genes=Immediate_early	EGR1	FOS	FOSB	ZFP36	JUNB	DUSP1
JAK_IL10_Ly10_Up	ZFP36	JUNB	IFITM2	PRDM1		
KRAS target genes=KRAS_Up	TAGLN	ADCY7	HSPG2	SPARC	SNAI1	SGK1
	TGFBI	SERPINE1	JUNB	CADM1		

Broad institute Molecular signatures Database (http://www.broadinstitute.org/gsea/msigdb/index.jsp)	ID							
HRAS Oncogenic Signature=BILD HRAS Oncogenic	msig_1335	NFKBIZ	EPHA2	EGR1	FOS	IL1B	ADAM8	CD274
		ZFP36	SDC4	KDM6B	IER2	JUNB	PLAUR	PTPRE
		ITPRIP	DUSP6	DUSP1	AHNAK2			
EGF signaling target genes=NAGASHIMA_EGF_SIG	msig_308	EPHA2	EGR2	EGR3	EGR1	FOS	FOSB	DNAJB1
		ZFP36	NR4A2	NR4A1	BHLHE40	KDM6B	IER2	JUNB
		DUSP1						
TGFB1 induced genes=VERRECCHIA_EARLY_RES	msig_2312	NOTCH2	LRP1	HSPG2	APC	JUP	SPARC	SERPINE1
		CD44	PAK1					
Serum Response genes=AMIT_SERUM_RESPONS	msig_977	ZC3H12A	EGR3	EGR1	NR4A2	PLK2	BHLHE40	SGK1
		IER2						
LPS (TLR4) induced genes=SEKI_INFLAMMATORY_	msig_1707	NFKBIZ	ZC3H12A	EGR2	EGR3	EGR1	VCAM1	PLK2

		PTPRE	CD44					
TNF induced genes=ZHANG_RESPONSE_TO_IKK_	msig_994	CDC42EP4	NFKBIZ	ZC3H12A	DSE	IL1B	SDC4	SGK1
		IRAK2	SNX9	PLAUR	SOCS3	GPR132		
CROONQUIST_NRAS_SIGNALING_UP	msig_1832	CX3CR1	CCR2	TBC1D9	DUSP6			
CHIARADONNA_NEOPLASTIC_TRANSFORMATIO	msig_398	NOTCH1	SLC4A3	FOS	KLF2	STK10	JUP	PER1
		RAB11FIP5	SOCS3	DUSP1				
PEREZ_TP53_AND_TP63_TARGETS	msig_556	ADAP2	NTN1	COL9A3	EGR2	EGR1	NRARP	BAMBI
		INSR	DFNB31	FAM46C	TNRC6C	FAM43A	VASN	CAPN3

Supp Table 4 (cont.). Leading edge genes from GSEA and genes associated with pathways

Leading Edge Genes from B220 ChIPseq Enhancer Figure 4c,d

400 leading edge genes determined by GSEA.

B220+ VavPBcl2-shKmt2d	KMT2D nonsense mutant FL
ABR	ACAD9
ACSL1	ADAMTSL4
ACVR1B	ADCK5
ACVRL1	ADORA2A
ADAMTSL4	ADRBK1
ADCY9	AGPAT4
AFF3	AHCYL2
AHCYL2	AKAP2
AKAP2	ALPK2
ANKRD11	ANKRD11
ANKRD44	AP1S3
APOBEC2	ARHGAP22
ARHGAP26	ARHGAP26
ARHGAP29	ARID3A
ARHGAP32	ARID5A
ARID3B	AXIN1
ARMC9	AZIN1
ASAP1	BCAR3
ASXL1	BCL9L
ATP11B	BFSP2
ATP8B4	BTG1
ATXN7L1	C10orf32
B4GALT5	C1orf95
BATF3	C9orf85
BCL9	CAPN10
BCL9L	CCRN4L
BEGAIN	CD69
BMP2K	CDADC1
BPTF	CDK5R1
C1orf95	CDYL
CACNA1H	CELF2
CACNG6	CEP164
CCDC38	CHD9
CCDC6	CHST12
CCDC88B	CIITA
CD69	CLIP2
CECR2	CMTM7
CELF2	CPM

Leading Edge Genes from B220 ChIPseq promoter from Suppl Figure 4e, f

400 leading edge genes determined by GSEA.

B220+ VavPBcl2-shKmt2d	KMT2D nonsense mutant FL
ABR	ABAT
ACACB	ABCB6
ACHE	ACACB
ADAR	ACHE
AEBP2	ACOT7
AGRN	ADCK5
AIM2	ADORA2A
AIRE	AGRN
AKT3	ALDH7A1
ALDH1L2	ALKBH7
APP	ANKRD9
ARHGAP23	APP
ARHGAP29	ARHGEF40
ARHGAP6	ARID2
ARID1A	ARMC5
ARID2	ATE1
ARID5B	B3GAT2
ATXN1	BAHD1
B3GAT2	BCAP31
BAHD1	BCL3
BCR	BMP1
BRD3	C19orf66
C19orf66	C1orf95
C1orf95	CASZ1
C3orf70	CBX6
CACNA1H	CCDC64
CAMK2A	CCDC88B
CASZ1	CCDC9
CCDC102A	CCR6
CCDC38	CD55
CCDC39	CDC42BPB
CCDC88B	CDH24
CCDC9	CEP68
CCR6	CHRM4
CDC42BPB	CHST7
CELSR1	CKAP4
CENPF	CLIP2
CEP68	COL1A1

CELSR2
CEP164
CHD9
CHST11
CIITA
CLASP1
CLIP2
CORO2A
CRB2
CREB1
CRYBG3
DCHS1
DDX6
DENND1B
DFNB31
DGKH
DIP2B
DLL1
DNAI2
DNMT3A
DOCK11
DOCK9
DUSP16
DYRK1A
EDARADD
EEPD1
EGR2
EIF2AK3
EIF4A2
EIF4G3
ELF4
EML4
EPHB2
ETV6
EXOC1
FAM129B
FAM91A1
FBXO10
FCHSD2
FGD6
FKBP15
FMNL3
FNBP1
FOSB
FOXK1

CRB2
CSRNP1
CXCR4
CXCR5
DFNB31
DIP2B
DLL1
DNASE1
DOCK11
DOCK9
DTNB
DYRK1A
EGR2
ELF4
ELK3
EMILIN2
ENPP1
ETV6
EXT1
FAM117A
FAM134B
FAM46C
FAM49B
FAM91A1
FMNL3
FOSB
FSCN1
FUT8
GADD45B
GDF11
GHRL
GLTSCR1
GNA15
GNG7
GPM6B
GPR157
GPR18
GYPC
HAAO
HDAC4
HDAC7
HEG1
HIPK2
HIVEP1
HMBOX1

CLIP2
CNST
CPD
CRAMP1L
DBNDD1
DCBLD2
DENND3
DNAI2
DNMBP
EEPD1
EHHADH
ELF4
EPHB2
ERBB2IP
ESAM
FAM105A
FAM179A
FAM89A
FARP2
FBXL2
FGR
FSCN1
FUT1
GBP6
GFOD1
GPR157
GYLTL1B
HCN3
HEMGN
HIC2
HIF3A
HINFP
HIP1R
HOXB6
HTATSF1
HTT
IGSF3
IL9R
IMPACT
INF2
INTS2
IQCE
IQSEC2
ITGB3
ITGB8

CRAMP1L
CRAT
CSRNP2
CXCR3
CXorf40A
DBNDD1
DCBLD2
DHRS13
EHHADH
ELF4
ENTPD7
EOMES
ERBB2IP
ESAM
FAAH
FABP5
FADS2
FAM105A
FAM110A
FAM132A
FAM83H
FARP2
FBXL2
FGF9
FGFRL1
FGR
FRAT2
FSCN1
GALNT12
GNGT2
GPR135
GPR157
GTPBP1
GTPBP4
GYLTL1B
HIC1
HIC2
HIP1R
HSD17B14
HSPB1
HTT
IGF1R
IGF2BP3
IGSF3
IL12RB1

FRY
GDA
GHRL
GLTSCR1
GNG7
GPR157
GRAMD1B
GXYLT1
HDAC4
HEG1
HIPK2
HIVEP1
HK3
HMBOX1
IL6R
IL9R
IQSEC1
ITGAL
ITGB3
ITPR2
JMJD1C
KATNAL1
KIF13B
KIF20B
KSR1
LNPEP
LPGAT1
LRIG2
LRRFIP1
LYST
MAP3K5
MAP3K8
MCTP2
MED13L
MEF2A
MGAT5
MICAL3
MINK1
MXD1
MYCBP2
NCOA2
NCOR2
NLRC5
NOD2
NOSTRIN

IDH2
IDO1
INPP5A
INPP5D
IQSEC1
IRAK2
ITGB2
ITPR2
JMJD1C
KDM2B
KIF13B
KLHL3
KSR1
LASP1
LRRFIP1
LY6E
MANBA
MAP3K5
MBP
MED13L
MGAT1
MICAL3
MTMR12
MXD1
MYO3B
NCEH1
NCOA2
NCOR2
NDUFA13
NFATC1
NFKBIA
NLRC5
NLRP2
NPRL3
NRARP
OGFRL1
OSBPL3
OSBPL8
PCNX
PFKFB3
PHF2
PIK3AP1
PIK3C2B
PIK3CD
PIP5K1C

KCP
KDM3B
KDM5B
KIAA0922
KIAA1522
KIAA2018
KIF19
KLF11
KLF13
KLF2
LATS2
LCP2
LIME1
MAFB
MAFK
MAPKBP1
MAST1
MCTP2
MED13L
MGAT4A
MGAT5
MICALL1
MYCBP2
MYO5B
NAA40
NAV2
NBEAL2
NFATC2
NFE2L1
NFE2L3
NFIC
NFIX
NFXL1
NOSTRIN
NQO1
NRP2
OSBPL6
PAK6
PAPLN
PARM1
PBX1
PCF11
PCGF3
PCMTD1
PDE4C

ING1
INPP5A
INPP5D
KAZALD1
KCNJ1
KDM3B
KIAA2018
KLF11
KLF13
KLF2
LCP2
LEPRE1
LGALS1
LGALS3BP
MAFK
MAPK8IP1
MAPKBP1
MCOLN1
MED13L
MEPCE
MICALL1
MMP17
MOCS3
MOV10
MSH5
MTL5
MYCBP2
MYO5B
NAV2
NBEAL2
NDRG1
NDRG4
NFATC2
NINJ1
NR3C2
NXPH4
PAOX
PCK2
PDE4C
PHRF1
PIK3CD
PIM3
PLEKHG2
PLXNB2
PLXNC1

NRIP1
NRP2
OSBPL8
PAG1
PAN3
PCMTD1
PCNX
PCYT1A
PCYT1B
PECAM1
PIK3C2B
PIK3R1
POFUT1
POU2F2
PREX1
PRRC2B
PVRL1
QPRT
RAB6B
RAD54B
RAP1GAP2
RASA2
RASGRP3
RERE
REV1
RIMKLA
RUNX1
SCN8A
SECISBP2L
SEMA4B
SERTAD2
SGK1
SH3PXD2A
SHB
SIPA1L1
SIPA1L2
SLC29A3
SLC4A8
SMAD3
SMAD7
SMARCA2
SOCS3
SPATA13
SPRED2
ST3GAL1

PLEKHO2
POPDC2
PPP1R13B
PREX1
PRICKLE1
PRR5
PSAP
PSTPIP1
PTP4A3
PTPN1
RAB6B
RAB8B
RAD54B
RALGDS
RAP1GAP2
RASA3
RERE
RIMKLA
RNF130
RNF19B
RUNX1
RUNX3
SECISBP2L
SEMA4B
SEMA7A
SERTAD1
SGK1
SH3BP5
SH3PXD2A
SIPA1L1
SLAMF1
SLC4A8
SLC9A3R1
SNX18
SNX9
SOCS3
ST3GAL1
ST6GALNAC6
STAT5B
TAF3
TBC1D14
TBC1D9
TBKBP1
TCP11L2
TEC

PEAR1
PFKFB4
PHRF1
PLCG1
PLEKHG2
PLXNB2
PPARGC1B
PPL
PPM1H
PRRC2B
PTPDC1
PTPN3
PVRL1
RAB6B
RAI1
RASGRF1
RASSF2
RCBTB1
RERE
RGS3
RIMKLA
SALL2
SCN11A
SEC14L2
SEC31B
SEMA4B
SGK223
SH3BP4
SHANK1
SHB
SIN3A
SIX1
SLC11A1
SLC12A9
SLC22A15
SLC26A8
SLC30A1
SLC43A2
SLC45A4
SLC4A3
SOAT2
SPATA1
SRMS
STARD9
SYNPO

POLD1
PPP1R3E
PPTC7
PRR5L
PTPDC1
RAB35
RAB36
RAB6B
RAI1
RALGDS
RASL11B
RASSF2
RBMX2
RDH10
REPIN1
RERE
RGS12
RGS14
RIMKLA
RMND5A
RND1
RPS6KA1
RRAGD
RUNX3
SALL2
SCN11A
SEC31B
SEMA4B
SEMA4D
SERHL2
SESN2
SETD4
SGTB
SIDT2
SIN3A
SLBP
SLC12A4
SLC12A9
SLC25A34
SLC25A43
SLC39A14
SLC4A2
SLC4A3
SP110
ST6GALNAC6

TAF3
TARSL2
TBC1D14
TBC1D9
TBKBP1
TCF4
TEF
TMEM131
TNFAIP3
TNFAIP8
TNFRSF14
TNRC18
TRAK1
TRERF1
TRIM2
TSNAXIP1
TTC39B
USP6NL
USP7
VAMP1
VAV2
WDFY1
WDFY4
ZBTB38
ZFYVE26
ZMIZ1
ZNF217

TMEM173
TMEM176B
TMEM189
TMEM2
TMEM201
TNFAIP3
TNFAIP8
TNFRSF14
TNIP1
TNRC18
TOX2
TRAF2
TRIM2
TRIM8
TSNAXIP1
TSPAN14
TTC39B
TUBA1B
USP15
VAMP1
WDFY1
WDFY4
WWP2
ZBTB38
ZMIZ1
ZNF469
ZNRF1

TBC1D2
TEAD2
TFCP2L1
THSD1
TOX
TRPM2
TRRAP
TSC1
TSPAN33
TTC28
TTC39B
TUFT1
USP2
USP51
WDFY1
WHSC1L1
ZBTB38
ZBTB4
ZC3H12A
ZDHHC23
ZMIZ1
ZNF275
ZNF280B
ZNF546
ZNF629
ZNFX1
ZNRF3

STARD9
SYNGR3
SYNPO
TCF3
TCTN2
TEX9
TMEM108
TNFRSF12A
TRAF4
TRPM2
TRRAP
TSC1
TSPAN18
TTC39B
UBE2D1
ULK1
UNC119
USP2
WDFY1
WDR6
WSB2
ZBTB38
ZC3H12A
ZFP82
ZMIZ1
ZNF629
ZNFX1

Supp Table 4 (cont.). Leading edge genes from GSEA and genes associated with pathways

Genes associated with significantly enriched pathways in Figure 4e (enhancers)

Lymphochip database pathways (http://lymphochip.nih.gov/signaturedb/index.html)						
NFkB targets=NFkB bothOCILy3andLY10	GADD45B	NFKBIA	TNFAIP3	SMARCA2		
IL6 induced genes=IL6_Ly10_Up_all	EGR2	CXCR5	PTPN1	SGK1	SOCS3	
IL10 induced genes=IL10_OCILy3_Up	CXCR5	NLRC5	FUT8	PTPN1	PFKFB3	TNFAIP3
	SGK1	CIITA	ADRBK1	SNX9	BCAR3	BCL9L
	SOCS3	POU2F2	BATF3			
TGFB induced genes=TGFbeta up epithelial large	GADD45B	SMAD7	EPHB2	SGK1	ST3GAL1	
KRAS induced genes=KRAS_Up	INPP4B	GADD45B	MAP3K8	EPHB2	SGK1	ACVR1B
PRDM1 repressed genes= Blimp_Bcell_repressed	CXCR5	GPR18	INPP5D	CIITA	PAG1	POU2F2

Broad institute Molecular signatures Database (http://www.broadinstitute.org/gsea/msigdb/index.jsp)	ID					
CD40 induced genes=BASSO_CD40_SIGNALING_UP	msig_1313	GADD45B	CXCR5	MAP3K8	NFKBIA	TNFAIP8
		TNFAIP3	PIK3CD	PTP4A3	SLAMF1	
LPS (TLR4) induced genes=SEKI_INFLAMMATORY_RESPONSE_LPS_UP	msig_1707	BTG1	GADD45B	EGR2	NFKBIA	TNFAIP3
		TMEM2				
TNF induced genes=ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP	msig_994	BTG1	ABTB2	SMAD3	RNF19B	B4GALT5
		SEMA7A	MXD1	NFKBIA	TNFAIP8	TNFAIP3
		SGK1	DUSP16	IRAK2	SNX9	PAG1
		SOCS3	HIVEP1			
EGF signaling target genes=AMIT_EGF_RESPONSE_480_HELA	msig_968	TSPAN14	EXT1	CDYL	MBP	AMIGO2
		CHST11	TRIO	BCAR3	LY6E	GRAMD1B
p53 and p63 target genes=PEREZ_TP53_AND_TP63_TARGETS	msig_556	PPP1R13B	SIPA1L2	EGR2	NRARP	SMAD7
		TAF3	TRIM8	KSR1	FAM105A	DFNB31
		FAM46C	TOX	FRY		

Genes associated with significantly enriched pathways in Suppl Figure 4g (promoters)

Lymphochip database pathways (http://lymphochip.nih.gov/signaturedb/index.html)						
KRAS target genes=KRAS_Up	COL1A1	ULK1	HSPB1	EPHB2	BMP1	TUFT1

Broad institute Molecular signatures Database (http://www.broadinstitute.org/gsea/msigdb/index.jsp)	ID					
KRAS regulated genes in neoplastic transformation=CHIARADONNA_NEOPLASTIC_TRAN	msig_398	SLC4A3	COL1A1	KAZALD1	KLF2	APP
		INPP5A	TCF3	NDRG4		
PEREZ_TP53_AND_TP63_TARGETS	msig_556	ULK1	MAFB	HIC2	TUFT1	FAM105A
		TOX	IGF1R	PAK6	CASZ1	SEMA4D
		CRAMP1L				

Genes associated with significantly enriched pathways in Figure 5e

Lymphochip database pathways (http://lymphochip.nih.gov/signaturedb/index.html)							
PRDM1 targets=Blimp_Bcell_repressed	FCER1G	FCRLA	MS4A1	ST6GAL1	CXCR5	VPREB3	CD22
	NR1H2	ZFP36L1	CIITA	BTK	CD19	PLEK	PAG1
	FCER2	POU2F2					
IL10 induced genes=IL10_OCILy3_Up	ST6GAL1	IL21R	CXCR5	RB1	DMD	HMOX1	ZFP36
	RAD51	MEF2D	CIITA	BCAR3	IFITM1	BCL9L	POU2F2

	PRDM1	MYB	CCND3				
KRAS target genesKRAS_Up	PGLS	PDXK	GADD45B	JAK1	HSPB1	PMEPA1	SNAI1
	NPTX1	EVL	NCF2	SOX4	ATP2B4	CADM1	
NFkB_bothOCILy3andLy10	GADD45B	RELB	BCL2L1	TRAF1	NFKBIA	NCF2	IRF4
Broad institute Molecular signatures Database (http://www.broadinstitute.org/gsea/msigdb/index.jsp)	**ID**						
IL6 induced genes=BROCKE_APOPTOSIS_REVERSED_BY_IL6	msig_1155	EPB41L2	GADD45B	MAPKAPK2	RB1	DAPK1	GNA13
		SF1	ZFP36	TMEM184B	HBEGF	MX1	SOX2
		CADPS	IRF1	IRF4	ATP2B4	ID3	POU2F2
		PRDM1	SLC2A3				
IRF4 induced genes in plasma cells=SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CEL	msig_1812	WHSC1	SSR1	ST6GAL1	GNG7	CD38	PPP1R2
		TXNDC5	IRF4	TNFRSF17	SUB1	MNAT1	PRDM1
		MYB					
CD40 induced genes in GCB-DLBCL=HOLLMAN_APOPTOSIS_VIA_CD40_UP	msig_28	CHMP7	FOXN3	EPB41L2	TUBA1C	FANCA	ITGB1
		PLEKHF2	CKAP4	CUX1	ALDH2	NRGN	CD38
		CD22	SGCB	CAB39L	KDM5D	MAP4K1	BLK
		BTK	ALDH4A1	NR3C1	TNFRSF17	MRPL34	PPP2CB
		INTS9	ENDOD1	NFIB			
NFkB target genes downregulated after IKKB inhibition=DUTTA_APOPTOSIS_VIA_NFKB	msig_587	GADD45B	TNFRSF21	BCL2L1	TNFRSF10B	TRAF1	MDM2
		TERT					

Supplementary Table 5 - ChIP peaks with H3K4$^{me1/me2}$ occupancy loss in B220+ lymphoma cells and mutant OCI-LY1 vs OCI-LY7

Enhancer peaks significant downregulated (25% loss) in H3K4$^{me1/me2}$ ChIPseq in vavP-Bcl2-shKmt2d B220 positive lymphoma cells (Figure 4b)

mgi_symbol	symbol	range	start	end	chr	loss	pval	peak	hgnc_symbol
Raf1	ENSMUSG00000000441	18104	115644272	115645243	chr6	-0.41	0.000150	chr6:115644272-115645243	RAF1
Tox2	ENSMUSG00000074607	41420	163104355	163105030	chr2	-0.42	0.000204	chr2:163104355-163105030	TOX2
Tbc1d9	ENSMUSG00000031709	12653	85676489	85676705	chr8	-0.32	0.000286	chr8:85676489-85676705	TBC1D9
Tnip1	ENSMUSG00000020400	10129	54786272	54786826	chr11	-0.42	0.000349	chr11:54786272-54786826	TNIP1
Sertad2	ENSMUSG00000049800	15636	20516226	20516462	chr11	-0.43	0.000377	chr11:20516226-20516462	SERTAD2
Slc41a1	ENSMUSG00000013275	5575	133733745	133733937	chr1	-0.62	0.000429	chr1:133733745-133733937	SLC41A1
Akap2	ENSMUSG00000038729	6987	57737354	57737676	chr4	-0.50	0.000480	chr4:57737354-57737676	AKAP2
Kcnn4	ENSMUSG00000054342	2368	25157622	25158022	chr7	-0.41	0.000537	chr7:25157622-25158022	KCNN4
Etv6	ENSMUSG00000030199	8762	133993970	133995654	chr6	-0.48	0.000556	chr6:133993970-133995654	ETV6
Klrg1	ENSMUSG00000030114	10914	122243226	122244401	chr6	-0.50	0.000621	chr6:122243226-122244401	KLRG1
D10Wsu102e	ENSMUSG00000020255	36514	82859331	82859626	chr10	-0.33	0.000751	chr10:82859331-82859626	C12orf45
Ankrd44	ENSMUSG00000052331	3850	54979252	54979512	chr1	-0.53	0.000777	chr1:54979252-54979512	ANKRD44
Il4ra	ENSMUSG00000030748	19012	132726745	132727404	chr7	-0.32	0.000835	chr7:132726745-132727404	IL4R
Nod2	ENSMUSG00000055994	15394	91190225	91191040	chr8	-0.41	0.000850	chr8:91190225-91191040	NOD2
Ext1	ENSMUSG00000061731	3888	52935354	52935717	chr15	-0.41	0.000891	chr15:52935354-52935717	EXT1
Hspa4	ENSMUSG00000020361	11775	53125007	53126463	chr11	-0.30	0.000903	chr11:53125007-53126463	HSPA4
Cd86	ENSMUSG00000022901	5776	36637067	36637165	chr16	-0.71	0.000940	chr16:36637067-36637165	CD86
Cdyl	ENSMUSG00000059288	7389	35913802	35914208	chr13	-0.40	0.000946	chr13:35913802-35914208	CDYL
Tnfaip3	ENSMUSG00000019850	15482	18750888	18751003	chr10	-0.60	0.000997	chr10:18750888-18751003	TNFAIP3
Olfr1423	ENSMUSG00000067529	27384	12083697	12083995	chr19	-0.26	0.001084	chr19:12083697-12083995	OR4D11
Ntn5	ENSMUSG00000070564	3252	52936355	52936705	chr7	-0.47	0.001084	chr7:52936355-52936705	NTN5
Chst11	ENSMUSG00000034612	6624	82454567	82455165	chr10	-0.47	0.001136	chr10:82454567-82455165	CHST11
Kcnk5	ENSMUSG00000023243	13628	20986646	20988107	chr14	-0.36	0.001197	chr14:20986646-20988107	KCNK5
Tmem184b	ENSMUSG00000009035	3860	79237237	79237952	chr15	-0.35	0.001268	chr15:79237237-79237952	TMEM184B
Nfkbia	ENSMUSG00000021025	24582	56568956	56569149	chr12	-0.51	0.001279	chr12:56568956-56569149	NFKBIA
Ghrl	ENSMUSG00000064177	5077	113664229	113664465	chr6	-0.50	0.001349	chr6:113664229-113664465	GHRL
Sertad2	ENSMUSG00000049800	12604	20455843	20456036	chr11	-0.41	0.001403	chr11:20455843-20456036	SERTAD2
Glis2	ENSMUSG00000014303	10698	4583938	4584090	chr16	-0.56	0.001504	chr16:4583938-4584090	GLIS2
Rph3al	ENSMUSG00000020847	28253	75780118	75780252	chr11	-0.66	0.001505	chr11:75780118-75780252	RPH3AL
Celf2	ENSMUSG00000002107	17089	6625523	6625619	chr2	-0.46	0.001511	chr2:6625523-6625619	CELF2
Stat5b	ENSMUSG00000020919	3230	100686914	100687231	chr11	-0.42	0.001521	chr11:100686914-100687231	STAT5B
Fmnl3	ENSMUSG00000023008	6716	99172821	99172927	chr15	-0.39	0.001537	chr15:99172821-99172927	FMNL3
Slc2a5	ENSMUSG00000028976	4114	149507003	149507334	chr4	-0.48	0.001588	chr4:149507003-149507334	SLC2A5
Xpo6	ENSMUSG00000000131	13686	133270272	133270708	chr7	-0.48	0.001643	chr7:133270272-133270708	XPO6

Bmp2k	ENSMUSG00000034663	6558	97432707	97433820	chr5	-0.30	0.001666	chr5:97432707-97433820	BMP2K
Susd1	ENSMUSG00000038578	6588	59457866	59458322	chr4	-0.30	0.001733	chr4:59457866-59458322	SUSD1
Alx3	ENSMUSG00000014603	13664	107411420	107411804	chr3	-0.57	0.001755	chr3:107411420-107411804	ALX3
Asap1	ENSMUSG00000022377	46436	64167882	64168211	chr15	-0.53	0.001771	chr15:64167882-64168211	ASAP1
Zmynd12	ENSMUSG00000070806	2682	119114591	119114692	chr4	-0.65	0.001809	chr4:119114591-119114692	ZMYND12
Ntn5	ENSMUSG00000070564	4009	52935693	52935853	chr7	-0.52	0.001877	chr7:52935693-52935853	NTN5
Ptcd2	ENSMUSG00000021650	6786	100107551	100108144	chr13	-0.40	0.001884	chr13:100107551-100108144	PTCD2
Tgfbr2	ENSMUSG00000032440	37754	116046527	116046732	chr9	-0.48	0.001916	chr9:116046527-116046732	TGFBR2
Acsl1	ENSMUSG00000018796	5009	47582922	47583464	chr8	-0.54	0.001935	chr8:47582922-47583464	ACSL1
Mtss1	ENSMUSG00000022353	12354	58925638	58926234	chr15	-0.46	0.002021	chr15:58925638-58926234	MTSS1
Slc4a8	ENSMUSG00000023032	5616	100606041	100606095	chr15	-0.66	0.002109	chr15:100606041-100606095	SLC4A8
Fam3c	ENSMUSG00000029672	4506	22301293	22301844	chr6	-0.54	0.002277	chr6:22301293-22301844	FAM3C
Parp8	ENSMUSG00000021725	23178	117837124	117837879	chr13	-0.27	0.002334	chr13:117837124-117837879	PARP8
Laptm5	ENSMUSG00000028581	4169	130475966	130476096	chr4	-0.45	0.002369	chr4:130475966-130476096	LAPTM5
Plcg2	ENSMUSG00000034330	16844	120004087	120006606	chr8	-0.32	0.002381	chr8:120004087-120006606	PLCG2
Adamtsl4	ENSMUSG00000015850	6386	95498098	95498353	chr3	-0.60	0.002458	chr3:95498098-95498353	ADAMTSL4
Bmp2k	ENSMUSG00000034663	8300	97434842	97435170	chr5	-0.39	0.002487	chr5:97434842-97435170	BMP2K
Hdac4	ENSMUSG00000026313	28854	94016004	94016228	chr1	-0.53	0.002506	chr1:94016004-94016228	HDAC4
Bcl9l	ENSMUSG00000063382	5268	44301822	44302077	chr9	-0.60	0.002601	chr9:44301822-44302077	BCL9L
Dchs1	ENSMUSG00000036862	9136	112926895	112926960	chr7	-0.40	0.002652	chr7:112926895-112926960	DCHS1
Cep164	ENSMUSG00000043987	12202	45598434	45598661	chr9	-0.45	0.002725	chr9:45598434-45598661	CEP164
Snx18	ENSMUSG00000042364	17472	114426128	114426360	chr13	-0.41	0.002754	chr13:114426128-114426360	SNX18
Laptm5	ENSMUSG00000028581	12338	130456079	130457322	chr4	-0.27	0.002767	chr4:130456079-130457322	LAPTM5
Ralgds	ENSMUSG00000026821	3066	28391978	28392290	chr2	-0.57	0.002787	chr2:28391978-28392290	RALGDS
Tuba1b	ENSMUSG00000023004	2624	98767336	98767905	chr15	-0.42	0.002806	chr15:98767336-98767905	TUBA1B
Lrmp	ENSMUSG00000030263	9648	145054466	145054582	chr6	-0.40	0.002819	chr6:145054466-145054582	LRMP
Arid5a	ENSMUSG00000037447	13144	36351230	36351635	chr1	-0.52	0.002995	chr1:36351230-36351635	ARID5A
Mmp15	ENSMUSG00000031790	7726	97884235	97884721	chr8	-0.42	0.003083	chr8:97884235-97884721	MMP15
Basp1	ENSMUSG00000045763	27906	25315518	25315710	chr15	-0.36	0.003103	chr15:25315518-25315710	BASP1
Hint3	ENSMUSG00000019791	9241	30347319	30347735	chr10	-0.34	0.003225	chr10:30347319-30347735	HINT3
Ccrn4l	ENSMUSG00000023087	30186	50998036	50998327	chr3	-0.46	0.003235	chr3:50998036-50998327	CCRN4L
Rabgap1l	ENSMUSG00000026721	2944	162242123	162242258	chr1	-0.44	0.003240	chr1:162242123-162242258	RABGAP1L
Coro2a	ENSMUSG00000028337	9492	46604929	46605616	chr4	-0.42	0.003245	chr4:46604929-46605616	CORO2A
Pde6a	ENSMUSG00000024575	3976	61384050	61384198	chr18	-0.70	0.003304	chr18:61384050-61384198	PDE6A
Slc28a3	ENSMUSG00000021553	12128	58724231	58724501	chr13	-0.63	0.003411	chr13:58724231-58724501	SLC28A3
S1pr2	ENSMUSG00000043895	11727	20792869	20793061	chr9	-0.52	0.003474	chr9:20792869-20793061	S1PR2
Wdfy1	ENSMUSG00000073643	6258	79764763	79764998	chr1	-0.35	0.003581	chr1:79764763-79764998	WDFY1
Acvrl1	ENSMUSG00000000530	9072	100976030	100978175	chr15	-0.42	0.003603	chr15:100976030-100978175	ACVRL1
Haao	ENSMUSG00000000673	15670	84230237	84230682	chr17	-0.37	0.003604	chr17:84230237-84230682	HAAO
Fam117a	ENSMUSG00000038893	11303	95212492	95212662	chr11	-0.56	0.003633	chr11:95212492-95212662	FAM117A

Lrrc43	ENSMUSG00000063409	8786	123947775	123948465	chr5	-0.30	0.003919	chr5:123947775-123948465	LRRC43
Nrp2	ENSMUSG00000025969	16445	62766636	62766802	chr1	-0.57	0.003923	chr1:62766636-62766802	NRP2
B4galt5	ENSMUSG00000017929	27008	167201536	167201849	chr2	-0.42	0.003982	chr2:167201536-167201849	B4GALT5
Ralb	ENSMUSG00000004451	12272	121388795	121389406	chr1	-0.35	0.004197	chr1:121388795-121389406	RALB
Eif4ebp1	ENSMUSG00000031490	3891	28374452	28374926	chr8	-0.33	0.004198	chr8:28374452-28374926	EIF4EBP1
Vrk1	ENSMUSG00000021115	6040	107254293	107254732	chr12	-0.38	0.004287	chr12:107254293-107254732	VRK1
Pstpip1	ENSMUSG00000032322	13968	55923748	55923853	chr9	-0.55	0.004358	chr9:55923748-55923853	PSTPIP1
Gnb4	ENSMUSG00000027669	2870	32512537	32512603	chr3	-0.67	0.004451	chr3:32512537-32512603	GNB4
Acad9	ENSMUSG00000027710	5634	35959122	35959411	chr3	-0.27	0.004453	chr3:35959122-35959411	ACAD9
Hmbox1	ENSMUSG00000021972	31800	65484121	65484251	chr14	-0.54	0.004462	chr14:65484121-65484251	HMBOX1
Kif20b	ENSMUSG00000024795	16738	34979842	34980374	chr19	-0.49	0.004578	chr19:34979842-34980374	KIF20B
Gramd1a	ENSMUSG00000001248	2606	31938409	31938943	chr7	-0.31	0.004678	chr7:31938409-31938943	GRAMD1A
Fam110a	ENSMUSG00000027459	5580	151811429	151811643	chr2	-0.63	0.004744	chr2:151811429-151811643	FAM110A
Bcl7b	ENSMUSG00000029681	2434	135646620	135646808	chr5	-0.62	0.004750	chr5:135646620-135646808	BCL7B
Tnfrsf14	ENSMUSG00000042333	15606	154317976	154318580	chr4	-0.40	0.004841	chr4:154317976-154318580	TNFRSF14
Mkl1	ENSMUSG00000042292	13834	80949238	80949457	chr15	-0.65	0.005064	chr15:80949238-80949457	MKL1
Stim2	ENSMUSG00000039156	2838	54463028	54463244	chr5	-0.43	0.005069	chr5:54463028-54463244	STIM2
Cacna1h	ENSMUSG00000024112	9030	25579616	25579901	chr17	-0.33	0.005076	chr17:25579616-25579901	CACNA1H
Gng7	ENSMUSG00000048240	7292	80453560	80453729	chr10	-0.47	0.005093	chr10:80453560-80453729	GNG7
Foxk1	ENSMUSG00000056493	19755	142897049	142897401	chr5	-0.40	0.005117	chr5:142897049-142897401	FOXK1
Trpc4ap	ENSMUSG00000038324	6808	155505251	155505942	chr2	-0.38	0.005151	chr2:155505251-155505942	TRPC4AP
Gdf15	ENSMUSG00000038508	3144	73159163	73159837	chr8	-0.53	0.005162	chr8:73159163-73159837	GDF15
Tnrc18	ENSMUSG00000039477	5176	143584441	143584596	chr5	-0.45	0.005173	chr5:143584441-143584596	TNRC18
Smarca4	ENSMUSG00000032187	9372	21429548	21430608	chr9	-0.32	0.005242	chr9:21429548-21430608	SMARCA4
Inpp5a	ENSMUSG00000025477	2414	146583718	146584227	chr7	-0.47	0.005315	chr7:146583718-146584227	INPP5A
Kctd1	ENSMUSG00000036225	10670	15210870	15211974	chr18	-0.32	0.005395	chr18:15210870-15211974	KCTD1
Atxn7l1	ENSMUSG00000020564	35229	33867376	33868418	chr12	-0.27	0.005531	chr12:33867376-33868418	ATXN7L1
Lyst	ENSMUSG00000019726	31504	13651005	13651336	chr13	-0.36	0.005569	chr13:13651005-13651336	LYST
Taf3	ENSMUSG00000025782	12068	9887159	9887546	chr2	-0.28	0.005606	chr2:9887159-9887546	TAF3
Rnf130	ENSMUSG00000020376	8416	49829597	49831262	chr11	-0.33	0.005684	chr11:49829597-49831262	RNF130
Bcl9	ENSMUSG00000038256	8916	97041303	97042068	chr3	-0.37	0.005718	chr3:97041303-97042068	BCL9
Fbxo34	ENSMUSG00000037536	8010	48134546	48135525	chr14	-0.34	0.005793	chr14:48134546-48135525	FBXO34
Idh2	ENSMUSG00000030541	31827	87208678	87209500	chr7	-0.41	0.005826	chr7:87208678-87209500	IDH2
Rsph1	ENSMUSG00000024033	11977	31402056	31402494	chr17	-0.39	0.005914	chr17:31402056-31402494	RSPH1
Sertad1	ENSMUSG00000008384	5610	28266257	28266380	chr7	-0.36	0.005996	chr7:28266257-28266380	SERTAD1
Lrrc8d	ENSMUSG00000046079	15455	106113251	106113811	chr5	-0.37	0.006028	chr5:106113251-106113811	LRRC8D
Osbpl3	ENSMUSG00000029822	19886	50366928	50367149	chr6	-0.36	0.006038	chr6:50366928-50367149	OSBPL3
Fndc7	ENSMUSG00000045326	2731	108689794	108690596	chr3	-0.40	0.006041	chr3:108689794-108690596	FNDC7
Abr	ENSMUSG00000017631	10146	76296666	76297906	chr11	-0.37	0.006287	chr11:76296666-76297906	ABR
Rasgrp3	ENSMUSG00000071042	14296	75878857	75879486	chr17	-0.27	0.006298	chr17:75878857-75879486	RASGRP3

Tmem110	ENSMUSG00000006526	3654	31642270	31642593	chr14	-0.58	0.006393	chr14:31642270-31642593	TMEM110-MUSTN1
Adap1	ENSMUSG00000056413	3246	139775677	139775874	chr5	-0.53	0.006416	chr5:139775677-139775874	ADAP1
Cecr2	ENSMUSG00000071226	30374	120585384	120586641	chr6	-0.44	0.006478	chr6:120585384-120586641	CECR2
Armc9	ENSMUSG00000062590	10691	88130247	88130651	chr1	-0.58	0.006676	chr1:88130247-88130651	ARMC9
Grtp1	ENSMUSG00000038515	12977	13213181	13214013	chr8	-0.36	0.006708	chr8:13213181-13214013	GRTP1
Psmc1	ENSMUSG00000021178	22853	101371044	101371450	chr12	-0.43	0.006756	chr12:101371044-101371450	PSMC1
Sgms1	ENSMUSG00000040451	9734	32244200	32244695	chr19	-0.30	0.006847	chr19:32244200-32244695	SGMS1
Azin1	ENSMUSG00000037458	25159	38473956	38474406	chr15	-0.46	0.006856	chr15:38473956-38474406	AZIN1
Zfyve26	ENSMUSG00000066440	42710	80354408	80354713	chr12	-0.42	0.006870	chr12:80354408-80354713	ZFYVE26
Parp1	ENSMUSG00000026496	38614	182459759	182461181	chr1	-0.34	0.006922	chr1:182459759-182461181	PARP1
Hs1bp3	ENSMUSG00000020605	34702	8354809	8355072	chr12	-0.58	0.006941	chr12:8354809-8355072	HS1BP3
Mtmr14	ENSMUSG00000030269	11926	113175422	113176399	chr6	-0.26	0.006943	chr6:113175422-113176399	MTMR14
Lyst	ENSMUSG00000019726	6350	13688952	13689095	chr13	-0.56	0.006993	chr13:13688952-13689095	LYST
M6pr	ENSMUSG00000007458	11530	122246234	122248178	chr6	-0.31	0.007002	chr6:122246234-122248178	M6PR
Rev1	ENSMUSG00000026082	9811	38195979	38196659	chr1	-0.33	0.007027	chr1:38195979-38196659	REV1
Smad2	ENSMUSG00000024563	18952	76382037	76382524	chr18	-0.29	0.007099	chr18:76382037-76382524	SMAD2
Cntn2	ENSMUSG00000053024	8636	134430659	134431100	chr1	-0.29	0.007140	chr1:134430659-134431100	CNTN2
Ephb2	ENSMUSG00000028664	35850	136355529	136356288	chr4	-0.63	0.007161	chr4:136355529-136356288	EPHB2
Cd81	ENSMUSG00000037706	6228	150232081	150232748	chr7	-0.37	0.007294	chr7:150232081-150232748	CD81
Col2a1	ENSMUSG00000022483	2528	97823222	97823649	chr15	-0.45	0.007386	chr15:97823222-97823649	COL2A1
Fam134b	ENSMUSG00000022270	15642	25788479	25788841	chr15	-0.26	0.007395	chr15:25788479-25788841	FAM134B
Slc25a12	ENSMUSG00000027010	5646	71176284	71176603	chr2	-0.35	0.007406	chr2:71176284-71176603	SLC25A12
Susd1	ENSMUSG00000038578	6096	59457483	59457722	chr4	-0.31	0.007428	chr4:59457483-59457722	SUSD1
Ube2e1	ENSMUSG00000021774	23122	19136490	19136879	chr14	-0.44	0.007460	chr14:19136490-19136879	UBE2E1
Grhl3	ENSMUSG00000037188	28312	135101015	135101454	chr4	-0.46	0.007515	chr4:135101015-135101454	GRHL3
Ube2g1	ENSMUSG00000020794	11692	72408823	72409360	chr11	-0.32	0.007518	chr11:72408823-72409360	UBE2G1
Grb2	ENSMUSG00000059923	6144	115575712	115576400	chr11	-0.26	0.007551	chr11:115575712-115576400	GRB2
Sema7a	ENSMUSG00000038264	12290	57775475	57775780	chr9	-0.50	0.007672	chr9:57775475-57775780	SEMA7A
Sema7a	ENSMUSG00000038264	27255	57814760	57815586	chr9	-0.42	0.007676	chr9:57814760-57815586	SEMA7A
Rassf3	ENSMUSG00000025795	6842	120906369	120906560	chr10	-0.58	0.007712	chr10:120906369-120906560	RASSF3
Fam83f	ENSMUSG00000022408	9547	80511641	80512005	chr15	-0.38	0.007737	chr15:80511641-80512005	FAM83F
Rimkla	ENSMUSG00000048899	14095	119150939	119151099	chr4	-0.40	0.007744	chr4:119150939-119151099	RIMKLA
Fam81a	ENSMUSG00000032224	8322	69942272	69942853	chr9	-0.30	0.007759	chr9:69942272-69942853	FAM81A
Fam49b	ENSMUSG00000022378	39716	63931696	63931757	chr15	-0.34	0.007864	chr15:63931696-63931757	FAM49B
Psma6	ENSMUSG00000021024	31542	56539688	56540131	chr12	-0.44	0.007915	chr12:56539688-56540131	PSMA6
Xrcc6bp1	ENSMUSG00000025436	27330	126365584	126365931	chr10	-0.44	0.007939	chr10:126365584-126365931	XRCC6BP1
Fchsd2	ENSMUSG00000030691	36384	108220642	108221166	chr7	-0.47	0.008063	chr7:108220642-108221166	FCHSD2
Mink1	ENSMUSG00000020827	7778	70400472	70401232	chr11	-0.50	0.008080	chr11:70400472-70401232	MINK1
Manba	ENSMUSG00000028164	5976	135231956	135232305	chr3	-0.48	0.008088	chr3:135231956-135232305	MANBA
Tox2	ENSMUSG00000074607	42266	163103719	163103974	chr2	-0.40	0.008162	chr2:163103719-163103974	TOX2

Fam160a1	ENSMUSG00000051000	19414	85497218	85497429	chr3	-0.50	0.008173	chr3:85497218-85497429	FAM160A1
Ccdc6	ENSMUSG00000048701	19430	69579205	69579390	chr10	-0.60	0.008231	chr10:69579205-69579390	CCDC6
Usp6nl	ENSMUSG00000039046	26142	6299528	6300311	chr2	-0.31	0.008306	chr2:6299528-6300311	USP6NL
Socs1	ENSMUSG00000038037	16499	10768985	10769277	chr16	-0.45	0.008320	chr16:10768985-10769277	SOCS1
D15Ertd621e	ENSMUSG00000037119	14233	58232640	58232938	chr15	-0.51	0.008335	chr15:58232640-58232938	FAM91A1
Dusp16	ENSMUSG00000030203	13614	134756069	134756448	chr6	-0.35	0.008482	chr6:134756069-134756448	DUSP16
Rhobtb1	ENSMUSG00000019944	11143	68716868	68717614	chr10	-0.39	0.008574	chr10:68716868-68717614	RHOBTB1
Cd81	ENSMUSG00000037706	14360	150223907	150224657	chr7	-0.35	0.008689	chr7:150223907-150224657	CD81
Hk3	ENSMUSG00000025877	4182	55117993	55118174	chr13	-0.44	0.008709	chr13:55117993-55118174	HK3
Egr2	ENSMUSG00000037868	31507	66966297	66967133	chr10	-0.33	0.008723	chr10:66966297-66967133	EGR2
Cmtm7	ENSMUSG00000032436	12290	114703172	114703337	chr9	-0.65	0.008843	chr9:114703172-114703337	CMTM7
Amdhd1	ENSMUSG00000015890	5914	92996672	92997056	chr10	-0.63	0.008863	chr10:92996672-92997056	AMDHD1
Erp44	ENSMUSG00000028343	12646	48279576	48279779	chr4	-0.44	0.008962	chr4:48279576-48279779	ERP44
St3gal2	ENSMUSG00000031749	3282	113452370	113452707	chr8	-0.58	0.009012	chr8:113452370-113452707	ST3GAL2
Tcp11l2	ENSMUSG00000020034	5238	84034063	84034201	chr10	-0.48	0.009015	chr10:84034063-84034201	TCP11L2
Heg1	ENSMUSG00000075254	20720	33705128	33705573	chr16	-0.36	0.009052	chr16:33705128-33705573	HEG1
Eif4a2	ENSMUSG00000022884	11324	23096090	23096294	chr16	-0.46	0.009064	chr16:23096090-23096294	EIF4A2
Pou2f2	ENSMUSG00000008496	9400	25892144	25892256	chr7	-0.64	0.009084	chr7:25892144-25892256	POU2F2
Dkk3	ENSMUSG00000030772	15616	119286762	119287151	chr7	-0.51	0.009125	chr7:119286762-119287151	DKK3
Chst12	ENSMUSG00000036599	3249	140984277	140985277	chr5	-0.41	0.009131	chr5:140984277-140985277	CHST12
Nprl3	ENSMUSG00000020289	4938	32144468	32145291	chr11	-0.36	0.009146	chr11:32144468-32145291	NPRL3
Il1r2	ENSMUSG00000026073	29328	40112072	40112495	chr1	-0.59	0.009155	chr1:40112072-40112495	IL1R2
Actb	ENSMUSG00000029580	4455	143672777	143673001	chr5	-0.54	0.009320	chr5:143672777-143673001	ACTB
Prex1	ENSMUSG00000039621	15427	166448857	166449225	chr2	-0.44	0.009379	chr2:166448857-166449225	PREX1
Asap1	ENSMUSG00000022377	9380	64204837	64205368	chr15	-0.45	0.009405	chr15:64204837-64205368	ASAP1
Parp8	ENSMUSG00000021725	5992	117819943	117820688	chr13	-0.26	0.009440	chr13:117819943-117820688	PARP8
Tnip1	ENSMUSG00000020400	10896	54787163	54787469	chr11	-0.46	0.009453	chr11:54787163-54787469	TNIP1
Gnaz	ENSMUSG00000040009	2744	74426890	74427463	chr10	-0.48	0.009478	chr10:74426890-74427463	GNAZ
Tmem184c	ENSMUSG00000031617	5210	80128831	80128996	chr8	-0.42	0.009576	chr8:80128831-80128996	TMEM184C
Foxf2	ENSMUSG00000038402	3772	31721344	31721568	chr13	-0.41	0.009660	chr13:31721344-31721568	FOXF2
Dnaic2	ENSMUSG00000034706	4716	114609187	114609357	chr11	-0.46	0.009676	chr11:114609187-114609357	DNAI2
Hspa4	ENSMUSG00000020361	8584	53122237	53122851	chr11	-0.44	0.009704	chr11:53122237-53122851	HSPA4
Ffar2	ENSMUSG00000051314	8565	31617148	31617570	chr7	-0.32	0.009709	chr7:31617148-31617570	FFAR2
Rnf19b	ENSMUSG00000028793	8862	128744811	128745024	chr4	-0.49	0.009728	chr4:128744811-128745024	RNF19B
Grhl3	ENSMUSG00000037188	3774	135125311	135126233	chr4	-0.26	0.009825	chr4:135125311-135126233	GRHL3
Lrig2	ENSMUSG00000032913	10172	104305118	104306097	chr3	-0.29	0.009833	chr3:104305118-104306097	LRIG2
Jkamp	ENSMUSG00000005078	10758	73211340	73211728	chr12	-0.56	0.009881	chr12:73211340-73211728	JKAMP
Aacs	ENSMUSG00000029482	12142	125968276	125968373	chr5	-0.66	0.009923	chr5:125968276-125968373	AACS
Gramd4	ENSMUSG00000035900	2844	85894848	85895947	chr15	-0.35	0.009962	chr15:85894848-85895947	GRAMD4
Fry	ENSMUSG00000056602	36222	151025841	151026724	chr5	-0.33	0.010159	chr5:151025841-151026724	FRY

Rapgef1	ENSMUSG00000039844	4302	29562189	29562415	chr2	-0.56	0.010173	chr2:29562189-29562415	RAPGEF1
Pcyt1b	ENSMUSG00000035246	25808	90946069	90946428	chrX	-0.36	0.010267	chrX:90946069-90946428	PCYT1B
Sema6b	ENSMUSG00000001227	7938	56287656	56287753	chr17	-0.61	0.010299	chr17:56287656-56287753	SEMA6B
Ptpn1	ENSMUSG00000027540	7026	167764719	167765120	chr2	-0.43	0.010593	chr2:167764719-167765120	PTPN1
Axin1	ENSMUSG00000024182	20040	26304961	26305150	chr17	-0.50	0.010675	chr17:26304961-26305150	AXIN1
Celsr2	ENSMUSG00000068740	2377	108192420	108192582	chr3	-0.52	0.010688	chr3:108192420-108192582	CELSR2
Lekr1	ENSMUSG00000074579	2852	65467017	65467576	chr3	-0.42	0.010789	chr3:65467017-65467576	LEKR1
Pik3r1	ENSMUSG00000041417	8496	102529251	102530101	chr13	-0.26	0.010841	chr13:102529251-102530101	PIK3R1
Btnl2	ENSMUSG00000024340	5774	34497488	34497593	chr17	-0.51	0.011154	chr17:34497488-34497593	BTNL2
Laptm4a	ENSMUSG00000020585	6113	8934193	8934741	chr12	-0.32	0.011357	chr12:8934193-8934741	LAPTM4A
Ffar2	ENSMUSG00000051314	15372	31624049	31624284	chr7	-0.46	0.011407	chr7:31624049-31624284	FFAR2
Lrrc8d	ENSMUSG00000046079	20426	106108376	106108743	chr5	-0.41	0.011452	chr5:106108376-106108743	LRRC8D
Fmnl3	ENSMUSG00000023008	7174	99173286	99173378	chr15	-0.47	0.011504	chr15:99173286-99173378	FMNL3
Smad3	ENSMUSG00000032402	9120	63550392	63550920	chr9	-0.48	0.011533	chr9:63550392-63550920	SMAD3
Mef2a	ENSMUSG00000030557	47135	74564562	74565196	chr7	-0.32	0.011627	chr7:74564562-74565196	MEF2A
Gpr157	ENSMUSG00000047875	9087	149470424	149470970	chr4	-0.37	0.011719	chr4:149470424-149470970	GPR157
Arx	ENSMUSG00000035277	12586	90544333	90544535	chrX	-0.37	0.011831	chrX:90544333-90544535	ARX
Enpp1	ENSMUSG00000037370	38529	24354968	24356102	chr10	-0.42	0.011867	chr10:24354968-24356102	ENPP1
Tmem120b	ENSMUSG00000054434	7157	123533328	123533742	chr5	-0.38	0.011924	chr5:123533328-123533742	TMEM120B
Cyth4	ENSMUSG00000018008	5133	78421772	78422914	chr15	-0.37	0.011952	chr15:78421772-78422914	CYTH4
Slc9a3r1	ENSMUSG00000020733	10358	115034898	115035125	chr11	-0.41	0.012095	chr11:115034898-115035125	SLC9A3R1
Arhgap8	ENSMUSG00000078954	4976	84557665	84559023	chr15	-0.38	0.012204	chr15:84557665-84559023	ARHGAP8
Arhgap8	ENSMUSG00000078954	4976	84557665	84559023	chr15	-0.38	0.012204	chr15:84557665-84559023	PRR5-ARHGAP8
Arhgap26	ENSMUSG00000036452	5326	39253454	39253821	chr18	-0.32	0.012242	chr18:39253454-39253821	ARHGAP26
BC017643	ENSMUSG00000039294	3751	121094155	121094619	chr11	-0.40	0.012282	chr11:121094155-121094619	C17orf62
Socs3	ENSMUSG00000053113	6146	117837476	117837541	chr11	-0.51	0.012293	chr11:117837476-117837541	SOCS3
Bcl2l14	ENSMUSG00000030200	29758	134316514	134316639	chr6	-0.70	0.012320	chr6:134316514-134316639	BCL2L14
Rap1a	ENSMUSG00000068798	2236	105606262	105606707	chr3	-0.45	0.012433	chr3:105606262-105606707	RAP1A
Il9r	ENSMUSG00000020279	3242	32096896	32097065	chr11	-0.37	0.012442	chr11:32096896-32097065	IL9R
Keap1	ENSMUSG00000003308	3534	21040127	21040357	chr9	-0.48	0.012524	chr9:21040127-21040357	KEAP1
Mgat1	ENSMUSG00000020346	2329	49055107	49055619	chr11	-0.42	0.012539	chr11:49055107-49055619	MGAT1
1700019O17Rik	ENSMUSG00000036574	11184	88333976	88334280	chr1	-0.58	0.012580	chr1:88333976-88334280	C2orf57
Sstr2	ENSMUSG00000047904	7064	113473488	113473693	chr11	-0.53	0.012595	chr11:113473488-113473693	SSTR2
Zbtb38	ENSMUSG00000040433	3632	96616162	96616301	chr9	-0.41	0.012631	chr9:96616162-96616301	ZBTB38
Pfkfb3	ENSMUSG00000026773	21962	11445504	11445877	chr2	-0.59	0.012638	chr2:11445504-11445877	PFKFB3
Scn8a	ENSMUSG00000090536	27748	100735532	100736688	chr15	-0.26	0.012668	chr15:100735532-100736688	SCN8A
Emilin2	ENSMUSG00000024053	22539	71637721	71637813	chr17	-0.39	0.012727	chr17:71637721-71637813	EMILIN2
Fut8	ENSMUSG00000021065	40396	78299493	78299815	chr12	-0.29	0.012743	chr12:78299493-78299815	FUT8
Arl5c	ENSMUSG00000038352	7404	97864713	97865088	chr11	-0.28	0.012797	chr11:97864713-97865088	ARL5C
Fam129b	ENSMUSG00000026796	6244	32737749	32738004	chr2	-0.58	0.012853	chr2:32737749-32738004	FAM129B

Paqr5	ENSMUSG00000032278	10952	61813245	61813612	chr9	-0.28	0.012873	chr9:61813245-61813612	PAQR5
Nrbf2	ENSMUSG00000075000	26332	66774179	66774594	chr10	-0.27	0.012932	chr10:66774179-66774594	NRBF2
Tsga10	ENSMUSG00000060771	2652	37924732	37924859	chr1	-0.47	0.013022	chr1:37924732-37924859	TSGA10
Tarsl2	ENSMUSG00000030515	3784	72826306	72827157	chr7	-0.34	0.013172	chr7:72826306-72827157	TARSL2
Vav2	ENSMUSG00000009621	10597	27210484	27210710	chr2	-0.45	0.013196	chr2:27210484-27210710	VAV2
Sipa1l1	ENSMUSG00000042700	3082	83266896	83267752	chr12	-0.29	0.013255	chr12:83266896-83267752	SIPA1L1
Tmem173	ENSMUSG00000024349	8148	35908204	35908509	chr18	-0.44	0.013286	chr18:35908204-35908509	TMEM173
Cacng6	ENSMUSG00000078815	14700	3410619	3410826	chr7	-0.46	0.013311	chr7:3410619-3410826	CACNG6
Sdccag8	ENSMUSG00000026504	3818	178748616	178749039	chr1	-0.39	0.013366	chr1:178748616-178749039	SDCCAG8
Tgfbr2	ENSMUSG00000032440	38096	116046153	116046422	chr9	-0.35	0.013373	chr9:116046153-116046422	TGFBR2
Pm20d1	ENSMUSG00000042251	2696	133696488	133696853	chr1	-0.29	0.013407	chr1:133696488-133696853	PM20D1
Rybp	ENSMUSG00000072872	48554	100285794	100286187	chr6	-0.33	0.013408	chr6:100285794-100286187	RYBP
Gadd45b	ENSMUSG00000015312	8183	80400726	80401308	chr10	-0.37	0.013410	chr10:80400726-80401308	GADD45B
Zmiz1	ENSMUSG00000007817	6952	26433957	26434590	chr14	-0.45	0.013411	chr14:26433957-26434590	ZMIZ1
Mycbp2	ENSMUSG00000033004	43067	103633789	103634009	chr14	-0.46	0.013586	chr14:103633789-103634009	MYCBP2
Ssbp3	ENSMUSG00000061887	2642	106611299	106612017	chr4	-0.43	0.013599	chr4:106611299-106612017	SSBP3
Zdhhc18	ENSMUSG00000037553	6943	133178287	133178563	chr4	-0.27	0.013669	chr4:133178287-133178563	ZDHHC18
Tec	ENSMUSG00000029217	15945	73243412	73243970	chr5	-0.44	0.013688	chr5:73243412-73243970	TEC
Rab7	ENSMUSG00000079477	19206	88014409	88014532	chr6	-0.27	0.013793	chr6:88014409-88014532	RAB7A
Prickle1	ENSMUSG00000036158	34904	93314999	93315101	chr15	-0.49	0.013822	chr15:93314999-93315101	PRICKLE1
Whrn	ENSMUSG00000039137	8104	63141271	63142486	chr4	-0.27	0.013884	chr4:63141271-63142486	DFNB31
Vav2	ENSMUSG00000009621	10243	27272156	27272222	chr2	-0.59	0.014202	chr2:27272156-27272222	VAV2
Fer	ENSMUSG00000000127	6158	64281083	64281240	chr17	-0.47	0.014209	chr17:64281083-64281240	FER
Mctp2	ENSMUSG00000032776	28117	79423080	79423650	chr7	-0.37	0.014251	chr7:79423080-79423650	MCTP2
Il6ra	ENSMUSG00000027947	7492	89708782	89710402	chr3	-0.28	0.014315	chr3:89708782-89710402	IL6R
Nostrin	ENSMUSG00000034738	6923	68966493	68967373	chr2	-0.35	0.014350	chr2:68966493-68967373	NOSTRIN
Prg2	ENSMUSG00000027073	16132	84803913	84805056	chr2	-0.26	0.014397	chr2:84803913-84805056	PRG2
Ido2	ENSMUSG00000031549	4804	25669712	25670036	chr8	-0.40	0.014446	chr8:25669712-25670036	IDO2
Irak2	ENSMUSG00000060477	11882	113600324	113600481	chr6	-0.28	0.014446	chr6:113600324-113600481	IRAK2
Gars	ENSMUSG00000029777	20959	54966555	54967515	chr6	-0.50	0.014467	chr6:54966555-54967515	GARS
Eif4g3	ENSMUSG00000028760	13502	137573765	137574571	chr4	-0.45	0.014534	chr4:137573765-137574571	EIF4G3
Tspan14	ENSMUSG00000037824	13380	41765577	41767855	chr14	-0.27	0.014640	chr14:41765577-41767855	TSPAN14
Iqsec1	ENSMUSG00000034312	4568	90691109	90691390	chr6	-0.31	0.014723	chr6:90691109-90691390	IQSEC1
Psap	ENSMUSG00000004207	5578	59752701	59752870	chr10	-0.56	0.014747	chr10:59752701-59752870	PSAP
Fkbp15	ENSMUSG00000066151	12569	62008598	62009272	chr4	-0.40	0.014780	chr4:62008598-62009272	FKBP15
Tmem110	ENSMUSG00000006526	4275	31643001	31643105	chr14	-0.58	0.014917	chr14:31643001-31643105	TMEM110-MUSTN1
Pcmtd1	ENSMUSG00000051285	22666	7101418	7101915	chr1	-0.41	0.014931	chr1:7101418-7101915	PCMTD1
Miox	ENSMUSG00000022613	3344	89170150	89170262	chr15	-0.39	0.015000	chr15:89170150-89170262	MIOX
Mink1	ENSMUSG00000020827	6402	70401907	70402548	chr11	-0.50	0.015017	chr11:70401907-70402548	MINK1
Slpi	ENSMUSG00000017002	10714	164192681	164193236	chr2	-0.36	0.015058	chr2:164192681-164193236	SLPI

Homez	ENSMUSG00000057156	14556	55462392	55462731	chr14	-0.42	0.015062	chr14:55462392-55462731	HOMEZ
Fnbp1	ENSMUSG00000075415	3308	30993908	30994121	chr2	-0.35	0.015067	chr2:30993908-30994121	FNBP1
Clip2	ENSMUSG00000063146	32196	134995689	134996526	chr5	-0.44	0.015111	chr5:134995689-134996526	CLIP2
Tmem64	ENSMUSG00000043252	13152	15179454	15180193	chr4	-0.38	0.015124	chr4:15179454-15180193	TMEM64
Bcl9	ENSMUSG00000038256	3878	97036391	97036905	chr3	-0.37	0.015331	chr3:97036391-97036905	BCL9
Adamtsl4	ENSMUSG00000015850	7291	95498553	95499709	chr3	-0.34	0.015389	chr3:95498553-95499709	ADAMTSL4
Dnmt3a	ENSMUSG00000020661	4785	3870868	3871082	chr12	-0.53	0.015588	chr12:3870868-3871082	DNMT3A
Mgat5	ENSMUSG00000036155	35342	129136376	129137432	chr1	-0.42	0.015601	chr1:129136376-129137432	MGAT5
Pou2af1	ENSMUSG00000032053	10686	51032357	51032602	chr9	-0.29	0.015602	chr9:51032357-51032602	POU2AF1
Hivep1	ENSMUSG00000021366	41928	42189226	42189406	chr13	-0.57	0.015626	chr13:42189226-42189406	HIVEP1
Rasgrp1	ENSMUSG00000027347	22454	117190890	117191493	chr2	-0.39	0.015663	chr2:117190890-117191493	RASGRP1
Stau2	ENSMUSG00000025920	14226	16524049	16524790	chr1	-0.43	0.015665	chr1:16524049-16524790	STAU2
Map2k6	ENSMUSG00000020623	26880	110311585	110312036	chr11	-0.47	0.015759	chr11:110311585-110312036	MAP2K6
Enpp6	ENSMUSG00000038173	6652	48147360	48147903	chr8	-0.35	0.015767	chr8:48147360-48147903	ENPP6
Itgb2	ENSMUSG00000000290	2963	76989457	76990609	chr10	-0.26	0.015811	chr10:76989457-76990609	ITGB2
Rere	ENSMUSG00000039852	10244	149852193	149852318	chr4	-0.40	0.015879	chr4:149852193-149852318	RERE
Eftud1	ENSMUSG00000038563	21197	89839802	89840068	chr7	-0.40	0.016063	chr7:89839802-89840068	EFTUD1
Sh3bp5	ENSMUSG00000021892	3326	32226935	32228140	chr14	-0.26	0.016069	chr14:32226935-32228140	SH3BP5
Slamf1	ENSMUSG00000015316	4812	173692106	173692782	chr1	-0.36	0.016090	chr1:173692106-173692782	SLAMF1
Mtss1	ENSMUSG00000022353	29806	58841678	58843015	chr15	-0.35	0.016163	chr15:58841678-58843015	MTSS1
Fance	ENSMUSG00000007570	4758	28445402	28446030	chr17	-0.33	0.016352	chr17:28445402-28446030	FANCE
Myo3b	ENSMUSG00000042064	17631	69951860	69952110	chr2	-0.58	0.016398	chr2:69951860-69952110	MYO3B
Wwp2	ENSMUSG00000031930	42117	110026540	110027154	chr8	-0.40	0.016492	chr8:110026540-110027154	WWP2
Tsnaxip1	ENSMUSG00000031893	9278	108360843	108360996	chr8	-0.40	0.016507	chr8:108360843-108360996	TSNAXIP1
Myo3b	ENSMUSG00000042064	22480	69956654	69957014	chr2	-0.44	0.016556	chr2:69956654-69957014	MYO3B
Pofut1	ENSMUSG00000046020	5556	153088477	153089247	chr2	-0.40	0.016610	chr2:153088477-153089247	POFUT1
Elk3	ENSMUSG00000008398	37260	92736217	92736374	chr10	-0.44	0.016633	chr10:92736217-92736374	ELK3
Gm22	ENSMUSG00000043903	38881	124754523	124754651	chr8	-0.45	0.016640	chr8:124754523-124754651	ZNF469
Clasp1	ENSMUSG00000064302	10520	120295266	120297042	chr1	-0.27	0.016687	chr1:120295266-120297042	CLASP1
Nlrc5	ENSMUSG00000074151	12878	97009231	97009850	chr8	-0.38	0.016704	chr8:97009231-97009850	NLRC5
Adap1	ENSMUSG00000056413	3733	139775008	139775570	chr5	-0.45	0.016790	chr5:139775008-139775570	ADAP1
Creb1	ENSMUSG00000025958	2470	64576633	64577178	chr1	-0.38	0.016797	chr1:64576633-64577178	CREB1
Tnip1	ENSMUSG00000020400	9631	54785990	54786112	chr11	-0.54	0.016804	chr11:54785990-54786112	TNIP1
Atp8b4	ENSMUSG00000060131	3539	126321753	126322337	chr2	-0.41	0.016813	chr2:126321753-126322337	ATP8B4
Mlycd	ENSMUSG00000074064	6080	121936784	121937048	chr8	-0.35	0.016850	chr8:121936784-121937048	MLYCD
Kpnb1	ENSMUSG00000001440	3212	97052164	97052651	chr11	-0.46	0.016853	chr11:97052164-97052651	KPNB1
Uvrag	ENSMUSG00000035354	18246	106271022	106271795	chr7	-0.31	0.016984	chr7:106271022-106271795	UVRAG
Adipor2	ENSMUSG00000030168	7078	119345294	119346270	chr6	-0.26	0.016988	chr6:119345294-119346270	ADIPOR2
Tmem50a	ENSMUSG00000028822	3626	134474281	134474851	chr4	-0.35	0.016997	chr4:134474281-134474851	TMEM50A
Arhgap26	ENSMUSG00000036452	6979	39251643	39252327	chr18	-0.29	0.017068	chr18:39251643-39252327	ARHGAP26

Cxcr4	ENSMUSG00000045382	8690	130479822	130480535	chr1	-0.28	0.017070	chr1:130479822-130480535	CXCR4
Ncor2	ENSMUSG00000029478	18392	125586734	125587021	chr5	-0.39	0.017086	chr5:125586734-125587021	NCOR2
Map2k6	ENSMUSG00000020623	37972	110298188	110298899	chr11	-0.48	0.017094	chr11:110298188-110298899	MAP2K6
Rassf3	ENSMUSG00000025795	43110	120869938	120870454	chr10	-0.53	0.017122	chr10:120869938-120870454	RASSF3
Ogfrl1	ENSMUSG00000026158	16636	23406412	23406888	chr1	-0.30	0.017264	chr1:23406412-23406888	OGFRL1
Dnmt3a	ENSMUSG00000020661	5274	3871238	3871691	chr12	-0.40	0.017334	chr12:3871238-3871691	DNMT3A
Tbc1d22a	ENSMUSG00000051864	16432	86061330	86061513	chr15	-0.66	0.017424	chr15:86061330-86061513	TBC1D22A
Gadd45b	ENSMUSG00000015312	7373	80399840	80400574	chr10	-0.47	0.017457	chr10:80399840-80400574	GADD45B
Arid3a	ENSMUSG00000019564	7090	79400166	79400351	chr10	-0.60	0.017619	chr10:79400166-79400351	ARID3A
Ak2	ENSMUSG00000028792	26101	128696129	128697265	chr4	-0.29	0.017647	chr4:128696129-128697265	AK2
Rgs10	ENSMUSG00000030844	6212	135525773	135526356	chr7	-0.43	0.017682	chr7:135525773-135526356	RGS10
Gxylt1	ENSMUSG00000036197	6860	93098547	93098897	chr15	-0.35	0.017902	chr15:93098547-93098897	GXYLT1
Trim2	ENSMUSG00000027993	29393	84138207	84139315	chr3	-0.26	0.017940	chr3:84138207-84139315	TRIM2
Mtss1	ENSMUSG00000022353	10895	58924246	58924708	chr15	-0.36	0.017944	chr15:58924246-58924708	MTSS1
Susd1	ENSMUSG00000038578	5542	59456757	59457338	chr4	-0.27	0.018011	chr4:59456757-59457338	SUSD1
Tpd52	ENSMUSG00000027506	4210	8984281	8984572	chr3	-0.38	0.018021	chr3:8984281-8984572	TPD52
Znrf1	ENSMUSG00000033545	10446	114096014	114096354	chr8	-0.56	0.018113	chr8:114096014-114096354	ZNRF1
Mrps30	ENSMUSG00000021731	31204	119207028	119207501	chr13	-0.54	0.018164	chr13:119207028-119207501	MRPS30
Ciita	ENSMUSG00000075404	26460	10516280	10516387	chr16	-0.55	0.018334	chr16:10516280-10516387	CIITA
Mkl1	ENSMUSG00000042292	7728	80943181	80943302	chr15	-0.51	0.018362	chr15:80943181-80943302	MKL1
St6gal1	ENSMUSG00000022885	3288	23286959	23287548	chr16	-0.27	0.018433	chr16:23286959-23287548	ST6GAL1
Mctp2	ENSMUSG00000032776	23070	79428000	79428825	chr7	-0.28	0.018595	chr7:79428000-79428825	MCTP2
Tef	ENSMUSG00000022389	10881	81662138	81662368	chr15	-0.34	0.018668	chr15:81662138-81662368	TEF
Pbk	ENSMUSG00000022033	46790	66377743	66378022	chr14	-0.51	0.018691	chr14:66377743-66378022	PBK
Lrig2	ENSMUSG00000032913	11692	104327290	104327775	chr3	-0.43	0.018755	chr3:104327290-104327775	LRIG2
Rusc1	ENSMUSG00000041263	5025	88888769	88889089	chr3	-0.49	0.018768	chr3:88888769-88889089	RUSC1
Slc19a2	ENSMUSG00000040918	30686	166148245	166148735	chr1	-0.34	0.018858	chr1:166148245-166148735	SLC19A2
Dapp1	ENSMUSG00000028159	35504	137679850	137680179	chr3	-0.41	0.018904	chr3:137679850-137680179	DAPP1
Fhad1	ENSMUSG00000051435	13031	141554165	141554877	chr4	-0.28	0.018967	chr4:141554165-141554877	FHAD1
Mef2b	ENSMUSG00000079033	5120	72681168	72682429	chr8	-0.31	0.019127	chr8:72681168-72682429	MEF2B
Tmem140	ENSMUSG00000057137	4697	34817741	34817941	chr6	-0.43	0.019227	chr6:34817741-34817941	TMEM140
Chd9	ENSMUSG00000056608	11214	93363394	93364497	chr8	-0.37	0.019307	chr8:93363394-93364497	CHD9
Ap1s2	ENSMUSG00000031367	9172	160337650	160337903	chrX	-0.42	0.019314	chrX:160337650-160337903	AP1S2
Cmtm7	ENSMUSG00000032436	12786	114703440	114704061	chr9	-0.37	0.019325	chr9:114703440-114704061	CMTM7
Znrf4	ENSMUSG00000044526	4807	56646538	56647660	chr17	-0.30	0.019385	chr17:56646538-56647660	ZNRF4
Rap1b	ENSMUSG00000052681	14386	117268576	117268637	chr10	-0.49	0.019484	chr10:117268576-117268637	RAP1B
Exoc1	ENSMUSG00000036435	4290	76953758	76954329	chr5	-0.61	0.019510	chr5:76953758-76954329	EXOC1
St3gal2	ENSMUSG00000031749	2464	113453023	113453688	chr8	-0.52	0.019565	chr8:113453023-113453688	ST3GAL2
Gpr84	ENSMUSG00000063234	2880	103137782	103138198	chr15	-0.31	0.019600	chr15:103137782-103138198	GPR84
Arhgap29	ENSMUSG00000039831	12716	121643048	121643812	chr3	-0.39	0.019652	chr3:121643048-121643812	ARHGAP29

Prr5	ENSMUSG00000036106	3864	84515192	84515395	chr15	-0.45	0.019660	chr15:84515192-84515395	PRR5
Cdh23	ENSMUSG00000012819	9178	60168350	60168481	chr10	-0.59	0.019684	chr10:60168350-60168481	CDH23
Ncoa2	ENSMUSG00000005886	11398	13278161	13278651	chr1	-0.29	0.019773	chr1:13278161-13278651	NCOA2
Dip2b	ENSMUSG00000023026	24928	99959478	99960319	chr15	-0.26	0.019784	chr15:99959478-99960319	DIP2B
Mtmr12	ENSMUSG00000039458	6756	12145738	12146967	chr15	-0.36	0.019810	chr15:12145738-12146967	MTMR12
Prrc2b	ENSMUSG00000039262	14964	32022174	32023846	chr2	-0.35	0.019856	chr2:32022174-32023846	PRRC2B
Rhbdl2	ENSMUSG00000043333	3099	123472062	123472632	chr4	-0.26	0.019976	chr4:123472062-123472632	RHBDL2
Mybph	ENSMUSG00000042451	2888	136092744	136093081	chr1	-0.49	0.020045	chr1:136092744-136093081	MYBPH
Vamp1	ENSMUSG00000030337	6991	125172338	125172840	chr6	-0.38	0.020049	chr6:125172338-125172840	VAMP1
Ksr1	ENSMUSG00000018334	34891	78908201	78908337	chr11	-0.35	0.020056	chr11:78908201-78908337	KSR1
Nat9	ENSMUSG00000015542	11256	115060044	115060817	chr11	-0.29	0.020086	chr11:115060044-115060817	NAT9
Cdadc1	ENSMUSG00000021982	41733	60174865	60175017	chr14	-0.56	0.020267	chr14:60174865-60175017	CDADC1
Tcf4	ENSMUSG00000053477	13297	69735752	69736818	chr18	-0.25	0.020289	chr18:69735752-69736818	TCF4
Igj	ENSMUSG00000067149	3058	88959930	88960018	chr5	-0.46	0.020541	chr5:88959930-88960018	IGJ
Azin1	ENSMUSG00000037458	48217	38497020	38497458	chr15	-0.25	0.020705	chr15:38497020-38497458	AZIN1
Atp11b	ENSMUSG00000037400	6738	35645970	35646661	chr3	-0.26	0.020749	chr3:35645970-35646661	ATP11B
1110059E24Rik	ENSMUSG00000035171	6001	21720718	21721844	chr19	-0.34	0.020937	chr19:21720718-21721844	C9orf85
Ppp2cb	ENSMUSG00000009630	7628	34717682	34717759	chr8	-0.41	0.021138	chr8:34717682-34717759	PPP2CB
Gpr18	ENSMUSG00000050350	12086	122302646	122303174	chr14	-0.42	0.021163	chr14:122302646-122303174	GPR18
Bfsp2	ENSMUSG00000032556	10697	103340405	103341053	chr9	-0.39	0.021329	chr9:103340405-103341053	BFSP2
Hipk2	ENSMUSG00000061436	29266	38663895	38664092	chr6	-0.46	0.021476	chr6:38663895-38664092	HIPK2
Spred2	ENSMUSG00000045671	30891	19885311	19885615	chr11	-0.44	0.021604	chr11:19885311-19885615	SPRED2
Txn2	ENSMUSG00000005354	10502	77735206	77736050	chr15	-0.37	0.021615	chr15:77735206-77736050	TXN2
Dennd1b	ENSMUSG00000056268	6121	140853782	140854000	chr1	-0.44	0.021744	chr1:140853782-140854000	DENND1B
Ankrd11	ENSMUSG00000035569	43864	125454584	125455035	chr8	-0.35	0.021755	chr8:125454584-125455035	ANKRD11
Treh	ENSMUSG00000032098	25659	44455589	44455721	chr9	-0.64	0.021916	chr9:44455589-44455721	TREH
Smarcal1	ENSMUSG00000039354	4458	72625184	72625548	chr1	-0.39	0.021919	chr1:72625184-72625548	SMARCAL1
Treh	ENSMUSG00000032098	24450	44456649	44457080	chr9	-0.34	0.022000	chr9:44456649-44457080	TREH
Spred2	ENSMUSG00000045671	14214	19868546	19869027	chr11	-0.41	0.022004	chr11:19868546-19869027	SPRED2
Itgb3	ENSMUSG00000020689	9370	104489014	104489651	chr11	-0.40	0.022009	chr11:104489014-104489651	ITGB3
D930015E06Rik	ENSMUSG00000033767	41996	83801760	83802415	chr3	-0.53	0.022116	chr3:83801760-83802415	KIAA0922
Rapgef1	ENSMUSG00000039844	3724	29554196	29554356	chr2	-0.45	0.022143	chr2:29554196-29554356	RAPGEF1
Armc9	ENSMUSG00000062590	15756	88125198	88125571	chr1	-0.39	0.022250	chr1:88125198-88125571	ARMC9
Slc45a4	ENSMUSG00000079020	2962	73457836	73458436	chr15	-0.43	0.022268	chr15:73457836-73458436	SLC45A4
Fam3c	ENSMUSG00000029672	5902	22299360	22300984	chr6	-0.44	0.022327	chr6:22299360-22300984	FAM3C
Sppl3	ENSMUSG00000029550	7875	115452902	115453636	chr5	-0.39	0.022379	chr5:115452902-115453636	SPPL3
Ly6e	ENSMUSG00000022587	27838	74757484	74757799	chr15	-0.49	0.022439	chr15:74757484-74757799	LY6E
Ndufa13	ENSMUSG00000036199	17602	72443972	72444149	chr8	-0.37	0.022484	chr8:72443972-72444149	NDUFA13
Pik3ap1	ENSMUSG00000025017	41952	41417277	41417940	chr19	-0.36	0.022547	chr19:41417277-41417940	PIK3AP1
Arid5a	ENSMUSG00000037447	8408	36355693	36356643	chr1	-0.34	0.022586	chr1:36355693-36356643	ARID5A

Socs1	ENSMUSG00000038037	2202	10783380	10783475	chr16	-0.59	0.022602	chr16:10783380-10783475	SOCS1
Jdp2	ENSMUSG00000034271	9793	86930500	86930642	chr12	-0.58	0.022706	chr12:86930500-86930642	JDP2
Ltbp1	ENSMUSG00000001870	3980	75787497	75787560	chr17	-0.42	0.022725	chr17:75787497-75787560	LTBP1
Nrip1	ENSMUSG00000048490	11012	76334763	76335070	chr16	-0.38	0.022777	chr16:76334763-76335070	NRIP1
Tnfaip8	ENSMUSG00000062210	9478	50169676	50169809	chr18	-0.41	0.022803	chr18:50169676-50169809	TNFAIP8
Hdac7	ENSMUSG00000022475	6502	97655273	97655523	chr15	-0.35	0.022808	chr15:97655273-97655523	HDAC7
Mical3	ENSMUSG00000051586	4382	120928201	120928511	chr6	-0.45	0.022819	chr6:120928201-120928511	MICAL3
Cplx4	ENSMUSG00000024519	9807	66119801	66120249	chr18	-0.32	0.023114	chr18:66119801-66120249	CPLX4
Alpk2	ENSMUSG00000032845	11925	65541228	65542006	chr18	-0.39	0.023169	chr18:65541228-65542006	ALPK2
Smarca2	ENSMUSG00000024921	2487	26828586	26829260	chr19	-0.37	0.023180	chr19:26828586-26829260	SMARCA2
Tgfbr2	ENSMUSG00000032440	38594	116045665	116045916	chr9	-0.39	0.023203	chr9:116045665-116045916	TGFBR2
Itgal	ENSMUSG00000030830	2554	134437167	134437269	chr7	-0.65	0.023246	chr7:134437167-134437269	ITGAL
Npffr1	ENSMUSG00000020090	26354	61084493	61084675	chr10	-0.65	0.023307	chr10:61084493-61084675	NPFFR1
Cxcr5	ENSMUSG00000047880	2220	44336636	44336812	chr9	-0.29	0.023386	chr9:44336636-44336812	CXCR5
Mreg	ENSMUSG00000039395	8742	72250097	72250183	chr1	-0.46	0.023410	chr1:72250097-72250183	MREG
Itpr2	ENSMUSG00000030287	22439	146220041	146220693	chr6	-0.28	0.023420	chr6:146220041-146220693	ITPR2
Mogat2	ENSMUSG00000052396	10927	106397794	106398320	chr7	-0.26	0.023469	chr7:106397794-106398320	MOGAT2
Katnal1	ENSMUSG00000041298	3920	149788673	149788826	chr5	-0.47	0.023532	chr5:149788673-149788826	KATNAL1
Lyst	ENSMUSG00000019726	36632	13645960	13646123	chr13	-0.45	0.023595	chr13:13645960-13646123	LYST
Map2k6	ENSMUSG00000020623	37840	110300413	110301287	chr11	-0.34	0.023625	chr11:110300413-110301287	MAP2K6
Fam134b	ENSMUSG00000022270	20540	25849885	25850316	chr15	-0.51	0.023650	chr15:25849885-25850316	FAM134B
Lrch1	ENSMUSG00000068015	18538	75328755	75329538	chr14	-0.31	0.023673	chr14:75328755-75329538	LRCH1
Stat5b	ENSMUSG00000020919	9146	100692919	100693057	chr11	-0.30	0.023720	chr11:100692919-100693057	STAT5B
Rasgrp1	ENSMUSG00000027347	38616	117129268	117130392	chr2	-0.34	0.023820	chr2:117129268-117130392	RASGRP1
Laptm5	ENSMUSG00000028581	3136	130474584	130475412	chr4	-0.32	0.023829	chr4:130474584-130475412	LAPTM5
D10Jhu81e	ENSMUSG00000053329	35127	77597051	77597723	chr10	-0.43	0.023943	chr10:77597051-77597723	C21orf33
D10Jhu81e	ENSMUSG00000053329	35127	77597051	77597723	chr10	-0.43	0.023943	chr10:77597051-77597723	LOC102724023
Plek2	ENSMUSG00000021118	4768	80012355	80013086	chr12	-0.30	0.024045	chr12:80012355-80013086	PLEK2
Rhobtb1	ENSMUSG00000019944	17376	68710778	68711239	chr10	-0.36	0.024049	chr10:68710778-68711239	RHOBTB1
St6gal1	ENSMUSG00000022885	8114	23234155	23234256	chr16	-0.45	0.024105	chr16:23234155-23234256	ST6GAL1
Shb	ENSMUSG00000044813	29700	45465507	45466442	chr4	-0.47	0.024509	chr4:45465507-45466442	SHB
Dgkh	ENSMUSG00000034731	39418	79085336	79085619	chr14	-0.46	0.024546	chr14:79085336-79085619	DGKH
Dll1	ENSMUSG00000014773	3696	15517286	15517778	chr17	-0.30	0.024577	chr17:15517286-15517778	DLL1
Rab8b	ENSMUSG00000036943	3184	66763937	66764619	chr9	-0.27	0.024582	chr9:66763937-66764619	RAB8B
Nudt3	ENSMUSG00000024213	8886	27729066	27729235	chr17	-0.33	0.024758	chr17:27729066-27729235	NUDT3
Bmp2k	ENSMUSG00000034663	9180	97435765	97436006	chr5	-0.38	0.024780	chr5:97435765-97436006	BMP2K
Csrnp1	ENSMUSG00000032515	3497	119889781	119889949	chr9	-0.55	0.024851	chr9:119889781-119889949	CSRNP1
10-Sep	ENSMUSG00000059248	8918	117178762	117178895	chr11	-0.59	0.024884	chr11:117178762-117178895	SEPT9
Kdm2b	ENSMUSG00000029475	5166	123345056	123345340	chr5	-0.43	0.024926	chr5:123345056-123345340	KDM2B
Rras2	ENSMUSG00000055723	16601	121244669	121244721	chr7	-0.48	0.025007	chr7:121244669-121244721	RRAS2

Usp7	ENSMUSG00000022710	8817	8748231	8748355	chr16	-0.50	0.025083	chr16:8748231-8748355	USP7
Il2rb	ENSMUSG00000068227	15268	78340695	78340833	chr15	-0.54	0.025120	chr15:78340695-78340833	IL2RB
Gltscr1	ENSMUSG00000070808	15488	16599750	16600915	chr7	-0.26	0.025180	chr7:16599750-16600915	GLTSCR1
Pou2af1	ENSMUSG00000032053	47866	50973717	50974140	chr9	-0.32	0.025249	chr9:50973717-50974140	POU2AF1
Sgk1	ENSMUSG00000019970	18550	21666670	21666978	chr10	-0.42	0.025262	chr10:21666670-21666978	SGK1
Irgm2	ENSMUSG00000069874	22599	58052941	58053233	chr11	-0.38	0.025292	chr11:58052941-58053233	IRGM
Runx3	ENSMUSG00000070691	8450	134684738	134685294	chr4	-0.41	0.025292	chr4:134684738-134685294	RUNX3
Lasp1	ENSMUSG00000038366	3182	97691188	97691441	chr11	-0.40	0.025418	chr11:97691188-97691441	LASP1
Rap1gap2	ENSMUSG00000038807	37776	74292999	74293132	chr11	-0.53	0.025552	chr11:74292999-74293132	RAP1GAP2
Jakmip1	ENSMUSG00000063646	16244	37459999	37460728	chr5	-0.44	0.025592	chr5:37459999-37460728	JAKMIP1
Sh3pxd2a	ENSMUSG00000053617	13424	47524947	47526010	chr19	-0.38	0.025605	chr19:47524947-47526010	SH3PXD2A
Med13l	ENSMUSG00000018076	29658	119040310	119040458	chr5	-0.38	0.025627	chr5:119040310-119040458	MED13L
St3gal1	ENSMUSG00000013846	33242	66979075	66979252	chr15	-0.42	0.025674	chr15:66979075-66979252	ST3GAL1
Wnk2	ENSMUSG00000037989	45110	49110732	49111551	chr13	-0.29	0.025760	chr13:49110732-49111551	WNK2
Sh2d6	ENSMUSG00000052631	2104	72463116	72463245	chr6	-0.45	0.025861	chr6:72463116-72463245	SH2D6
Fbxo10	ENSMUSG00000048232	7919	45082549	45083041	chr4	-0.35	0.025882	chr4:45082549-45083041	FBXO10
Irak2	ENSMUSG00000060477	13838	113604830	113605177	chr6	-0.53	0.025930	chr6:113604830-113605177	IRAK2
Armc9	ENSMUSG00000062590	19244	88160189	88160579	chr1	-0.53	0.026033	chr1:88160189-88160579	ARMC9
Jakmip1	ENSMUSG00000063646	17062	37458643	37459788	chr5	-0.37	0.026150	chr5:37458643-37459788	JAKMIP1
Mab21l3	ENSMUSG00000044313	35876	101604158	101604382	chr3	-0.26	0.026176	chr3:101604158-101604382	MAB21L3
Qprt	ENSMUSG00000030674	8688	134255932	134257755	chr7	-0.30	0.026237	chr7:134255932-134257755	QPRT
Vps8	ENSMUSG00000033653	32580	21660147	21660416	chr16	-0.50	0.026356	chr16:21660147-21660416	VPS8
Ccrn4l	ENSMUSG00000023087	27150	51000576	51001861	chr3	-0.34	0.026501	chr3:51000576-51001861	CCRN4L
Rab21	ENSMUSG00000020132	17652	114769902	114770697	chr10	-0.48	0.026555	chr10:114769902-114770697	RAB21
Socs3	ENSMUSG00000053113	5247	117825027	117825479	chr11	-0.32	0.026645	chr11:117825027-117825479	SOCS3
Arl5c	ENSMUSG00000038352	2322	97859756	97859881	chr11	-0.50	0.026775	chr11:97859756-97859881	ARL5C
Insig2	ENSMUSG00000003721	29687	123173822	123174596	chr1	-0.44	0.026802	chr1:123173822-123174596	INSIG2
Kalrn	ENSMUSG00000061751	14325	34111387	34111615	chr16	-0.36	0.026833	chr16:34111387-34111615	KALRN
Cpne5	ENSMUSG00000024008	8002	29305219	29306034	chr17	-0.39	0.026839	chr17:29305219-29306034	CPNE5
Pdlim5	ENSMUSG00000028273	35029	142019681	142019889	chr3	-0.40	0.026900	chr3:142019681-142019889	PDLIM5
Chst11	ENSMUSG00000034612	19454	82467088	82468303	chr10	-0.47	0.026904	chr10:82467088-82468303	CHST11
Pecam1	ENSMUSG00000020717	10600	106601264	106601421	chr11	-0.38	0.026938	chr11:106601264-106601421	PECAM1
Vav2	ENSMUSG00000009621	11590	27211383	27211798	chr2	-0.48	0.027110	chr2:27211383-27211798	VAV2
Eif1b	ENSMUSG00000006941	13988	120387379	120388088	chr9	-0.27	0.027193	chr9:120387379-120388088	EIF1B
Osbpl10	ENSMUSG00000040875	22676	114953271	114954170	chr9	-0.25	0.027199	chr9:114953271-114954170	OSBPL10
2700060E02Rik	ENSMUSG00000021807	26795	20616192	20616310	chr14	-0.32	0.027321	chr14:20616192-20616310	C14orf166
Hspa4	ENSMUSG00000020361	7268	53120998	53121459	chr11	-0.44	0.027356	chr11:53120998-53121459	HSPA4
Lamc3	ENSMUSG00000026840	6194	31736584	31736649	chr2	-0.49	0.027391	chr2:31736584-31736649	LAMC3
Rnf157	ENSMUSG00000052949	3364	116270921	116270986	chr11	-0.51	0.027428	chr11:116270921-116270986	RNF157
Adamtsl4	ENSMUSG00000015850	4974	95496690	95496939	chr3	-0.30	0.027450	chr3:95496690-95496939	ADAMTSL4

Tekt4	ENSMUSG00000024175	18443	25589982	25590200	chr17	-0.30	0.027506	chr17:25589982-25590200	TEKT4
Eepd1	ENSMUSG00000036611	27634	25317913	25318255	chr9	-0.44	0.027508	chr9:25317913-25318255	EEPD1
Fam83a	ENSMUSG00000051225	12097	57804691	57805059	chr15	-0.46	0.027558	chr15:57804691-57805059	FAM83A
Rnf145	ENSMUSG00000019189	17882	44352353	44352546	chr11	-0.51	0.027835	chr11:44352353-44352546	RNF145
Pik3ap1	ENSMUSG00000025017	17850	41477360	41477512	chr19	-0.35	0.027961	chr19:41477360-41477512	PIK3AP1
Asxl1	ENSMUSG00000042548	2878	153175767	153177064	chr2	-0.30	0.027974	chr2:153175767-153177064	ASXL1
Eml4	ENSMUSG00000032624	27098	83722832	83723511	chr17	-0.37	0.027982	chr17:83722832-83723511	EML4
Nlrp2	ENSMUSG00000035177	12770	5315313	5315504	chr7	-0.33	0.028005	chr7:5315313-5315504	NLRP2
Tmem189	ENSMUSG00000090213	4594	167475162	167475381	chr2	-0.41	0.028039	chr2:167475162-167475381	TMEM189
Rad54b	ENSMUSG00000066307	2351	11504383	11504535	chr4	-0.39	0.028155	chr4:11504383-11504535	RAD54B
Vrk1	ENSMUSG00000021115	42520	107205385	107206518	chr12	-0.37	0.028233	chr12:107205385-107206518	VRK1
Snx9	ENSMUSG00000002365	21220	5862140	5862988	chr17	-0.31	0.028366	chr17:5862140-5862988	SNX9
Pecam1	ENSMUSG00000020717	6589	106605306	106605400	chr11	-0.31	0.028387	chr11:106605306-106605400	PECAM1
Os9	ENSMUSG00000040462	2368	126560518	126560649	chr10	-0.46	0.028407	chr10:126560518-126560649	OS9
Pag1	ENSMUSG00000027508	45359	9878974	9879104	chr3	-0.53	0.028512	chr3:9878974-9879104	PAG1
Nxnl2	ENSMUSG00000021396	9010	51257045	51257718	chr13	-0.30	0.028632	chr13:51257045-51257718	NXNL2
Aff3	ENSMUSG00000037138	27436	38623758	38624490	chr1	-0.38	0.028752	chr1:38623758-38624490	AFF3
Ciita	ENSMUSG00000075404	6575	10496262	10496636	chr16	-0.43	0.028785	chr16:10496262-10496636	CIITA
Nufip1	ENSMUSG00000022009	37832	76548259	76548797	chr14	-0.37	0.028813	chr14:76548259-76548797	NUFIP1
Adcy9	ENSMUSG00000005580	37920	4381219	4382118	chr16	-0.30	0.028849	chr16:4381219-4382118	ADCY9
Plcl2	ENSMUSG00000038910	9705	50639122	50639208	chr17	-0.51	0.028849	chr17:50639122-50639208	PLCL2
Smap2	ENSMUSG00000032870	6862	120696489	120696939	chr4	-0.38	0.028875	chr4:120696489-120696939	SMAP2
Otp	ENSMUSG00000021685	37284	95608125	95608466	chr13	-0.31	0.028913	chr13:95608125-95608466	OTP
Rasa2	ENSMUSG00000032413	18341	96550200	96550554	chr9	-0.41	0.029024	chr9:96550200-96550554	RASA2
Lrch1	ENSMUSG00000068015	13402	75248389	75248582	chr14	-0.44	0.029033	chr14:75248389-75248582	LRCH1
Jmjd1c	ENSMUSG00000037876	15436	66663818	66664055	chr10	-0.26	0.029086	chr10:66663818-66664055	JMJD1C
Tbc1d22a	ENSMUSG00000051864	15252	86059553	86060932	chr15	-0.32	0.029091	chr15:86059553-86060932	TBC1D22A
Slc1a3	ENSMUSG00000005360	17520	8575592	8575865	chr15	-0.27	0.029193	chr15:8575592-8575865	SLC1A3
Phf2	ENSMUSG00000038025	7442	48958615	48959010	chr13	-0.37	0.029207	chr13:48958615-48959010	PHF2
Pan3	ENSMUSG00000029647	18380	148260267	148260800	chr5	-0.37	0.029405	chr5:148260267-148260800	PAN3
Agpat4	ENSMUSG00000023827	9830	12354414	12354517	chr17	-0.57	0.029461	chr17:12354414-12354517	AGPAT4
Stk40	ENSMUSG00000042608	6442	125787152	125788289	chr4	-0.40	0.029656	chr4:125787152-125788289	STK40
Plg	ENSMUSG00000059481	14310	12556861	12557466	chr17	-0.48	0.029721	chr17:12556861-12557466	PLG
Rnf130	ENSMUSG00000020376	13474	49852192	49852452	chr11	-0.29	0.029751	chr11:49852192-49852452	RNF130
Manba	ENSMUSG00000028164	5551	135231581	135231829	chr3	-0.27	0.029823	chr3:135231581-135231829	MANBA
Srsf9	ENSMUSG00000029538	7494	115769365	115770016	chr5	-0.41	0.029824	chr5:115769365-115770016	SRSF9
Cdyl	ENSMUSG00000059288	3123	35909602	35909876	chr13	-0.40	0.029941	chr13:35909602-35909876	CDYL
Gramd1b	ENSMUSG00000040111	46496	40385384	40385543	chr9	-0.50	0.030076	chr9:40385384-40385543	GRAMD1B
Tox2	ENSMUSG00000074607	25886	163076913	163077236	chr2	-0.35	0.030084	chr2:163076913-163077236	TOX2
Snx10	ENSMUSG00000038301	12185	51506630	51506868	chr6	-0.63	0.030192	chr6:51506630-51506868	SNX10

Acvrl1	ENSMUSG00000000530	12598	100980505	100980752	chr15	-0.41	0.030202	chr15:100980505-100980752	ACVRL1
Adora2a	ENSMUSG00000020178	10135	74789671	74789971	chr10	-0.54	0.030245	chr10:74789671-74789971	ADORA2A
Dennd1b	ENSMUSG00000056268	8128	140851593	140852175	chr1	-0.33	0.030251	chr1:140851593-140852175	DENND1B
Adck5	ENSMUSG00000022550	2950	76420749	76421084	chr15	-0.57	0.030274	chr15:76420749-76421084	ADCK5
Mchr1	ENSMUSG00000050164	42514	81108371	81108514	chr15	-0.46	0.030316	chr15:81108371-81108514	MCHR1
Slc29a3	ENSMUSG00000020100	7906	60207447	60207802	chr10	-0.41	0.030338	chr10:60207447-60207802	SLC29A3
Pcyt1a	ENSMUSG00000005615	3084	32434345	32434451	chr16	-0.56	0.030339	chr16:32434345-32434451	PCYT1A
Acvr1b	ENSMUSG00000000532	14178	101018303	101019161	chr15	-0.27	0.030384	chr15:101018303-101019161	ACVR1B
Chrac1	ENSMUSG00000068391	46940	72967497	72968063	chr15	-0.42	0.030388	chr15:72967497-72968063	CHRAC1
Crb2	ENSMUSG00000035403	9060	37622115	37623302	chr2	-0.36	0.030552	chr2:37622115-37623302	CRB2
Nufip1	ENSMUSG00000022009	38950	76549385	76549908	chr14	-0.54	0.030586	chr14:76549385-76549908	NUFIP1
Gltscr1	ENSMUSG00000070808	19166	16603520	16604499	chr7	-0.28	0.030615	chr7:16603520-16604499	GLTSCR1
Lbx1	ENSMUSG00000025216	5906	45303985	45304806	chr19	-0.29	0.030653	chr19:45303985-45304806	LBX1
Popdc2	ENSMUSG00000022803	27928	38399487	38400533	chr16	-0.31	0.030672	chr16:38399487-38400533	POPDC2
Ccdc38	ENSMUSG00000036168	2508	93029861	93030303	chr10	-0.39	0.030675	chr10:93029861-93030303	CCDC38
Rab6b	ENSMUSG00000032549	19596	102994716	102994897	chr9	-0.61	0.030828	chr9:102994716-102994897	RAB6B
Trim8	ENSMUSG00000025034	27414	46602852	46604247	chr19	-0.34	0.030878	chr19:46602852-46604247	TRIM8
Alpk2	ENSMUSG00000032845	17894	65490735	65491853	chr18	-0.26	0.031016	chr18:65490735-65491853	ALPK2
Dnase1	ENSMUSG00000005980	6776	4029678	4030649	chr16	-0.52	0.031043	chr16:4029678-4030649	DNASE1
Tmem173	ENSMUSG00000024349	5380	35905331	35905844	chr18	-0.36	0.031086	chr18:35905331-35905844	TMEM173
Phc2	ENSMUSG00000028796	7096	128412017	128412624	chr4	-0.36	0.031281	chr4:128412017-128412624	PHC2
Cd69	ENSMUSG00000030156	8112	129233429	129233572	chr6	-0.58	0.031453	chr6:129233429-129233572	CD69
Bcl9	ENSMUSG00000038256	27504	97059944	97060605	chr3	-0.37	0.031569	chr3:97059944-97060605	BCL9
Tbc1d14	ENSMUSG00000029192	14654	36891802	36892301	chr5	-0.34	0.031577	chr5:36891802-36892301	TBC1D14
Dmbx1	ENSMUSG00000028707	23406	115635882	115635993	chr4	-0.50	0.031604	chr4:115635882-115635993	DMBX1
St6galnac6	ENSMUSG00000026811	2954	32457971	32458533	chr2	-0.29	0.031659	chr2:32457971-32458533	ST6GALNAC6
Cyth1	ENSMUSG00000017132	10138	118098375	118098489	chr11	-0.70	0.031672	chr11:118098375-118098489	CYTH1
Asb2	ENSMUSG00000021200	3172	104579668	104579844	chr12	-0.62	0.031672	chr12:104579668-104579844	ASB2
Gng7	ENSMUSG00000048240	7586	80453289	80453412	chr10	-0.63	0.031688	chr10:80453289-80453412	GNG7
Elmo1	ENSMUSG00000041112	8258	20285401	20285698	chr13	-0.25	0.031689	chr13:20285401-20285698	ELMO1
Ptk2b	ENSMUSG00000059456	25985	66814887	66815323	chr14	-0.27	0.031692	chr14:66814887-66815323	PTK2B
Ehd4	ENSMUSG00000027293	18702	119936424	119937097	chr2	-0.31	0.031738	chr2:119936424-119937097	EHD4
Micu1	ENSMUSG00000020111	8172	59156967	59157136	chr10	-0.50	0.031818	chr10:59156967-59157136	MICU1
Zfp664	ENSMUSG00000079215	38520	125403221	125403696	chr5	-0.32	0.031826	chr5:125403221-125403696	ZNF664
Prrc2b	ENSMUSG00000039262	4112	32010662	32010761	chr2	-0.51	0.031831	chr2:32010662-32010761	PRRC2B
Fscn1	ENSMUSG00000029581	32358	143763721	143764519	chr5	-0.48	0.031864	chr5:143763721-143764519	FSCN1
Dnajb12	ENSMUSG00000020109	6280	59348487	59348817	chr10	-0.34	0.031890	chr10:59348487-59348817	DNAJB12
Prex1	ENSMUSG00000039621	8210	166456117	166456400	chr2	-0.50	0.031919	chr2:166456117-166456400	PREX1
Tmem131	ENSMUSG00000026116	12865	36983418	36983596	chr1	-0.30	0.031933	chr1:36983418-36983596	TMEM131
Dbf4	ENSMUSG00000002297	5665	8416750	8417084	chr5	-0.49	0.031968	chr5:8416750-8417084	DBF4

Tmem201	ENSMUSG00000044700	3962	149116028	149116203	chr4	-0.26	0.032116	chr4:149116028-149116203	TMEM201
Abcc4	ENSMUSG00000032849	6050	119099068	119099715	chr14	-0.34	0.032137	chr14:119099068-119099715	ABCC4
Trak1	ENSMUSG00000032536	3452	121209951	121210188	chr9	-0.36	0.032187	chr9:121209951-121210188	TRAK1
Neurl1a	ENSMUSG00000006435	6830	47296424	47296580	chr19	-0.61	0.032405	chr19:47296424-47296580	NEURL1
Setd3	ENSMUSG00000056770	27341	109325754	109325880	chr12	-0.78	0.032422	chr12:109325754-109325880	SETD3
Arhgap32	ENSMUSG00000041444	30238	31953739	31954176	chr9	-0.32	0.032445	chr9:31953739-31954176	ARHGAP32
Glrx	ENSMUSG00000021591	7082	75970054	75970409	chr13	-0.41	0.032458	chr13:75970054-75970409	GLRX
Lrrfip1	ENSMUSG00000026305	9112	92959082	92959465	chr1	-0.44	0.032489	chr1:92959082-92959465	LRRFIP1
Pacsin2	ENSMUSG00000016664	15091	83278048	83278694	chr15	-0.28	0.032503	chr15:83278048-83278694	PACSIN2
Sema4b	ENSMUSG00000030539	6820	87324847	87324964	chr7	-0.30	0.032514	chr7:87324847-87324964	SEMA4B
Car13	ENSMUSG00000027555	12522	14654069	14654427	chr3	-0.55	0.032631	chr3:14654069-14654427	CA13
Arid3a	ENSMUSG00000019564	6602	79399514	79400026	chr10	-0.46	0.032697	chr10:79399514-79400026	ARID3A
Mctp2	ENSMUSG00000032776	35034	79416128	79416768	chr7	-0.37	0.032824	chr7:79416128-79416768	MCTP2
Stx7	ENSMUSG00000019998	13211	23882090	23882576	chr10	-0.40	0.032928	chr10:23882090-23882576	STX7
Arhgap8	ENSMUSG00000078954	14070	84536344	84536476	chr15	-0.51	0.032954	chr15:84536344-84536476	ARHGAP8
Arhgap8	ENSMUSG00000078954	14070	84536344	84536476	chr15	-0.51	0.032954	chr15:84536344-84536476	PRR5-ARHGAP8
Cotl1	ENSMUSG00000031827	28648	122335633	122335916	chr8	-0.31	0.032958	chr8:122335633-122335916	COTL1
Bptf	ENSMUSG00000040481	8694	107001903	107002370	chr11	-0.34	0.033062	chr11:107001903-107002370	BPTF
Tnfrsf8	ENSMUSG00000028602	14678	144890009	144890735	chr4	-0.26	0.033093	chr4:144890009-144890735	TNFRSF8
Zmiz1	ENSMUSG00000007817	6480	26433750	26433853	chr14	-0.49	0.033166	chr14:26433750-26433853	ZMIZ1
Bcl9l	ENSMUSG00000063382	11447	44318583	44318747	chr9	-0.40	0.033185	chr9:44318583-44318747	BCL9L
Strbp	ENSMUSG00000026915	27738	37586798	37587437	chr2	-0.35	0.033253	chr2:37586798-37587437	STRBP
Pik3c2b	ENSMUSG00000026447	39112	134981580	134981821	chr1	-0.48	0.033268	chr1:134981580-134981821	PIK3C2B
Sox13	ENSMUSG00000070643	5813	135315082	135315200	chr1	-0.57	0.033334	chr1:135315082-135315200	SOX13
Lnpep	ENSMUSG00000023845	16932	17744474	17744570	chr17	-0.56	0.033455	chr17:17744474-17744570	LNPEP
Sipa1l2	ENSMUSG00000001995	35408	128051925	128052111	chr8	-0.48	0.033578	chr8:128051925-128052111	SIPA1L2
Ccdc12	ENSMUSG00000019659	4818	110563532	110564117	chr9	-0.52	0.033588	chr9:110563532-110564117	CCDC12
Zbtb38	ENSMUSG00000040433	5926	96638888	96639344	chr9	-0.47	0.033673	chr9:96638888-96639344	ZBTB38
Dock11	ENSMUSG00000031093	3644	33432363	33432577	chrX	-0.34	0.033773	chrX:33432363-33432577	DOCK11
Plekho2	ENSMUSG00000050721	5338	65422440	65422579	chr9	-0.42	0.033811	chr9:65422440-65422579	PLEKHO2
Ccdc88b	ENSMUSG00000047810	13429	6945938	6946324	chr19	-0.36	0.033934	chr19:6945938-6946324	CCDC88B
Stt3b	ENSMUSG00000032437	18584	115200312	115201599	chr9	-0.26	0.034023	chr9:115200312-115201599	STT3B
Grik3	ENSMUSG00000001985	9228	125158639	125158788	chr4	-0.70	0.034027	chr4:125158639-125158788	GRIK3
Sh3bp2	ENSMUSG00000054520	4758	34863383	34864073	chr5	-0.27	0.034124	chr5:34863383-34864073	SH3BP2
Lrrfip1	ENSMUSG00000026305	32786	92982597	92983298	chr1	-0.46	0.034181	chr1:92982597-92983298	LRRFIP1
6330403A02Rik	ENSMUSG00000053963	25344	182438804	182439079	chr1	-0.52	0.034252	chr1:182438804-182439079	C1orf95
Usp15	ENSMUSG00000020124	41102	122592757	122593024	chr10	-0.36	0.034354	chr10:122592757-122593024	USP15
Ahcyl1	ENSMUSG00000027893	9076	107489528	107490084	chr3	-0.45	0.034375	chr3:107489528-107490084	AHCYL1
Mxd1	ENSMUSG00000001156	14414	86604611	86604870	chr6	-0.40	0.034448	chr6:86604611-86604870	MXD1
Ccdc12	ENSMUSG00000019659	9059	110566969	110569161	chr9	-0.30	0.034453	chr9:110566969-110569161	CCDC12

Apobec2	ENSMUSG00000040694	5060	48566245	48567744	chr17	-0.38	0.034474	chr17:48566245-48567744	APOBEC2
Map3k5	ENSMUSG00000071369	3508	19674222	19674515	chr10	-0.44	0.034574	chr10:19674222-19674515	MAP3K5
Capn10	ENSMUSG00000026270	10182	94853552	94853732	chr1	-0.29	0.034602	chr1:94853552-94853732	CAPN10
Lpgat1	ENSMUSG00000026623	2594	193538747	193539490	chr1	-0.34	0.034610	chr1:193538747-193539490	LPGAT1
Papss1	ENSMUSG00000028032	3748	131223731	131224233	chr3	-0.28	0.034620	chr3:131223731-131224233	PAPSS1
Bcar3	ENSMUSG00000028121	17317	122105210	122105548	chr3	-0.36	0.034738	chr3:122105210-122105548	BCAR3
Lrrc3	ENSMUSG00000051652	9588	77355631	77355756	chr10	-0.62	0.034837	chr10:77355631-77355756	LRRC3
Plekho2	ENSMUSG00000050721	4550	65422685	65423912	chr9	-0.31	0.034897	chr9:65422685-65423912	PLEKHO2
Inpp5d	ENSMUSG00000026288	17392	89554994	89555845	chr1	-0.39	0.034962	chr1:89554994-89555845	INPP5D
Kcnv2	ENSMUSG00000047298	41958	27438849	27439220	chr19	-0.43	0.034965	chr19:27438849-27439220	KCNV2
Il17d	ENSMUSG00000050222	12542	58156639	58156737	chr14	-0.43	0.034977	chr14:58156639-58156737	IL17D
Otub2	ENSMUSG00000021203	6442	104633563	104633710	chr12	-0.36	0.035072	chr12:104633563-104633710	OTUB2
Dock11	ENSMUSG00000031093	16540	33445315	33445417	chrX	-0.45	0.035166	chrX:33445315-33445417	DOCK11
Osbpl8	ENSMUSG00000020189	4729	110596994	110597260	chr10	-0.46	0.035172	chr10:110596994-110597260	OSBPL8
Wdr73	ENSMUSG00000025722	10666	88034425	88035024	chr7	-0.40	0.035207	chr7:88034425-88035024	WDR73
Ube2g1	ENSMUSG00000020794	12164	72408550	72408691	chr11	-0.41	0.035273	chr11:72408550-72408691	UBE2G1
Golim4	ENSMUSG00000034109	43423	75639326	75639688	chr3	-0.45	0.035306	chr3:75639326-75639688	GOLIM4
Mttp	ENSMUSG00000028158	12712	137781552	137781709	chr3	-0.57	0.035309	chr3:137781552-137781709	MTTP
Cdk5r1	ENSMUSG00000048895	12721	80303053	80303501	chr11	-0.48	0.035343	chr11:80303053-80303501	CDK5R1
Rasa3	ENSMUSG00000031453	5651	13671591	13672011	chr8	-0.29	0.035460	chr8:13671591-13672011	RASA3
Runx1	ENSMUSG00000022952	41546	92867758	92867958	chr16	-0.33	0.035520	chr16:92867758-92867958	RUNX1
Fam46c	ENSMUSG00000044468	8855	100284070	100284456	chr3	-0.45	0.035524	chr3:100284070-100284456	FAM46C
Trim8	ENSMUSG00000025034	22960	46598796	46599396	chr19	-0.45	0.035536	chr19:46598796-46599396	TRIM8
Trim8	ENSMUSG00000025034	16930	46593022	46593109	chr19	-0.60	0.035561	chr19:46593022-46593109	TRIM8
Dnajb12	ENSMUSG00000020109	31566	59373840	59374035	chr10	-0.31	0.035564	chr10:59373840-59374035	DNAJB12
Pkib	ENSMUSG00000019876	9700	57380386	57380586	chr10	-0.27	0.035610	chr10:57380386-57380586	PKIB
Kif13b	ENSMUSG00000060012	2448	65268876	65269103	chr14	-0.50	0.035617	chr14:65268876-65269103	KIF13B
Rab35	ENSMUSG00000029518	3572	116085199	116086240	chr5	-0.32	0.035645	chr5:116085199-116086240	RAB35
Arhgap22	ENSMUSG00000063506	14920	34044669	34045186	chr14	-0.52	0.035673	chr14:34044669-34045186	ARHGAP22
Uvrag	ENSMUSG00000035354	2542	106291672	106292721	chr7	-0.25	0.035701	chr7:106291672-106292721	UVRAG
Mpp6	ENSMUSG00000038388	33864	50096191	50096677	chr6	-0.28	0.035743	chr6:50096191-50096677	MPP6
Iqsec1	ENSMUSG00000034312	3748	90670206	90670338	chr6	-0.44	0.035841	chr6:90670206-90670338	IQSEC1
Prex1	ENSMUSG00000039621	13502	166450889	166451043	chr2	-0.51	0.035862	chr2:166450889-166451043	PREX1
Fam134b	ENSMUSG00000022270	18904	25791849	25791995	chr15	-0.57	0.035866	chr15:25791849-25791995	FAM134B
Usp7	ENSMUSG00000022710	8160	8729859	8729960	chr16	-0.43	0.035931	chr16:8729859-8729960	USP7
Vps53	ENSMUSG00000017288	26204	75879916	75880041	chr11	-0.41	0.035968	chr11:75879916-75880041	VPS53
Klrg1	ENSMUSG00000030114	12312	122245122	122245301	chr6	-0.48	0.036172	chr6:122245122-122245301	KLRG1
Pde6h	ENSMUSG00000064330	21260	136928891	136929190	chr6	-0.27	0.036228	chr6:136928891-136929190	PDE6H
Tbc1d9	ENSMUSG00000031709	33461	85655430	85656148	chr8	-0.30	0.036264	chr8:85655430-85656148	TBC1D9
Rwdd3	ENSMUSG00000028133	4948	120866497	120866874	chr3	-0.27	0.036309	chr3:120866497-120866874	RWDD3

Mgll	ENSMUSG00000033174	6652	88681340	88681603	chr6	-0.36	0.036353	chr6:88681340-88681603	MGLL
Mrpl15	ENSMUSG00000033845	17168	4758554	4758658	chr1	-0.43	0.036369	chr1:4758554-4758658	MRPL15
Mbp	ENSMUSG00000041607	4324	82649049	82649118	chr18	-0.42	0.036462	chr18:82649049-82649118	MBP
Foxk1	ENSMUSG00000056493	29516	142847885	142847982	chr5	-0.44	0.036484	chr5:142847885-142847982	FOXK1
Rassf3	ENSMUSG00000025795	7521	120905641	120905929	chr10	-0.58	0.036540	chr10:120905641-120905929	RASSF3
Rapgef1	ENSMUSG00000039844	39268	29518632	29518831	chr2	-0.47	0.036548	chr2:29518632-29518831	RAPGEF1
Igf2bp3	ENSMUSG00000029814	3448	49168046	49168759	chr6	-0.30	0.036559	chr6:49168046-49168759	IGF2BP3
Srgap2	ENSMUSG00000026425	46197	133275804	133275886	chr1	-0.38	0.036647	chr1:133275804-133275886	SRGAP2
D930015E06Rik	ENSMUSG00000033767	5194	83838701	83839079	chr3	-0.26	0.036653	chr3:83838701-83839079	KIAA0922
Bmp10	ENSMUSG00000030046	18216	87396387	87398032	chr6	-0.25	0.036662	chr6:87396387-87398032	BMP10
Fscn1	ENSMUSG00000029581	30766	143762240	143762816	chr5	-0.52	0.036855	chr5:143762240-143762816	FSCN1
Fam129a	ENSMUSG00000026483	12154	153536407	153536492	chr1	-0.69	0.037007	chr1:153536407-153536492	FAM129A
Nfatc1	ENSMUSG00000033016	17950	80886607	80887318	chr18	-0.47	0.037195	chr18:80886607-80887318	NFATC1
Tmem189	ENSMUSG00000090213	4058	167474597	167474874	chr2	-0.33	0.037232	chr2:167474597-167474874	TMEM189
Elf4	ENSMUSG00000031103	25609	45781642	45781832	chrX	-0.50	0.037588	chrX:45781642-45781832	ELF4
Ppp2r2a	ENSMUSG00000022052	24368	67666840	67666955	chr14	-0.40	0.037671	chr14:67666840-67666955	PPP2R2A
Socs1	ENSMUSG00000038037	15716	10769511	10770318	chr16	-0.50	0.037697	chr16:10769511-10770318	SOCS1
Cryz	ENSMUSG00000028199	7153	154267378	154267728	chr3	-0.58	0.037719	chr3:154267378-154267728	CRYZ
Cyth1	ENSMUSG00000017132	7642	118101891	118102456	chr11	-0.30	0.037756	chr11:118101891-118102456	CYTH1
Uvrag	ENSMUSG00000035354	6162	106295250	106296383	chr7	-0.28	0.037789	chr7:106295250-106296383	UVRAG
Begain	ENSMUSG00000040867	17750	110309286	110309395	chr12	-0.45	0.037800	chr12:110309286-110309395	BEGAIN
Lrrc32	ENSMUSG00000090958	6931	105635514	105636084	chr7	-0.30	0.037834	chr7:105635514-105636084	LRRC32
Plcg2	ENSMUSG00000034330	32719	120054712	120055106	chr8	-0.39	0.037992	chr8:120054712-120055106	PLCG2
Elmo1	ENSMUSG00000041112	30446	20212669	20213195	chr13	-0.27	0.038065	chr13:20212669-20213195	ELMO1
Vgll4	ENSMUSG00000030315	3119	114868542	114868900	chr6	-0.50	0.038175	chr6:114868542-114868900	VGLL4
Fgd6	ENSMUSG00000020021	6408	93528826	93528931	chr10	-0.50	0.038219	chr10:93528826-93528931	FGD6
Etv6	ENSMUSG00000030199	25494	134158053	134158190	chr6	-0.37	0.038224	chr6:134158053-134158190	ETV6
Dtnb	ENSMUSG00000071454	3016	3771065	3771532	chr12	-0.34	0.038232	chr12:3771065-3771532	DTNB
Fam49b	ENSMUSG00000022378	40238	63932176	63932319	chr15	-0.52	0.038284	chr15:63932176-63932319	FAM49B
Mtss1	ENSMUSG00000022353	3174	58875232	58875420	chr15	-0.35	0.038330	chr15:58875232-58875420	MTSS1
Cpm	ENSMUSG00000020183	10904	117077334	117077583	chr10	-0.46	0.038359	chr10:117077334-117077583	CPM
Acvr1b	ENSMUSG00000000532	16486	101020358	101021723	chr15	-0.25	0.038476	chr15:101020358-101021723	ACVR1B
Ido1	ENSMUSG00000031551	9632	25716767	25717461	chr8	-0.38	0.038775	chr8:25716767-25717461	IDO1
Pcnx	ENSMUSG00000021140	6090	82954858	82954994	chr12	-0.48	0.038903	chr12:82954858-82954994	PCNX
Uck2	ENSMUSG00000026558	15844	169198650	169200178	chr1	-0.26	0.038951	chr1:169198650-169200178	UCK2
Fgfbp3	ENSMUSG00000047632	15336	36978446	36979093	chr19	-0.43	0.038993	chr19:36978446-36979093	FGFBP3
Lefty2	ENSMUSG00000066652	8519	182814482	182814956	chr1	-0.41	0.039000	chr1:182814482-182814956	LEFTY2
Stap1	ENSMUSG00000029254	3806	86504590	86504695	chr5	-0.55	0.039185	chr5:86504590-86504695	STAP1
Stat5b	ENSMUSG00000020919	4063	100687454	100688356	chr11	-0.26	0.039348	chr11:100687454-100688356	STAT5B
Ppa2	ENSMUSG00000028013	3812	132997690	132998482	chr3	-0.31	0.039402	chr3:132997690-132998482	PPA2

10-Sep	ENSMUSG00000059248	3216	117210902	117211651	chr11	-0.37	0.039462	chr11:117210902-117211651	SEPT9
Mob3a	ENSMUSG00000003348	9040	80154789	80156264	chr10	-0.39	0.039489	chr10:80154789-80156264	MOB3A
Nkd1	ENSMUSG00000031661	43030	91094340	91094781	chr8	-0.51	0.039496	chr8:91094340-91094781	NKD1
Gna15	ENSMUSG00000034792	4906	80979863	80980717	chr10	-0.34	0.039533	chr10:80979863-80980717	GNA15
Smap1	ENSMUSG00000026155	13150	23942227	23942384	chr1	-0.35	0.039652	chr1:23942227-23942384	SMAP1
Nceh1	ENSMUSG00000027698	5452	27092616	27093012	chr3	-0.40	0.039756	chr3:27092616-27093012	NCEH1
Bmp2k	ENSMUSG00000034663	28720	97397711	97398260	chr5	-0.29	0.039792	chr5:97397711-97398260	BMP2K
Fam3c	ENSMUSG00000029672	2586	22303406	22303571	chr6	-0.35	0.039793	chr6:22303406-22303571	FAM3C
Ncor2	ENSMUSG00000029478	3218	125532683	125533598	chr5	-0.37	0.039819	chr5:125532683-125533598	NCOR2
Mgst3	ENSMUSG00000026688	19048	169304597	169305250	chr1	-0.48	0.039891	chr1:169304597-169305250	MGST3
Fscn1	ENSMUSG00000029581	4834	143736191	143737002	chr5	-0.45	0.039921	chr5:143736191-143737002	FSCN1
Zfp217	ENSMUSG00000052056	4470	169951863	169952636	chr2	-0.26	0.039940	chr2:169951863-169952636	ZNF217
Ptp4a3	ENSMUSG00000059895	4904	73548612	73548727	chr15	-0.42	0.039960	chr15:73548612-73548727	PTP4A3
Yipf2	ENSMUSG00000032182	8508	21405634	21405831	chr9	-0.55	0.039965	chr9:21405634-21405831	YIPF2
Ahcyl2	ENSMUSG00000029772	14962	29788747	29788862	chr6	-0.54	0.040034	chr6:29788747-29788862	AHCYL2
Id2	ENSMUSG00000020644	47620	25828310	25828845	chr12	-0.36	0.040057	chr12:25828310-25828845	ID2
Tmem139	ENSMUSG00000071506	4572	42207313	42207479	chr6	-0.39	0.040064	chr6:42207313-42207479	TMEM139
Smad7	ENSMUSG00000025880	44560	75578956	75579297	chr18	-0.34	0.040233	chr18:75578956-75579297	SMAD7
Pvrl1	ENSMUSG00000032012	17334	43569907	43570077	chr9	-0.47	0.040239	chr9:43569907-43570077	PVRL1
Tram1	ENSMUSG00000025935	9825	13589091	13590451	chr1	-0.27	0.040240	chr1:13589091-13590451	TRAM1
Eif2ak3	ENSMUSG00000031668	13774	70780666	70780803	chr6	-0.50	0.040297	chr6:70780666-70780803	EIF2AK3
Fam134b	ENSMUSG00000022270	18638	25791592	25791720	chr15	-0.39	0.040506	chr15:25791592-25791720	FAM134B
Acsf2	ENSMUSG00000076435	11944	94450713	94451567	chr11	-0.31	0.040621	chr11:94450713-94451567	ACSF2
Ddx6	ENSMUSG00000032097	29928	44382757	44383334	chr9	-0.35	0.040690	chr9:44382757-44383334	DDX6
Rbm38	ENSMUSG00000027510	4568	172852517	172853718	chr2	-0.40	0.040757	chr2:172852517-172853718	RBM38
Crybg3	ENSMUSG00000022723	8082	59516913	59517804	chr16	-0.28	0.040855	chr16:59516913-59517804	CRYBG3
4930523C07Rik	ENSMUSG00000050883	9634	161983732	161984963	chr1	-0.28	0.040886	chr1:161983732-161984963	KIAA0040
Ttc39b	ENSMUSG00000038172	5300	82919744	82920279	chr4	-0.32	0.040938	chr4:82919744-82920279	TTC39B
Spata13	ENSMUSG00000021990	9525	61342083	61342351	chr14	-0.36	0.040944	chr14:61342083-61342351	SPATA13
Arhgdib	ENSMUSG00000030220	4684	136894936	136895273	chr6	-0.32	0.040977	chr6:136894936-136895273	ARHGDIB
Sorcs2	ENSMUSG00000029093	48214	36660204	36660505	chr5	-0.33	0.040983	chr5:36660204-36660505	SORCS2
Plcg2	ENSMUSG00000034330	29985	120050232	120054118	chr8	-0.29	0.041034	chr8:120050232-120054118	PLCG2
Tec	ENSMUSG00000029217	35439	73223638	73224756	chr5	-0.29	0.041094	chr5:73223638-73224756	TEC
Adrbk1	ENSMUSG00000024858	4448	4300664	4300856	chr19	-0.28	0.041156	chr19:4300664-4300856	ADRBK1
Usp7	ENSMUSG00000022710	7158	8728478	8729339	chr16	-0.33	0.041159	chr16:8728478-8729339	USP7
Fgl2	ENSMUSG00000039899	2180	20880536	20880741	chr5	-0.43	0.041213	chr5:20880536-20880741	FGL2
Suclg2	ENSMUSG00000061838	44424	95564581	95564959	chr6	-0.42	0.041250	chr6:95564581-95564959	SUCLG2
Mpp6	ENSMUSG00000038388	2235	50062883	50063303	chr6	-0.35	0.041281	chr6:50062883-50063303	MPP6
Secisbp2l	ENSMUSG00000035093	9004	125617432	125617787	chr2	-0.44	0.041382	chr2:125617432-125617787	SECISBP2L
Ppp1r13b	ENSMUSG00000021285	44300	113154877	113155375	chr12	-0.43	0.041384	chr12:113154877-113155375	PPP1R13B

Tmem2	ENSMUSG00000024754	46072	21898745	21899060	chr19	-0.33	0.041444	chr19:21898745-21899060	TMEM2
Bbc3	ENSMUSG00000002083	33468	16932245	16932418	chr7	-0.57	0.041709	chr7:16932245-16932418	BBC3
Fnbp1	ENSMUSG00000075415	13918	30937906	30938295	chr2	-0.27	0.041853	chr2:30937906-30938295	FNBP1
Kmo	ENSMUSG00000039783	8046	177570330	177570499	chr1	-0.42	0.042012	chr1:177570330-177570499	KMO
Bbs5	ENSMUSG00000063145	26564	69458565	69458760	chr2	-0.55	0.042093	chr2:69458565-69458760	BBS5
Edaradd	ENSMUSG00000039309	21872	12634125	12635052	chr13	-0.31	0.042094	chr13:12634125-12635052	EDARADD
Sdhaf2	ENSMUSG00000024668	3166	10596437	10596632	chr19	-0.33	0.042097	chr19:10596437-10596632	SDHAF2
Adam18	ENSMUSG00000031552	8432	25776635	25776956	chr8	-0.48	0.042150	chr8:25776635-25776956	ADAM18
Map3k8	ENSMUSG00000024235	21160	4313606	4314165	chr18	-0.40	0.042156	chr18:4313606-4314165	MAP3K8
Ido2	ENSMUSG00000031549	6745	25657898	25658128	chr8	-0.43	0.042193	chr8:25657898-25658128	IDO2
Neurog2	ENSMUSG00000027967	7170	127328521	127329242	chr3	-0.27	0.042195	chr3:127328521-127329242	NEUROG2
Actb	ENSMUSG00000029580	4899	143673258	143673408	chr5	-0.49	0.042202	chr5:143673258-143673408	ACTB
Mgat5	ENSMUSG00000036155	8804	129211810	129212475	chr1	-0.38	0.042222	chr1:129211810-129212475	MGAT5
E2f8	ENSMUSG00000046179	27631	56164290	56164904	chr7	-0.31	0.042295	chr7:56164290-56164904	E2F8
Asb2	ENSMUSG00000021200	5468	104581879	104582226	chr12	-0.33	0.042506	chr12:104581879-104582226	ASB2
Itgb3	ENSMUSG00000020689	6044	104492552	104492765	chr11	-0.27	0.042568	chr11:104492552-104492765	ITGB3
Akap2	ENSMUSG00000038729	8108	57738172	57739100	chr4	-0.41	0.042599	chr4:57738172-57739100	AKAP2
Gda	ENSMUSG00000058624	34466	21582310	21582495	chr19	-0.52	0.042636	chr19:21582310-21582495	GDA
Batf3	ENSMUSG00000026630	27520	192949702	192949922	chr1	-0.39	0.042891	chr1:192949702-192949922	BATF3
Smoc1	ENSMUSG00000021136	27866	82099710	82100146	chr12	-0.34	0.042930	chr12:82099710-82100146	SMOC1
Odc1	ENSMUSG00000011179	37668	17513877	17514144	chr12	-0.45	0.042947	chr12:17513877-17514144	ODC1
Lax1	ENSMUSG00000051998	5354	135591897	135592184	chr1	-0.34	0.043074	chr1:135591897-135592184	LAX1
Tmem176b	ENSMUSG00000029810	7594	48780469	48780956	chr6	-0.51	0.043121	chr6:48780469-48780956	TMEM176B
Atp11b	ENSMUSG00000037400	2998	35649921	35650192	chr3	-0.35	0.043133	chr3:35649921-35650192	ATP11B
Wee1	ENSMUSG00000031016	35332	117300840	117301547	chr7	-0.28	0.043150	chr7:117300840-117301547	WEE1
Gfod2	ENSMUSG00000013150	12174	108270160	108270485	chr8	-0.32	0.043248	chr8:108270160-108270485	GFOD2
Tmprss11e	ENSMUSG00000054537	4390	87170192	87170708	chr5	-0.36	0.043259	chr5:87170192-87170708	TMPRSS11E
Yy1	ENSMUSG00000021264	31672	109999290	109999729	chr12	-0.41	0.043283	chr12:109999290-109999729	YY1
Siah1a	ENSMUSG00000036840	33354	89303105	89303416	chr8	-0.26	0.043598	chr8:89303105-89303416	SIAH1
Nprl3	ENSMUSG00000020289	3620	32143478	32143647	chr11	-0.57	0.043644	chr11:32143478-32143647	NPRL3
Pon2	ENSMUSG00000032667	16880	5265021	5265651	chr6	-0.30	0.043704	chr6:5265021-5265651	PON2
Socs2	ENSMUSG00000020027	20958	94834473	94834816	chr10	-0.38	0.043707	chr10:94834473-94834816	SOCS2
Sumf1	ENSMUSG00000030101	2292	108104314	108104829	chr6	-0.29	0.043713	chr6:108104314-108104829	SUMF1
Begain	ENSMUSG00000040867	14200	110305576	110306005	chr12	-0.39	0.043730	chr12:110305576-110306005	BEGAIN
Gnb5	ENSMUSG00000032192	2321	75161474	75161568	chr9	-0.55	0.043880	chr9:75161474-75161568	GNB5
Tmem158	ENSMUSG00000054871	21024	123148542	123149227	chr9	-0.39	0.043943	chr9:123148542-123149227	TMEM158
Psma6	ENSMUSG00000021024	39762	56547705	56548554	chr12	-0.37	0.043944	chr12:56547705-56548554	PSMA6
4-Mar	ENSMUSG00000032656	16256	57068622	57069205	chr18	-0.36	0.043962	chr18:57068622-57069205	MARCH3
Stim2	ENSMUSG00000039156	2846	54492729	54492990	chr5	-0.32	0.044033	chr5:54492729-54492990	STIM2
Alg8	ENSMUSG00000035704	16026	104503756	104504419	chr7	-0.42	0.044092	chr7:104503756-104504419	ALG8

Cldn5	ENSMUSG00000041378	43706	18733145	18733320	chr16	-0.68	0.044245	chr16:18733145-18733320	CLDN5
Ap1s3	ENSMUSG00000054702	41806	79626567	79626900	chr1	-0.30	0.044257	chr1:79626567-79626900	AP1S3
Ciita	ENSMUSG00000075404	5718	10495069	10496114	chr16	-0.35	0.044356	chr16:10495069-10496114	CIITA
Ptp4a3	ENSMUSG00000059895	5229	73573191	73573259	chr15	-0.30	0.044379	chr15:73573191-73573259	PTP4A3
Lrch1	ENSMUSG00000068015	9032	75275635	75276425	chr14	-0.33	0.044486	chr14:75275635-75276425	LRCH1
Traf2	ENSMUSG00000026942	2633	25404684	25405502	chr2	-0.34	0.044508	chr2:25404684-25405502	TRAF2
Ccdc12	ENSMUSG00000019659	3626	110562247	110563018	chr9	-0.34	0.044538	chr9:110562247-110563018	CCDC12
Dock9	ENSMUSG00000025558	10628	122127329	122127720	chr14	-0.26	0.044675	chr14:122127329-122127720	DOCK9
Ptpn14	ENSMUSG00000026604	4660	191690969	191691424	chr1	-0.47	0.044793	chr1:191690969-191691424	PTPN14
Ciita	ENSMUSG00000075404	7068	10496833	10497052	chr16	-0.31	0.044846	chr16:10496833-10497052	CIITA
Gdf11	ENSMUSG00000025352	3956	128332682	128332777	chr10	-0.57	0.044854	chr10:128332682-128332777	GDF11
Sdccag8	ENSMUSG00000026504	4236	178749153	178749339	chr1	-0.45	0.044890	chr1:178749153-178749339	SDCCAG8
Slc9a3r1	ENSMUSG00000020733	10078	115034672	115034792	chr11	-0.45	0.045255	chr11:115034672-115034792	SLC9A3R1
Fnbp1	ENSMUSG00000075415	4076	30993070	30993423	chr2	-0.48	0.045293	chr2:30993070-30993423	FNBP1
Fmnl3	ENSMUSG00000023008	2584	99163145	99164003	chr15	-0.40	0.045299	chr15:99163145-99164003	FMNL3
Rapgef1	ENSMUSG00000039844	29559	29527857	29529025	chr2	-0.28	0.045310	chr2:29527857-29529025	RAPGEF1
Ccnd3	ENSMUSG00000034165	36609	47693733	47693877	chr17	-0.58	0.045334	chr17:47693733-47693877	CCND3
Gpm6b	ENSMUSG00000031342	15372	162767024	162767476	chrX	-0.29	0.045376	chrX:162767024-162767476	GPM6B
Phc2	ENSMUSG00000028796	5507	128410585	128410877	chr4	-0.36	0.045456	chr4:128410585-128410877	PHC2
Nup93	ENSMUSG00000032939	2712	96748683	96749014	chr8	-0.40	0.045572	chr8:96748683-96749014	NUP93
Scn4b	ENSMUSG00000046480	7840	44954234	44954482	chr9	-0.33	0.045835	chr9:44954234-44954482	SCN4B
Dnajb12	ENSMUSG00000020109	28360	59370668	59370796	chr10	-0.43	0.046021	chr10:59370668-59370796	DNAJB12
Mppe1	ENSMUSG00000062526	9868	67415287	67415417	chr18	-0.46	0.046053	chr18:67415287-67415417	MPPE1
Socs3	ENSMUSG00000053113	9124	117821229	117821523	chr11	-0.40	0.046438	chr11:117821229-117821523	SOCS3
1810055G02Rik	ENSMUSG00000035372	22828	3731008	3731311	chr19	-0.31	0.046475	chr19:3731008-3731311	C11orf24
Btg1	ENSMUSG00000036478	16922	96096401	96096711	chr10	-0.38	0.046494	chr10:96096401-96096711	BTG1
Rasa3	ENSMUSG00000031453	22430	13628219	13628858	chr8	-0.35	0.046575	chr8:13628219-13628858	RASA3
Ccin	ENSMUSG00000070999	11346	43984940	43985115	chr4	-0.37	0.046575	chr4:43984940-43985115	CCIN
Dyrk1a	ENSMUSG00000022897	18142	94810202	94811105	chr16	-0.32	0.046709	chr16:94810202-94811105	DYRK1A
Lpcat1	ENSMUSG00000021608	32295	73572293	73572405	chr13	-0.43	0.046731	chr13:73572293-73572405	LPCAT1
Chst12	ENSMUSG00000036599	5923	140993541	140993757	chr5	-0.41	0.046763	chr5:140993541-140993757	CHST12
Gypc	ENSMUSG00000090523	4462	32723916	32724384	chr18	-0.30	0.046831	chr18:32723916-32724384	GYPC
Cd247	ENSMUSG00000005763	9199	167778793	167779501	chr1	-0.39	0.046891	chr1:167778793-167779501	CD247
Tnfrsf17	ENSMUSG00000022496	2930	11316577	11317091	chr16	-0.34	0.047103	chr16:11316577-11317091	TNFRSF17
Klhl3	ENSMUSG00000014164	27600	58168813	58169211	chr13	-0.39	0.047136	chr13:58168813-58169211	KLHL3
Tbkbp1	ENSMUSG00000038517	16212	96994702	96994925	chr11	-0.52	0.047192	chr11:96994702-96994925	TBKBP1
Rassf3	ENSMUSG00000025795	22302	120935325	120935891	chr10	-0.38	0.047228	chr10:120935325-120935891	RASSF3
Nkd1	ENSMUSG00000031661	40082	91091540	91091684	chr8	-0.50	0.047233	chr8:91091540-91091684	NKD1
Ubqln1	ENSMUSG00000005312	13452	58303343	58303749	chr13	-0.38	0.047256	chr13:58303343-58303749	UBQLN1
2010012O05Rik	ENSMUSG00000062376	8378	46772233	46773312	chr19	-0.33	0.047369	chr19:46772233-46773312	C10orf32

Ston1	ENSMUSG00000033855	15788	88980907	88981560	chr17	-0.31	0.047445	chr17:88980907-88981560	STON1
Wdfy4	ENSMUSG00000051506	12752	33985448	33985551	chr14	-0.41	0.047521	chr14:33985448-33985551	WDFY4
Tekt5	ENSMUSG00000039179	11108	10384046	10384821	chr16	-0.40	0.047531	chr16:10384046-10384821	TEKT5
Tgfbr2	ENSMUSG00000032440	39040	116045250	116045437	chr9	-0.52	0.047746	chr9:116045250-116045437	TGFBR2
Pik3cd	ENSMUSG00000039936	3170	149079264	149080437	chr4	-0.33	0.047781	chr4:149079264-149080437	PIK3CD
Mapk14	ENSMUSG00000053436	5084	28834395	28834796	chr17	-0.39	0.047989	chr17:28834395-28834796	MAPK14
Sh3kbp1	ENSMUSG00000040990	49924	156196356	156196555	chrX	-0.31	0.048095	chrX:156196356-156196555	SH3KBP1
Crygs	ENSMUSG00000033501	8160	22803254	22803395	chr16	-0.63	0.048131	chr16:22803254-22803395	CRYGS
Rras2	ENSMUSG00000055723	13188	121247924	121248292	chr7	-0.32	0.048141	chr7:121247924-121248292	RRAS2
Fosb	ENSMUSG00000003545	16852	19911911	19912581	chr7	-0.32	0.048211	chr7:19911911-19912581	FOSB
Cacng6	ENSMUSG00000078815	2429	3422675	3423311	chr7	-0.26	0.048233	chr7:3422675-3423311	CACNG6
Trerf1	ENSMUSG00000064043	2099	47279926	47280052	chr17	-0.45	0.048359	chr17:47279926-47280052	TRERF1
Gpr18	ENSMUSG00000050350	14206	122300612	122300968	chr14	-0.27	0.048438	chr14:122300612-122300968	GPR18
Tubg2	ENSMUSG00000045007	15568	101001363	101001942	chr11	-0.35	0.048615	chr11:101001363-101001942	TUBG2
Snx13	ENSMUSG00000020590	5064	35726511	35727080	chr12	-0.27	0.048631	chr12:35726511-35727080	SNX13
Ube2q1	ENSMUSG00000042572	11812	89589153	89589532	chr3	-0.36	0.048653	chr3:89589153-89589532	UBE2Q1
Tmem131	ENSMUSG00000026116	12452	36983820	36984019	chr1	-0.52	0.048703	chr1:36983820-36984019	TMEM131
Tbc1d1	ENSMUSG00000029174	2686	64624122	64624322	chr5	-0.30	0.049004	chr5:64624122-64624322	TBC1D1
Arid3b	ENSMUSG00000004661	2488	57679481	57679632	chr9	-0.40	0.049049	chr9:57679481-57679632	ARID3B
Il27	ENSMUSG00000044701	2885	133741189	133741493	chr7	-0.44	0.049160	chr7:133741189-133741493	IL27
Pip5k1c	ENSMUSG00000034902	4534	80759597	80760968	chr10	-0.37	0.049201	chr10:80759597-80760968	PIP5K1C
Ankrd44	ENSMUSG00000052331	19127	54963659	54964551	chr1	-0.27	0.049221	chr1:54963659-54964551	ANKRD44
Rev1	ENSMUSG00000026082	8384	38178038	38178209	chr1	-0.38	0.049238	chr1:38178038-38178209	REV1
Whrn	ENSMUSG00000039137	3556	63150681	63151476	chr4	-0.28	0.049633	chr4:63150681-63151476	DFNB31
Nrarp	ENSMUSG00000078202	5107	25041146	25041620	chr2	-0.42	0.049740	chr2:25041146-25041620	NRARP
Tmem131	ENSMUSG00000026116	19441	36976408	36977454	chr1	-0.27	0.049756	chr1:36976408-36977454	TMEM131
Gnai2	ENSMUSG00000032562	5712	107531614	107532275	chr9	-0.39	0.049894	chr9:107531614-107532275	GNAI2
Ppcdc	ENSMUSG00000063849	6338	57281410	57281758	chr9	-0.30	0.049967	chr9:57281410-57281758	PPCDC
St3gal6	ENSMUSG00000022747	10348	58534421	58534988	chr16	-0.33	0.049973	chr16:58534421-58534988	ST3GAL6

Supplementary Table 5 (cont.). ChIP peaks with H3K4$^{me1/me2}$ occupancy loss in B220+ lymphoma cells and mutant OCI-LY1 vs OCI-LY7

Peaks with at least 25% H3K4me1/me2 occupancy loss in OCI-LY1 (KMT2Dmut) vs OCI-LY7 (KMT2Dwt) lymphoma cells (for figure 5a)

symbol	range	peak	label	start	end	chr	loss
SASS6	1867	chr1:100369150-10036931	pro	100369150	100369316	chr1	-0.66
TRMT13	1502	chr1:100372433-10037315	pro	100372433	100373154	chr1	-0.49
C1orf159	1067	chr1:1040468-1040598	pro	1040468	1040598	chr1	-0.38
DFFA	1180	chr1:10456281-10456480	pro	10456281	10456480	chr1	-0.52
PEX14	735	chr1:10456751-10456955	pro	10456751	10456955	chr1	-0.69
LINC01342	489	chr1:1061687-1061851	pro	1061687	1061851	chr1	-0.78
FAM102B	1834	chr1:108901326-10890398	pro	108901326	108903989	chr1	-0.63
FAM102B	1818	chr1:108906173-10890644	pro	108906173	108906446	chr1	-0.84
SORT1	1039	chr1:109734997-10973792	pro	109734997	109737929	chr1	-0.93
SORT1	1198	chr1:109740279-10974149	pro	109740279	109741496	chr1	-0.64
TARDBP	1418	chr1:10996562-10996801	pro	10996562	10996801	chr1	-0.49
AHCYL1	1913	chr1:110330633-11033100	pro	110330633	110331009	chr1	-0.68
AHCYL1	24	chr1:110347838-11034829	pro	110347838	110348299	chr1	-0.43
STRIP1	851	chr1:110374737-11037500	pro	110374737	110375001	chr1	-0.34
KCNC4	2028	chr1:110556729-11055704	pro	110556729	110557044	chr1	-0.66
LAMTOR5-AS1	1592	chr1:110750012-11075070	pro	110750012	110750707	chr1	-0.49
KCNA2	76	chr1:110974595-11097679	pro	110974595	110976798	chr1	-0.93
KCNA3	586	chr1:111011991-11101867	pro	111011991	111018677	chr1	-0.84
CEPT1	1431	chr1:111482055-11148262	pro	111482055	111482623	chr1	-0.50
DENND2D	773	chr1:111549080-11154983	pro	111549080	111549834	chr1	-0.58
ADORA3	304	chr1:111847561-11184836	pro	111847561	111848362	chr1	-0.27
ADORA3	1916	chr1:111849429-11185093	pro	111849429	111850934	chr1	-0.32
FAM212B	1676	chr1:112101504-11210173	pro	112101504	112101733	chr1	-0.78
MIR4256	1064	chr1:112806797-11280728	pro	112806797	112807286	chr1	-0.69
RHOC	1970	chr1:113048561-11304990	pro	113048561	113049903	chr1	-0.60
AP4B1-AS1	1098	chr1:114201720-11420203	pro	114201720	114202031	chr1	-0.86
AP4B1-AS1	1810	chr1:114202397-11420277	pro	114202397	114202778	chr1	-0.80
PTPN22	318	chr1:114215077-11421735	pro	114215077	114217356	chr1	-0.28
TRIM33	1371	chr1:114856477-11485687	pro	114856477	114856873	chr1	-0.59
BCAS2	1199	chr1:114924492-11492468	pro	114924492	114924686	chr1	-0.51
SLC22A15	580	chr1:116319703-11632041	pro	116319703	116320417	chr1	-0.50
LOC101928977	173	chr1:116321042-11632214	pro	116321042	116322144	chr1	-0.98
MAB21L3	244	chr1:116455227-11645608	pro	116455227	116456081	chr1	-0.97
ATP1A1	2540	chr1:116718333-11672276	pro	116718333	116722766	chr1	-0.67
ATP1A1-AS1	1501	chr1:116761125-11676128	pro	116761125	116761281	chr1	-0.82
WARS2	1018	chr1:119485404-11948626	pro	119485404	119486269	chr1	-0.55
EMBP1	1014	chr1:120961206-12096162	pro	120961206	120961629	chr1	-0.29
PDE4DIP	3978	chr1:143636345-14364314	pro	143636345	143643144	chr1	-0.46
PDE4DIP	2648	chr1:143643535-14364920	pro	143643535	143649206	chr1	-0.71
PDE4DIP	2117	chr1:143710056-14371111	pro	143710056	143711114	chr1	-0.69
LIX1L	1138	chr1:144188756-14419036	pro	144188756	144190363	chr1	-0.28
NUDT17	1071	chr1:144301704-14430202	pro	144301704	144302022	chr1	-0.78
POLR3C	1596	chr1:144320225-14432106	pro	144320225	144321068	chr1	-0.54
BCL9	1054	chr1:145478189-14547949	pro	145478189	145479492	chr1	-0.80
BCL9	867	chr1:145479672-14548185	pro	145479672	145481850	chr1	-0.88
GJA5	2140	chr1:145701053-14570190	pro	145701053	145701904	chr1	-0.97
ANP32E	1777	chr1:148471800-14847194	pro	148471800	148471946	chr1	-0.70

C1orf54	235	chr1:148511204-14851193	pro	148511204	148511938	chr1	-0.79
FALEC	818	chr1:148755309-14875604	pro	148755309	148756040	chr1	-0.57
ADAMTSL4-AS1	1230	chr1:148812031-14881281	pro	148812031	148812812	chr1	-0.78
ENSA	1254	chr1:148866892-14886706	pro	148866892	148867067	chr1	-0.39
GOLPH3L	1374	chr1:148934858-14893498	pro	148934858	148934987	chr1	-0.67
GOLPH3L	766	chr1:148935162-14893589	pro	148935162	148935897	chr1	-0.29
ANXA9	2114	chr1:149218846-14921917	pro	149218846	149219170	chr1	-0.55
FAM63A	1836	chr1:149243921-14924420	pro	149243921	149244202	chr1	-0.72
GABPB2	1339	chr1:149310870-14931121	pro	149310870	149311212	chr1	-0.44
RFX5	657	chr1:149586618-14958748	pro	149586618	149587484	chr1	-0.39
POGZ	1677	chr1:149682893-14968307	pro	149682893	149683073	chr1	-0.77
POGZ	2487	chr1:149683239-14968434	pro	149683239	149684347	chr1	-0.81
POGZ	2206	chr1:149695979-14969674	pro	149695979	149696740	chr1	-0.41
POGZ	441	chr1:149698715-14969929	pro	149698715	149699299	chr1	-0.48
S100A11	1970	chr1:150273880-15027445	pro	150273880	150274453	chr1	-0.32
S100A13	1804	chr1:151874936-15187505	pro	151874936	151875057	chr1	-0.48
ILF2	1284	chr1:151911314-15191151	pro	151911314	151911510	chr1	-0.45
NPR1	990	chr1:151916737-15191685	pro	151916737	151916854	chr1	-0.50
INTS3	2222	chr1:151969058-15196976	pro	151969058	151969766	chr1	-0.63
RPS27	2164	chr1:152231833-15223221	pro	152231833	152232219	chr1	-0.75
TPM3	792	chr1:152417670-15241855	pro	152417670	152418557	chr1	-0.27
TPM3	1975	chr1:152419921-15242082	pro	152419921	152420829	chr1	-0.40
ADAR	1121	chr1:152847707-15284923	pro	152847707	152849231	chr1	-0.33
KCNN3	1862	chr1:153100326-15310132	pro	153100326	153101323	chr1	-0.47
PMVK	1716	chr1:153177754-15317789	pro	153177754	153177893	chr1	-0.60
FLAD1	1539	chr1:153223787-15322407	pro	153223787	153224075	chr1	-0.43
GBAP1	1738	chr1:153462026-15346239	pro	153462026	153462399	chr1	-0.56
GON4L	912	chr1:154094103-15409514	pro	154094103	154095140	chr1	-0.47
KIAA0907	2114	chr1:154168228-15416916	pro	154168228	154169169	chr1	-0.49
KIAA0907	1247	chr1:154169359-15416977	pro	154169359	154169771	chr1	-0.51
RXFP4	695	chr1:154177166-15417764	pro	154177166	154177648	chr1	-0.50
RXFP4	1670	chr1:154179687-15417985	pro	154179687	154179856	chr1	-0.72
LMNA	345	chr1:154362539-15436321	pro	154362539	154363211	chr1	-0.88
SEMA4A	1734	chr1:154384030-15438521	pro	154384030	154385217	chr1	-0.41
CCT3	973	chr1:154575728-15457587	pro	154575728	154575878	chr1	-0.67
MEF2D	1144	chr1:154724357-15473196	pro	154724357	154731964	chr1	-0.52
MEF2D	3042	chr1:154732154-15473627	pro	154732154	154736278	chr1	-0.27
MEF2D	1763	chr1:154738650-15473939	pro	154738650	154739392	chr1	-0.91
IQGAP3	588	chr1:154807553-15480931	pro	154807553	154809310	chr1	-0.54
GPATCH4	1619	chr1:154836138-15483643	pro	154836138	154836432	chr1	-0.58
FCRL4	2444	chr1:155831579-15583252	pro	155831579	155832522	chr1	-0.91
FCRL1	1293	chr1:156053406-15605713	pro	156053406	156057136	chr1	-0.35
CD5L	1368	chr1:156079292-15607996	pro	156079292	156079961	chr1	-0.94
CD1D	1049	chr1:156414421-15641620	pro	156414421	156416201	chr1	-0.74
CD1C	598	chr1:156525736-15652783	pro	156525736	156527833	chr1	-0.82
OR6P1	1217	chr1:156801045-15680142	pro	156801045	156801425	chr1	-0.68
PYHIN1	336	chr1:157166913-15716968	pro	157166913	157169680	chr1	-0.93
PYHIN1	2479	chr1:157169785-15717109	pro	157169785	157171093	chr1	-0.94
IFI16	3900	chr1:157247823-15725258	pro	157247823	157252585	chr1	-0.38
AIM2	606	chr1:157311107-15731422	pro	157311107	157314224	chr1	-0.28
PIGM	1640	chr1:158266671-15826686	pro	158266671	158266865	chr1	-0.71
PEA15	770	chr1:158440242-15844168	pro	158440242	158441682	chr1	-0.40
NCSTN	1964	chr1:158577365-15857808	pro	158577365	158578080	chr1	-0.53
CD84	919	chr1:158816732-15881696	pro	158816732	158816966	chr1	-0.73
CD48	1150	chr1:158949163-15894966	pro	158949163	158949669	chr1	-0.80

LY9	29	chr1:159032042-15903287	pro	159032042	159032872	chr1	-0.36
LY9	2874	chr1:159032991-15903772	pro	159032991	159037728	chr1	-0.47
USF1	1782	chr1:159279141-15928000	pro	159279141	159280000	chr1	-0.75
ARHGAP30	275	chr1:159306465-15930685	pro	159306465	159306853	chr1	-0.26
KLHDC9	784	chr1:159333881-15933409	pro	159333881	159334099	chr1	-0.77
NIT1	1898	chr1:159356311-15935654	pro	159356311	159356544	chr1	-0.61
NDUFS2	1292	chr1:159439776-15943992	pro	159439776	159439928	chr1	-0.55
FCER1G	2604	chr1:159453526-15945510	pro	159453526	159455101	chr1	-0.77
FCRLA	1796	chr1:159941412-15994176	pro	159941412	159941764	chr1	-0.62
FCRLA	1222	chr1:159941970-15994235	pro	159941970	159942353	chr1	-0.42
FCRLB	2454	chr1:159954963-15995604	pro	159954963	159956040	chr1	-0.52
FCRLB	1060	chr1:159956643-15995715	pro	159956643	159957150	chr1	-0.33
DUSP12	1210	chr1:159987326-15998750	pro	159987326	159987501	chr1	-0.63
SPEN	1161	chr1:16045644-16045922	pro	16045644	16045922	chr1	-0.65
UHMK1	1948	chr1:160736056-16073627	pro	160736056	160736277	chr1	-0.68
ZBTB17	1661	chr1:16173454-16173652	pro	16173454	16173652	chr1	-0.59
POU2F1	956	chr1:165563094-16556480	pro	165563094	165564801	chr1	-0.44
CREG1	1930	chr1:165786864-16578863	pro	165786864	165788637	chr1	-0.72
NECAP2	1844	chr1:16641419-16641774	pro	16641419	16641774	chr1	-0.41
ATP1B1	2330	chr1:167342993-16734680	pro	167342993	167346806	chr1	-0.64
GORAB	1098	chr1:168766614-16876696	pro	168766614	168766961	chr1	-0.52
FMO1	1706	chr1:169485287-16948658	pro	169485287	169486589	chr1	-0.98
FMO4	644	chr1:169549184-16954974	pro	169549184	169549744	chr1	-0.65
FMO4	173	chr1:169549913-16955064	pro	169549913	169550649	chr1	-0.27
METTL13	1156	chr1:170018319-17001875	pro	170018319	170018758	chr1	-0.63
NADK	1574	chr1:1702778-1703107	pro	1702778	1703107	chr1	-0.58
CROCC	70	chr1:17120524-17121677	pro	17120524	17121677	chr1	-0.80
CENPL	1510	chr1:172058209-17205855	pro	172058209	172058559	chr1	-0.72
DARS2	1176	chr1:172061539-17206164	pro	172061539	172061649	chr1	-0.34
DARS2	1734	chr1:172062021-17206228	pro	172062021	172062282	chr1	-0.90
GAS5-AS1	332	chr1:172099109-17209957	pro	172099109	172099571	chr1	-0.72
SNORD78	15	chr1:172099957-17210296	pro	172099957	172102969	chr1	-0.38
LOC102724601	1718	chr1:172392846-17239381	pro	172392846	172393815	chr1	-0.41
RABGAP1L	2078	chr1:173107273-17310886	pro	173107273	173108863	chr1	-0.50
LOC101928696	133	chr1:173189017-17319129	pro	173189017	173191293	chr1	-0.34
RABGAP1L	310	chr1:173199005-17320266	pro	173199005	173202667	chr1	-0.50
KIAA0040	1890	chr1:173430570-17343091	pro	173430570	173430913	chr1	-0.60
PADI1	2218	chr1:17406113-17406736	pro	17406113	17406736	chr1	-0.86
RCC2	1236	chr1:17639005-17641144	pro	17639005	17641144	chr1	-0.60
FAM20B	1546	chr1:177262466-17726401	pro	177262466	177264018	chr1	-0.48
TOR3A	1946	chr1:177319435-17731992	pro	177319435	177319924	chr1	-0.29
ACBD6	1752	chr1:178736671-17873711	pro	178736671	178737116	chr1	-0.35
XPR1	484	chr1:178867008-17886755	pro	178867008	178867559	chr1	-0.50
XPR1	1228	chr1:178868378-17886961	pro	178868378	178869614	chr1	-0.27
STX6	274	chr1:179258963-17925934	pro	179258963	179259346	chr1	-0.28
MR1	658	chr1:179268970-17927071	pro	179268970	179270710	chr1	-0.96
RGS8	90	chr1:180908331-18090886	pro	180908331	180908868	chr1	-0.61
SMG7-AS1	2055	chr1:181705443-18170592	pro	181705443	181705927	chr1	-0.83
NCF2	795	chr1:181824474-18182666	pro	181824474	181826660	chr1	-0.94
TSEN15	1868	chr1:182289205-18228934	pro	182289205	182289344	chr1	-0.81
IVNS1ABP	1554	chr1:183554560-18355471	pro	183554560	183554717	chr1	-0.64
LINC01036	805	chr1:185327567-18532801	pro	185327567	185328015	chr1	-0.48
LINC01036	355	chr1:185328146-18532833	pro	185328146	185328336	chr1	-0.75
KLHDC7A	1445	chr1:18678259-18678871	pro	18678259	18678871	chr1	-0.95
RGS18	638	chr1:190393871-19039583	pro	190393871	190395834	chr1	-0.96

RGS18	1946	chr1:190396009-19039631	pro	190396009	190396312	chr1	-0.90
ALDH4A1	748	chr1:19100818-19101447	pro	19100818	19101447	chr1	-0.96
ALDH4A1	90	chr1:19101678-19101903	pro	19101678	19101903	chr1	-0.68
ALDH4A1	538	chr1:19102071-19102764	pro	19102071	19102764	chr1	-0.95
UCHL5	2104	chr1:191292378-1912937	pro	191292378	191293705	chr1	-0.60
CDC73	2218	chr1:191359263-1913605	pro	191359263	191360593	chr1	-0.45
UBR4	2186	chr1:19411232-19411809	pro	19411232	19411809	chr1	-0.61
MRTO4	1699	chr1:19451882-19452836	pro	19451882	19452836	chr1	-0.30
DENND1B	1704	chr1:196012523-1960133	pro	196012523	196013378	chr1	-0.89
MIR181A1HG	390	chr1:197173300-19717384	pro	197173300	197173845	chr1	-0.34
NR5A2	1092	chr1:198263987-1982649	pro	198263987	198264902	chr1	-0.46
NR5A2	2658	chr1:198265064-1982669	pro	198265064	198266955	chr1	-0.61
NR5A2	366	chr1:198278700-1982791	pro	198278700	198279179	chr1	-0.54
LINC00862	444	chr1:198609038-1986109	pro	198609038	198610939	chr1	-0.91
ZNF281	2446	chr1:198642618-19864411	pro	198642618	198644111	chr1	-0.75
CAMSAP2	1429	chr1:198975481-1989779	pro	198975481	198977993	chr1	-0.72
KIF21B	2255	chr1:199255436-1992589	pro	199255436	199258958	chr1	-0.44
KIF21B	2076	chr1:199261446-1992616	pro	199261446	199261609	chr1	-0.77
TNNI1	796	chr1:199657693-1996588	pro	199657693	199658894	chr1	-0.98
CSRP1	806	chr1:199740819-1997427	pro	199740819	199742749	chr1	-0.36
RNF186	274	chr1:20014306-20014958	pro	20014306	20014958	chr1	-0.65
RNF186	948	chr1:20015109-20015504	pro	20015109	20015504	chr1	-0.82
TIMM17A	871	chr1:200190311-20019042	pro	200190311	200190427	chr1	-0.75
PTPN7	699	chr1:200394410-2003988	pro	200394410	200398872	chr1	-0.40
UBE2T	1036	chr1:200578683-2005788	pro	200578683	200578826	chr1	-0.79
UBE2T	1628	chr1:200579024-2005796	pro	200579024	200579668	chr1	-0.55
ATP2B4	820	chr1:201861418-2018652	pro	201861418	201865294	chr1	-0.54
ZBED6	526	chr1:202032200-2020332	pro	202032200	202033292	chr1	-0.25
MDM4	1464	chr1:202750242-2027510	pro	202750242	202751086	chr1	-0.74
MDM4	2090	chr1:202753384-2027550	pro	202753384	202755051	chr1	-0.65
PLA2G2D	77	chr1:20318436-20318702	pro	20318436	20318702	chr1	-0.92
PLA2G2C	232	chr1:20373972-20374113	pro	20373972	20374113	chr1	-0.80
UBXN10	422	chr1:20384601-20384882	pro	20384601	20384882	chr1	-0.71
UBXN10-AS1	59	chr1:20385409-20385841	pro	20385409	20385841	chr1	-0.87
SLC45A3	1650	chr1:203914504-2039147	pro	203914504	203914703	chr1	-0.89
PM20D1	301	chr1:204086073-2040863	pro	204086073	204086329	chr1	-0.46
C1orf186	851	chr1:204455407-2044568	pro	204455407	204456835	chr1	-0.66
C1orf186	2480	chr1:204457201-2044583	pro	204457201	204458300	chr1	-0.82
MIR6769B	2189	chr1:204712178-2047129	pro	204712178	204712980	chr1	-0.67
RASSF5	980	chr1:204795222-2047970	pro	204795222	204797046	chr1	-0.38
MAPKAPK2	1730	chr1:204921747-2049247	pro	204921747	204924765	chr1	-0.67
FAIM3	708	chr1:205161074-2051612	pro	205161074	205161226	chr1	-0.72
FAIM3	736	chr1:205161501-2051639	pro	205161501	205163974	chr1	-0.42
PFKFB2	1689	chr1:205294317-2052955	pro	205294317	205295545	chr1	-0.62
CR2	244	chr1:205693861-2056941	pro	205693861	205694183	chr1	-0.28
CR2	891	chr1:205694456-2056958	pro	205694456	205695858	chr1	-0.41
CD46	1839	chr1:205988439-2059918	pro	205988439	205991891	chr1	-0.78
CD46	1214	chr1:205993141-2059932	pro	205993141	205993295	chr1	-0.28
CD46	2052	chr1:205993611-2059945	pro	205993611	205994501	chr1	-0.77
FAM43B	1014	chr1:20749872-20751137	pro	20749872	20751137	chr1	-0.99
TRAF3IP3	556	chr1:207995308-2079978	pro	207995308	207997800	chr1	-0.41
TRAF3IP3	926	chr1:208008984-2080097	pro	208008984	208009776	chr1	-0.71
DIEXF	1336	chr1:208069126-2080694	pro	208069126	208069413	chr1	-0.51
HHAT	1020	chr1:208569989-2085705	pro	208569989	208570574	chr1	-0.96
DDOST	1860	chr1:20858643-20858885	pro	20858643	20858885	chr1	-0.48

TMEM206	540	chr1:210654984-21065587	pro	210654984	210655877	chr1	-0.28
NSL1	1972	chr1:211029543-21103003	pro	211029543	211030037	chr1	-0.48
TATDN3	1110	chr1:211032629-21103317	pro	211032629	211033174	chr1	-0.38
TATDN3	1929	chr1:211033554-21103388	pro	211033554	211033888	chr1	-0.85
FLVCR1-AS1	1000	chr1:211096739-21109747	pro	211096739	211097470	chr1	-0.30
VASH2	400	chr1:211189801-21119036	pro	211189801	211190367	chr1	-0.96
VASH2	586	chr1:211190854-21119128	pro	211190854	211191285	chr1	-0.85
KCTD3	380	chr1:213806759-2138071	pro	213806759	213807194	chr1	-0.33
KCTD3	808	chr1:213807915-2138084	pro	213807915	213808414	chr1	-0.38
EPRS	1609	chr1:218284712-2182853	pro	218284712	218285318	chr1	-0.53
IARS2	1506	chr1:218335456-2183357	pro	218335456	218335709	chr1	-0.52
TAF1A-AS1	1378	chr1:220828419-2208285	pro	220828419	220828594	chr1	-0.87
AIDA	1705	chr1:220950601-2209509	pro	220950601	220950965	chr1	-0.34
TLR5	276	chr1:221383360-2213836	pro	221383360	221383687	chr1	-0.41
TP53BP2	1302	chr1:222098260-2220997	pro	222098260	222099732	chr1	-0.30
DEGS1	1307	chr1:222435986-2224364	pro	222435986	222436464	chr1	-0.90
DEGS1	2464	chr1:222439142-2224408	pro	222439142	222440849	chr1	-0.49
CDC42	2004	chr1:22253604-22253817	pro	22253604	22253817	chr1	-0.55
NVL	1458	chr1:222582811-2225833	pro	222582811	222583302	chr1	-0.47
ENAH	1436	chr1:223905941-2239061	pro	223905941	223906124	chr1	-0.73
ENAH	898	chr1:223906240-2239069	pro	223906240	223906901	chr1	-0.51
SRP9	610	chr1:224031122-2240319	pro	224031122	224031931	chr1	-0.29
SRP9	1952	chr1:224033723-2240344	pro	224033723	224034454	chr1	-0.66
PYCR2	974	chr1:224179480-2241797	pro	224179480	224179797	chr1	-0.39
LEFTY2	537	chr1:224195705-2241967	pro	224195705	224196781	chr1	-0.97
LEFTY2	1784	chr1:224197151-2241978	pro	224197151	224197828	chr1	-0.95
SDE2	2632	chr1:224250287-2242518	pro	224250287	224251829	chr1	-0.63
SDE2	1561	chr1:224252012-2242522	pro	224252012	224252246	chr1	-0.39
H3F3AP4	2299	chr1:224318819-22431987	pro	224318819	224319879	chr1	-0.38
LIN9	408	chr1:224563784-22456517	pro	224563784	224565175	chr1	-0.31
ITPKB-IT1	2402	chr1:224926541-2249274	pro	224926541	224927440	chr1	-0.42
ITPKB	830	chr1:224993813-2249948	pro	224993813	224994848	chr1	-0.37
ITPKB	2174	chr1:224995230-22499611	pro	224995230	224996119	chr1	-0.63
ZNF678	200	chr1:225817540-2258177	pro	225817540	225817743	chr1	-0.27
GUK1	1980	chr1:226392312-2263925	pro	226392312	226392539	chr1	-0.65
GUK1	1946	chr1:226396980-2263971	pro	226396980	226397181	chr1	-0.68
HIST3H2A	1497	chr1:226709699-22671167	pro	226709699	226711675	chr1	-0.97
HIST3H2BB	602	chr1:226712895-2267131	pro	226712895	226713169	chr1	-0.71
HIST3H2BB	1455	chr1:226713467-2267143	pro	226713467	226714303	chr1	-0.92
MIR4666A	698	chr1:226714691-2267167	pro	226714691	226716704	chr1	-0.98
MIR4666A	1280	chr1:226716814-2267185	pro	226716814	226718537	chr1	-0.92
RNF187	1696	chr1:226739903-2267400	pro	226739903	226740086	chr1	-0.96
RNF187	1278	chr1:226740347-22674047	pro	226740347	226740476	chr1	-0.61
RNF187	2248	chr1:226742422-2267454	pro	226742422	226745453	chr1	-0.35
LINC00582	325	chr1:229814433-2298151	pro	229814433	229815137	chr1	-0.43
LINC00582	1068	chr1:229815332-2298157	pro	229815332	229815723	chr1	-0.32
MORN1	1452	chr1:2311130-2312066	pro	2311130	2312066	chr1	-0.72
PCNXL2	793	chr1:231496894-2314976	pro	231496894	231497684	chr1	-0.32
PCNXL2	646	chr1:231498334-2314991	pro	231498334	231499123	chr1	-0.53
TARBP1	338	chr1:232681618-2326820	pro	232681618	232682003	chr1	-0.28
LOC101927787	1083	chr1:232849572-2328499	pro	232849572	232849906	chr1	-0.84
LOC101927851	1696	chr1:233163671-23316567	pro	233163671	233165678	chr1	-0.63
LOC101927851	146	chr1:233165781-2331666	pro	233165781	233166667	chr1	-0.61
PEX10	1702	chr1:2334871-2336273	pro	2334871	2336273	chr1	-0.26
ERO1LB	2636	chr1:234513757-2345154	pro	234513757	234515438	chr1	-0.42

ASAP3	892	chr1:23683876-23684583	pro	23683876	23684583	chr1	-0.35
E2F2	792	chr1:23730581-23731603	pro	23730581	23731603	chr1	-0.39
E2F2	2112	chr1:23732097-23732726	pro	23732097	23732726	chr1	-0.75
ID3	1506	chr1:23758785-23761970	pro	23758785	23761970	chr1	-0.51
MDS2	711	chr1:23825537-23825861	pro	23825537	23825861	chr1	-0.97
MDS2	2000	chr1:23828068-23828751	pro	23828068	23828751	chr1	-0.76
TCEB3-AS1	939	chr1:23976310-23976560	pro	23976310	23976560	chr1	-0.49
CHML	192	chr1:239865616-23986648	pro	239865616	239866480	chr1	-0.71
OPN3	1445	chr1:239868190-23986956	pro	239868190	239869568	chr1	-0.41
EXO1	1823	chr1:240080414-24008054	pro	240080414	240080540	chr1	-0.85
ZBTB18	2	chr1:242281109-24228126	pro	242281109	242281260	chr1	-0.47
COX20	1477	chr1:243063554-24306401	pro	243063554	243064012	chr1	-0.50
IFNLR1	1276	chr1:24387482-24387773	pro	24387482	24387773	chr1	-0.70
IFNLR1	1761	chr1:24387963-24388263	pro	24387963	24388263	chr1	-0.57
LOC284632	400	chr1:24399450-24399981	pro	24399450	24399981	chr1	-0.84
LOC284632	978	chr1:24400095-24400492	pro	24400095	24400492	chr1	-0.94
LOC284632	2134	chr1:24400745-24402155	pro	24400745	24402155	chr1	-0.79
ZNF669	1269	chr1:245332811-24533324	pro	245332811	245333247	chr1	-0.73
ZNF124	450	chr1:245402342-24540244	pro	245402342	245402443	chr1	-0.43
RCAN3	930	chr1:24702449-24703355	pro	24702449	24703355	chr1	-0.27
RCAN3	1922	chr1:24703505-24704282	pro	24703505	24704282	chr1	-0.97
RCAN3	1072	chr1:24704738-24706457	pro	24704738	24706457	chr1	-0.96
NCMAP	1972	chr1:24756952-24757295	pro	24756952	24757295	chr1	-0.72
SRRM1	1302	chr1:24840504-24841253	pro	24840504	24841253	chr1	-0.47
LDLRAP1	1256	chr1:25743205-25744632	pro	25743205	25744632	chr1	-0.37
PAQR7	1670	chr1:26071885-26072119	pro	26071885	26072119	chr1	-0.80
CEP85	2066	chr1:26435040-26435553	pro	26435040	26435553	chr1	-0.56
UBXN11	1873	chr1:26507409-26507901	pro	26507409	26507901	chr1	-0.27
UBXN11	2592	chr1:26519150-26520722	pro	26519150	26520722	chr1	-0.61
HMGN2	1614	chr1:26672424-26673781	pro	26672424	26673781	chr1	-0.28
RPS6KA1	2840	chr1:26740623-26743553	pro	26740623	26743553	chr1	-0.30
RPS6KA1	865	chr1:26743898-26744228	pro	26743898	26744228	chr1	-0.55
PIGV	1354	chr1:26988497-26988738	pro	26988497	26988738	chr1	-0.60
ZDHHC18	1541	chr1:27026463-27028191	pro	27026463	27028191	chr1	-0.28
SYTL1	1564	chr1:27539425-27539583	pro	27539425	27539583	chr1	-0.39
FGR	2090	chr1:27831870-27832577	pro	27831870	27832577	chr1	-0.42
EYA3	1071	chr1:28288698-28288916	pro	28288698	28288916	chr1	-0.48
PTAFR	2660	chr1:28372672-28374093	pro	28372672	28374093	chr1	-0.53
PTAFR	22	chr1:28375500-28376627	pro	28375500	28376627	chr1	-0.39
PTAFR	924	chr1:28376884-28377047	pro	28376884	28377047	chr1	-0.74
SESN2	428	chr1:28457845-28458396	pro	28457845	28458396	chr1	-0.30
MED18	1941	chr1:28525795-28526519	pro	28525795	28526519	chr1	-0.85
MED18	1431	chr1:28529451-28529607	pro	28529451	28529607	chr1	-0.82
TRNAU1AP	1308	chr1:28753261-28753582	pro	28753261	28753582	chr1	-0.62
SNORA61	144	chr1:28778507-28779189	pro	28778507	28779189	chr1	-0.41
TAF12	1320	chr1:28843124-28843900	pro	28843124	28843900	chr1	-0.53
EPB41	1552	chr1:29084551-29084721	pro	29084551	29084721	chr1	-0.30
LAPTM5	2732	chr1:31004701-31007304	pro	31004701	31007304	chr1	-0.49
PTP4A2	1546	chr1:32177600-32178643	pro	32177600	32178643	chr1	-0.54
KHDRBS1	593	chr1:32250926-32251648	pro	32250926	32251648	chr1	-0.26
TMEM39B	1258	chr1:32312292-32312400	pro	32312292	32312400	chr1	-0.68
FAM167B	1186	chr1:32485969-32487211	pro	32485969	32487211	chr1	-0.33
MARCKSL1	1643	chr1:32575963-32576179	pro	32575963	32576179	chr1	-0.47
ZBTB8OS	2320	chr1:32886026-32886878	pro	32886026	32886878	chr1	-0.65
ZBTB8OS	1200	chr1:32887393-32887750	pro	32887393	32887750	chr1	-0.35

RBBP4	1832	chr1:32890939-32891814	pro	32890939	32891814	chr1	-0.54
S100PBP	1784	chr1:33053636-33054052	pro	33053636	33054052	chr1	-0.40
YARS	1843	chr1:33057733-33058393	pro	33057733	33058393	chr1	-0.80
FNDC5	118	chr1:33110357-33111239	pro	33110357	33111239	chr1	-0.34
ZSCAN20	1818	chr1:33708919-33709081	pro	33708919	33709081	chr1	-0.76
ZSCAN20	489	chr1:33711029-33711585	pro	33711029	33711585	chr1	-0.47
ZMYM1	1294	chr1:35318717-35318970	pro	35318717	35318970	chr1	-0.66
ZMYM4	652	chr1:35506232-35506771	pro	35506232	35506771	chr1	-0.27
AGO1	1530	chr1:36122847-36123005	pro	36122847	36123005	chr1	-0.36
GRIK3	3088	chr1:37267734-37270954	pro	37267734	37270954	chr1	-1.00
CEP104	1332	chr1:3762062-3762591	pro	3762062	3762591	chr1	-0.31
GNL2	1655	chr1:37832378-37832660	pro	37832378	37832660	chr1	-0.37
LINC01134	3972	chr1:3808584-3813011	pro	3808584	3813011	chr1	-0.91
INPP5B	1166	chr1:38186294-38186669	pro	38186294	38186669	chr1	-0.83
SF3A3	1386	chr1:38226600-38227324	pro	38226600	38227324	chr1	-0.63
KIAA0754	1852	chr1:39645869-39645952	pro	39645869	39645952	chr1	-0.43
MFSD2A	2046	chr1:40195247-40195584	pro	40195247	40195584	chr1	-0.77
SMAP2	1233	chr1:40629665-40631073	pro	40629665	40631073	chr1	-0.44
SMAP2	12	chr1:40631400-40631781	pro	40631400	40631781	chr1	-0.45
ZFP69B	1788	chr1:40690458-40690962	pro	40690458	40690962	chr1	-0.95
RIMS3	1858	chr1:40900592-40903517	pro	40900592	40903517	chr1	-0.39
CITED4	420	chr1:41100828-41101225	pro	41100828	41101225	chr1	-0.98
FOXJ3	1993	chr1:42571108-42571354	pro	42571108	42571354	chr1	-0.38
CCDC23	384	chr1:43055743-43056317	pro	43055743	43056317	chr1	-0.27
EBNA1BP2	289	chr1:43411005-43411229	pro	43411005	43411229	chr1	-0.41
CDC20	2273	chr1:43599196-43599774	pro	43599196	43599774	chr1	-0.73
MIR6079	3218	chr1:44072420-44074905	pro	44072420	44074905	chr1	-0.26
MIR6079	1588	chr1:44075020-44075564	pro	44075020	44075564	chr1	-0.25
C1orf228	2252	chr1:44914543-44915922	pro	44914543	44915922	chr1	-0.82
PLK3	1762	chr1:45040061-45040706	pro	45040061	45040706	chr1	-0.65
TCTEX1D4	452	chr1:45045894-45046097	pro	45045894	45046097	chr1	-0.51
BTBD19	442	chr1:45046211-45046386	pro	45046211	45046386	chr1	-0.56
BTBD19	996	chr1:45047490-45047983	pro	45047490	45047983	chr1	-0.82
BTBD19	1448	chr1:45048087-45048289	pro	45048087	45048289	chr1	-0.81
HPDL	856	chr1:45564681-45567291	pro	45564681	45567291	chr1	-0.33
MMACHC	1052	chr1:45739103-45739886	pro	45739103	45739886	chr1	-0.30
AKR1A1	1754	chr1:45790668-45790921	pro	45790668	45790921	chr1	-0.71
RPS15AP10	1660	chr1:45882704-45883865	pro	45882704	45883865	chr1	-0.90
TMEM69	1112	chr1:45927377-45927711	pro	45927377	45927711	chr1	-0.50
POMGNT1	950	chr1:46437443-46437873	pro	46437443	46437873	chr1	-0.69
RAD54L	1154	chr1:46486355-46487856	pro	46486355	46487856	chr1	-0.32
NSUN4	342	chr1:46577930-46578253	pro	46577930	46578253	chr1	-0.67
STIL	1372	chr1:47550738-47551331	pro	47550738	47551331	chr1	-0.60
FOXD2	124	chr1:47673956-47674841	pro	47673956	47674841	chr1	-0.36
BEND5	1479	chr1:49016341-49017073	pro	49016341	49017073	chr1	-0.99
OSBPL9	90	chr1:51854847-51855237	pro	51854847	51855237	chr1	-0.40
OSBPL9	2091	chr1:51970055-51970271	pro	51970055	51970271	chr1	-0.62
NRD1	1960	chr1:52114171-52114509	pro	52114171	52114509	chr1	-0.29
NRD1	1370	chr1:52114778-52115083	pro	52114778	52115083	chr1	-0.38
ZFYVE9	1029	chr1:52380980-52381782	pro	52380980	52381782	chr1	-0.41
ORC1	1922	chr1:52640692-52640928	pro	52640692	52640928	chr1	-0.60
PRPF38A	1934	chr1:52644673-52644808	pro	52644673	52644808	chr1	-0.67
GPX7	1840	chr1:52842362-52842577	pro	52842362	52842577	chr1	-0.54
SCP2	1796	chr1:53254908-53255075	pro	53254908	53255075	chr1	-0.80
NDC1	1973	chr1:54074770-54074912	pro	54074770	54074912	chr1	-0.29

NDC1	1438	chr1:54075242-54075511	pro	54075242	54075511	chr1	-0.32
SSBP3	2188	chr1:54642251-54642685	pro	54642251	54642685	chr1	-0.65
SSBP3	1786	chr1:54642814-54642927	pro	54642814	54642927	chr1	-0.78
PPAP2B	2580	chr1:56813694-56816839	pro	56813694	56816839	chr1	-0.96
PPAP2B	87	chr1:56817512-56818006	pro	56817512	56818006	chr1	-0.34
PPAP2B	427	chr1:56818130-56818416	pro	56818130	56818416	chr1	-0.85
LINC01358	162	chr1:59258239-59258905	pro	59258239	59258905	chr1	-0.61
DOCK7	993	chr1:62927526-62927716	pro	62927526	62927716	chr1	-0.72
ACOT7	1260	chr1:6374744-6375565	pro	6374744	6375565	chr1	-0.43
ROR1	1100	chr1:64011021-64011330	pro	64011021	64011330	chr1	-0.90
JAK1	2040	chr1:65201328-65204145	pro	65201328	65204145	chr1	-0.54
JAK1	955	chr1:65205005-65206457	pro	65205005	65206457	chr1	-0.28
WDR78	1182	chr1:67161409-67162543	pro	67161409	67162543	chr1	-0.43
MIER1	1803	chr1:67166599-67166819	pro	67166599	67166819	chr1	-0.73
SRSF11	1754	chr1:70445486-70445927	pro	70445486	70445927	chr1	-0.27
CTH	1666	chr1:70650847-70651462	pro	70650847	70651462	chr1	-0.39
TYW3	1382	chr1:74969987-74970092	pro	74969987	74970092	chr1	-0.43
SNORD45B	204	chr1:76026806-76029099	pro	76026806	76029099	chr1	-0.53
SNORD45B	1746	chr1:76029416-76029571	pro	76029416	76029571	chr1	-0.85
ZZZ3	1870	chr1:77918199-77919926	pro	77918199	77919926	chr1	-0.42
USP33	2752	chr1:77994401-77996398	pro	77994401	77996398	chr1	-0.84
USP33	286	chr1:77998269-77998608	pro	77998269	77998608	chr1	-0.37
FAM73A	2054	chr1:78019758-78020143	pro	78019758	78020143	chr1	-0.50
FUBP1	1548	chr1:78218404-78219424	pro	78218404	78219424	chr1	-0.35
LOC101927412	1077	chr1:80877828-80879134	pro	80877828	80879134	chr1	-0.94
LOC101927412	12	chr1:80879321-80879770	pro	80879321	80879770	chr1	-0.94
LOC102724552	2391	chr1:8409146-8410216	pro	8409146	8410216	chr1	-0.64
PRKACB	924	chr1:84314700-84315941	pro	84314700	84315941	chr1	-0.49
PRKACB	1125	chr1:84403971-84404099	pro	84403971	84404099	chr1	-0.84
LOC100130417	1268	chr1:845993-846416	pro	845993	846416	chr1	-0.63
GNG5	774	chr1:84745071-84746177	pro	84745071	84746177	chr1	-0.27
RERE	1711	chr1:8797421-8799729	pro	8797421	8799729	chr1	-0.44
RERE	844	chr1:8800735-8801526	pro	8800735	8801526	chr1	-0.33
ENO1	812	chr1:8861962-8863137	pro	8861962	8863137	chr1	-0.35
GTF2B	2074	chr1:89127644-89127988	pro	89127644	89127988	chr1	-0.51
GBP3	170	chr1:89260620-89261315	pro	89260620	89261315	chr1	-0.52
SLC2A5	807	chr1:9052982-9053580	pro	9052982	9053580	chr1	-0.39
GPR157	817	chr1:9110457-9111541	pro	9110457	9111541	chr1	-0.72
GPR157	894	chr1:9112343-9113078	pro	9112343	9113078	chr1	-0.72
ZNF644	484	chr1:91260323-91261445	pro	91260323	91261445	chr1	-0.25
H6PD	126	chr1:9222282-9222441	pro	9222282	9222441	chr1	-0.31
SNORD21	1427	chr1:93073947-93074063	pro	93073947	93074063	chr1	-0.37
FAM69A	520	chr1:93115210-93116422	pro	93115210	93116422	chr1	-0.71
FAM69A	1378	chr1:93200126-93201965	pro	93200126	93201965	chr1	-0.25
CCDC18	2054	chr1:93420067-93421761	pro	93420067	93421761	chr1	-0.70
LOC100129046	308	chr1:93829627-93829982	pro	93829627	93829982	chr1	-0.82
LOC100129046	163	chr1:93830083-93830467	pro	93830083	93830467	chr1	-0.83
BCAR3	880	chr1:93918314-93918953	pro	93918314	93918953	chr1	-0.87
BCAR3	334	chr1:93919059-93919301	pro	93919059	93919301	chr1	-0.45
BCAR3	104	chr1:93919547-93919689	pro	93919547	93919689	chr1	-0.71
BCAR3	380	chr1:93920068-93920655	pro	93920068	93920655	chr1	-0.96
LOC100506022	1378	chr1:9409980-9410389	pro	9409980	9410389	chr1	-0.39
DNTTIP2	1462	chr1:94115747-94116028	pro	94115747	94116028	chr1	-0.65
COX15	1030	chr10:101483146-1014837	pro	101483146	101483743	chr10	-0.69
CWF19L1	1671	chr10:102015580-102015	pro	102015580	102015934	chr10	-0.35

BLOC1S2	1170	chr10:102034821-1020350	pro	102034821	102035063	chr10	-0.77
SCD	990	chr10:102095263-1020962	pro	102095263	102096277	chr10	-0.39
LINC00263	2534	chr10:102120045-1021215	pro	102120045	102121530	chr10	-0.60
LINC00263	726	chr10:102122079-1021231	pro	102122079	102123114	chr10	-0.41
LINC00263	1546	chr10:102124800-1021249	pro	102124800	102124935	chr10	-0.58
LINC00263	1962	chr10:102125072-1021254	pro	102125072	102125495	chr10	-0.69
HIF1AN	670	chr10:102284420-1022854	pro	102284420	102285499	chr10	-0.75
HIF1AN	1683	chr10:102287174-1022874	pro	102287174	102287452	chr10	-0.29
FAM178A	1138	chr10:102661125-1026612	pro	102661125	102661228	chr10	-0.72
FAM178A	306	chr10:102661542-1026624	pro	102661542	102662475	chr10	-0.39
FAM178A	1584	chr10:102663152-1026646	pro	102663152	102664643	chr10	-0.33
KAZALD1	680	chr10:102810941-1028123	pro	102810941	102812396	chr10	-0.45
KAZALD1	2194	chr10:102812577-1028137	pro	102812577	102813788	chr10	-0.60
BTRC	958	chr10:103104272-1031052	pro	103104272	103105201	chr10	-0.28
FBXW4	1438	chr10:103442567-1034440	pro	103442567	103444024	chr10	-0.33
FBXW4	1361	chr10:103445958-1034462	pro	103445958	103446232	chr10	-0.89
C10orf76	352	chr10:103806076-1038064	pro	103806076	103806472	chr10	-0.47
HPS6	565	chr10:103814156-1038149	pro	103814156	103814938	chr10	-0.41
NFKB2	260	chr10:104143434-1041437	pro	104143434	104143757	chr10	-0.25
PSD	752	chr10:104167838-1041684	pro	104167838	104168441	chr10	-0.90
CUEDC2	984	chr10:104183244-1041835	pro	104183244	104183551	chr10	-0.89
RPARP-AS1	338	chr10:104198953-1041994	pro	104198953	104199495	chr10	-0.62
ACTR1A	536	chr10:104252556-1042535	pro	104252556	104253521	chr10	-0.28
ARL3	1584	chr10:104461470-1044637	pro	104461470	104463723	chr10	-0.65
SFXN2	1320	chr10:104465029-1044661	pro	104465029	104466182	chr10	-0.33
CNNM2	2454	chr10:104669542-1046714	pro	104669542	104671493	chr10	-0.44
MIR1307	737	chr10:105144744-1051450	pro	105144744	105145026	chr10	-0.57
PDCD11	1370	chr10:105147475-1051480	pro	105147475	105148066	chr10	-0.39
NEURL1-AS1	1806	chr10:105265079-1052656	pro	105265079	105265689	chr10	-0.65
SLK	2184	chr10:105718987-1057202	pro	105718987	105720296	chr10	-0.26
LOC101927472	875	chr10:106071244-1060732	pro	106071244	106073226	chr10	-0.63
ITPRIP	1092	chr10:106088868-1060898	pro	106088868	106089801	chr10	-0.67
ITPRIP	1840	chr10:106089941-1060902	pro	106089941	106090222	chr10	-0.84
CCDC147-AS1	456	chr10:106102333-1061034	pro	106102333	106103404	chr10	-0.76
SMNDC1	1278	chr10:112055917-1120560	pro	112055917	112056036	chr10	-0.33
SMNDC1	1575	chr10:112056144-1120564	pro	112056144	112056402	chr10	-0.67
RBM20	784	chr10:112393111-1123936	pro	112393111	112393610	chr10	-0.57
RBM20	717	chr10:112394409-1123953	pro	112394409	112395313	chr10	-0.34
PDCD4-AS1	1592	chr10:112618547-1126195	pro	112618547	112619573	chr10	-0.65
BBIP1	883	chr10:112667279-1126683	pro	112667279	112668323	chr10	-0.44
SHOC2	3116	chr10:112670631-1126741	pro	112670631	112674181	chr10	-0.60
NHLRC2	2427	chr10:115605468-1156081	pro	115605468	115608146	chr10	-0.39
PDZD8	2710	chr10:119121424-1191230	pro	119121424	119123011	chr10	-0.57
FAM45A	362	chr10:120853084-1208533	pro	120853084	120853393	chr10	-0.32
RGS10	1044	chr10:121290407-1212919	pro	121290407	121291930	chr10	-0.28
BAG3	1202	chr10:121401890-1214022	pro	121401890	121402253	chr10	-0.77
INPP5F	1351	chr10:121476805-1214769	pro	121476805	121476993	chr10	-0.54
SEC23IP	1515	chr10:121643262-1216439	pro	121643262	121643916	chr10	-0.46
NUDT5	2044	chr10:12279796-12280592	pro	12279796	12280592	chr10	-0.60
FAM53B-AS1	372	chr10:126382615-1263833	pro	126382615	126383302	chr10	-0.45
METTL10	1224	chr10:126469083-1264693	pro	126469083	126469328	chr10	-0.28
EDRF1	2212	chr10:127399341-1274012	pro	127399341	127401227	chr10	-0.75
MKI67	1060	chr10:129815327-1298157	pro	129815327	129815709	chr10	-0.44
GLRX3	2214	chr10:131826615-1318270	pro	131826615	131827069	chr10	-0.49
PWWP2B	572	chr10:134061177-1340613	pro	134061177	134061346	chr10	-0.56

PWWP2B	965	chr10:134061512-1340617	pro	134061512	134061798	chr10	-0.74
C10orf91	2191	chr10:134110514-1341112	pro	134110514	134111272	chr10	-0.86
INPP5A	1284	chr10:134199687-1342004	pro	134199687	134200429	chr10	-0.98
ADAM8	1250	chr10:134938207-1349400	pro	134938207	134940090	chr10	-0.79
MTG1	1555	chr10:135055729-1350563	pro	135055729	135056381	chr10	-0.95
PRPF18	336	chr10:13668433-13668784	pro	13668433	13668784	chr10	-0.49
ADARB2-AS1	228	chr10:1558874-1559230	pro	1558874	1559230	chr10	-0.38
TRDMT1	1648	chr10:17281485-17283372	pro	17281485	17283372	chr10	-0.25
VIM	464	chr10:17309486-17310109	pro	17309486	17310109	chr10	-0.69
VIM	73	chr10:17310257-17310413	pro	17310257	17310413	chr10	-0.35
VIM-AS1	1065	chr10:17312605-17313505	pro	17312605	17313505	chr10	-0.31
STAM-AS1	1262	chr10:17724452-17724873	pro	17724452	17724873	chr10	-0.75
ARL5B	2369	chr10:18990086-18991288	pro	18990086	18991288	chr10	-0.40
DNAJC1	1915	chr10:22334363-22334779	pro	22334363	22334779	chr10	-0.91
SPAG6	1137	chr10:22673136-22673346	pro	22673136	22673346	chr10	-0.93
OTUD1	2292	chr10:23769174-23771813	pro	23769174	23771813	chr10	-0.37
ENKUR	135	chr10:25344538-25345376	pro	25344538	25345376	chr10	-0.78
THNSL1	863	chr10:25345573-25347177	pro	25345573	25347177	chr10	-0.73
APBB1IP	1826	chr10:26765135-26765752	pro	26765135	26765752	chr10	-0.71
ANKRD26	1100	chr10:27428256-27428413	pro	27428256	27428413	chr10	-0.60
MPP7	312	chr10:28610302-28612469	pro	28610302	28612469	chr10	-0.99
BAMBI	1708	chr10:29007843-29008430	pro	29007843	29008430	chr10	-0.48
MTPAP	2235	chr10:30675436-30676642	pro	30675436	30676642	chr10	-0.47
ZNF438	690	chr10:31359819-31360546	pro	31359819	31360546	chr10	-0.62
ZNF438	284	chr10:31360976-31361336	pro	31360976	31361336	chr10	-0.52
ZNF438	768	chr10:31361503-31361778	pro	31361503	31361778	chr10	-0.88
ITGB1	2652	chr10:33281986-33286366	pro	33281986	33286366	chr10	-0.76
ITGB1	1556	chr10:33287525-33290187	pro	33287525	33290187	chr10	-0.54
CREM	1898	chr10:35457797-35458779	pro	35457797	35458779	chr10	-0.94
CREM	1492	chr10:35464753-35465691	pro	35464753	35465691	chr10	-0.71
CREM	1320	chr10:35526007-35526300	pro	35526007	35526300	chr10	-0.45
CCNY	2176	chr10:35663346-35663913	pro	35663346	35663913	chr10	-0.63
CCNY	1385	chr10:35666421-35667961	pro	35666421	35667961	chr10	-0.48
ZNF37BP	1380	chr10:42366851-42367037	pro	42366851	42367037	chr10	-0.47
CSGALNACT2	3258	chr10:42948603-42952676	pro	42948603	42952676	chr10	-0.98
CSGALNACT2	2221	chr10:42955606-42956632	pro	42955606	42956632	chr10	-0.96
HNRNPF	2038	chr10:43210066-43210430	pro	43210066	43210430	chr10	-0.67
HNRNPF	2080	chr10:43214149-43215612	pro	43214149	43215612	chr10	-0.53
HNRNPF	950	chr10:43225399-43225905	pro	43225399	43225905	chr10	-0.39
C10orf25	1032	chr10:44816767-44818249	pro	44816767	44818249	chr10	-0.26
ANTXRLP1	2093	chr10:47108595-47108919	pro	47108595	47108919	chr10	-0.61
ANTXRLP1	1410	chr10:47109118-47109761	pro	47109118	47109761	chr10	-0.26
ANTXRLP1	442	chr10:47111056-47111527	pro	47111056	47111527	chr10	-0.53
FAM170B	324	chr10:50012316-50012476	pro	50012316	50012476	chr10	-0.80
FAM170B	744	chr10:50012602-50013029	pro	50012602	50013029	chr10	-0.68
FAM170B	1897	chr10:50013402-50014536	pro	50013402	50014536	chr10	-0.56
C10orf128	67	chr10:50066090-50066948	pro	50066090	50066948	chr10	-0.68
C10orf128	2422	chr10:50068086-50069662	pro	50068086	50069662	chr10	-0.69
SGMS1	3416	chr10:52047778-52052879	pro	52047778	52052879	chr10	-0.52
NET1	1175	chr10:5445062-5446312	pro	5445062	5446312	chr10	-0.39
ASB13	2947	chr10:5744582-5746652	pro	5744582	5746652	chr10	-0.96
ASB13	916	chr10:5747076-5748219	pro	5747076	5748219	chr10	-0.51
ZWINT	1376	chr10:57792082-57792751	pro	57792082	57792751	chr10	-0.61
FBXO18	1809	chr10:5977435-5978891	pro	5977435	5978891	chr10	-0.59
RBM17	1280	chr10:6168590-6170758	pro	6168590	6170758	chr10	-0.48

RBM17	2768	chr10:6173289-6174875	pro	6173289	6174875	chr10	-0.30
MIR548AV	2038	chr10:63402633-6340542	pro	63402633	63405423	chr10	-0.44
ADO	2422	chr10:64235462-6423842	pro	64235462	64238422	chr10	-0.59
REEP3	1008	chr10:64949277-6495096	pro	64949277	64950963	chr10	-0.39
PRKCQ-AS1	1498	chr10:6663805-6663976	pro	6663805	6663976	chr10	-0.85
DNAJC12	1579	chr10:69266108-6926662	pro	69266108	69266622	chr10	-0.89
DNAJC12	910	chr10:69266778-6926728	pro	69266778	69267289	chr10	-0.88
DNAJC12	256	chr10:69267423-6926795	pro	69267423	69267952	chr10	-0.44
HNRNPH3	1778	chr10:69759726-6976026	pro	69759726	69760263	chr10	-0.90
SRGN	360	chr10:70517347-7051903	pro	70517347	70519036	chr10	-0.30
SUPV3L1	1102	chr10:70608789-7060893	pro	70608789	70608936	chr10	-0.59
HKDC1	2473	chr10:70651994-7065308	pro	70651994	70653080	chr10	-0.64
SAR1A	866	chr10:71600986-71601331	pro	71600986	71601331	chr10	-0.69
C10orf105	1963	chr10:73165175-7316607	pro	73165175	73166075	chr10	-0.61
C10orf54	2004	chr10:73205261-7320543	pro	73205261	73205435	chr10	-0.86
MIR7152	248	chr10:73220583-7322093	pro	73220583	73220930	chr10	-0.84
PSAP	301	chr10:73281241-7328153	pro	73281241	73281537	chr10	-0.51
PSAP	1172	chr10:73282083-7328243	pro	73282083	73282436	chr10	-0.43
ASCC1	630	chr10:73647170-7364788	pro	73647170	73647886	chr10	-0.35
ASCC1	1716	chr10:73647988-7364924	pro	73647988	73649240	chr10	-0.67
MRPS16	1502	chr10:74680774-7468113	pro	74680774	74681137	chr10	-0.37
PPP3CB	1988	chr10:74923496-7492410	pro	74923496	74924103	chr10	-0.42
SAMD8	948	chr10:76540267-7654063	pro	76540267	76540633	chr10	-0.48
POLR3A	1104	chr10:79458083-7945831	pro	79458083	79458318	chr10	-0.33
ZMIZ1	1663	chr10:80500361-8050055	pro	80500361	80500557	chr10	-0.85
PPIF	434	chr10:80776517-8077706	pro	80776517	80777062	chr10	-0.41
ANXA11	2008	chr10:81951962-8195247	pro	81951962	81952479	chr10	-0.47
GRID1	718	chr10:88115381-88115643	pro	88115381	88115643	chr10	-0.69
WAPAL	1732	chr10:88272009-8827449	pro	88272009	88274498	chr10	-0.39
LDB3	141	chr10:88418436-8841865	pro	88418436	88418654	chr10	-0.60
LDB3	572	chr10:88418790-8841916	pro	88418790	88419163	chr10	-0.93
FAM35A	1464	chr10:88846099-8884669	pro	88846099	88846692	chr10	-0.65
ATAD1	1759	chr10:89564637-89567641	pro	89564637	89567641	chr10	-0.40
PTEN	2222	chr10:89609852-8961205	pro	89609852	89612052	chr10	-0.41
STAMBPL1	484	chr10:90629011-9062986	pro	90629011	90629865	chr10	-0.60
STAMBPL1	1768	chr10:90630699-9063268	pro	90630699	90632682	chr10	-0.71
FAS-AS1	741	chr10:90739468-9074447	pro	90739468	90744474	chr10	-0.56
LIPA	202	chr10:91001820-9100213	pro	91001820	91002137	chr10	-0.79
IFIT2	446	chr10:91051156-91051321	pro	91051156	91051321	chr10	-0.31
IFIT2	406	chr10:91051468-9105271	pro	91051468	91052713	chr10	-0.43
IFIT3	334	chr10:91081846-9108325	pro	91081846	91083250	chr10	-0.73
IFIT3	1378	chr10:91083475-9108371	pro	91083475	91083710	chr10	-0.87
IFIT3	1840	chr10:91083965-9108414	pro	91083965	91084144	chr10	-0.80
IFIT1	158	chr10:91141705-91142544	pro	91141705	91142544	chr10	-0.36
PANK1	412	chr10:91392732-91393701	pro	91392732	91393701	chr10	-0.45
PANK1	310	chr10:91395023-9139621	pro	91395023	91396216	chr10	-0.39
KIF20B	716	chr10:91450120-9145109	pro	91450120	91451099	chr10	-0.46
RPP30	1054	chr10:92621955-9262352	pro	92621955	92623528	chr10	-0.25
PCGF5	846	chr10:92911425-9291238	pro	92911425	92912380	chr10	-0.25
PCGF5	190	chr10:92969170-9297022	pro	92969170	92970223	chr10	-0.46
PCGF5	1559	chr10:92970927-9297286	pro	92970927	92972867	chr10	-0.26
TNKS2-AS1	1906	chr10:93545931-9354612	pro	93545931	93546125	chr10	-0.58
FGFBP3	1524	chr10:93657339-9365809	pro	93657339	93658090	chr10	-0.27
LOC101928272	1251	chr10:9376227-9376395	pro	9376227	9376395	chr10	-0.55
CEP55	760	chr10:95245040-9524615	pro	95245040	95246156	chr10	-0.32

CEP55	2108	chr10:95247871-95249101	pro	95247871	95249101	chr10	-0.56
FRA10AC1	792	chr10:95450932-95452125	pro	95450932	95452125	chr10	-0.26
SLC35G1	1109	chr10:95644093-95645561	pro	95644093	95645561	chr10	-0.39
PDLIM1	1684	chr10:97042459-97042702	pro	97042459	97042702	chr10	-0.91
LOC101927762	1846	chr10:970639-970982	pro	970639	970982	chr10	-0.70
ALDH18A1	1843	chr10:97404591-97404839	pro	97404591	97404839	chr10	-0.68
ALDH18A1	312	chr10:97406637-97407102	pro	97406637	97407102	chr10	-0.44
TCTN3	366	chr10:97444049-97444462	pro	97444049	97444462	chr10	-0.42
ENTPD1	756	chr10:97505382-97507453	pro	97505382	97507453	chr10	-0.94
CCNJ	388	chr10:97792397-97793122	pro	97792397	97793122	chr10	-0.38
ENTPD1-AS1	824	chr10:97838746-97839569	pro	97838746	97839569	chr10	-0.35
TM9SF3	1260	chr10:98336997-98339123	pro	98336997	98339123	chr10	-0.32
PIK3AP1	737	chr10:98470431-98471583	pro	98470431	98471583	chr10	-0.33
LCOR	1123	chr10:98580067-98581699	pro	98580067	98581699	chr10	-0.30
ARHGAP19-SLI	305	chr10:99042609-99042841	pro	99042609	99042841	chr10	-0.45
PI4K2A	363	chr10:99389959-99390179	pro	99389959	99390179	chr10	-0.28
R3HCC1L	1260	chr10:99883031-99883190	pro	99883031	99883190	chr10	-0.73
R3HCC1L	330	chr10:99883771-99884310	pro	99883771	99884310	chr10	-0.49
MIR548G	1074	chr11:100286463-1002877	pro	100286463	100287789	chr11	-0.97
TRPC6	907	chr11:100960522-1009610	pro	100960522	100961032	chr11	-0.97
LOC643733	94	chr11:104294074-1042943	pro	104294074	104294339	chr11	-0.44
AMPD3	155	chr11:10438811-10439383	pro	10438811	10439383	chr11	-0.91
MSANTD4	2312	chr11:105395366-1053963	pro	105395366	105396338	chr11	-0.54
ALKBH8	2156	chr11:106943099-1069445	pro	106943099	106944558	chr11	-0.64
ACAT1	1950	chr11:107499228-1074996	pro	107499228	107499603	chr11	-0.59
DDX10	1230	chr11:108039493-1080399	pro	108039493	108039968	chr11	-0.89
ZW10	1262	chr11:113148223-1131486	pro	113148223	113148644	chr11	-0.52
ZW10	488	chr11:113149864-1131505	pro	113149864	113150504	chr11	-0.38
HTR3A	38	chr11:113352671-1133542	pro	113352671	113354264	chr11	-0.83
CADM1	2738	chr11:114876465-1148789	pro	114876465	114878964	chr11	-0.96
CEP164	487	chr11:116703144-1167034	pro	116703144	116703442	chr11	-0.77
TMPRSS13	1210	chr11:117306514-1173066	pro	117306514	117306663	chr11	-0.46
SCN2B	95	chr11:117552333-1175525	pro	117552333	117552573	chr11	-0.42
AMICA1	1433	chr11:117590066-1175913	pro	117590066	117591368	chr11	-0.69
MPZL3	1145	chr11:117627082-1176272	pro	117627082	117627216	chr11	-0.46
UBE4A	336	chr11:117734950-1177353	pro	117734950	117735385	chr11	-0.32
ATP5L	754	chr11:117776256-1177768	pro	117776256	117776859	chr11	-0.67
ATP5L	1651	chr11:117778895-1177790	pro	117778895	117779031	chr11	-0.51
LOC101929089	493	chr11:117905896-1179065	pro	117905896	117906518	chr11	-0.26
IFT46	193	chr11:117942086-1179423	pro	117942086	117942304	chr11	-0.49
ARCN1	740	chr11:117947379-1179477	pro	117947379	117947761	chr11	-0.65
BCL9L	1922	chr11:118288053-1182894	pro	118288053	118289439	chr11	-0.69
MIR3656	1142	chr11:118395652-1183963	pro	118395652	118396357	chr11	-0.32
H2AFX	678	chr11:118471687-1184724	pro	118471687	118472446	chr11	-0.64
H2AFX	2150	chr11:118473024-1184740	pro	118473024	118474053	chr11	-0.94
DPAGT1	1188	chr11:118479026-1184793	pro	118479026	118479343	chr11	-0.73
CBL	825	chr11:118580901-1185818	pro	118580901	118581837	chr11	-0.26
USP2	1882	chr11:118736667-1187397	pro	118736667	118739773	chr11	-0.87
USP2	952	chr11:118740356-1187417	pro	118740356	118741751	chr11	-0.94
PVRL1	1712	chr11:119102255-1191036	pro	119102255	119103612	chr11	-0.43
OAF	698	chr11:119585948-1195865	pro	119585948	119586567	chr11	-0.36
ARHGEF12	935	chr11:119712779-1197147	pro	119712779	119714743	chr11	-0.45
TBCEL	228	chr11:120399655-1203999	pro	120399655	120399913	chr11	-0.35
UBASH3B	478	chr11:122030723-1220315	pro	122030723	122031534	chr11	-0.49
NRGN	313	chr11:124114546-1241149	pro	124114546	124114904	chr11	-0.54

MSANTD2	1410	chr11:124173576-1241746	pro	124173576	124174624	chr11	-0.52
STT3A	2099	chr11:124969679-1249703	pro	124969679	124970315	chr11	-0.76
HYLS1	1350	chr11:125260696-1252609	pro	125260696	125260932	chr11	-0.96
HYLS1	665	chr11:125261176-1252618	pro	125261176	125261822	chr11	-0.93
HYLS1	2002	chr11:125263896-1252644	pro	125263896	125264435	chr11	-0.91
PUS3	176	chr11:125278437-1252785	pro	125278437	125278566	chr11	-0.41
FOXRED1	1011	chr11:125645124-1256453	pro	125645124	125645394	chr11	-0.62
TIRAP	1896	chr11:125659934-1256602	pro	125659934	125660239	chr11	-0.29
ST3GAL4-AS1	1859	chr11:125728409-1257292	pro	125728409	125729257	chr11	-0.89
KCNJ1	888	chr11:128215905-1282176	pro	128215905	128217600	chr11	-0.76
PRDM10	2109	chr11:129320068-1293211	pro	129320068	129321170	chr11	-0.65
PRDM10	1763	chr11:129324284-1293246	pro	129324284	129324698	chr11	-0.84
LINC00167	1938	chr11:129375649-1293759	pro	129375649	129375931	chr11	-0.56
PRDM10	2180	chr11:129379742-1293804	pro	129379742	129380497	chr11	-0.84
NCAPD3	1875	chr11:133596803-1335987	pro	133596803	133598719	chr11	-0.28
ACAD8	865	chr11:133629195-1336298	pro	133629195	133629819	chr11	-0.34
INSC	1073	chr11:15091781-15092189	pro	15091781	15092189	chr11	-0.82
RPS13	1755	chr11:17053804-17054278	pro	17053804	17054278	chr11	-0.60
SAAL1	1233	chr11:18082528-18083434	pro	18082528	18083434	chr11	-0.37
SAA3P	590	chr11:18093570-18093761	pro	18093570	18093761	chr11	-0.81
E2F8	1812	chr11:19216583-19217961	pro	19216583	19217961	chr11	-0.48
E2F8	585	chr11:19219926-19220800	pro	19219926	19220800	chr11	-0.33
E2F8	1747	chr11:19221122-19221928	pro	19221122	19221928	chr11	-0.86
PRMT3	986	chr11:20364583-20364746	pro	20364583	20364746	chr11	-0.34
CDKN1C	158	chr11:2863332-2863495	pro	2863332	2863495	chr11	-0.65
IFITM1	1844	chr11:301822-302471	pro	301822	302471	chr11	-0.91
IFITM1	424	chr11:302818-304315	pro	302818	304315	chr11	-0.65
ARL14EP	890	chr11:30299597-30301062	pro	30299597	30301062	chr11	-0.34
IFITM1	1320	chr11:304983-305636	pro	304983	305636	chr11	-0.93
HIPK3	1404	chr11:33236685-33239026	pro	33236685	33239026	chr11	-0.26
KIAA1549L	1722	chr11:33517454-33520007	pro	33517454	33520007	chr11	-0.98
ZNF195	1449	chr11:3355336-3355822	pro	3355336	3355822	chr11	-0.67
ZNF195	413	chr11:3357207-3357675	pro	3357207	3357675	chr11	-0.34
LMO2	508	chr11:33869690-33870118	pro	33869690	33870118	chr11	-0.83
LMO2	2084	chr11:33871725-33873267	pro	33871725	33873267	chr11	-0.61
TRIM44	1366	chr11:35641494-35643093	pro	35641494	35643093	chr11	-0.29
API5	1513	chr11:43291279-43291907	pro	43291279	43291907	chr11	-0.26
MIR129-2	784	chr11:43558613-43558856	pro	43558613	43558856	chr11	-0.42
HSD17B12	2971	chr11:43660638-43662740	pro	43660638	43662740	chr11	-0.60
PTDSS2	742	chr11:439360-439713	pro	439360	439713	chr11	-0.43
EXT2	1270	chr11:44072335-44072474	pro	44072335	44072474	chr11	-0.41
EXT2	630	chr11:44074632-44075273	pro	44074632	44075273	chr11	-0.47
PEX16	1535	chr11:45894643-45894787	pro	45894643	45894787	chr11	-0.54
DGKZ	530	chr11:46323593-46324252	pro	46323593	46324252	chr11	-0.78
CKAP5	1844	chr11:46822456-46822729	pro	46822456	46822729	chr11	-0.32
LRP4	1238	chr11:46897889-46898088	pro	46897889	46898088	chr11	-0.46
FNBP4	2273	chr11:47742891-47743703	pro	47742891	47743703	chr11	-0.58
NUP160	2090	chr11:47828488-47828959	pro	47828488	47828959	chr11	-0.49
TRIM34	131	chr11:5609542-5610316	pro	5609542	5610316	chr11	-0.49
UBE2L6	215	chr11:57092411-57092779	pro	57092411	57092779	chr11	-0.26
YPEL4	596	chr11:57172956-57173839	pro	57172956	57173839	chr11	-0.29
ZDHHC5	1932	chr11:57193908-57194052	pro	57193908	57194052	chr11	-0.55
MED19	980	chr11:57235140-57235399	pro	57235140	57235399	chr11	-0.42
OR5B21	1158	chr11:58030581-58031411	pro	58030581	58031411	chr11	-0.93
FAM111A	2436	chr11:58670378-58672147	pro	58670378	58672147	chr11	-0.72

MPEG1	50	chr11:58736640-58737601	pro	58736640	58737601	chr11	-0.37
MRPL16	1752	chr11:59333110-59333229	pro	59333110	59333229	chr11	-0.81
MRPL16	1124	chr11:59333554-59334041	pro	59333554	59334041	chr11	-0.37
MS4A7	130	chr11:59901592-59903211	pro	59901592	59903211	chr11	-0.58
MS4A14	1074	chr11:59921054-59921217	pro	59921054	59921217	chr11	-0.87
MS4A1	998	chr11:59978156-59979559	pro	59978156	59979559	chr11	-0.55
TMEM109	1680	chr11:60436178-60436355	pro	60436178	60436355	chr11	-0.80
IRF7	649	chr11:606592-606706	pro	606592	606706	chr11	-0.60
FEN1	2238	chr11:61318583-61319260	pro	61318583	61319260	chr11	-0.50
GANAB	1596	chr11:62169137-62169218	pro	62169137	62169218	chr11	-0.38
LBHD1	1519	chr11:62197154-62197520	pro	62197154	62197520	chr11	-0.38
UBXN1	2025	chr11:62205112-62205270	pro	62205112	62205270	chr11	-0.28
TAF6L	1180	chr11:62294096-62294244	pro	62294096	62294244	chr11	-0.51
WDR74	1274	chr11:62365396-62365560	pro	62365396	62365560	chr11	-0.28
SNORD22	778	chr11:62375961-62376650	pro	62375961	62376650	chr11	-0.65
SLC3A2	1339	chr11:62406747-62407423	pro	62406747	62407423	chr11	-0.37
APBB1	794	chr11:6395828-6396419	pro	6395828	6396419	chr11	-0.36
LOC100996455	180	chr11:63972123-63973725	pro	63972123	63973725	chr11	-0.49
PYGM	2830	chr11:64286680-64288508	pro	64286680	64288508	chr11	-0.70
SF1	1320	chr11:64303733-64304691	pro	64303733	64304691	chr11	-0.57
C11orf85	1719	chr11:64497566-64498152	pro	64497566	64498152	chr11	-0.86
BATF2	2068	chr11:64512168-64512349	pro	64512168	64512349	chr11	-0.74
BATF2	110	chr11:64513983-64514890	pro	64513983	64514890	chr11	-0.48
BATF2	88	chr11:64520654-64521359	pro	64520654	64521359	chr11	-0.48
BATF2	1630	chr11:64522416-64523032	pro	64522416	64523032	chr11	-0.96
ARL2-SNX15	828	chr11:64537022-64537643	pro	64537022	64537643	chr11	-0.62
CDCA5	1980	chr11:64605992-64606431	pro	64605992	64606431	chr11	-0.84
MRPL49	2027	chr11:64643767-64644639	pro	64643767	64644639	chr11	-0.68
MIR6751	346	chr11:64654085-64654660	pro	64654085	64654660	chr11	-0.35
MIR612	2803	chr11:64964853-64966549	pro	64964853	64966549	chr11	-0.43
MALAT1	887	chr11:65020352-65021490	pro	65020352	65021490	chr11	-0.53
EHBP1L1	1038	chr11:65100366-65101877	pro	65100366	65101877	chr11	-0.64
RBM14	1124	chr11:66139374-66139633	pro	66139374	66139633	chr11	-0.67
RBM4B	2090	chr11:66198969-66200787	pro	66198969	66200787	chr11	-0.26
POLD4	2128	chr11:66877956-66881587	pro	66877956	66881587	chr11	-0.34
TBC1D10C	782	chr11:66927096-66927255	pro	66927096	66927255	chr11	-0.62
CABP4	1999	chr11:66974197-66974725	pro	66974197	66974725	chr11	-0.79
GSTP1	870	chr11:67106468-67107073	pro	67106468	67107073	chr11	-0.43
ACY3	743	chr11:67175256-67175642	pro	67175256	67175642	chr11	-0.71
C11orf24	1228	chr11:67796965-67797584	pro	67796965	67797584	chr11	-0.39
TPCN2	469	chr11:68572167-68572743	pro	68572167	68572743	chr11	-0.55
MYEOV	2334	chr11:68818158-68822871	pro	68818158	68822871	chr11	-0.73
ZNF215	450	chr11:6903374-6904181	pro	6903374	6904181	chr11	-0.51
ZNF215	3022	chr11:6905329-6909172	pro	6905329	6909172	chr11	-0.76
STARD10	607	chr11:72181210-72182372	pro	72181210	72182372	chr11	-0.34
MRPL48	628	chr11:73175347-73176524	pro	73175347	73176524	chr11	-0.27
PAAF1	1010	chr11:73266562-73266779	pro	73266562	73266779	chr11	-0.30
LIPT2	1370	chr11:73880743-73881325	pro	73880743	73881325	chr11	-0.90
GDPD5	2061	chr11:74911747-74912627	pro	74911747	74912627	chr11	-0.90
GDPD5	1046	chr11:74912728-74913675	pro	74912728	74913675	chr11	-0.68
UVRAG	1319	chr11:75202359-75202719	pro	75202359	75202719	chr11	-0.63
KCTD21-AS1	1046	chr11:77529352-77529711	pro	77529352	77529711	chr11	-0.75
USP35	1328	chr11:77578774-77578891	pro	77578774	77578891	chr11	-0.74
LOC101928865	1860	chr11:77816377-77816962	pro	77816377	77816962	chr11	-0.44
CEND1	810	chr11:778774-779858	pro	778774	779858	chr11	-0.68

NARS2	1852	chr11:77961488-77961924	pro	77961488	77961924	chr11	-0.69
CEND1	142	chr11:780190-780347	pro	780190	780347	chr11	-0.26
EIF3F	1749	chr11:7967106-7967276	pro	7967106	7967276	chr11	-0.32
RPLP2	1972	chr11:797878-798046	pro	797878	798046	chr11	-0.75
PRCP	2000	chr11:82286948-82287464	pro	82286948	82287464	chr11	-0.79
DDIAS	1926	chr11:82290655-82293966	pro	82290655	82293966	chr11	-0.42
CCDC90B	1128	chr11:82676063-82676388	pro	82676063	82676388	chr11	-0.66
DLG2	1593	chr11:85014021-85014717	pro	85014021	85014717	chr11	-0.85
DLG2	608	chr11:85015262-85015445	pro	85015262	85015445	chr11	-0.82
SYTL2	1990	chr11:85197795-85197925	pro	85197795	85197925	chr11	-0.78
SYTL2	955	chr11:85198062-85199728	pro	85198062	85199728	chr11	-0.46
STK33	376	chr11:8571540-8571971	pro	8571540	8571971	chr11	-0.35
STK33	346	chr11:8572471-8573046	pro	8572471	8573046	chr11	-0.38
CTSC	1918	chr11:87708283-87709061	pro	87708283	87709061	chr11	-0.81
AKIP1	1274	chr11:8890365-8890810	pro	8890365	8890810	chr11	-0.78
SNORA40	1444	chr11:93109301-93109687	pro	93109301	93109687	chr11	-0.71
PANX1	1833	chr11:93503486-93503660	pro	93503486	93503660	chr11	-0.30
MRE11A	1912	chr11:93864711-93864842	pro	93864711	93864842	chr11	-0.69
FUT4	274	chr11:93916142-93916639	pro	93916142	93916639	chr11	-0.78
AMOTL1	1591	chr11:94142272-94143218	pro	94142272	94143218	chr11	-0.98
ZNF143	2432	chr11:9441062-9441974	pro	9441062	9441974	chr11	-0.47
SRSF8	134	chr11:94439272-94439837	pro	94439272	94439837	chr11	-0.41
ENDOD1	2282	chr11:94462926-94466878	pro	94462926	94466878	chr11	-0.64
SBF2-AS1	2245	chr11:9733584-9734754	pro	9733584	9734754	chr11	-0.28
ARL1	1074	chr12:100326691-1003269	pro	100326691	100326918	chr12	-0.51
GNPTAB	1888	chr12:100746600-1007471	pro	100746600	100747176	chr12	-0.83
PARPBP	2124	chr12:101039679-1010407	pro	101039679	101040738	chr12	-0.84
IGF1	456	chr12:101396396-1013976	pro	101396396	101397637	chr12	-0.69
TDG	766	chr12:102882354-1028835	pro	102882354	102883557	chr12	-0.34
TDG	1077	chr12:102884251-1028853	pro	102884251	102885347	chr12	-0.35
NFYB	1588	chr12:103053791-1030553	pro	103053791	103055374	chr12	-0.42
TXNRD1	282	chr12:103203812-1032047	pro	103203812	103204799	chr12	-0.68
TXNRD1	1830	chr12:103206108-1032067	pro	103206108	103206727	chr12	-0.28
CHST11	557	chr12:103373835-1033746	pro	103373835	103374691	chr12	-0.40
C12orf45	1228	chr12:103904640-1039062	pro	103904640	103906268	chr12	-0.31
LOC414300	608	chr12:104024386-1040254	pro	104024386	104025498	chr12	-0.39
KIAA1033	2012	chr12:104026200-1040290	pro	104026200	104029064	chr12	-0.40
APPL2	1240	chr12:104152114-1041536	pro	104152114	104153682	chr12	-0.59
C12orf75	2176	chr12:104245758-1042469	pro	104245758	104246974	chr12	-0.99
C12orf75	542	chr12:104247605-1042483	pro	104247605	104248396	chr12	-0.57
C12orf75	1342	chr12:104249295-1042504	pro	104249295	104250474	chr12	-0.64
KLRK1	3138	chr12:10435522-10438595	pro	10435522	10438595	chr12	-0.46
CKAP4	1670	chr12:105163965-1051643	pro	105163965	105164384	chr12	-0.94
CKAP4	1031	chr12:105164602-1051650	pro	105164602	105165024	chr12	-0.60
CKAP4	1596	chr12:105166398-1051684	pro	105166398	105168482	chr12	-0.68
TCP11L2	1026	chr12:105219172-1052201	pro	105219172	105220171	chr12	-0.35
POLR3B	230	chr12:105275147-1052755	pro	105275147	105275522	chr12	-0.54
TMEM263	1771	chr12:105874255-1058766	pro	105874255	105876631	chr12	-0.27
MAGOHB	1863	chr12:10654914-10655048	pro	10654914	10655048	chr12	-0.73
PWP1	572	chr12:106602702-1066035	pro	106602702	106603591	chr12	-0.39
PWP1	1316	chr12:106604956-1066051	pro	106604956	106605111	chr12	-0.58
LOC101929162	416	chr12:106654753-1066549	pro	106654753	106654999	chr12	-0.70
LOC101929162	812	chr12:106655181-1066553	pro	106655181	106655364	chr12	-0.69
PRDM4	1546	chr12:106676504-1066784	pro	106676504	106678493	chr12	-0.26
LOC728739	1214	chr12:106819374-1068215	pro	106819374	106821553	chr12	-0.99

LOC728739	336	chr12:106821820-1068222	pro	106821820	106822209	chr12	-0.91
SART3	2130	chr12:107477015-1074773	pro	107477015	107477318	chr12	-0.56
ISCU	2333	chr12:107480892-1074825	pro	107480892	107482510	chr12	-0.39
SELPLG	1118	chr12:107548592-1075491	pro	107548592	107549140	chr12	-0.96
SELPLG	28	chr12:107549420-1075504	pro	107549420	107550493	chr12	-0.82
SELPLG	649	chr12:107550721-1075515	pro	107550721	107551581	chr12	-0.73
SELPLG	516	chr12:107551760-1075528	pro	107551760	107552872	chr12	-0.57
SELPLG	1587	chr12:107553152-1075536	pro	107553152	107553622	chr12	-0.29
SELPLG	2410	chr12:107553769-1075546	pro	107553769	107554651	chr12	-0.41
CORO1C	774	chr12:107647325-1076486	pro	107647325	107648623	chr12	-0.61
CORO1C	902	chr12:107650089-1076506	pro	107650089	107650628	chr12	-0.51
YBX3	722	chr12:10767406-1076847	pro	10767406	10768477	chr12	-0.64
SSH1	1092	chr12:107776135-1077770	pro	107776135	107777025	chr12	-0.72
USP30	366	chr12:107974140-1079746	pro	107974140	107974640	chr12	-0.47
USP30-AS1	31	chr12:107975029-1079773	pro	107975029	107977341	chr12	-0.31
ALKBH2	2360	chr12:108012905-1080137	pro	108012905	108013727	chr12	-0.88
ALKBH2	288	chr12:108015820-1080161	pro	108015820	108016107	chr12	-0.36
UNG	289	chr12:108019314-1080196	pro	108019314	108019668	chr12	-0.28
FOXN4	253	chr12:108230836-1082314	pro	108230836	108231474	chr12	-0.53
FOXN4	1648	chr12:108232334-1082337	pro	108232334	108233777	chr12	-0.69
TCHP	339	chr12:108821821-1088224	pro	108821821	108822421	chr12	-0.38
GIT2	1850	chr12:108915394-1089180	pro	108915394	108918061	chr12	-0.37
GIT2	234	chr12:108918613-1089190	pro	108918613	108919010	chr12	-0.53
ANKRD13A	1056	chr12:108919566-1089215	pro	108919566	108921555	chr12	-0.50
ANKRD13A	2244	chr12:108923183-1089245	pro	108923183	108924538	chr12	-0.54
IFT81	300	chr12:109046109-1090463	pro	109046109	109046336	chr12	-0.51
ATP2A2	2824	chr12:109204384-1092080	pro	109204384	109208091	chr12	-0.49
ANAPC7	456	chr12:109325932-1093268	pro	109325932	109326815	chr12	-0.33
ARPC3	1222	chr12:109371293-1093714	pro	109371293	109371462	chr12	-0.46
GPN3	1357	chr12:109388991-1093892	pro	109388991	109389239	chr12	-0.58
GPN3	1198	chr12:109391899-1093923	pro	109391899	109392317	chr12	-0.31
VPS29	2030	chr12:109421546-1094230	pro	109421546	109423050	chr12	-0.78
PPTC7	538	chr12:109505667-1095063	pro	109505667	109506304	chr12	-0.49
PPTC7	2016	chr12:109507353-1095075	pro	109507353	109507574	chr12	-0.44
TCTN1	491	chr12:109536354-1095372	pro	109536354	109537216	chr12	-0.35
TCTN1	1260	chr12:109537328-1095377	pro	109537328	109537781	chr12	-0.78
TCTN1	1710	chr12:109537903-1095381	pro	109537903	109538105	chr12	-0.70
PPP1CC	2262	chr12:109661506-1096643	pro	109661506	109664303	chr12	-0.40
PPP1CC	586	chr12:109665359-1096661	pro	109665359	109666146	chr12	-0.31
LINC01405	806	chr12:109859500-1098596	pro	109859500	109859688	chr12	-0.86
FAM109A	554	chr12:110291435-1102922	pro	110291435	110292290	chr12	-0.64
SH2B3	1246	chr12:110326166-1103276	pro	110326166	110327611	chr12	-0.56
SH2B3	1442	chr12:110328556-1103305	pro	110328556	110330595	chr12	-0.45
SH2B3	218	chr12:110356070-1103575	pro	110356070	110357589	chr12	-0.80
ATXN2	2563	chr12:110518526-1105200	pro	110518526	110520076	chr12	-0.26
BRAP	1815	chr12:110606289-1106064	pro	110606289	110606449	chr12	-0.53
BRAP	1492	chr12:110606560-1106068	pro	110606560	110606825	chr12	-0.60
ACAD10	1104	chr12:110608826-1106098	pro	110608826	110609857	chr12	-0.57
ALDH2	408	chr12:110688438-1106888	pro	110688438	110688889	chr12	-0.46
ALDH2	830	chr12:110689314-1106904	pro	110689314	110690490	chr12	-0.65
MAPKAPK5	2006	chr12:110762256-1107625	pro	110762256	110762561	chr12	-0.71
RPL6	2230	chr12:111329224-1113299	pro	111329224	111329967	chr12	-0.50
OAS1	1105	chr12:111827721-1118283	pro	111827721	111828309	chr12	-0.84
DDX54	1843	chr12:112105591-1121060	pro	112105591	112106059	chr12	-0.47
IQCD	1623	chr12:112141455-1121418	pro	112141455	112141863	chr12	-0.45

MED13L	1998	chr12:115197305-1151974	pro	115197305	115197447	chr12	-0.40
LINC01252	1920	chr12:11589625-11590994	pro	11589625	11590994	chr12	-0.80
FBXO21	237	chr12:116112810-1161130	pro	116112810	116113032	chr12	-0.30
RFC5	1633	chr12:116940458-1169405	pro	116940458	116940584	chr12	-0.81
ETV6	2300	chr12:11694712-11697995	pro	11694712	11697995	chr12	-0.62
GCN1L1	1426	chr12:119115374-1191155	pro	119115374	119115566	chr12	-0.87
GCN1L1	1496	chr12:119118211-11911857	pro	119118211	119118573	chr12	-0.50
RPLP0	1916	chr12:119120550-1191224	pro	119120550	119122414	chr12	-0.37
PXN-AS1	978	chr12:119124288-1191246	pro	119124288	119124619	chr12	-0.44
COX6A1	1869	chr12:119361813-1193624	pro	119361813	119362473	chr12	-0.25
COQ5	768	chr12:119450417-1194507	pro	119450417	119450744	chr12	-0.35
RNF10	157	chr12:119456255-1194564	pro	119456255	119456459	chr12	-0.33
CABP1	1006	chr12:119571171-1195722	pro	119571171	119572201	chr12	-0.40
UNC119B	1610	chr12:119634158-1196343	pro	119634158	119634302	chr12	-0.27
MIR4700	1125	chr12:119643855-1196446	pro	119643855	119644651	chr12	-0.77
HNF1A-AS1	198	chr12:119894198-1198943	pro	119894198	119894362	chr12	-0.59
P2RX4	334	chr12:120131669-1201317	pro	120131669	120131756	chr12	-0.43
CAMKK2	2238	chr12:120222266-1202231	pro	120222266	120223197	chr12	-0.90
BCL7A	2180	chr12:120941767-1209423	pro	120941767	120942357	chr12	-0.68
MLXIP	1752	chr12:120999147-1209993	pro	120999147	120999382	chr12	-0.83
MLXIP	1360	chr12:120999488-1209998	pro	120999488	120999824	chr12	-0.69
ZCCHC8	1350	chr12:121552748-1215530	pro	121552748	121553099	chr12	-0.29
MPHOSPH9	1772	chr12:122281835-1222820	pro	122281835	122282096	chr12	-0.66
C12orf65	1249	chr12:122285161-1222858	pro	122285161	122285821	chr12	-0.37
RILPL2	1921	chr12:122485208-1224853	pro	122485208	122485386	chr12	-0.84
RILPL2	1330	chr12:122485804-1224859	pro	122485804	122485973	chr12	-0.62
RILPL1	1247	chr12:122582919-1225830	pro	122582919	122583023	chr12	-0.51
LOC101927415	1695	chr12:122632844-1226334	pro	122632844	122633422	chr12	-0.75
DDX55	1030	chr12:122651457-1226517	pro	122651457	122651731	chr12	-0.42
SCARB1	1445	chr12:123912157-1239138	pro	123912157	123913897	chr12	-0.63
DHX37	266	chr12:124039806-1240399	pro	124039806	124039966	chr12	-0.52
GPR19	650	chr12:12739062-12740415	pro	12739062	12740415	chr12	-0.67
GPR19	1301	chr12:12740557-12742821	pro	12740557	12742821	chr12	-0.31
ANKLE2	1178	chr12:131849591-1318498	pro	131849591	131849862	chr12	-0.34
LOC101928530	780	chr12:131975223-1319753	pro	131975223	131975336	chr12	-0.54
ZNF10	926	chr12:132218078-1322183	pro	132218078	132218345	chr12	-0.25
ATF7IP	1196	chr12:14428645-14432275	pro	14428645	14432275	chr12	-0.93
PLBD1	103	chr12:14612086-14612236	pro	14612086	14612236	chr12	-0.44
HIST4H4	2676	chr12:14811871-14813442	pro	14811871	14813442	chr12	-0.38
MGP	1483	chr12:14928091-14929183	pro	14928091	14929183	chr12	-0.66
PTPRO	38	chr12:15590310-15590853	pro	15590310	15590853	chr12	-0.75
EPS8	196	chr12:15833784-15834163	pro	15833784	15834163	chr12	-0.88
DERA	1395	chr12:15956514-15957020	pro	15956514	15957020	chr12	-0.54
MGST1	863	chr12:16391972-16393710	pro	16391972	16393710	chr12	-0.99
LMO3	122	chr12:16649730-16651633	pro	16649730	16651633	chr12	-0.99
LMO3	896	chr12:16652578-16654046	pro	16652578	16654046	chr12	-0.99
AEBP2	2071	chr12:19486663-19487039	pro	19486663	19487039	chr12	-0.35
BCAT1	1320	chr12:24994866-24995094	pro	24994866	24995094	chr12	-0.78
C12orf77	360	chr12:25039631-25044369	pro	25039631	25044369	chr12	-0.28
KRAS	2608	chr12:25297124-25298356	pro	25297124	25298356	chr12	-0.53
CACNA1C-AS1	1094	chr12:2671323-2672032	pro	2671323	2672032	chr12	-0.28
RHNO1	726	chr12:2854800-2855116	pro	2854800	2855116	chr12	-0.86
RHNO1	1300	chr12:2857503-2858344	pro	2857503	2858344	chr12	-0.35
DDX11	1077	chr12:31116711-31117223	pro	31116711	31117223	chr12	-0.53
DENND5B-AS1	868	chr12:31632175-31634333	pro	31632175	31634333	chr12	-0.34

METTL20	660	chr12:31704350-3170471	pro	31704350	31704719	chr12	-0.29
AMN1	1649	chr12:31771650-3177180	pro	31771650	31771804	chr12	-0.29
ALG10B	564	chr12:36996191-3699632	pro	36996191	36996326	chr12	-0.53
ABCD2	1287	chr12:38297519-3830012	pro	38297519	38300127	chr12	-0.56
ABCD2	1628	chr12:38301294-3830218	pro	38301294	38302181	chr12	-0.83
PARP11	2045	chr12:3849324-3852338	pro	3849324	3852338	chr12	-0.26
LRRK2	1972	chr12:38906546-3890755	pro	38906546	38907553	chr12	-0.27
PDZRN4	1952	chr12:40117328-4012218	pro	40117328	40122187	chr12	-1.00
TWF1	2082	chr12:42484045-4248468	pro	42484045	42484682	chr12	-0.59
PLEKHA8P1	1570	chr12:43896891-4389836	pro	43896891	43898361	chr12	-0.64
C12orf4	2382	chr12:4514163-4516868	pro	4514163	4516868	chr12	-0.89
RPAP3	1926	chr12:46384005-4638436	pro	46384005	46384367	chr12	-0.52
PFKM	346	chr12:46798590-4679927	pro	46798590	46799274	chr12	-0.27
CCNT1	1740	chr12:47395182-4739543	pro	47395182	47395435	chr12	-0.57
CCNT1	681	chr12:47397470-4739798	pro	47397470	47397988	chr12	-0.32
DDX23	1302	chr12:47530537-4753130	pro	47530537	47531306	chr12	-0.28
TUBA1A	437	chr12:47869366-4787025	pro	47869366	47870256	chr12	-0.53
TUBA1C	1265	chr12:47943700-4794403	pro	47943700	47944030	chr12	-0.59
TUBA1C	1940	chr12:47946950-4794719	pro	47946950	47947191	chr12	-0.53
TROAP	865	chr12:48002066-4800267	pro	48002066	48002676	chr12	-0.51
TMBIM6	2006	chr12:48423624-4842410	pro	48423624	48424105	chr12	-0.57
CERS5	1682	chr12:48845761-4884604	pro	48845761	48846044	chr12	-0.42
LIMA1	942	chr12:48900355-4890327	pro	48900355	48903274	chr12	-0.85
LIMA1	916	chr12:48903524-4890381	pro	48903524	48903819	chr12	-0.88
LIMA1	1740	chr12:48904121-4890487	pro	48904121	48904872	chr12	-0.96
DIP2B	1880	chr12:49186763-4918706	pro	49186763	49187064	chr12	-0.92
ATF1	1358	chr12:49442537-4944285	pro	49442537	49442856	chr12	-0.89
TFCP2	1910	chr12:49851200-4985136	pro	49851200	49851367	chr12	-0.69
BIN2	854	chr12:50002732-5000405	pro	50002732	50004059	chr12	-0.84
SLC4A8	364	chr12:50104211-5010478	pro	50104211	50104782	chr12	-0.25
SLC4A8	454	chr12:50105302-5010593	pro	50105302	50105938	chr12	-0.88
ACVR1B	4	chr12:50633002-5063386	pro	50633002	50633866	chr12	-0.62
ACVR1B	596	chr12:50633989-5063406	pro	50633989	50634062	chr12	-0.64
NR4A1	944	chr12:50731565-5073322	pro	50731565	50733228	chr12	-0.44
ATG101	2010	chr12:50751964-5075210	pro	50751964	50752103	chr12	-0.74
OR7E47P	1817	chr12:50761099-5076202	pro	50761099	50762027	chr12	-0.76
OR7E47P	1313	chr12:50763397-5076356	pro	50763397	50763569	chr12	-0.61
KRT78	1960	chr12:51530722-5153129	pro	51530722	51531290	chr12	-0.97
EIF4B	1093	chr12:51684878-5168555	pro	51684878	51685552	chr12	-0.51
RARG	1884	chr12:51902072-5190262	pro	51902072	51902625	chr12	-0.53
ESPL1	2031	chr12:51950178-5195058	pro	51950178	51950580	chr12	-0.67
MAP3K12	916	chr12:52178195-5217939	pro	52178195	52179396	chr12	-0.66
HOXC6	326	chr12:52708035-5270823	pro	52708035	52708233	chr12	-0.94
HOXC6	466	chr12:52708460-5270939	pro	52708460	52709393	chr12	-0.93
HOXC4	916	chr12:52734501-5273518	pro	52734501	52735184	chr12	-0.45
HOXC4	2113	chr12:52735421-5273665	pro	52735421	52736657	chr12	-0.92
SMUG1	842	chr12:52868040-5286829	pro	52868040	52868293	chr12	-0.30
ZNF385A	240	chr12:53064529-5306551	pro	53064529	53065514	chr12	-0.92
ZNF385A	781	chr12:53070531-5307061	pro	53070531	53070619	chr12	-0.56
GTSF1	1233	chr12:53154752-5315502	pro	53154752	53155022	chr12	-0.68
NCKAP1L	864	chr12:53179241-5318015	pro	53179241	53180155	chr12	-0.46
NCKAP1L	1832	chr12:53180504-5318082	pro	53180504	53180829	chr12	-0.87
NTF3	862	chr12:5409996-5411359	pro	5409996	5411359	chr12	-0.99
GDF11	1504	chr12:54423688-5442597	pro	54423688	54425979	chr12	-0.34
TMEM198B	1460	chr12:54507222-5450917	pro	54507222	54509174	chr12	-0.30

WIBG	1174	chr12:54608749-54609526	pro	54608749	54609526	chr12	-0.33
DGKA	1101	chr12:54609750-54610472	pro	54609750	54610472	chr12	-0.34
RPS26	692	chr12:54720816-54721704	pro	54720816	54721704	chr12	-0.54
PA2G4	736	chr12:54783028-54784235	pro	54783028	54784235	chr12	-0.32
RPL41	991	chr12:54795349-54795949	pro	54795349	54795949	chr12	-0.25
ESYT1	1216	chr12:54806081-54807991	pro	54806081	54807991	chr12	-0.46
SMARCC2	1292	chr12:54870818-54871003	pro	54870818	54871003	chr12	-0.52
CS	2142	chr12:54982352-54982817	pro	54982352	54982817	chr12	-0.49
IL23A	2012	chr12:55016584-55017249	pro	55016584	55017249	chr12	-0.91
IL23A	168	chr12:55018214-55019978	pro	55018214	55019978	chr12	-0.78
STAT2	874	chr12:55040825-55041532	pro	55040825	55041532	chr12	-0.53
TIMELESS	1578	chr12:55127657-55128124	pro	55127657	55128124	chr12	-0.59
RBMS2	180	chr12:55201610-55201777	pro	55201610	55201777	chr12	-0.50
RBMS2	428	chr12:55202119-55202484	pro	55202119	55202484	chr12	-0.70
SNORD59B	470	chr12:55324177-55324376	pro	55324177	55324376	chr12	-0.66
PRIM1	2502	chr12:55429338-55430487	pro	55429338	55430487	chr12	-0.55
TMEM194A	1100	chr12:55757580-55757903	pro	55757580	55757903	chr12	-0.27
INHBE	58	chr12:56135350-56135491	pro	56135350	56135491	chr12	-0.49
ARHGAP9	849	chr12:56160646-56160852	pro	56160646	56160852	chr12	-0.82
DDIT3	2052	chr12:56198364-56198668	pro	56198364	56198668	chr12	-0.38
AGAP2	308	chr12:56422381-56422658	pro	56422381	56422658	chr12	-0.26
CDK4	567	chr12:56432723-56433407	pro	56432723	56433407	chr12	-0.32
LOC100506844	1042	chr12:56614220-56616125	pro	56614220	56616125	chr12	-0.47
XRCC6BP1	1420	chr12:56622864-56623397	pro	56622864	56623397	chr12	-0.87
MIRLET7I	1006	chr12:61283923-61285553	pro	61283923	61285553	chr12	-0.56
PPM1H	776	chr12:61614054-61614257	pro	61614054	61614257	chr12	-0.26
TMEM5	1310	chr12:62461374-62461591	pro	62461374	62461591	chr12	-0.67
TNFRSF1A	1246	chr12:6318494-6322102	pro	6318494	6322102	chr12	-0.93
GNS	1376	chr12:63438058-63438177	pro	63438058	63438177	chr12	-0.52
SCNN1A	264	chr12:6356441-6356599	pro	6356441	6356599	chr12	-0.79
HELB	1857	chr12:64983636-64985278	pro	64983636	64985278	chr12	-0.69
CHD4	390	chr12:6587146-6587355	pro	6587146	6587355	chr12	-0.48
ING4	465	chr12:6642822-6643248	pro	6642822	6643248	chr12	-0.30
PIANP	3146	chr12:6675020-6678404	pro	6675020	6678404	chr12	-0.47
PIANP	699	chr12:6678805-6679513	pro	6678805	6679513	chr12	-0.71
PIANP	340	chr12:6680313-6680908	pro	6680313	6680908	chr12	-0.39
SNORA70G	3303	chr12:67309353-67312097	pro	67309353	67312097	chr12	-0.53
MLF2	520	chr12:6733267-6733570	pro	6733267	6733570	chr12	-0.48
SLC35E3	2546	chr12:67427593-67429902	pro	67427593	67429902	chr12	-0.31
PTMS	1554	chr12:6743938-6744553	pro	6743938	6744553	chr12	-0.41
MDM2	1082	chr12:67486799-67487472	pro	67486799	67487472	chr12	-0.65
CPM	776	chr12:67611833-67613106	pro	67611833	67613106	chr12	-0.77
CPSF6	2050	chr12:67920444-67922821	pro	67920444	67922821	chr12	-0.32
GPR162	344	chr12:6800806-6800949	pro	6800806	6800949	chr12	-0.43
YEATS4	2057	chr12:68041671-68041955	pro	68041671	68041955	chr12	-0.81
GNB3	1237	chr12:6818744-6819338	pro	6818744	6819338	chr12	-0.60
GNB3	364	chr12:6820471-6820812	pro	6820471	6820812	chr12	-0.65
CDCA3	2126	chr12:6829159-6829574	pro	6829159	6829574	chr12	-0.84
BEST3	1482	chr12:68376177-68379786	pro	68376177	68379786	chr12	-0.99
LRRC23	688	chr12:6883413-6883524	pro	6883413	6883524	chr12	-0.74
ATN1	2065	chr12:6900956-6902686	pro	6900956	6902686	chr12	-0.81
ATN1	178	chr12:6903621-6903796	pro	6903621	6903796	chr12	-0.42
EMG1	1666	chr12:6951655-6952085	pro	6951655	6952085	chr12	-0.77
PEX5	2030	chr12:7236167-7236340	pro	7236167	7236340	chr12	-0.83
WNK1	2499	chr12:729030-730668	pro	729030	730668	chr12	-0.43

NAP1L1	898	chr12:74764911-74766898	pro	74764911	74766898	chr12	-0.34
ZDHHC17	982	chr12:75680925-75681078	pro	75680925	75681078	chr12	-0.62
NAV3	1736	chr12:76747273-76747651	pro	76747273	76747651	chr12	-0.48
NAV3	582	chr12:76748321-76748911	pro	76748321	76748911	chr12	-0.26
SLC2A3	2012	chr12:7977324-7978972	pro	7977324	7978972	chr12	-0.92
SLC2A3	486	chr12:7979251-7980098	pro	7979251	7980098	chr12	-0.80
SLC2A3	406	chr12:7980375-7980758	pro	7980375	7980758	chr12	-0.73
FOXJ2	1330	chr12:8077914-8077994	pro	8077914	8077994	chr12	-0.31
NECAP1	1429	chr12:8124342-8124944	pro	8124342	8124944	chr12	-0.71
TMTC2	1453	chr12:81603520-81603702	pro	81603520	81603702	chr12	-0.63
EEA1	1512	chr12:91844828-91846623	pro	91844828	91846623	chr12	-0.26
NUDT4	1567	chr12:92296577-92299469	pro	92296577	92299469	chr12	-0.26
UBE2N	3861	chr12:92353542-92359052	pro	92353542	92359052	chr12	-0.78
RAD52	1426	chr12:927490-927959	pro	927490	927959	chr12	-0.45
PLXNC1	884	chr12:93065537-93065950	pro	93065537	93065950	chr12	-0.26
NR2C1	224	chr12:93991680-93991841	pro	93991680	93991841	chr12	-0.32
FGD6	1215	chr12:94133263-94135051	pro	94133263	94135051	chr12	-0.40
USP44	1092	chr12:94464073-94466104	pro	94464073	94466104	chr12	-0.89
USP44	34	chr12:94468606-94470122	pro	94468606	94470122	chr12	-0.99
LTA4H	705	chr12:94953983-94954567	pro	94953983	94954567	chr12	-0.46
ELK3	1914	chr12:95113854-95114646	pro	95113854	95114646	chr12	-0.51
LOC374443	1496	chr12:9658997-9660303	pro	9658997	9660303	chr12	-0.92
LOC374443	210	chr12:9660820-9661891	pro	9660820	9661891	chr12	-0.99
LOC374443	1301	chr12:9678338-9678824	pro	9678338	9678824	chr12	-0.76
LOC374443	560	chr12:9690581-9691858	pro	9690581	9691858	chr12	-0.34
CLEC2D	1978	chr12:9711292-9711893	pro	9711292	9711893	chr12	-0.44
LOC643770	770	chr12:97422240-97422829	pro	97422240	97422829	chr12	-0.38
IKBIP	1504	chr12:97561144-97561767	pro	97561144	97561767	chr12	-0.36
CLECL1	634	chr12:9777667-9777926	pro	9777667	9777926	chr12	-0.74
CD69	2646	chr12:9801381-9802856	pro	9801381	9802856	chr12	-0.57
CD69	464	chr12:9803005-9805595	pro	9803005	9805595	chr12	-0.52
UHRF1BP1L	707	chr12:99061373-99061589	pro	99061373	99061589	chr12	-0.56
CLEC2B	3163	chr12:9909192-9911934	pro	9909192	9911934	chr12	-0.94
CLEC2B	475	chr12:9912098-9914404	pro	9912098	9914404	chr12	-0.61
GAS2L3	298	chr12:99491147-99491493	pro	99491147	99491493	chr12	-0.36
GAS2L3	588	chr12:99491622-99492789	pro	99491622	99492789	chr12	-0.49
LIG4	1202	chr13:107666880-1076672	pro	107666880	107667293	chr13	-0.43
RAB20	448	chr13:110012354-1100126	pro	110012354	110012687	chr13	-0.33
MRPL57	1340	chr13:20646946-20647114	pro	20646946	20647114	chr13	-0.79
FGF9	1358	chr13:21143316-21145829	pro	21143316	21145829	chr13	-0.40
SPATA13	652	chr13:23632161-23632242	pro	23632161	23632242	chr13	-0.36
SPATA13	820	chr13:23633005-23634342	pro	23633005	23634342	chr13	-0.39
LINC01053	211	chr13:24652524-24653990	pro	24652524	24653990	chr13	-0.97
MTMR6	1643	chr13:24761174-24761520	pro	24761174	24761520	chr13	-0.77
CDK8	1051	chr13:25725483-25725923	pro	25725483	25725923	chr13	-0.26
USP12	2430	chr13:26640021-26643187	pro	26640021	26643187	chr13	-0.36
MTUS2	354	chr13:28900876-28901385	pro	28900876	28901385	chr13	-0.98
UBL3	282	chr13:29322940-29323265	pro	29322940	29323265	chr13	-0.33
LINC00544	531	chr13:29407712-29408558	pro	29407712	29408558	chr13	-0.78
KATNAL1	1356	chr13:29776691-29778982	pro	29776691	29778982	chr13	-0.39
LINC00426	12	chr13:29845229-29846851	pro	29845229	29846851	chr13	-0.32
LINC01058	1831	chr13:29895767-29896659	pro	29895767	29896659	chr13	-0.37
FRY-AS1	1280	chr13:31503729-31506384	pro	31503729	31506384	chr13	-0.69
PDS5B	2216	chr13:32059438-32062119	pro	32059438	32062119	chr13	-0.45
RFC3	364	chr13:33289533-33290147	pro	33289533	33290147	chr13	-0.44

RFC3	1860	chr13:33291291-3329283	pro	33291291	33292838	chr13	-0.77
NBEA	1924	chr13:34415087-3441760	pro	34415087	34417605	chr13	-0.68
RFXAP	564	chr13:36290280-3629126	pro	36290280	36291267	chr13	-0.25
RFXAP	1318	chr13:36291754-3629355	pro	36291754	36293558	chr13	-0.34
SMAD9	1382	chr13:36390280-3639177	pro	36390280	36391775	chr13	-0.88
SMAD9	780	chr13:36392733-3639364	pro	36392733	36393648	chr13	-0.82
ALG5	1198	chr13:36469671-3647094	pro	36469671	36470942	chr13	-0.41
ALG5	438	chr13:36471623-3647226	pro	36471623	36472260	chr13	-0.32
EXOSC8	1502	chr13:36473508-3647484	pro	36473508	36474847	chr13	-0.42
SUPT20H	292	chr13:36531944-3653234	pro	36531944	36532340	chr13	-0.28
NHLRC3	2512	chr13:38512357-3851355	pro	38512357	38513559	chr13	-0.92
LHFP	2405	chr13:39071057-3907484	pro	39071057	39074845	chr13	-0.93
SLC25A15	1651	chr13:40263050-4026334	pro	40263050	40263344	chr13	-0.88
WBP4	2744	chr13:40529650-4053225	pro	40529650	40532254	chr13	-0.26
VWA8	2112	chr13:41430638-4143158	pro	41430638	41431582	chr13	-0.59
TNFSF11	685	chr13:42046913-4204703	pro	42046913	42047037	chr13	-0.40
TNFSF11	1183	chr13:42047385-42047561	pro	42047385	42047561	chr13	-0.73
LACC1	892	chr13:43349705-4335134	pro	43349705	43351348	chr13	-0.34
MED4-AS1	1454	chr13:47550646-4755080	pro	47550646	47550806	chr13	-0.57
MED4	1955	chr13:47565282-4756536	pro	47565282	47565364	chr13	-0.29
RB1	1663	chr13:47776903-4777818	pro	47776903	47778187	chr13	-0.51
LINC00462	1592	chr13:48050750-48052141	pro	48050750	48052141	chr13	-0.48
FNDC3A	2616	chr13:48448819-4845390	pro	48448819	48453902	chr13	-0.72
CAB39L	732	chr13:48914958-4891610	pro	48914958	48916105	chr13	-0.29
SETDB2	3200	chr13:48918066-48921191	pro	48918066	48921191	chr13	-0.30
SETDB2	1360	chr13:48921935-48922721	pro	48921935	48922721	chr13	-0.79
RNASEH2B	1462	chr13:50379610-5038109	pro	50379610	50381095	chr13	-0.94
RNASEH2B-AS	4214	chr13:50384386-5038974	pro	50384386	50389742	chr13	-0.68
MRPS31P5	1206	chr13:51665166-5166563	pro	51665166	51665630	chr13	-0.46
CKAP2	1455	chr13:51929423-5192969	pro	51929423	51929699	chr13	-0.79
CKAP2	1948	chr13:51930010-5193009	pro	51930010	51930099	chr13	-0.80
HNRNPA1L2	1031	chr13:52090325-5209094	pro	52090325	52090945	chr13	-0.33
DIAPH3	1223	chr13:59634136-5963565	pro	59634136	59635658	chr13	-0.35
PCDH9	2513	chr13:66698626-6670128	pro	66698626	66701288	chr13	-0.91
PCDH9	526	chr13:66701466-66702421	pro	66701466	66702421	chr13	-0.87
PCDH9	1356	chr13:66703424-6670422	pro	66703424	66704229	chr13	-0.98
BORA	1939	chr13:72197554-7219834	pro	72197554	72198340	chr13	-0.64
TBC1D4	2742	chr13:74949884-7495313	pro	74949884	74953136	chr13	-0.96
COMMD6	728	chr13:75020197-7502149	pro	75020197	75021499	chr13	-0.39
SLAIN1	1484	chr13:77172444-7717255	pro	77172444	77172556	chr13	-0.35
MIR4500HG	738	chr13:87119369-8712159	pro	87119369	87121596	chr13	-0.99
SLITRK5	1710	chr13:87122926-8712623	pro	87122926	87126235	chr13	-0.99
MIR17HG	1080	chr13:90796248-9079774	pro	90796248	90797740	chr13	-0.37
MIR19A	1	chr13:90799402-9080288	pro	90799402	90802888	chr13	-0.52
MIR92A1	2010	chr13:90803501-9080365	pro	90803501	90803654	chr13	-0.87
GPC5	356	chr13:90848224-9084880	pro	90848224	90848807	chr13	-0.31
LINC00359	236	chr13:96434432-9643489	pro	96434432	96434897	chr13	-0.96
DOCK9	2037	chr13:98426007-9842659	pro	98426007	98426599	chr13	-0.87
DOCK9	1838	chr13:98534213-9853543	pro	98534213	98535435	chr13	-0.78
UBAC2	1637	chr13:98652355-9865324	pro	98652355	98653243	chr13	-0.39
LINC00239	1484	chr14:101267559-101268	pro	101267559	101268460	chr14	-0.78
PPP2R5C	1545	chr14:101296151-101296	pro	101296151	101296531	chr14	-0.60
HSP90AA1	1776	chr14:101621030-101621	pro	101621030	101621950	chr14	-0.54
HSP90AA1	986	chr14:101674363-101675	pro	101674363	101675346	chr14	-0.26
ZNF839	833	chr14:101852205-101853	pro	101852205	101853061	chr14	-0.32

ZNF839	838	chr14:101856327-1018570	pro	101856327	101857029	chr14	-0.55
RCOR1	1499	chr14:102126852-1021276	pro	102126852	102127646	chr14	-0.68
RCOR1	1750	chr14:102129677-1021313	pro	102129677	102131318	chr14	-0.33
EXOC3L4	564	chr14:102636684-1026369	pro	102636684	102636908	chr14	-0.58
EIF5	1517	chr14:102868299-1028688	pro	102868299	102868847	chr14	-0.66
INF2	2116	chr14:104224251-1042254	pro	104224251	104225489	chr14	-0.90
PLD4	258	chr14:104462269-1044627	pro	104462269	104462708	chr14	-0.77
PLD4	1651	chr14:104463708-1044640	pro	104463708	104464054	chr14	-0.53
C14orf80	813	chr14:105029251-1050296	pro	105029251	105029635	chr14	-0.40
TTC5	1340	chr14:19842490-19842818	pro	19842490	19842818	chr14	-0.57
SNORD126	1184	chr14:19865536-19865909	pro	19865536	19865909	chr14	-0.42
CCNB1IP1	1802	chr14:19869074-19869945	pro	19869074	19869945	chr14	-0.70
CCNB1IP1	465	chr14:19871396-19872158	pro	19871396	19872158	chr14	-0.41
RPPH1	1529	chr14:19879586-19880176	pro	19879586	19880176	chr14	-0.82
RNASE6	732	chr14:20318808-20320752	pro	20318808	20320752	chr14	-0.95
METTL17	1490	chr14:20529113-20529476	pro	20529113	20529476	chr14	-0.64
SALL2	713	chr14:21063347-21063991	pro	21063347	21063991	chr14	-0.51
SALL2	620	chr14:21064333-21065670	pro	21064333	21065670	chr14	-0.29
DAD1	1646	chr14:22126243-22126432	pro	22126243	22126432	chr14	-0.75
OXA1L	810	chr14:22304676-22304845	pro	22304676	22304845	chr14	-0.53
SLC7A7	1742	chr14:22353138-22353263	pro	22353138	22353263	chr14	-0.83
SLC7A7	584	chr14:22353465-22355250	pro	22353465	22355250	chr14	-0.52
SLC7A7	154	chr14:22358004-22359407	pro	22358004	22359407	chr14	-0.69
REM2	612	chr14:22421190-22422125	pro	22421190	22422125	chr14	-0.77
REM2	258	chr14:22422284-22422771	pro	22422284	22422771	chr14	-0.56
RBM23	1794	chr14:22456315-22456569	pro	22456315	22456569	chr14	-0.43
PRMT5	2038	chr14:22466400-22466793	pro	22466400	22466793	chr14	-0.73
AJUBA	275	chr14:22515692-22516302	pro	22515692	22516302	chr14	-0.41
CEBPE	1029	chr14:22658499-22660879	pro	22658499	22660879	chr14	-0.47
SLC7A8	620	chr14:22721173-22723008	pro	22721173	22723008	chr14	-0.30
AP1G2	650	chr14:23106918-23108153	pro	23106918	23108153	chr14	-0.34
IRF9	205	chr14:23699985-23700125	pro	23699985	23700125	chr14	-0.39
IPO4	336	chr14:23728033-23728567	pro	23728033	23728567	chr14	-0.27
TM9SF1	936	chr14:23733389-23734304	pro	23733389	23734304	chr14	-0.33
TM9SF1	1573	chr14:23736154-23736556	pro	23736154	23736556	chr14	-0.47
TM9SF1	2100	chr14:23736735-23737030	pro	23736735	23737030	chr14	-0.74
CHMP4A	372	chr14:23752654-23753842	pro	23752654	23753842	chr14	-0.39
GMPR2	1384	chr14:23773191-23773409	pro	23773191	23773409	chr14	-0.77
TINF2	1036	chr14:23782451-23783062	pro	23782451	23783062	chr14	-0.59
RABGGTA	2122	chr14:23812673-23812920	pro	23812673	23812920	chr14	-0.85
NFATC4	1394	chr14:23904365-23904758	pro	23904365	23904758	chr14	-0.74
HEATR5A	1400	chr14:30958056-30958224	pro	30958056	30958224	chr14	-0.83
GPR33	2041	chr14:31028804-31029082	pro	31028804	31029082	chr14	-0.65
NUBPL	1969	chr14:31102138-31102480	pro	31102138	31102480	chr14	-0.70
EAPP	551	chr14:34079191-34079299	pro	34079191	34079299	chr14	-0.30
CFL2	1473	chr14:34249455-34253147	pro	34249455	34253147	chr14	-0.39
BAZ1A	235	chr14:34414375-34415303	pro	34414375	34415303	chr14	-0.32
PSMA6	2070	chr14:34828972-34829433	pro	34828972	34829433	chr14	-0.92
PSMA6	1522	chr14:34829597-34829902	pro	34829597	34829902	chr14	-0.76
CTAGE5	324	chr14:38804198-38805658	pro	38804198	38805658	chr14	-0.29
C14orf28	522	chr14:44435538-44435931	pro	44435538	44435931	chr14	-0.45
RPS29	1986	chr14:49120719-49121078	pro	49120719	49121078	chr14	-0.41
RPS29	870	chr14:49123569-49123940	pro	49123569	49123940	chr14	-0.54
LRR1	2148	chr14:49132725-49133308	pro	49132725	49133308	chr14	-0.76
POLE2	1568	chr14:49222974-49223587	pro	49222974	49223587	chr14	-0.66

C14orf182	918	chr14:49544848-49544964	pro	49544848	49544964	chr14	-0.87
C14orf182	1691	chr14:49545279-49546079	pro	49545279	49546079	chr14	-0.55
FRMD6-AS1	1472	chr14:51186675-51186806	pro	51186675	51186806	chr14	-0.80
FRMD6	1572	chr14:51189133-51190658	pro	51189133	51190658	chr14	-0.67
GNG2	1672	chr14:51396745-51400139	pro	51396745	51400139	chr14	-0.45
GMFB	2243	chr14:54022934-54023568	pro	54022934	54023568	chr14	-0.89
GMFB	952	chr14:54026336-54026557	pro	54026336	54026557	chr14	-0.89
FBXO34	402	chr14:54807093-54807648	pro	54807093	54807648	chr14	-0.53
KTN1	2369	chr14:55117439-55120651	pro	55117439	55120651	chr14	-0.27
TMEM260	469	chr14:56115692-56115894	pro	56115692	56115894	chr14	-0.44
EXOC5	2234	chr14:56806610-56808598	pro	56806610	56808598	chr14	-0.59
C14orf37	581	chr14:57688828-57689534	pro	57688828	57689534	chr14	-0.34
DAAM1	1612	chr14:58722223-58724818	pro	58722223	58724818	chr14	-0.29
JKAMP	1571	chr14:59022402-59022564	pro	59022402	59022564	chr14	-0.28
JKAMP	1945	chr14:59022705-59023009	pro	59022705	59023009	chr14	-0.47
DHRS7	510	chr14:59702046-59702901	pro	59702046	59702901	chr14	-0.44
PPM1A	2270	chr14:59786607-59789368	pro	59786607	59789368	chr14	-0.25
MNAT1	205	chr14:60270869-60271141	pro	60270869	60271141	chr14	-0.64
LOC101927780	1996	chr14:61104224-61105117	pro	61104224	61105117	chr14	-0.51
WDR89	1889	chr14:63176010-63177000	pro	63176010	63177000	chr14	-0.74
ESR2	1213	chr14:63872902-63874716	pro	63872902	63874716	chr14	-0.27
MTHFD1	1826	chr14:63922364-63923003	pro	63922364	63923003	chr14	-0.62
MTHFD1	1914	chr14:63926127-63926722	pro	63926127	63926722	chr14	-0.39
MIR4708	650	chr14:64870444-64871565	pro	64870444	64871565	chr14	-0.63
TMEM229B	1392	chr14:67049336-67051427	pro	67049336	67051427	chr14	-0.51
RDH11	1610	chr14:67230470-67230839	pro	67230470	67230839	chr14	-0.56
SYNJ2BP-COX1	1226	chr14:69952280-69952389	pro	69952280	69952389	chr14	-0.54
MED6	1596	chr14:70135514-70135614	pro	70135514	70135614	chr14	-0.48
PCNX	1794	chr14:70445039-70446296	pro	70445039	70446296	chr14	-0.37
SNORD56B	801	chr14:70935183-70936031	pro	70935183	70936031	chr14	-0.87
MIR7843	2438	chr14:72055219-72056218	pro	72055219	72056218	chr14	-0.55
ZNF410	1778	chr14:73421118-73421466	pro	73421118	73421466	chr14	-0.85
ZNF410	1086	chr14:73421712-73422255	pro	73421712	73422255	chr14	-0.39
ABCD4	596	chr14:73839934-73840299	pro	73839934	73840299	chr14	-0.45
ISCA2	1852	chr14:74031891-74032160	pro	74031891	74032160	chr14	-0.72
AREL1	1210	chr14:74248262-74248439	pro	74248262	74248439	chr14	-0.36
DLST	1962	chr14:74419739-74420877	pro	74419739	74420877	chr14	-0.41
RPS6KL1	1201	chr14:74460020-74460178	pro	74460020	74460178	chr14	-0.38
TMED10	2218	chr14:74710628-74711139	pro	74710628	74711139	chr14	-0.88
TMED10	1325	chr14:74711517-74712037	pro	74711517	74712037	chr14	-0.56
GPATCH2L	725	chr14:75691030-75691316	pro	75691030	75691316	chr14	-0.53
GPATCH2L	1546	chr14:75691446-75692542	pro	75691446	75692542	chr14	-0.62
POMT2	973	chr14:76855573-76856437	pro	76855573	76856437	chr14	-0.31
CEP128	570	chr14:80475745-80476671	pro	80475745	80476671	chr14	-0.59
TSHR	1772	chr14:80491094-80495690	pro	80491094	80495690	chr14	-0.62
GTF2A1	2372	chr14:80753921-80755436	pro	80753921	80755436	chr14	-0.30
GPR65	328	chr14:87540560-87541224	pro	87540560	87541224	chr14	-0.78
GPR65	1226	chr14:87541334-87543557	pro	87541334	87543557	chr14	-0.66
FOXN3	1378	chr14:89152668-89155072	pro	89152668	89155072	chr14	-0.36
TDP1	1286	chr14:89492934-89493635	pro	89492934	89493635	chr14	-0.28
LGMN	752	chr14:92283558-92284539	pro	92283558	92284539	chr14	-0.94
LGMN	356	chr14:92284880-92285433	pro	92284880	92285433	chr14	-0.99
CHGA	1139	chr14:92460164-92460506	pro	92460164	92460506	chr14	-0.80
CHGA	1661	chr14:92460655-92461059	pro	92460655	92461059	chr14	-0.81
ITPK1-AS1	1720	chr14:92601256-92602399	pro	92601256	92602399	chr14	-0.57

UBR7	1907	chr14:92741013-9274147	pro	92741013	92741477	chr14	-0.66
ASB2	2294	chr14:93494784-9349684	pro	93494784	93496845	chr14	-0.59
ASB2	1751	chr14:93514185-9351497	pro	93514185	93514977	chr14	-0.37
OTUB2	296	chr14:93562074-9356228	pro	93562074	93562286	chr14	-0.38
PPP4R4	2079	chr14:93708152-9370849	pro	93708152	93708490	chr14	-0.98
DICER1	1698	chr14:94690769-9469285	pro	94690769	94692858	chr14	-0.44
LOC101929080	2106	chr14:94863064-9486406	pro	94863064	94864068	chr14	-0.87
LOC101929080	469	chr14:94864455-94865951	pro	94864455	94865951	chr14	-0.96
TCL6	920	chr14:95188111-95188260	pro	95188111	95188260	chr14	-0.73
TCL6	1388	chr14:95188418-9518889	pro	95188418	95188890	chr14	-0.84
TCL6	1850	chr14:95189009-9518922	pro	95189009	95189223	chr14	-0.87
BDKRB2	929	chr14:95741013-9574261	pro	95741013	95742617	chr14	-0.88
PAPOLA	1934	chr14:96040773-9604100	pro	96040773	96041003	chr14	-0.49
CCDC85C	1814	chr14:99138424-9913890	pro	99138424	99138907	chr14	-0.93
CCDC85C	606	chr14:99139785-9913996	pro	99139785	99139963	chr14	-0.88
CCDC85C	1485	chr14:99141567-9914236	pro	99141567	99142363	chr14	-0.35
CYP46A1	2058	chr14:99220687-99224441	pro	99220687	99224441	chr14	-0.85
EVL	946	chr14:99600403-9960070	pro	99600403	99600708	chr14	-0.89
EVL	1936	chr14:99600900-9960597	pro	99600900	99605975	chr14	-0.37
DEGS2	2262	chr14:99693111-99693898	pro	99693111	99693898	chr14	-0.78
TARSL2	980	chr15:100080692-100081	pro	100080692	100081685	chr15	-0.49
NIPA2	2360	chr15:20583069-2058394	pro	20583069	20583946	chr15	-0.33
NIPA1	1991	chr15:20635825-2063594	pro	20635825	20635949	chr15	-0.59
NIPA1	598	chr15:20638725-2063903	pro	20638725	20639038	chr15	-0.50
MIR4715	1584	chr15:23643134-2364383	pro	23643134	23643830	chr15	-0.95
MIR4715	2032	chr15:23647013-2364718	pro	23647013	23647182	chr15	-0.49
NDNL2	2829	chr15:27345164-2734780	pro	27345164	27347802	chr15	-0.89
NDNL2	886	chr15:27349482-2735091	pro	27349482	27350914	chr15	-0.37
LOC283710	553	chr15:29310569-29311221	pro	29310569	29311221	chr15	-0.66
AVEN	736	chr15:32118781-32119884	pro	32118781	32119884	chr15	-0.53
C15orf41	944	chr15:34658068-34658231	pro	34658068	34658231	chr15	-0.43
FSIP1	704	chr15:37861321-3786193	pro	37861321	37861936	chr15	-0.38
KNSTRN	1858	chr15:38463973-3846416	pro	38463973	38464167	chr15	-0.62
RAD51	1452	chr15:38775717-3877652	pro	38775717	38776523	chr15	-0.70
OIP5-AS1	771	chr15:39362593-3936284	pro	39362593	39362849	chr15	-0.58
OIP5-AS1	1777	chr15:39365177-39365361	pro	39365177	39365361	chr15	-0.49
EHD4	1759	chr15:40049083-4005149	pro	40049083	40051495	chr15	-0.41
TMEM87A	2172	chr15:40350638-4035116	pro	40350638	40351166	chr15	-0.49
SNAP23	1461	chr15:40572942-4057372	pro	40572942	40573724	chr15	-0.44
STARD9	1946	chr15:40657041-4065714	pro	40657041	40657146	chr15	-0.67
UBR1	1554	chr15:41183860-41184188	pro	41183860	41184188	chr15	-0.40
ZSCAN29	474	chr15:41449012-4144913	pro	41449012	41449139	chr15	-0.43
MAP1A	1342	chr15:41598276-4159860	pro	41598276	41598600	chr15	-0.48
ELL3	1095	chr15:41857819-4185795	pro	41857819	41857959	chr15	-0.56
MIR1282	1618	chr15:41874714-41875021	pro	41874714	41875021	chr15	-0.50
MFAP1	340	chr15:41904335-4190483	pro	41904335	41904834	chr15	-0.31
SPG11	1622	chr15:42741104-4274198	pro	42741104	42741989	chr15	-0.64
SPG11	520	chr15:42743339-4274403	pro	42743339	42744038	chr15	-0.30
B2M	2216	chr15:42792424-4279396	pro	42792424	42793960	chr15	-0.58
TRIM69	165	chr15:42814953-4281641	pro	42814953	42816417	chr15	-0.71
TRIM69	1202	chr15:42816880-4281722	pro	42816880	42817223	chr15	-0.95
LOC101928414	450	chr15:43357846-4335867	pro	43357846	43358679	chr15	-0.51
LOC101928414	608	chr15:43358929-4335971	pro	43358929	43359710	chr15	-0.50
DUT	1988	chr15:46411965-46415324	pro	46411965	46415324	chr15	-0.41
CEP152	1906	chr15:46888522-4688893	pro	46888522	46888938	chr15	-0.60

EID1	1950	chr15:46959115-46959945	pro	46959115	46959945	chr15	-0.92
USP8	808	chr15:48502985-48503128	pro	48502985	48503128	chr15	-0.51
LOC100129973	1692	chr15:50261153-50261259	pro	50261153	50261259	chr15	-0.76
LOC100129973	2324	chr15:50261494-50262181	pro	50261494	50262181	chr15	-0.58
FAM214A	3422	chr15:50759357-50763734	pro	50759357	50763734	chr15	-0.27
ONECUT1	256	chr15:50859752-50860483	pro	50859752	50860483	chr15	-0.31
PIGB	1100	chr15:53397226-53397421	pro	53397226	53397421	chr15	-0.58
TEX9	2012	chr15:54445035-54448814	pro	54445035	54448814	chr15	-0.72
ANXA2	1078	chr15:58476243-58476558	pro	58476243	58476558	chr15	-0.74
SNX1	534	chr15:62174131-62175070	pro	62174131	62175070	chr15	-0.29
SNX1	1904	chr15:62176909-62177168	pro	62176909	62177168	chr15	-0.61
KIAA0101	1649	chr15:62458839-62459387	pro	62458839	62459387	chr15	-0.51
KIAA0101	652	chr15:62466138-62466437	pro	62466138	62466437	chr15	-0.47
PIF1	1278	chr15:62906033-62906362	pro	62906033	62906362	chr15	-0.88
MTFMT	1610	chr15:63107298-63107542	pro	63107298	63107542	chr15	-0.60
PDCD7	1897	chr15:63211221-63211441	pro	63211221	63211441	chr15	-0.25
PTPLAD1	1580	chr15:63611235-63611680	pro	63611235	63611680	chr15	-0.26
VWA9	1364	chr15:63688865-63689486	pro	63688865	63689486	chr15	-0.36
RAB11A	672	chr15:63947877-63948480	pro	63947877	63948480	chr15	-0.48
TIPIN	2084	chr15:64433741-64434306	pro	64433741	64434306	chr15	-0.75
TIPIN	414	chr15:64436283-64436762	pro	64436283	64436762	chr15	-0.38
SNORD18B	114	chr15:64581517-64581678	pro	64581517	64581678	chr15	-0.64
CORO2B	1734	chr15:66656526-66656725	pro	66656526	66656725	chr15	-0.79
CORO2B	2260	chr15:66659015-66662224	pro	66659015	66662224	chr15	-0.87
CORO2B	1200	chr15:66709344-66711017	pro	66709344	66711017	chr15	-0.65
CORO2B	316	chr15:66711319-66712074	pro	66711319	66712074	chr15	-0.46
CORO2B	2437	chr15:66712214-66715420	pro	66712214	66715420	chr15	-0.67
RPLP1	1924	chr15:67533678-67534594	pro	67533678	67534594	chr15	-0.33
ADPGK-AS1	746	chr15:70861297-70861668	pro	70861297	70861668	chr15	-0.40
NPTN	1714	chr15:71710031-71712153	pro	71710031	71712153	chr15	-0.36
PML	2208	chr15:72075439-72077110	pro	72075439	72077110	chr15	-0.33
LOC283731	1394	chr15:72207211-72207344	pro	72207211	72207344	chr15	-0.42
UBL7-AS1	2074	chr15:72542174-72543289	pro	72542174	72543289	chr15	-0.62
PPCDC	1772	chr15:73104506-73104933	pro	73104506	73104933	chr15	-0.66
PPCDC	363	chr15:73122718-73123332	pro	73122718	73123332	chr15	-0.55
MAN2C1	1021	chr15:73446653-73447349	pro	73446653	73447349	chr15	-0.30
SIN3A	2038	chr15:73528682-73529202	pro	73528682	73529202	chr15	-0.49
IMP3	2284	chr15:73716632-73718239	pro	73716632	73718239	chr15	-0.48
PSTPIP1	740	chr15:75074937-75075580	pro	75074937	75075580	chr15	-0.44
HMG20A	1940	chr15:75502171-75502302	pro	75502171	75502302	chr15	-0.59
RASGRF1	773	chr15:77083579-77084991	pro	77083579	77084991	chr15	-0.46
RASGRF1	1612	chr15:77086460-77086880	pro	77086460	77086880	chr15	-0.79
ZFAND6	626	chr15:78152018-78153146	pro	78152018	78153146	chr15	-0.29
MESDC2	1608	chr15:79070812-79070951	pro	79070812	79070951	chr15	-0.71
IL16	2954	chr15:79370459-79376250	pro	79370459	79376250	chr15	-0.45
STARD5	1144	chr15:79402201-79402670	pro	79402201	79402670	chr15	-0.56
FAM154B	662	chr15:80342747-80342989	pro	80342747	80342989	chr15	-0.43
FSD2	335	chr15:81270531-81272551	pro	81270531	81272551	chr15	-0.70
FSD2	1380	chr15:81272973-81273540	pro	81272973	81273540	chr15	-0.92
FAM103A1	1163	chr15:81447059-81447183	pro	81447059	81447183	chr15	-0.73
TM6SF1	1122	chr15:81567752-81569145	pro	81567752	81569145	chr15	-0.81
HDGFRP3	1714	chr15:81665381-81666740	pro	81665381	81666740	chr15	-0.98
HDGFRP3	474	chr15:81668126-81668369	pro	81668126	81668369	chr15	-0.81
WDR73	1430	chr15:82997037-82997155	pro	82997037	82997155	chr15	-0.75
SEC11A	852	chr15:83061250-83061845	pro	83061250	83061845	chr15	-0.46

ZNF592	2309	chr15:83094482-83095776	pro	83094482	83095776	chr15	-0.37
PDE8A	316	chr15:83324243-83324616	pro	83324243	83324616	chr15	-0.32
PDE8A	1283	chr15:83326670-83328312	pro	83326670	83328312	chr15	-0.86
ABHD2	1874	chr15:87434204-87434313	pro	87434204	87434313	chr15	-0.27
FANCI	2074	chr15:87589690-87590849	pro	87589690	87590849	chr15	-0.70
CIB1	2024	chr15:88611801-88612238	pro	88611801	88612238	chr15	-0.56
LOC101929765	526	chr15:89004654-89005333	pro	89004654	89005333	chr15	-0.48
FURIN	1346	chr15:89214088-89214253	pro	89214088	89214253	chr15	-0.82
HDDC3	245	chr15:89276932-89277166	pro	89276932	89277166	chr15	-0.44
UNC45A	762	chr15:89278262-89278649	pro	89278262	89278649	chr15	-0.68
SLCO3A1	3016	chr15:90198581-90203332	pro	90198581	90203332	chr15	-0.66
CHD2	760	chr15:91243129-91244458	pro	91243129	91244458	chr15	-0.34
IGF1R	1528	chr15:97007372-97008152	pro	97007372	97008152	chr15	-0.97
IGF1R	1117	chr15:97010343-97010471	pro	97010343	97010471	chr15	-0.82
TTC23	131	chr15:97606049-97608909	pro	97606049	97608909	chr15	-0.83
MEF2A	1562	chr15:97988537-97989747	pro	97988537	97989747	chr15	-0.36
LRRK1	2190	chr15:99273758-99275826	pro	99273758	99275826	chr15	-0.28
CIITA	1738	chr16:10876649-10876983	pro	10876649	10876983	chr16	-0.93
CIITA	576	chr16:10877600-10878356	pro	10877600	10878356	chr16	-0.39
RMI2	1618	chr16:11347892-11348963	pro	11347892	11348963	chr16	-0.65
TXNDC11	902	chr16:11744859-11745246	pro	11744859	11745246	chr16	-0.34
ZC3H7A	1867	chr16:11800348-11800618	pro	11800348	11800618	chr16	-0.75
TNFRSF17	1176	chr16:11964748-11965828	pro	11964748	11965828	chr16	-0.55
TNFRSF17	1452	chr16:11967455-11968377	pro	11967455	11968377	chr16	-0.34
CPPED1	1902	chr16:12803008-12803680	pro	12803008	12803680	chr16	-0.87
CPPED1	856	chr16:12803908-12804872	pro	12803908	12804872	chr16	-0.97
UNKL	414	chr16:1405058-1405214	pro	1405058	1405214	chr16	-0.36
MIR365A	1326	chr16:14306172-14312461	pro	14306172	14312461	chr16	-0.77
PARN	314	chr16:14631772-14632116	pro	14631772	14632116	chr16	-0.37
MIR484	782	chr16:15644661-15646203	pro	15644661	15646203	chr16	-0.26
MYH11	1007	chr16:15856349-15858413	pro	15856349	15858413	chr16	-0.97
MYH11	586	chr16:15858556-15859392	pro	15858556	15859392	chr16	-0.85
FOPNL	542	chr16:15890181-15890800	pro	15890181	15890800	chr16	-0.34
RPS15A	2362	chr16:18706238-18707353	pro	18706238	18707353	chr16	-0.35
COQ7	1018	chr16:18987416-18988095	pro	18987416	18988095	chr16	-0.56
GDE1	478	chr16:19441024-19441835	pro	19441024	19441835	chr16	-0.28
CCP110	212	chr16:19442413-19442520	pro	19442413	19442520	chr16	-0.39
C16orf62	1004	chr16:19473074-19473389	pro	19473074	19473389	chr16	-0.65
SNORA10	1440	chr16:1950433-1951622	pro	1950433	1951622	chr16	-0.35
SNORA10	524	chr16:1951800-1952088	pro	1951800	1952088	chr16	-0.51
TBL3	983	chr16:1960971-1961191	pro	1960971	1961191	chr16	-0.36
IQCK	156	chr16:19635189-19635678	pro	19635189	19635678	chr16	-0.47
THUMPD1	230	chr16:20660843-20661017	pro	20660843	20661017	chr16	-0.40
ACSM3	156	chr16:20682171-20683140	pro	20682171	20683140	chr16	-0.35
ERI2	1440	chr16:20726533-20726940	pro	20726533	20726940	chr16	-0.61
CRYM	305	chr16:21221955-21222571	pro	21221955	21222571	chr16	-0.65
PGP	1520	chr16:2206271-2206416	pro	2206271	2206416	chr16	-0.81
DCTN5	1527	chr16:23561577-23561849	pro	23561577	23561849	chr16	-0.31
PRKCB	1790	chr16:23755506-23757674	pro	23755506	23757674	chr16	-0.46
NTN3	1940	chr16:2459071-2460048	pro	2459071	2460048	chr16	-0.54
NTN3	678	chr16:2460656-2460988	pro	2460656	2460988	chr16	-0.92
TBC1D24	1720	chr16:2463172-2463680	pro	2463172	2463680	chr16	-0.65
ARHGAP17	786	chr16:24934686-24935285	pro	24934686	24935285	chr16	-0.31
LCMT1-AS1	1140	chr16:25028683-25029792	pro	25028683	25029792	chr16	-0.54
AMDHD2	1114	chr16:2511450-2511503	pro	2511450	2511503	chr16	-0.44

KDM8	1302	chr16:27123809-27124387	pro	27123809	27124387	chr16	-0.72
KDM8	2064	chr16:27124662-27125057	pro	27124662	27125057	chr16	-0.64
NSMCE1	968	chr16:27188157-27189008	pro	27188157	27189008	chr16	-0.46
IL21R	1190	chr16:27319557-27320026	pro	27319557	27320026	chr16	-0.74
IL21R	259	chr16:27344923-27347751	pro	27344923	27347751	chr16	-0.61
SRRM2	1360	chr16:2740786-2741153	pro	2740786	2741153	chr16	-0.32
SRRM2-AS1	2561	chr16:2744520-2745806	pro	2744520	2745806	chr16	-0.29
SBK1	644	chr16:28210348-28211045	pro	28210348	28211045	chr16	-0.42
CLN3	682	chr16:28411690-28411922	pro	28411690	28411922	chr16	-0.80
APOBR	1154	chr16:28412130-28412502	pro	28412130	28412502	chr16	-0.79
APOBR	208	chr16:28412682-28413843	pro	28412682	28413843	chr16	-0.45
SULT1A1	1782	chr16:28540531-28540721	pro	28540531	28540721	chr16	-0.94
FLYWCH2	794	chr16:2873726-2874255	pro	2873726	2874255	chr16	-0.40
SH2B1	1625	chr16:28780744-28781162	pro	28780744	28781162	chr16	-0.63
CD19	1034	chr16:28849164-28850289	pro	28849164	28850289	chr16	-0.64
LAT	360	chr16:28903930-28904562	pro	28903930	28904562	chr16	-0.47
SPN	696	chr16:29580961-29581186	pro	29580961	29581186	chr16	-0.85
SPN	132	chr16:29581308-29581967	pro	29581308	29581967	chr16	-0.31
ALDOA	1225	chr16:29970621-29970749	pro	29970621	29970749	chr16	-0.85
TBX6	1129	chr16:30011586-30012084	pro	30011586	30012084	chr16	-0.44
LOC606724	1072	chr16:30106374-30106491	pro	30106374	30106491	chr16	-0.40
CD2BP2	1692	chr16:30271988-30272140	pro	30271988	30272140	chr16	-0.55
TBC1D10B	1894	chr16:30289987-30291850	pro	30289987	30291850	chr16	-0.52
ZNF48	1796	chr16:30298802-30299058	pro	30298802	30299058	chr16	-0.62
2-Sep	818	chr16:30302331-30302650	pro	30302331	30302650	chr16	-0.68
ZNF771	1983	chr16:30328071-30328363	pro	30328071	30328363	chr16	-0.32
ZNF747	1242	chr16:30452389-30452518	pro	30452389	30452518	chr16	-0.40
ZNF688	1764	chr16:30489403-30489529	pro	30489403	30489529	chr16	-0.73
ZNF688	1057	chr16:30492033-30492541	pro	30492033	30492541	chr16	-0.50
ZSCAN10	695	chr16:3083508-3083606	pro	3083508	3083606	chr16	-0.51
ZSCAN10	1488	chr16:3090690-3090925	pro	3090690	3090925	chr16	-0.55
ZSCAN10	2180	chr16:3091277-3091723	pro	3091277	3091723	chr16	-0.64
VKORC1	1814	chr16:31011902-31012027	pro	31011902	31012027	chr16	-0.65
ZNF213	962	chr16:3126010-3126181	pro	3126010	3126181	chr16	-0.55
ARMC5	1272	chr16:31375398-31376246	pro	31375398	31376246	chr16	-0.79
ZNF720	284	chr16:31631624-31631909	pro	31631624	31631909	chr16	-0.33
OR1F2P	124	chr16:3205049-3205828	pro	3205049	3205828	chr16	-0.75
ZNF200	1208	chr16:3223910-3224051	pro	3223910	3224051	chr16	-0.42
LINC00921	430	chr16:3253280-3253395	pro	3253280	3253395	chr16	-0.51
ZNF263	2036	chr16:3275346-3275697	pro	3275346	3275697	chr16	-0.74
NLRC3	1218	chr16:3568212-3569037	pro	3568212	3569037	chr16	-0.50
NLRC3	2636	chr16:3569274-3570810	pro	3569274	3570810	chr16	-0.64
MRPL28	378	chr16:360714-361181	pro	360714	361181	chr16	-0.30
POLR3K	2122	chr16:41284-41735	pro	41284	41735	chr16	-0.66
POLR3K	1512	chr16:41996-42245	pro	41996	42245	chr16	-0.65
LOC100507501	548	chr16:4244247-4244432	pro	4244247	4244432	chr16	-0.32
DNAJA3	1595	chr16:4417127-4417675	pro	4417127	4417675	chr16	-0.70
HMOX2	1458	chr16:4462824-4463669	pro	4462824	4463669	chr16	-0.54
NMRAL1	384	chr16:4465235-4465329	pro	4465235	4465329	chr16	-0.36
CNEP1R1	462	chr16:48615940-48616369	pro	48615940	48616369	chr16	-0.27
BRD7	2331	chr16:48957579-48958451	pro	48957579	48958451	chr16	-0.57
CRNDE	1918	chr16:53516833-53519714	pro	53516833	53519714	chr16	-0.71
NUP93	2254	chr16:55323124-55324417	pro	55323124	55324417	chr16	-0.75
MIR138-2	2056	chr16:55451260-55452711	pro	55451260	55452711	chr16	-0.71
NHLRC4	52	chr16:556630-557462	pro	556630	557462	chr16	-0.25

POLR2C	200	chr16:56053791-5605390	pro	56053791	56053909	chr16	-0.64
LOC101926950	134	chr16:5606011-5606224	pro	5606011	5606224	chr16	-0.85
GPR114	88	chr16:56134123-5613425	pro	56134123	56134253	chr16	-0.52
GPR114	1512	chr16:56135445-5613578	pro	56135445	56135780	chr16	-0.97
CFAP20	1963	chr16:56717449-56720221	pro	56717449	56720221	chr16	-0.31
GINS3	1690	chr16:56985255-56985721	pro	56985255	56985721	chr16	-0.82
LINC00920	200	chr16:64999937-6500031	pro	64999937	65000316	chr16	-0.35
BEAN1-AS1	64	chr16:65067657-6506782	pro	65067657	65067828	chr16	-0.79
NAE1	1449	chr16:65420507-6542135	pro	65420507	65421355	chr16	-0.44
PDP2	2113	chr16:65469441-6547009	pro	65469441	65470097	chr16	-0.86
KIAA0895L	933	chr16:65773914-6577498	pro	65773914	65774988	chr16	-0.31
KCTD19	1868	chr16:65916086-6591650	pro	65916086	65916502	chr16	-0.94
KCTD19	1038	chr16:65916938-6591731	pro	65916938	65917310	chr16	-0.57
CTCF	2056	chr16:66151522-6615198	pro	66151522	66151987	chr16	-0.60
C16orf86	1924	chr16:66259642-6626063	pro	66259642	66260638	chr16	-0.73
DDX28	626	chr16:66615751-6661604	pro	66615751	66616045	chr16	-0.50
NIP7	905	chr16:67929849-6793016	pro	67929849	67930169	chr16	-0.32
SNORD111B	2470	chr16:69117806-69119057	pro	69117806	69119057	chr16	-0.26
SNORD111B	212	chr16:69120627-6912075	pro	69120627	69120752	chr16	-0.67
TAT-AS1	246	chr16:70156799-7015807	pro	70156799	70158077	chr16	-0.39
ATXN1L	808	chr16:70436509-7043666	pro	70436509	70436664	chr16	-0.57
ZNF821	2220	chr16:70472316-7047313	pro	70472316	70473137	chr16	-0.84
ZNF821	1307	chr16:70476720-7047708	pro	70476720	70477082	chr16	-0.74
LOC101927957	2277	chr16:71253403-7125486	pro	71253403	71254863	chr16	-0.98
PSMD7	1614	chr16:72889573-7288999	pro	72889573	72889999	chr16	-0.64
FA2H	620	chr16:73365278-73365941	pro	73365278	73365941	chr16	-0.27
ZNRF1	1281	chr16:73591443-7359194	pro	73591443	73591947	chr16	-0.47
ZFP1	336	chr16:73739402-7373976	pro	73739402	73739767	chr16	-0.48
CTRB1	943	chr16:73811125-73811529	pro	73811125	73811529	chr16	-0.67
TMEM170A	1624	chr16:74054236-7405468	pro	74054236	74054689	chr16	-0.35
TMEM170A	390	chr16:74056398-7405655	pro	74056398	74056554	chr16	-0.41
GABARAPL2	1156	chr16:74156286-7415689	pro	74156286	74156897	chr16	-0.42
ADAT1	1714	chr16:74212760-7421325	pro	74212760	74213255	chr16	-0.42
NUDT7	378	chr16:76313322-7631369	pro	76313322	76313697	chr16	-0.59
WWOX	1152	chr16:76691577-7669234	pro	76691577	76692346	chr16	-0.69
CENPN	1776	chr16:79595315-7959633	pro	79595315	79596336	chr16	-0.49
GCSH	1697	chr16:79685701-7968586	pro	79685701	79685869	chr16	-0.48
MPHOSPH6	994	chr16:80760029-8076064	pro	80760029	80760643	chr16	-0.34
TAF1C	238	chr16:82778317-8277851	pro	82778317	82778516	chr16	-0.60
MIR5093	1492	chr16:83895813-8389606	pro	83895813	83896067	chr16	-0.53
MIR5093	411	chr16:83897574-8389811	pro	83897574	83898112	chr16	-0.50
MIR5093	952	chr16:83898322-8389844	pro	83898322	83898446	chr16	-0.63
TMEM114	1931	chr16:8557984-8558170	pro	8557984	8558170	chr16	-0.51
LOC102724467	1059	chr16:86368800-8636959	pro	86368800	86369594	chr16	-0.33
LOC102724467	1491	chr16:86371436-8637205	pro	86371436	86372058	chr16	-0.52
SLC7A5	2061	chr16:86462568-8646275	pro	86462568	86462758	chr16	-0.41
BANP	1080	chr16:86541370-8654154	pro	86541370	86541545	chr16	-0.35
ZFPM1	1076	chr16:87048079-8704910	pro	87048079	87049100	chr16	-0.89
SNAI3-AS1	1912	chr16:87258786-8725959	pro	87258786	87259597	chr16	-0.51
SNAI3	1314	chr16:87278969-8727917	pro	87278969	87279170	chr16	-0.58
RNF166	248	chr16:87296938-8729860	pro	87296938	87298609	chr16	-0.38
PIEZO1	1520	chr16:87376294-8737841	pro	87376294	87378413	chr16	-0.73
PIEZO1	934	chr16:87379643-8737997	pro	87379643	87379972	chr16	-0.26
CDT1	1654	chr16:87395560-8739650	pro	87395560	87396504	chr16	-0.50
LOC100129697	717	chr16:87532637-87533821	pro	87532637	87533821	chr16	-0.33

CBFA2T3	2807	chr16:87565408-87570990	pro	87565408	87570990	chr16	-0.35
CBFA2T3	2176	chr16:87572851-87573514	pro	87572851	87573514	chr16	-0.34
SNORD68	2325	chr16:88156993-88158333	pro	88156993	88158333	chr16	-0.36
FANCA	1490	chr16:88411449-88412663	pro	88411449	88412663	chr16	-0.74
DEF8	1733	chr16:88544934-88545188	pro	88544934	88545188	chr16	-0.87
DBNDD1	1184	chr16:88602767-88602926	pro	88602767	88602926	chr16	-0.27
CARHSP1	2164	chr16:8872284-8872784	pro	8872284	8872784	chr16	-0.56
LMF1	429	chr16:961241-961589	pro	961241	961589	chr16	-0.36
BHLHA9	1457	chr17:1119018-1119280	pro	1119018	1119280	chr17	-0.65
ZNF18	971	chr17:11840377-11840509	pro	11840377	11840509	chr17	-0.67
ARHGAP44	297	chr17:12633047-12633463	pro	12633047	12633463	chr17	-0.64
LOC100128006	56	chr17:12634179-12634584	pro	12634179	12634584	chr17	-0.26
PITPNA-AS1	926	chr17:1367723-1368052	pro	1367723	1368052	chr17	-0.40
WDR81	1372	chr17:1573059-1573361	pro	1573059	1573361	chr17	-0.72
TTC19	963	chr17:15842282-15842628	pro	15842282	15842628	chr17	-0.84
SNORD65	359	chr17:16284915-16286331	pro	16284915	16286331	chr17	-0.57
SNORD65	1416	chr17:16286445-16286916	pro	16286445	16286916	chr17	-0.54
ZNF287	348	chr17:16413355-16413833	pro	16413355	16413833	chr17	-0.36
ZNF624	283	chr17:16497980-16498370	pro	16497980	16498370	chr17	-0.38
TNFRSF13B	1775	chr17:16813550-16815156	pro	16813550	16815156	chr17	-0.96
TNFRSF13B	362	chr17:16815472-16816059	pro	16815472	16816059	chr17	-0.98
TNFRSF13B	352	chr17:16816275-16816684	pro	16816275	16816684	chr17	-0.96
TNFRSF13B	1986	chr17:16817770-16818457	pro	16817770	16818457	chr17	-0.72
PEMT	1429	chr17:17436910-17437432	pro	17436910	17437432	chr17	-0.78
RAI1	410	chr17:17524941-17525260	pro	17524941	17525260	chr17	-0.32
RAI1	1950	chr17:17527011-17527910	pro	17527011	17527910	chr17	-0.71
SREBF1	412	chr17:17681145-17681779	pro	17681145	17681779	chr17	-0.39
SREBF1	951	chr17:17681918-17682084	pro	17681918	17682084	chr17	-0.78
SREBF1	1496	chr17:17682332-17682761	pro	17682332	17682761	chr17	-0.70
SHMT1	1467	chr17:18205886-18206384	pro	18205886	18206384	chr17	-0.54
CCDC144B	458	chr17:18469970-18470257	pro	18469970	18470257	chr17	-0.51
EPN2	1189	chr17:19082008-19082934	pro	19082008	19082934	chr17	-0.81
EPN2-IT1	146	chr17:19114770-19115533	pro	19114770	19115533	chr17	-0.82
EPN2-AS1	1956	chr17:19148117-19148306	pro	19148117	19148306	chr17	-0.88
EPN2-AS1	1434	chr17:19148442-19149026	pro	19148442	19149026	chr17	-0.89
EPN2-AS1	424	chr17:19149221-19150266	pro	19149221	19150266	chr17	-0.89
EPN2-AS1	676	chr17:19150545-19151142	pro	19150545	19151142	chr17	-0.84
B9D1	460	chr17:19206985-19207214	pro	19206985	19207214	chr17	-0.26
SMG6	837	chr17:1937905-1938033	pro	1937905	1938033	chr17	-0.33
AKAP10	1799	chr17:19819901-19820025	pro	19819901	19820025	chr17	-0.62
KSR1	1922	chr17:22824979-22825188	pro	22824979	22825188	chr17	-0.75
LYRM9	516	chr17:23244637-23245467	pro	23244637	23245467	chr17	-0.76
NLK	1757	chr17:23391878-23392236	pro	23391878	23392236	chr17	-0.25
NLK	1856	chr17:23394442-23396899	pro	23394442	23396899	chr17	-0.30
METTL16	853	chr17:2362640-2362966	pro	2362640	2362966	chr17	-0.38
SARM1	447	chr17:23722243-23722479	pro	23722243	23722479	chr17	-0.41
SARM1	1318	chr17:23723665-23724587	pro	23723665	23724587	chr17	-0.50
UNC119	694	chr17:23902892-23903269	pro	23902892	23903269	chr17	-0.25
SDF2	1349	chr17:24011868-24012070	pro	24011868	24012070	chr17	-0.25
SNORD42A	338	chr17:24073523-24074944	pro	24073523	24074944	chr17	-0.53
TRAF4	2644	chr17:24091597-24093411	pro	24091597	24093411	chr17	-0.67
TAOK1	1992	chr17:24743376-24744743	pro	24743376	24744743	chr17	-0.47
SSH2	1628	chr17:25282731-25283270	pro	25282731	25283270	chr17	-0.61
TMIGD1	1742	chr17:25683409-25683490	pro	25683409	25683490	chr17	-0.41
CRLF3	1162	chr17:26176885-26177246	pro	26176885	26177246	chr17	-0.56

EVI2B	98	chr17:26664933-26665775	pro	26664933	26665775	chr17	-0.25
MIR4724	1070	chr17:26886473-26887706	pro	26886473	26887706	chr17	-0.28
MIR193A	1367	chr17:26909582-26909936	pro	26909582	26909936	chr17	-0.29
CCL1	2076	chr17:29715608-29717276	pro	29715608	29717276	chr17	-1.00
ZNF830	1645	chr17:30314228-30314382	pro	30314228	30314382	chr17	-0.75
RFFL	30	chr17:30414625-30415058	pro	30414625	30415058	chr17	-0.71
NLE1	1186	chr17:30491979-30492417	pro	30491979	30492417	chr17	-0.53
SLFN11	1130	chr17:30725722-30726205	pro	30725722	30726205	chr17	-0.27
AP2B1	1572	chr17:30939531-30940400	pro	30939531	30940400	chr17	-0.65
TAF15	1742	chr17:31162155-31162468	pro	31162155	31162468	chr17	-0.28
CCL3	333	chr17:31441874-31442032	pro	31441874	31442032	chr17	-0.55
GGNBP2	1336	chr17:31973434-31973590	pro	31973434	31973590	chr17	-0.57
AATF	2024	chr17:32382216-32382405	pro	32382216	32382405	chr17	-0.27
ACACA	1551	chr17:32839233-32839697	pro	32839233	32839697	chr17	-0.47
SYNRG	2991	chr17:33039528-33041690	pro	33039528	33041690	chr17	-0.46
SOCS7	2222	chr17:33763380-33764129	pro	33763380	33764129	chr17	-0.82
ARHGAP23	625	chr17:33837204-33838034	pro	33837204	33838034	chr17	-0.54
TRPV3	1197	chr17:3408863-3409611	pro	3408863	3409611	chr17	-0.38
MIR4734	676	chr17:34110899-34111969	pro	34110899	34111969	chr17	-0.46
CISD3	1898	chr17:34137906-34138367	pro	34137906	34138367	chr17	-0.74
PCGF2	1934	chr17:34155272-34157029	pro	34155272	34157029	chr17	-0.63
PSMB3	1624	chr17:34160187-34161546	pro	34160187	34161546	chr17	-0.36
SNORA21	1396	chr17:34260818-34261937	pro	34260818	34261937	chr17	-0.41
RPL23	860	chr17:34264286-34264594	pro	34264286	34264594	chr17	-0.68
ARL5C	1565	chr17:34577130-34577880	pro	34577130	34577880	chr17	-0.96
CACNB1	922	chr17:34607684-34609125	pro	34607684	34609125	chr17	-0.38
RPL19	1788	chr17:34611598-34612097	pro	34611598	34612097	chr17	-0.55
ZPBP2	1644	chr17:35275722-35276950	pro	35275722	35276950	chr17	-0.41
LRRC3C	1726	chr17:35349129-35349924	pro	35349129	35349924	chr17	-0.70
MED24	989	chr17:35463200-35463654	pro	35463200	35463654	chr17	-0.29
P2RX5	456	chr17:3546747-3547061	pro	3546747	3547061	chr17	-0.53
THRA	1676	chr17:35474110-35474426	pro	35474110	35474426	chr17	-0.75
NR1D1	1976	chr17:35508267-35508789	pro	35508267	35508789	chr17	-0.29
CDC6	1436	chr17:35698775-35699438	pro	35698775	35699438	chr17	-0.61
RARA	190	chr17:35718691-35718826	pro	35718691	35718826	chr17	-0.42
GSG2	1662	chr17:3574616-3576597	pro	3574616	3576597	chr17	-0.52
CCR7	576	chr17:35974499-35974872	pro	35974499	35974872	chr17	-0.38
CCR7	133	chr17:35974990-35975268	pro	35974990	35975268	chr17	-0.40
CCR7	292	chr17:35975386-35975722	pro	35975386	35975722	chr17	-0.64
TMEM99	480	chr17:36228973-36229912	pro	36228973	36229912	chr17	-0.32
C17orf85	377	chr17:3696504-3696838	pro	3696504	3696838	chr17	-0.51
EIF1	1504	chr17:37099780-37100531	pro	37099780	37100531	chr17	-0.44
JUP	2139	chr17:37194190-37194512	pro	37194190	37194512	chr17	-0.92
JUP	1138	chr17:37194696-37196009	pro	37194696	37196009	chr17	-0.30
P2RX1	2134	chr17:3764097-3765055	pro	3764097	3765055	chr17	-0.75
P2RX1	88	chr17:3766440-3766804	pro	3766440	3766804	chr17	-0.73
STAT5B	1261	chr17:37679911-37681467	pro	37679911	37681467	chr17	-0.29
ATP6V0A1	1634	chr17:37861963-37863541	pro	37861963	37863541	chr17	-0.54
PSMC3IP	1268	chr17:37981921-37982063	pro	37981921	37982063	chr17	-0.66
PSMC3IP	1725	chr17:37984765-37985437	pro	37984765	37985437	chr17	-0.66
PLEKHH3	943	chr17:38079836-38081546	pro	38079836	38081546	chr17	-0.75
CCR10	195	chr17:38086937-38087417	pro	38086937	38087417	chr17	-0.39
COA3	1178	chr17:38203016-38203168	pro	38203016	38203168	chr17	-0.64
AOC3	326	chr17:38258769-38259452	pro	38258769	38259452	chr17	-0.79
RUNDC1	1865	chr17:38387814-38388128	pro	38387814	38388128	chr17	-0.74

BRCA1	104	chr17:38529466-38529641	pro	38529466	38529641	chr17	-0.87
DHX8	1400	chr17:38917786-38918634	pro	38917786	38918634	chr17	-0.33
C17orf53	428	chr17:39574270-39574471	pro	39574270	39574471	chr17	-0.32
ASB16-AS1	1446	chr17:39617999-39618332	pro	39617999	39618332	chr17	-0.53
GRN	2094	chr17:39779985-39780234	pro	39779985	39780234	chr17	-0.93
KIF18B	1272	chr17:40378928-40379740	pro	40378928	40379740	chr17	-0.29
DCAKD	1462	chr17:40492468-40492615	pro	40492468	40492615	chr17	-0.67
FMNL1	2394	chr17:40655570-40659366	pro	40655570	40659366	chr17	-0.70
KANSL1-AS1	1139	chr17:41627295-41628411	pro	41627295	41628411	chr17	-0.32
UBE2G1	1766	chr17:4218360-4218607	pro	4218360	4218607	chr17	-0.82
RPRML	710	chr17:42412249-42412398	pro	42412249	42412398	chr17	-0.87
MYL4	1358	chr17:42639565-42640570	pro	42639565	42640570	chr17	-0.89
SPNS3	108	chr17:4283221-4284496	pro	4283221	4284496	chr17	-0.29
SPNS3	1752	chr17:4285615-4285821	pro	4285615	4285821	chr17	-0.91
KPNB1	480	chr17:43083332-43084749	pro	43083332	43084749	chr17	-0.26
TBKBP1	2120	chr17:43124876-43126140	pro	43124876	43126140	chr17	-0.25
SP2-AS1	288	chr17:43373224-43373739	pro	43373224	43373739	chr17	-0.28
CDK5RAP3	1404	chr17:43404261-43405188	pro	43404261	43405188	chr17	-0.44
HOXB4	888	chr17:44009463-44010246	pro	44009463	44010246	chr17	-0.98
HOXB4	728	chr17:44011039-44011901	pro	44011039	44011901	chr17	-0.98
HOXB5	44	chr17:44025975-44026141	pro	44025975	44026141	chr17	-0.90
HOXB5	490	chr17:44026548-44026636	pro	44026548	44026636	chr17	-0.65
MYBBP1A	1524	chr17:4406840-4407069	pro	4406840	4407069	chr17	-0.69
GGT6	1772	chr17:4411978-4412847	pro	4411978	4412847	chr17	-0.52
UBE2Z	1417	chr17:44341590-44342700	pro	44341590	44342700	chr17	-0.27
SPOP	1943	chr17:45108407-45108755	pro	45108407	45108755	chr17	-0.28
FAM117A	593	chr17:45196849-45197373	pro	45196849	45197373	chr17	-0.37
PDK2	460	chr17:45526560-45526715	pro	45526560	45526715	chr17	-0.51
PELP1	708	chr17:4554957-4555222	pro	4554957	4555222	chr17	-0.66
MRPL27	1181	chr17:45804102-45804660	pro	45804102	45804660	chr17	-0.57
SPATA20	179	chr17:45979189-45979349	pro	45979189	45979349	chr17	-0.43
ANKRD40	1373	chr17:46138793-46139001	pro	46138793	46139001	chr17	-0.53
RNF167	1780	chr17:4785913-4786394	pro	4785913	4786394	chr17	-0.65
LOC100130950	624	chr17:5036428-5037024	pro	5036428	5037024	chr17	-0.66
COX11	1984	chr17:50398927-50399234	pro	50398927	50399234	chr17	-0.55
SCIMP	1754	chr17:5077021-5077232	pro	5077021	5077232	chr17	-0.67
MMD	1370	chr17:50855314-50856107	pro	50855314	50856107	chr17	-0.62
TMEM100	2315	chr17:51157178-51157900	pro	51157178	51157900	chr17	-0.82
PCTP	234	chr17:51182957-51183250	pro	51182957	51183250	chr17	-0.82
PCTP	553	chr17:51183689-51184345	pro	51183689	51184345	chr17	-0.60
DGKE	2389	chr17:52267366-52270328	pro	52267366	52270328	chr17	-0.45
COIL	285	chr17:52393530-52393860	pro	52393530	52393860	chr17	-0.67
CUEDC1	391	chr17:53334654-53336064	pro	53334654	53336064	chr17	-0.69
BZRAP1-AS1	300	chr17:53761480-53761847	pro	53761480	53761847	chr17	-0.27
RNF43	180	chr17:53849464-53850037	pro	53849464	53850037	chr17	-0.60
RNF43	432	chr17:53850171-53850554	pro	53850171	53850554	chr17	-0.52
NLRP1	1400	chr17:5427106-5427206	pro	5427106	5427206	chr17	-0.75
TRIM37	1566	chr17:54540499-54540729	pro	54540499	54540729	chr17	-0.87
MIR301A	4	chr17:54583277-54583443	pro	54583277	54583443	chr17	-0.65
MIR301A	1542	chr17:54583831-54585981	pro	54583831	54585981	chr17	-0.44
PRR11	1656	chr17:54589035-54589556	pro	54589035	54589556	chr17	-0.72
SMG8	1690	chr17:54643779-54643905	pro	54643779	54643905	chr17	-0.63
GDPD1	1182	chr17:54653696-54653884	pro	54653696	54653884	chr17	-0.75
MIR4729	290	chr17:54797694-54798173	pro	54797694	54798173	chr17	-0.57
VMP1	1755	chr17:55141328-55141470	pro	55141328	55141470	chr17	-0.62

MIR21	1547	chr17:55271490-55272232	pro	55271490	55272232	chr17	-0.82
HEATR6	726	chr17:55511599-55512001	pro	55511599	55512001	chr17	-0.33
WFDC21P	1196	chr17:55521159-55522452	pro	55521159	55522452	chr17	-0.72
MED13	1076	chr17:57498335-57498668	pro	57498335	57498668	chr17	-0.28
STRADA	1457	chr17:59174442-59174596	pro	59174442	59174596	chr17	-0.49
SMARCD2	1156	chr17:59274782-59275698	pro	59274782	59275698	chr17	-0.66
GH1	1243	chr17:59351097-59351277	pro	59351097	59351277	chr17	-0.42
PRR29	417	chr17:59428895-59429155	pro	59428895	59429155	chr17	-0.41
ICAM2	2084	chr17:59449458-59449825	pro	59449458	59449825	chr17	-0.41
ICAM2	630	chr17:59452155-59452557	pro	59452155	59452557	chr17	-0.86
ERN1	1226	chr17:59559390-59560626	pro	59559390	59560626	chr17	-0.64
ERN1	1128	chr17:59561498-59563225	pro	59561498	59563225	chr17	-0.34
MILR1	1794	chr17:59877396-59877592	pro	59877396	59877592	chr17	-0.81
POLG2	1770	chr17:59921814-59921939	pro	59921814	59921939	chr17	-0.41
POLG2	1428	chr17:59922081-59922356	pro	59922081	59922356	chr17	-0.34
LRRC37A3	1414	chr17:60346739-60346820	pro	60346739	60346820	chr17	-0.54
AMZ2P1	2272	chr17:60399490-60400299	pro	60399490	60400299	chr17	-0.50
GNA13	842	chr17:60484122-60484327	pro	60484122	60484327	chr17	-0.61
AXIN2	1828	chr17:60986313-60986434	pro	60986313	60986434	chr17	-0.85
CEP112	1220	chr17:61619796-61619993	pro	61619796	61619993	chr17	-0.34
CEP112	1821	chr17:61620404-61620586	pro	61620404	61620586	chr17	-0.70
AMZ2	1191	chr17:63754459-63754635	pro	63754459	63754635	chr17	-0.71
AMZ2	1583	chr17:63757238-63757404	pro	63757238	63757404	chr17	-0.70
AMZ2	2342	chr17:63757737-63758422	pro	63757737	63758422	chr17	-0.64
ARSG	278	chr17:63766572-63766704	pro	63766572	63766704	chr17	-0.53
WIPI1	1338	chr17:63963860-63963960	pro	63963860	63963960	chr17	-0.30
PRKAR1A	1646	chr17:64017451-64018286	pro	64017451	64018286	chr17	-0.35
C17orf100	913	chr17:6496330-6497060	pro	6496330	6497060	chr17	-0.74
C17orf100	1688	chr17:6497259-6497682	pro	6497259	6497682	chr17	-0.82
ALOX12P2	1680	chr17:6698343-6700252	pro	6698343	6700252	chr17	-0.47
LOC102723505	876	chr17:67533455-67535729	pro	67533455	67535729	chr17	-0.97
LINC01152	660	chr17:67536306-67539151	pro	67536306	67539151	chr17	-0.83
LINC01152	994	chr17:67539287-67539476	pro	67539287	67539476	chr17	-0.92
ALOX12-AS1	1049	chr17:6855211-6855447	pro	6855211	6855447	chr17	-0.33
COG1	1541	chr17:68699133-68699317	pro	68699133	68699317	chr17	-0.47
RPL38	1640	chr17:69712654-69713401	pro	69712654	69713401	chr17	-0.47
ASGR1	1749	chr17:7021712-7022006	pro	7021712	7022006	chr17	-0.36
ACADVL	1912	chr17:7058670-7059839	pro	7058670	7059839	chr17	-0.57
ACADVL	518	chr17:7060024-7061271	pro	7060024	7061271	chr17	-0.95
DLG4	414	chr17:7061707-7062425	pro	7061707	7062425	chr17	-0.81
MIF4GD	908	chr17:70776928-70777099	pro	70776928	70777099	chr17	-0.51
SLC25A19	1794	chr17:70795091-70795573	pro	70795091	70795573	chr17	-0.74
PHF23	1362	chr17:7081369-7081855	pro	7081369	7081855	chr17	-0.26
MIR3678	2176	chr17:70915675-70916166	pro	70915675	70916166	chr17	-0.94
KIAA0195	2184	chr17:70961847-70962302	pro	70961847	70962302	chr17	-0.92
SMIM5	413	chr17:71141457-71141585	pro	71141457	71141585	chr17	-0.62
SAP30BP	1928	chr17:71172621-71173103	pro	71172621	71173103	chr17	-0.76
H3F3B	1445	chr17:71285954-71286068	pro	71285954	71286068	chr17	-0.25
H3F3B	500	chr17:71287744-71288169	pro	71287744	71288169	chr17	-0.56
YBX2	686	chr17:7139002-7139569	pro	7139002	7139569	chr17	-0.29
TRIM65	1383	chr17:71402799-71403795	pro	71402799	71403795	chr17	-0.38
SRP68	2055	chr17:71578036-71578258	pro	71578036	71578258	chr17	-0.92
NEURL4	1089	chr17:7172013-7172533	pro	7172013	7172533	chr17	-0.46
UBALD2	2098	chr17:71770178-71771387	pro	71770178	71771387	chr17	-0.50
UBALD2	672	chr17:71771817-71772598	pro	71771817	71772598	chr17	-0.47

ACAP1	1454	chr17:7181852-7182195	pro	7181852	7182195	chr17	-0.89
AANAT	184	chr17:71961081-71961338	pro	71961081	71961338	chr17	-0.36
RHBDF2	2109	chr17:71993285-71993669	pro	71993285	71993669	chr17	-0.89
TMEM95	1208	chr17:7200362-7200494	pro	7200362	7200494	chr17	-0.81
RHBDF2	1840	chr17:72006011-72008517	pro	72006011	72008517	chr17	-0.69
SNHG16	1114	chr17:72064195-72064458	pro	72064195	72064458	chr17	-0.85
SNORD1C	806	chr17:72067126-72067421	pro	72067126	72067421	chr17	-0.40
SNORD1B	918	chr17:72067681-72068052	pro	72067681	72068052	chr17	-0.59
SNORD1B	30	chr17:72068689-72068820	pro	72068689	72068820	chr17	-0.62
MGAT5B	856	chr17:72375455-72375617	pro	72375455	72375617	chr17	-0.59
MIR6516	1356	chr17:72598294-72598601	pro	72598294	72598601	chr17	-0.38
FLJ45079	1696	chr17:73389469-73390668	pro	73389469	73390668	chr17	-0.68
C17orf99	1400	chr17:73655043-73655812	pro	73655043	73655812	chr17	-0.65
BIRC5	1474	chr17:73723081-73723606	pro	73723081	73723606	chr17	-0.58
LOC100996291	1948	chr17:73783898-73784543	pro	73783898	73784543	chr17	-0.30
DNAH17-AS1	420	chr17:73991909-73992423	pro	73991909	73992423	chr17	-0.98
LOC101928710	1117	chr17:74138386-74138848	pro	74138386	74138848	chr17	-0.40
CYTH1	260	chr17:74222043-74227896	pro	74222043	74227896	chr17	-0.43
CYTH1	2200	chr17:74228992-74229463	pro	74228992	74229463	chr17	-0.52
CYTH1	1902	chr17:74232937-74233723	pro	74232937	74233723	chr17	-0.30
CD68	114	chr17:7423327-7423501	pro	7423327	7423501	chr17	-0.68
CYTH1	2306	chr17:74287101-74288327	pro	74287101	74288327	chr17	-0.56
WRAP53	965	chr17:7528701-7529593	pro	7528701	7529593	chr17	-0.28
BAIAP2	79	chr17:76623548-76623690	pro	76623548	76623690	chr17	-0.31
KDM6B	203	chr17:7682540-7685782	pro	7682540	7685782	chr17	-0.35
CHD3	2658	chr17:7723961-7728414	pro	7723961	7728414	chr17	-0.41
ANAPC11	1736	chr17:77444746-77444921	pro	77444746	77444921	chr17	-0.82
FASN	2224	chr17:77651368-77651871	pro	77651368	77651871	chr17	-0.39
SECTM1	1001	chr17:77885804-77886618	pro	77885804	77886618	chr17	-0.50
TEX19	248	chr17:77910080-77910243	pro	77910080	77910243	chr17	-0.42
C17orf62	1604	chr17:77999109-77999467	pro	77999109	77999467	chr17	-0.59
FN3KRP	1250	chr17:78268886-78269354	pro	78268886	78269354	chr17	-0.42
GUCY2D	464	chr17:7846052-7846444	pro	7846052	7846444	chr17	-0.31
PER1	1713	chr17:7998068-7998314	pro	7998068	7998314	chr17	-0.29
AURKB	1786	chr17:8052695-8053073	pro	8052695	8053073	chr17	-0.79
AURKB	720	chr17:8055156-8055624	pro	8055156	8055624	chr17	-0.54
CTC1	1649	chr17:8090233-8090745	pro	8090233	8090745	chr17	-0.78
RPL26	2366	chr17:8224122-8225726	pro	8224122	8225726	chr17	-0.51
RPL26	1350	chr17:8228468-8228811	pro	8228468	8228811	chr17	-0.66
NXN	1704	chr17:831292-831612	pro	831292	831612	chr17	-0.33
NTN1	716	chr17:8864609-8865123	pro	8864609	8865123	chr17	-0.77
IMPA2	1514	chr18:11972814-11973066	pro	11972814	11973066	chr18	-0.80
IMPA2	1832	chr18:11973176-11973341	pro	11973176	11973341	chr18	-0.78
SLMO1	1896	chr18:12399475-12400105	pro	12399475	12400105	chr18	-0.53
SEH1L	1279	chr18:12939165-12939357	pro	12939165	12939357	chr18	-0.27
USP14	2103	chr18:150275-150895	pro	150275	150895	chr18	-0.79
SNRPD1	1736	chr18:17447896-17448027	pro	17447896	17448027	chr18	-0.47
SNRPD1	2423	chr18:17448164-17449134	pro	17448164	17449134	chr18	-0.68
MIR320C1	1628	chr18:17518697-17519496	pro	17518697	17519496	chr18	-0.50
ABHD3	2407	chr18:17534742-17537972	pro	17534742	17537972	chr18	-0.30
MIB1	1550	chr18:17575810-17577861	pro	17575810	17577861	chr18	-0.45
CABLES1	4	chr18:18967694-18969361	pro	18967694	18969361	chr18	-0.79
CABLES1	1932	chr18:18970351-18972962	pro	18970351	18972962	chr18	-0.90
TMEM241	455	chr18:19272028-19272730	pro	19272028	19272730	chr18	-0.60
LAMA3	1664	chr18:19704734-19705899	pro	19704734	19705899	chr18	-0.77

TTC39C-AS1	2472	chr18:19848988-1985480	pro	19848988	19854800	chr18	-0.64
ZNF521	1346	chr18:21184762-2118496	pro	21184762	21184969	chr18	-0.81
KCTD1	3338	chr18:22377670-2238064	pro	22377670	22380649	chr18	-0.67
METTL4	1159	chr18:2559678-2560984	pro	2559678	2560984	chr18	-0.40
NDC80	1719	chr18:2561591-2564863	pro	2561591	2564863	chr18	-0.36
THOC1	1736	chr18:256247-256400	pro	256247	256400	chr18	-0.78
CBX3P2	706	chr18:2643846-2645530	pro	2643846	2645530	chr18	-0.44
DSG2-AS1	642	chr18:27390072-2739038	pro	27390072	27390388	chr18	-0.74
B4GALT6	1741	chr18:27515377-2751850	pro	27515377	27518509	chr18	-0.93
B4GALT6	1935	chr18:27519617-2752162	pro	27519617	27521621	chr18	-0.90
RNF125	553	chr18:27851806-2785197	pro	27851806	27851972	chr18	-0.84
RNF125	94	chr18:27852075-2785262	pro	27852075	27852621	chr18	-0.45
RNF125	926	chr18:27852779-2785395	pro	27852779	27853958	chr18	-0.46
GAREM	1279	chr18:28302123-28304211	pro	28302123	28304211	chr18	-0.67
ASXL3	1073	chr18:29412876-2941434	pro	29412876	29414346	chr18	-0.99
LPIN2	1768	chr18:3003543-3003884	pro	3003543	3003884	chr18	-0.31
MAPRE2	1928	chr18:30873005-3087378	pro	30873005	30873780	chr18	-0.56
MIR3975	952	chr18:31425699-3142760	pro	31425699	31427602	chr18	-0.93
C18orf21	2286	chr18:31804003-3180459	pro	31804003	31804592	chr18	-0.76
ELP2	1834	chr18:31965596-3196574	pro	31965596	31965740	chr18	-0.46
MYL12A	1340	chr18:3235041-3237331	pro	3235041	3237331	chr18	-0.32
MYL12A	1388	chr18:3238204-3239624	pro	3238204	3239624	chr18	-0.38
MYL12B	1018	chr18:3250567-3251616	pro	3250567	3251616	chr18	-0.28
MYL12B	2477	chr18:3252721-3257665	pro	3252721	3257665	chr18	-0.78
KIAA1328	1491	chr18:32661254-3266191	pro	32661254	32661916	chr18	-0.45
TGIF1	710	chr18:3437151-3439432	pro	3437151	3439432	chr18	-0.33
TGIF1	668	chr18:3443701-3445174	pro	3443701	3445174	chr18	-0.66
DLGAP1-AS1	1176	chr18:3582981-3587590	pro	3582981	3587590	chr18	-0.42
DLGAP1-AS2	866	chr18:3592611-3596590	pro	3592611	3596590	chr18	-0.82
SMAD7	1244	chr18:44727874-4472904	pro	44727874	44729042	chr18	-0.29
SNORD58C	617	chr18:45268912-4526923	pro	45268912	45269238	chr18	-0.56
RPL17	280	chr18:45273012-4527341	pro	45273012	45273415	chr18	-0.41
CFAP53	1610	chr18:46048047-4604890	pro	46048047	46048900	chr18	-0.92
SKA1	884	chr18:46155677-4615686	pro	46155677	46156868	chr18	-0.26
SNORA37	1780	chr18:50000413-5000158	pro	50000413	50001587	chr18	-0.34
POLI	723	chr18:50048796-5004945	pro	50048796	50049450	chr18	-0.81
C18orf54	612	chr18:50140087-5014047	pro	50140087	50140476	chr18	-0.80
SEC11C	692	chr18:54957243-54957581	pro	54957243	54957581	chr18	-0.57
PIGN	2160	chr18:58002677-5800354	pro	58002677	58003544	chr18	-0.72
PIGN	1288	chr18:58003697-5800426	pro	58003697	58004268	chr18	-0.44
PHLPP1	3449	chr18:58535326-5853887	pro	58535326	58538872	chr18	-0.80
CLUL1	424	chr18:586430-586713	pro	586430	586713	chr18	-0.83
BCL2	1353	chr18:59138873-59139021	pro	59138873	59139021	chr18	-0.29
TMX3	1856	chr18:64531047-6453190	pro	64531047	64531908	chr18	-0.27
TYMSOS	716	chr18:648442-649669	pro	648442	649669	chr18	-0.36
ENOSF1	798	chr18:701353-702087	pro	701353	702087	chr18	-0.89
CNDP2	1506	chr18:70316127-7031646	pro	70316127	70316465	chr18	-0.34
TSHZ1	1670	chr18:71053137-7105359	pro	71053137	71053595	chr18	-0.31
C18orf65	446	chr18:72336428-7233739	pro	72336428	72337392	chr18	-0.99
C18orf65	3126	chr18:72337542-7234163	pro	72337542	72341638	chr18	-0.84
ANKRD12	2490	chr18:9128460-9131639	pro	9128460	9131639	chr18	-0.52
RALBP1	2092	chr18:9467152-9468089	pro	9467152	9468089	chr18	-0.58
MIR4322	1588	chr19:10200014-1020098	pro	10200014	10200986	chr19	-0.31
MRPL4	1800	chr19:10221786-10221891	pro	10221786	10221891	chr19	-0.39
CDC37	1889	chr19:10376732-1037759	pro	10376732	10377590	chr19	-0.95

PDE4A	602	chr19:10387488-10388205	pro	10387488	10388205	chr19	-0.48
PDE4A	1291	chr19:10388845-10390633	pro	10388845	10390633	chr19	-0.93
PDE4A	876	chr19:10391103-10391810	pro	10391103	10391810	chr19	-0.55
PDE4A	1546	chr19:10392965-10394791	pro	10392965	10394791	chr19	-0.98
MIR1238	1699	chr19:10525405-10525585	pro	10525405	10525585	chr19	-0.55
GPX4	2072	chr19:1052687-1053016	pro	1052687	1053016	chr19	-0.58
SBNO2	640	chr19:1082516-1082753	pro	1082516	1082753	chr19	-0.33
SMARCA4	1834	chr19:10934480-10934801	pro	10934480	10934801	chr19	-0.31
LDLR	400	chr19:11060242-11061030	pro	11060242	11061030	chr19	-0.31
SPC24	1102	chr19:11126174-11126591	pro	11126174	11126591	chr19	-0.45
SWSAP1	1921	chr19:11348223-11348383	pro	11348223	11348383	chr19	-0.73
CCDC151	2138	chr19:11409541-11409942	pro	11409541	11409942	chr19	-0.44
ELOF1	1520	chr19:11532231-11532913	pro	11532231	11532913	chr19	-0.58
ACP5	2196	chr19:11552709-11553288	pro	11552709	11553288	chr19	-0.75
ZNF491	646	chr19:11770911-11771160	pro	11770911	11771160	chr19	-0.45
ZNF69	259	chr19:11859322-11859496	pro	11859322	11859496	chr19	-0.69
ZNF20	927	chr19:12111248-12111342	pro	12111248	12111342	chr19	-0.69
ZNF44	530	chr19:12267135-12267354	pro	12267135	12267354	chr19	-0.49
ZNF563	1488	chr19:12303024-12305067	pro	12303024	12305067	chr19	-0.55
ZNF709	2148	chr19:12454064-12454904	pro	12454064	12454904	chr19	-0.80
ZNF564	1028	chr19:12524252-12524515	pro	12524252	12524515	chr19	-0.75
DNASE2	1146	chr19:12852099-12852280	pro	12852099	12852280	chr19	-0.76
CALR	1800	chr19:12908408-12908815	pro	12908408	12908815	chr19	-0.31
GADD45GIP1	748	chr19:12929737-12929895	pro	12929737	12929895	chr19	-0.58
LYL1	1488	chr19:13073126-13073847	pro	13073126	13073847	chr19	-0.44
LYL1	1158	chr19:13076019-13076244	pro	13076019	13076244	chr19	-0.34
NDUFS7	718	chr19:1334015-1334314	pro	1334015	1334314	chr19	-0.40
ZSWIM4	964	chr19:13767632-13768841	pro	13767632	13768841	chr19	-0.42
MIR23A	163	chr19:13808496-13808778	pro	13808496	13808778	chr19	-0.64
MIR23A	582	chr19:13808918-13809194	pro	13808918	13809194	chr19	-0.54
APC2	496	chr19:1400321-1400979	pro	1400321	1400979	chr19	-0.84
MIR1199	2052	chr19:14047131-14047316	pro	14047131	14047316	chr19	-0.61
ASF1B	1956	chr19:14106263-14106705	pro	14106263	14106705	chr19	-0.75
CD97	86	chr19:14352737-14352998	pro	14352737	14352998	chr19	-0.32
CD97	1136	chr19:14353662-14354519	pro	14353662	14354519	chr19	-0.81
PKN1	1102	chr19:14403980-14404143	pro	14403980	14404143	chr19	-0.49
DNAJB1	1440	chr19:14488060-14488408	pro	14488060	14488408	chr19	-0.44
NDUFB7	260	chr19:14544027-14544273	pro	14544027	14544273	chr19	-0.36
CLEC17A	122	chr19:14554917-14555116	pro	14554917	14555116	chr19	-0.94
ZNF333	892	chr19:14660466-14661449	pro	14660466	14661449	chr19	-0.42
ILVBL	482	chr19:15097845-15098340	pro	15097845	15098340	chr19	-0.43
RASAL3	303	chr19:15436413-15436957	pro	15436413	15436957	chr19	-0.47
TCF3	2428	chr19:1598216-1599499	pro	1598216	1599499	chr19	-0.42
KLF2	2088	chr19:16294271-16294852	pro	16294271	16294852	chr19	-0.90
KLF2	539	chr19:16296035-16296187	pro	16296035	16296187	chr19	-0.59
KLF2	1660	chr19:16297822-16298797	pro	16297822	16298797	chr19	-0.79
TMEM38A	1702	chr19:16634543-16634734	pro	16634543	16634734	chr19	-0.89
NWD1	270	chr19:16691221-16691810	pro	16691221	16691810	chr19	-0.27
USE1	578	chr19:17187558-17187905	pro	17187558	17187905	chr19	-0.28
NR2F6	1373	chr19:17215420-17216138	pro	17215420	17216138	chr19	-0.38
USHBP1	0	chr19:17236294-17236794	pro	17236294	17236794	chr19	-0.77
ANKLE1	1421	chr19:17254718-17255028	pro	17254718	17255028	chr19	-0.34
MRPL34	412	chr19:17276874-17277255	pro	17276874	17277255	chr19	-0.55
PGLS	1065	chr19:17481953-17482777	pro	17481953	17482777	chr19	-0.83
FAM129C	262	chr19:17494682-17495009	pro	17494682	17495009	chr19	-0.67

ATP8B3	354	chr19:1762743-1763022	pro	1762743	1763022	chr19	-0.36
FCHO1	1552	chr19:17719861-17722296	pro	17719861	17722296	chr19	-0.74
FCHO1	1926	chr19:17725104-17725317	pro	17725104	17725317	chr19	-0.78
JAK3	614	chr19:17819040-17819416	pro	17819040	17819416	chr19	-0.77
IL12RB1	948	chr19:18071215-18071933	pro	18071215	18071933	chr19	-0.75
IL12RB1	2124	chr19:18072390-18073111	pro	18072390	18073111	chr19	-0.96
PDE4C	1634	chr19:18199777-18200064	pro	18199777	18200064	chr19	-0.93
LSM4	498	chr19:18295188-18295811	pro	18295188	18295811	chr19	-0.35
SSBP4	2002	chr19:18392644-18393648	pro	18392644	18393648	chr19	-0.91
KXD1	1606	chr19:18531107-18531245	pro	18531107	18531245	chr19	-0.33
ADAT3	1954	chr19:1854335-1854496	pro	1854335	1854496	chr19	-0.84
ADAT3	670	chr19:1855246-1856153	pro	1855246	1856153	chr19	-0.70
KLHL26	1095	chr19:18607580-18607902	pro	18607580	18607902	chr19	-0.52
KLHL26	650	chr19:18608966-18610006	pro	18608966	18610006	chr19	-0.60
HOMER3	77	chr19:18911738-18912740	pro	18911738	18912740	chr19	-0.28
HOMER3	438	chr19:18913281-18913678	pro	18913281	18913678	chr19	-0.60
SUGP2	1506	chr19:19003802-19003946	pro	19003802	19003946	chr19	-0.29
MEF2B	2411	chr19:19139262-19140112	pro	19139262	19140112	chr19	-0.44
MEF2B	1740	chr19:19143693-19143982	pro	19143693	19143982	chr19	-0.74
ATP13A1	1582	chr19:19636985-19637186	pro	19636985	19637186	chr19	-0.79
ZNF253	1586	chr19:19839189-19839408	pro	19839189	19839408	chr19	-0.72
MKNK2	947	chr19:2002921-2003461	pro	2002921	2003461	chr19	-0.73
ZNF85	300	chr19:20897530-20897666	pro	20897530	20897666	chr19	-0.49
ZNF85	950	chr19:20898764-20898932	pro	20898764	20898932	chr19	-0.54
ZNF431	878	chr19:21117388-21117723	pro	21117388	21117723	chr19	-0.46
DOT1L	583	chr19:2114462-2114664	pro	2114462	2114664	chr19	-0.29
DOT1L	1442	chr19:2116403-2116772	pro	2116403	2116772	chr19	-0.34
ZNF493	930	chr19:21372439-21372941	pro	21372439	21372941	chr19	-0.33
ZNF429	948	chr19:21481123-21481325	pro	21481123	21481325	chr19	-0.52
ZNF100	1068	chr19:21741093-21741312	pro	21741093	21741312	chr19	-0.41
ZNF43	374	chr19:21811053-21811396	pro	21811053	21811396	chr19	-0.27
ZNF43	1004	chr19:21825595-21825816	pro	21825595	21825816	chr19	-0.88
ZNF43	338	chr19:21826848-21827247	pro	21826848	21827247	chr19	-0.31
SF3A2	1886	chr19:2189347-2190054	pro	2189347	2190054	chr19	-0.58
JSRP1	1788	chr19:2209065-2209354	pro	2209065	2209354	chr19	-0.61
ZNF730	1172	chr19:23092141-23093436	pro	23092141	23093436	chr19	-0.80
ZNF724P	1253	chr19:23223695-23223823	pro	23223695	23223823	chr19	-0.74
IPO5P1	1179	chr19:23247514-23247916	pro	23247514	23247916	chr19	-0.34
ZNF675	1266	chr19:23660311-23660874	pro	23660311	23660874	chr19	-0.39
GNG7	1375	chr19:2651403-2653339	pro	2651403	2653339	chr19	-0.63
ZNF555	662	chr19:2791685-2791856	pro	2791685	2791856	chr19	-0.34
ZNF555	958	chr19:2793104-2793676	pro	2793104	2793676	chr19	-0.53
TLE6	659	chr19:2927476-2928274	pro	2927476	2928274	chr19	-0.95
TLE6	433	chr19:2928597-2929337	pro	2928597	2929337	chr19	-0.92
MIER2	306	chr19:295972-296224	pro	295972	296224	chr19	-0.34
AES	185	chr19:3014055-3014243	pro	3014055	3014243	chr19	-0.35
LOC100996351	114	chr19:3105899-3106221	pro	3105899	3106221	chr19	-0.93
LOC101927151	2228	chr19:32973749-32974223	pro	32973749	32974223	chr19	-0.80
LINC00662	1296	chr19:32977943-32978025	pro	32977943	32978025	chr19	-0.29
SMIM24	1490	chr19:3429907-3430194	pro	3429907	3430194	chr19	-0.52
SMIM24	300	chr19:3431118-3431363	pro	3431118	3431363	chr19	-0.29
SMIM24	191	chr19:3431466-3431996	pro	3431466	3431996	chr19	-0.29
SMIM24	960	chr19:3432158-3432841	pro	3432158	3432841	chr19	-0.32
FZR1	1318	chr19:3455772-3456180	pro	3455772	3456180	chr19	-0.85
POP4	1092	chr19:34787738-34788094	pro	34787738	34788094	chr19	-0.83

CCNE1	1486	chr19:34993146-34993363	pro	34993146	34993363	chr19	-0.72
URI1	578	chr19:35106382-35107553	pro	35106382	35107553	chr19	-0.51
HMG20B	1237	chr19:3525095-3525263	pro	3525095	3525263	chr19	-0.49
FXYD3	1222	chr19:40297250-40297447	pro	40297250	40297447	chr19	-0.67
FXYD1	1387	chr19:40323598-40323928	pro	40323598	40323928	chr19	-0.43
CD22	1217	chr19:40510577-40510805	pro	40510577	40510805	chr19	-0.46
MIR5196	1749	chr19:40529578-40530428	pro	40529578	40530428	chr19	-0.48
IGFLR1	128	chr19:40924821-40925819	pro	40924821	40925819	chr19	-0.31
HCST	406	chr19:41083861-41085767	pro	41083861	41085767	chr19	-0.34
HCST	1622	chr19:41086734-41086949	pro	41086734	41086949	chr19	-0.31
TYROBP	1180	chr19:41091832-41092633	pro	41091832	41092633	chr19	-0.66
LRFN3	72	chr19:41119576-41120000	pro	41119576	41120000	chr19	-0.44
WDR62	1588	chr19:41238935-41239485	pro	41238935	41239485	chr19	-0.52
SIRT6	1894	chr19:4131616-4131789	pro	4131616	4131789	chr19	-0.42
SIRT6	1336	chr19:4131964-4132557	pro	4131964	4132557	chr19	-0.59
CAPNS1	1510	chr19:41324040-41324493	pro	41324040	41324493	chr19	-0.46
CCDC94	1212	chr19:4199260-4199385	pro	4199260	4199385	chr19	-0.55
ZNF570	12	chr19:42650324-42650676	pro	42650324	42650676	chr19	-0.28
DPF1	372	chr19:43412397-43412734	pro	43412397	43412734	chr19	-0.84
CHAF1A	1832	chr19:4355103-4355876	pro	4355103	4355876	chr19	-0.35
HNRNPL	2112	chr19:44030128-44030564	pro	44030128	44030564	chr19	-0.27
HDGFRP2	1636	chr19:4421392-4421720	pro	4421392	4421720	chr19	-0.71
PAK4	970	chr19:44308937-44309518	pro	44308937	44309518	chr19	-0.50
GMFG	1372	chr19:44517060-44517328	pro	44517060	44517328	chr19	-0.89
ZFP36	1714	chr19:44587571-44587654	pro	44587571	44587654	chr19	-0.82
ZFP36	1158	chr19:44587898-44588437	pro	44587898	44588437	chr19	-0.57
PLEKHG2	1623	chr19:44593232-44594698	pro	44593232	44594698	chr19	-0.28
RPS16	1370	chr19:44616616-44617559	pro	44616616	44617559	chr19	-0.49
SUPT5H	1611	chr19:44629563-44629911	pro	44629563	44629911	chr19	-0.48
EID2	1572	chr19:44721042-44721171	pro	44721042	44721171	chr19	-0.70
EID2	293	chr19:44722831-44723111	pro	44722831	44723111	chr19	-0.41
LRG1	360	chr19:4491179-4491614	pro	4491179	4491614	chr19	-0.83
AKT2	1228	chr19:45484185-45484554	pro	45484185	45484554	chr19	-0.64
AKT2	1584	chr19:45484658-45484795	pro	45484658	45484795	chr19	-0.72
C19orf47	1324	chr19:45544760-45544904	pro	45544760	45544904	chr19	-0.34
C19orf47	744	chr19:45546631-45547404	pro	45546631	45547404	chr19	-0.36
PLD3	812	chr19:45556420-45556731	pro	45556420	45556731	chr19	-0.86
LTBP4	1386	chr19:45796242-45796489	pro	45796242	45796489	chr19	-0.79
C19orf54	1228	chr19:45946165-45946715	pro	45946165	45946715	chr19	-0.26
TMEM91	1038	chr19:46575972-46576120	pro	46575972	46576120	chr19	-0.71
LINC01480	831	chr19:46732648-46733086	pro	46732648	46733086	chr19	-0.94
LINC01480	374	chr19:46733356-46734789	pro	46733356	46734789	chr19	-0.92
CEACAM21	636	chr19:46745845-46750875	pro	46745845	46750875	chr19	-0.60
RPS19	599	chr19:47054992-47055462	pro	47054992	47055462	chr19	-0.44
CD79A	1271	chr19:47071436-47072078	pro	47071436	47072078	chr19	-0.33
CD79A	322	chr19:47072454-47072958	pro	47072454	47072958	chr19	-0.39
ARHGEF1	1712	chr19:47077307-47077482	pro	47077307	47077482	chr19	-0.42
SMG9	1763	chr19:48948996-48949442	pro	48948996	48949442	chr19	-0.84
SMG9	1470	chr19:48952057-48952846	pro	48952057	48952846	chr19	-0.76
KCNN4	1828	chr19:48974533-48976312	pro	48974533	48976312	chr19	-0.76
KCNN4	58	chr19:48976727-48977657	pro	48976727	48977657	chr19	-0.58
ZNF235	292	chr19:49501183-49501436	pro	49501183	49501436	chr19	-0.30
MIR4531	726	chr19:49849485-49849651	pro	49849485	49849651	chr19	-0.65
BCL3	1435	chr19:49942196-49942566	pro	49942196	49942566	chr19	-0.26
BCL3	2431	chr19:49945764-49946730	pro	49945764	49946730	chr19	-0.48

PVRL2	1307	chr19:50039855-50039995	pro	50039855	50039995	chr19	-0.32
PVRL2	922	chr19:50040130-50040490	pro	50040130	50040490	chr19	-0.79
APOC1	222	chr19:50109806-50110159	pro	50109806	50110159	chr19	-0.94
APOC1	590	chr19:50110281-50110420	pro	50110281	50110420	chr19	-0.34
RELB	1502	chr19:50194964-50195123	pro	50194964	50195123	chr19	-0.92
RELB	1075	chr19:50195279-50195663	pro	50195279	50195663	chr19	-0.84
ZNF296	1648	chr19:50269396-50270363	pro	50269396	50270363	chr19	-0.39
ZNF296	744	chr19:50271688-50272855	pro	50271688	50272855	chr19	-0.46
PPP1R37	1695	chr19:50286479-50286671	pro	50286479	50286671	chr19	-0.57
ERCC1	454	chr19:50618913-50620032	pro	50618913	50620032	chr19	-0.33
RTN2	630	chr19:50687621-50687808	pro	50687621	50687808	chr19	-0.49
PPM1N	1276	chr19:50694792-50694900	pro	50694792	50694900	chr19	-0.64
DMWD	406	chr19:50988165-50988447	pro	50988165	50988447	chr19	-0.30
SYMPK	2117	chr19:51055987-51056555	pro	51055987	51056555	chr19	-0.69
PPP5C	1803	chr19:51543834-51543952	pro	51543834	51543952	chr19	-0.59
SLC1A5	371	chr19:51983968-51984138	pro	51983968	51984138	chr19	-0.38
MIR3190	1058	chr19:52420809-52421152	pro	52420809	52421152	chr19	-0.39
C5AR2	104	chr19:52531941-52532051	pro	52531941	52532051	chr19	-0.70
KPTN	586	chr19:52678641-52678855	pro	52678641	52678855	chr19	-0.47
NAPA-AS1	1103	chr19:52680012-52680894	pro	52680012	52680894	chr19	-0.58
NAPA	1694	chr19:52708471-52708796	pro	52708471	52708796	chr19	-0.43
NAPA	940	chr19:52711061-52711475	pro	52711061	52711475	chr19	-0.84
PTPRS	208	chr19:5291527-5291684	pro	5291527	5291684	chr19	-0.77
LOC100505812	1686	chr19:53448969-53449143	pro	53448969	53449143	chr19	-0.72
CARD8	1438	chr19:53452362-53452545	pro	53452362	53452545	chr19	-0.61
CARD8	2196	chr19:53452819-53453606	pro	53452819	53453606	chr19	-0.39
EMP3	482	chr19:53520362-53521483	pro	53520362	53521483	chr19	-0.53
TMEM143	1011	chr19:53557717-53558257	pro	53557717	53558257	chr19	-0.56
LMTK3	2359	chr19:53705452-53706346	pro	53705452	53706346	chr19	-0.75
CA11	934	chr19:53842078-53842317	pro	53842078	53842317	chr19	-0.46
IZUMO1	166	chr19:53942009-53942279	pro	53942009	53942279	chr19	-0.38
IZUMO1	512	chr19:53942390-53942589	pro	53942390	53942589	chr19	-0.68
PLEKHA4	1906	chr19:54061711-54061870	pro	54061711	54061870	chr19	-0.87
PPP1R15A	1446	chr19:54067817-54069995	pro	54067817	54069995	chr19	-0.27
NUCB1-AS1	476	chr19:54113026-54113942	pro	54113026	54113942	chr19	-0.89
RUVBL2	1218	chr19:54190019-54190349	pro	54190019	54190349	chr19	-0.54
SLC6A16	407	chr19:54520642-54520744	pro	54520642	54520744	chr19	-0.76
SLC6A16	1336	chr19:54521443-54521801	pro	54521443	54521801	chr19	-0.41
DKKL1	413	chr19:54558191-54558579	pro	54558191	54558579	chr19	-0.43
DKKL1	121	chr19:54558922-54559024	pro	54558922	54559024	chr19	-0.54
LOC101928295	568	chr19:54582448-54582716	pro	54582448	54582716	chr19	-0.50
CCDC155	574	chr19:54583714-54584006	pro	54583714	54584006	chr19	-0.83
PTH2	1916	chr19:54616375-54616814	pro	54616375	54616814	chr19	-0.92
GFY	298	chr19:54621007-54621393	pro	54621007	54621393	chr19	-0.75
SLC17A7	1065	chr19:54637623-54637747	pro	54637623	54637747	chr19	-0.40
PIH1D1	519	chr19:54647110-54647784	pro	54647110	54647784	chr19	-0.62
PRR12	1900	chr19:54784702-54784943	pro	54784702	54784943	chr19	-0.52
PRMT1	2056	chr19:54870008-54870320	pro	54870008	54870320	chr19	-0.82
PNKP	1961	chr19:55060608-55060738	pro	55060608	55060738	chr19	-0.58
PNKP	1536	chr19:55061024-55061173	pro	55061024	55061173	chr19	-0.38
PNKP	1628	chr19:55064013-55064511	pro	55064013	55064511	chr19	-0.48
IL4I1	545	chr19:55091862-55093148	pro	55091862	55093148	chr19	-0.43
ATF5	1054	chr19:55126230-55126423	pro	55126230	55126423	chr19	-0.54
ZNF473	978	chr19:55221920-55222080	pro	55221920	55222080	chr19	-0.51
KCNC3	2048	chr19:55521675-55523122	pro	55521675	55523122	chr19	-0.54

NAPSB	1672	chr19:55537731-55538560	pro	55537731	55538560	chr19	-0.49
NAPSB	857	chr19:55538879-55539043	pro	55538879	55539043	chr19	-0.45
NAPSA	69	chr19:55560378-55561248	pro	55560378	55561248	chr19	-0.94
NAPSA	2062	chr19:55562693-55562920	pro	55562693	55562920	chr19	-0.95
NR1H2	992	chr19:55572234-55572729	pro	55572234	55572729	chr19	-0.61
SPIB	1607	chr19:55612286-55612512	pro	55612286	55612512	chr19	-0.34
MYBPC2	1718	chr19:55629372-55630003	pro	55629372	55630003	chr19	-0.80
FAM71E1	812	chr19:55672484-55672771	pro	55672484	55672771	chr19	-0.28
MGC45922	104	chr19:56012772-56012932	pro	56012772	56012932	chr19	-0.50
MGC45922	1090	chr19:56013633-56014044	pro	56013633	56014044	chr19	-0.67
MGC45922	1552	chr19:56014232-56014367	pro	56014232	56014367	chr19	-0.88
SIGLEC9	1207	chr19:56318533-56318949	pro	56318533	56318949	chr19	-0.84
RPL36	264	chr19:5640955-5641057	pro	5640955	5641057	chr19	-0.45
SIGLEC10	106	chr19:56612765-56613187	pro	56612765	56613187	chr19	-0.57
LONP1	2069	chr19:5668993-5669221	pro	5668993	5669221	chr19	-0.44
ZNF175	374	chr19:56765769-56766166	pro	56765769	56766166	chr19	-0.41
ZNF613	952	chr19:57123392-57123508	pro	57123392	57123508	chr19	-0.61
ZNF616	404	chr19:57335239-57335576	pro	57335239	57335576	chr19	-0.27
ZNF808	801	chr19:57723432-57723610	pro	57723432	57723610	chr19	-0.47
ZNF701	180	chr19:57765768-57766047	pro	57765768	57766047	chr19	-0.54
ZNF331	777	chr19:58716595-58716935	pro	58716595	58716935	chr19	-0.95
LOC100128568	1364	chr19:5930578-5930974	pro	5930578	5930974	chr19	-0.46
LENG8	1698	chr19:59650253-59650651	pro	59650253	59650651	chr19	-0.46
KIR3DX1	74	chr19:59735219-59736073	pro	59735219	59736073	chr19	-0.98
LILRA2	318	chr19:59776034-59777150	pro	59776034	59777150	chr19	-0.99
LILRB4	1642	chr19:59864145-59864735	pro	59864145	59864735	chr19	-0.97
RDH13	244	chr19:60266565-60266720	pro	60266565	60266720	chr19	-0.58
PPP1R12C	920	chr19:60321433-60321967	pro	60321433	60321967	chr19	-0.55
DNAAF3	374	chr19:60370090-60370463	pro	60370090	60370463	chr19	-0.96
PPP6R1	1325	chr19:60463082-60463268	pro	60463082	60463268	chr19	-0.30
PPP6R1	1937	chr19:60463597-60463977	pro	60463597	60463977	chr19	-0.83
HSPBP1	1460	chr19:60481420-60481736	pro	60481420	60481736	chr19	-0.28
HSPBP1	714	chr19:60483735-60484822	pro	60483735	60484822	chr19	-0.40
BRSK1	667	chr19:60486270-60487084	pro	60486270	60487084	chr19	-0.86
ZNF628	1531	chr19:60680955-60681127	pro	60680955	60681127	chr19	-0.34
FIZ1	716	chr19:60801743-60802238	pro	60801743	60802238	chr19	-0.74
ZNF784	564	chr19:60827080-60827300	pro	60827080	60827300	chr19	-0.58
EPN1	2499	chr19:60881572-60883030	pro	60881572	60883030	chr19	-0.35
NLRP11	1736	chr19:61032845-61034226	pro	61032845	61034226	chr19	-0.97
NLRP11	234	chr19:61034776-61036237	pro	61034776	61036237	chr19	-0.99
KHSRP	1024	chr19:6376602-6377089	pro	6376602	6377089	chr19	-0.34
C3	784	chr19:6672276-6672616	pro	6672276	6672616	chr19	-0.53
ZNF557	412	chr19:7019925-7020192	pro	7019925	7020192	chr19	-0.35
INSR	1029	chr19:7243532-7244434	pro	7243532	7244434	chr19	-0.99
INSR	1088	chr19:7245615-7246585	pro	7245615	7246585	chr19	-0.99
MCEMP1	309	chr19:7647389-7647877	pro	7647389	7647877	chr19	-0.84
FCER2	56	chr19:7672794-7673381	pro	7672794	7673381	chr19	-0.80
EVI5L	976	chr19:7799972-7800395	pro	7799972	7800395	chr19	-0.42
TIMM44	1020	chr19:7915663-7915793	pro	7915663	7915793	chr19	-0.59
CCL25	1741	chr19:8021804-8022002	pro	8021804	8022002	chr19	-0.73
CCL25	452	chr19:8022985-8023398	pro	8022985	8023398	chr19	-0.78
MIR4999	42	chr19:8360118-8360494	pro	8360118	8360494	chr19	-0.57
ZNF559	46	chr19:9295081-9295718	pro	9295081	9295718	chr19	-0.49
ZNF559-ZNF177	154	chr19:9296286-9296763	pro	9296286	9296763	chr19	-0.46
FBXL12	1204	chr19:9789414-9789643	pro	9789414	9789643	chr19	-0.60

PIN1	668	chr19:9805940-9806489	pro	9805940	9806489	chr19	-0.85
PDCL3	1068	chr2:100544278-10054528	pro	100544278	100545282	chr2	-0.50
KLF11	382	chr2:10101965-10102442	pro	10101965	10102442	chr2	-0.98
CYS1	800	chr2:10138449-10139131	pro	10138449	10139131	chr2	-0.43
RRM2	2102	chr2:10181871-10182956	pro	10181871	10182956	chr2	-0.58
HPCAL1	2246	chr2:10384640-10386343	pro	10384640	10386343	chr2	-0.94
HPCAL1	726	chr2:10386959-10389970	pro	10386959	10389970	chr2	-0.45
LINC01158	712	chr2:104834553-10483560	pro	104834553	104835604	chr2	-0.81
LINC01158	1684	chr2:104835788-10483631	pro	104835788	104836313	chr2	-0.82
LOC102724691	994	chr2:105022318-10502244	pro	105022318	105022442	chr2	-0.63
SNORA80B	1560	chr2:10502536-10503196	pro	10502536	10503196	chr2	-0.72
SNORA80B	834	chr2:10503402-10503781	pro	10503402	10503781	chr2	-0.27
NCK2	1089	chr2:105726254-10572746	pro	105726254	105727468	chr2	-0.26
NCK2	2056	chr2:105832329-10583282	pro	105832329	105832826	chr2	-0.86
NOL10	1161	chr2:10748631-10748819	pro	10748631	10748819	chr2	-0.70
LIMS1	1019	chr2:108516114-10851633	pro	108516114	108516332	chr2	-0.45
LIMS1	59	chr2:108571186-10857163	pro	108571186	108571636	chr2	-0.63
PDIA6	164	chr2:10889835-10889962	pro	10889835	10889962	chr2	-0.38
BUB1	1875	chr2:111148828-111151734	pro	111148828	111151734	chr2	-0.34
ANAPC1	754	chr2:112358896-11235903	pro	112358896	112359035	chr2	-0.35
CKAP2L	2179	chr2:113236292-11323680	pro	113236292	113236802	chr2	-0.80
SLC35F5	906	chr2:114231558-11423199	pro	114231558	114231994	chr2	-0.29
E2F6	1407	chr2:11522291-11522403	pro	11522291	11522403	chr2	-0.55
PTPN4	2154	chr2:120234485-12023717	pro	120234485	120237174	chr2	-0.47
TMEM185B	1958	chr2:120694922-12069606	pro	120694922	120696069	chr2	-0.38
TFCP2L1	1696	chr2:121756577-12175852	pro	121756577	121758526	chr2	-0.89
TFCP2L1	2161	chr2:121761171-12176164	pro	121761171	121761647	chr2	-0.52
RNU4ATAC	2358	chr2:122006924-12200764	pro	122006924	122007640	chr2	-0.55
GYPC	58	chr2:127129717-12713012	pro	127129717	127130126	chr2	-0.90
GYPC	455	chr2:127130360-12713051	pro	127130360	127130510	chr2	-0.63
GYPC	2236	chr2:127130627-12713380	pro	127130627	127133804	chr2	-0.94
SFT2D3	1931	chr2:128176269-12817772	pro	128176269	128177725	chr2	-0.36
WDR33	1948	chr2:128283104-12828346	pro	128283104	128283463	chr2	-0.37
POLR2D	2366	chr2:128329409-12833026	pro	128329409	128330260	chr2	-0.44
AMMECR1L	1408	chr2:128361129-12836165	pro	128361129	128361656	chr2	-0.61
HS6ST1	1560	chr2:128790583-12879158	pro	128790583	128791580	chr2	-0.25
ZRANB3	1454	chr2:136002581-13600405	pro	136002581	136004050	chr2	-0.44
DARS	1711	chr2:136461283-13646158	pro	136461283	136461587	chr2	-0.66
KYNU	744	chr2:143352325-14335249	pro	143352325	143352490	chr2	-0.37
GTDC1	756	chr2:144711897-14471236	pro	144711897	144712367	chr2	-0.45
GTDC1	3558	chr2:144713290-14471657	pro	144713290	144716578	chr2	-0.42
TEX41	2064	chr2:145143592-14514453	pro	145143592	145144539	chr2	-0.47
RIF1	1804	chr2:151976454-15197685	pro	151976454	151976850	chr2	-0.77
DDX1	1785	chr2:15650660-15651298	pro	15650660	15651298	chr2	-0.62
PKP4	1770	chr2:159022893-15902408	pro	159022893	159024087	chr2	-0.34
BAZ2B	928	chr2:160275715-16027681	pro	160275715	160276813	chr2	-0.41
MIR4785	1851	chr2:160969834-16097174	pro	160969834	160971744	chr2	-0.65
IFIH1	976	chr2:162883509-16288537	pro	162883509	162885370	chr2	-0.27
SCN3A	1859	chr2:165766113-16576781	pro	165766113	165767817	chr2	-0.99
SCN3A	436	chr2:165767967-16576880	pro	165767967	165768809	chr2	-0.98
SCN3A	203	chr2:165768935-16576911	pro	165768935	165769119	chr2	-0.91
SCN2A	98	chr2:165858388-16585858	pro	165858388	165858587	chr2	-0.68
TTC21B	1790	chr2:166516750-16651685	pro	166516750	166516858	chr2	-0.53
DHRS9	56	chr2:169636925-16963762	pro	169636925	169637623	chr2	-0.83
SSB	1678	chr2:170365335-17036558	pro	170365335	170365586	chr2	-0.31

METTL5	1510	chr2:170388046-17038831	pro	170388046	170388310	chr2	-0.52
LOC101929753	698	chr2:170916033-17091676	pro	170916033	170916764	chr2	-0.88
ZAK	412	chr2:173648203-17364859	pro	173648203	173648594	chr2	-0.41
CDCA7	2304	chr2:173925185-17392582	pro	173925185	173925820	chr2	-0.88
RAD51AP2	719	chr2:17561723-17563215	pro	17561723	17563215	chr2	-0.41
RAD51AP2	438	chr2:17563392-17563861	pro	17563392	17563861	chr2	-0.41
SMC6	1476	chr2:17796211-17797994	pro	17796211	17797994	chr2	-0.34
MIR1258	3243	chr2:180427479-18043379	pro	180427479	180433795	chr2	-0.98
ZNF385B	1474	chr2:180434545-18043736	pro	180434545	180437360	chr2	-0.94
MIR4437	247	chr2:181877098-18188064	pro	181877098	181880644	chr2	-0.42
FRZB	1638	chr2:183441029-18344173	pro	183441029	183441734	chr2	-0.65
WDR75	1468	chr2:190015756-19001598	pro	190015756	190015985	chr2	-0.30
WDR75	1842	chr2:190016155-19001633	pro	190016155	190016333	chr2	-0.45
ASNSD1	434	chr2:190233737-19023413	pro	190233737	190234130	chr2	-0.80
TMEM194B	956	chr2:191107970-19110937	pro	191107970	191109370	chr2	-0.28
NABP1	1980	chr2:192248540-19224958	pro	192248540	192249584	chr2	-0.45
NABP1	2496	chr2:192252625-19225458	pro	192252625	192254580	chr2	-0.28
SLC39A10	2125	chr2:196231050-19623339	pro	196231050	196233392	chr2	-0.38
HSPD1	2552	chr2:198068688-19807198	pro	198068688	198071981	chr2	-0.35
HSPD1	2114	chr2:198074758-19807595	pro	198074758	198075959	chr2	-0.51
LOC101927619	2	chr2:198947751-19894837	pro	198947751	198948377	chr2	-0.70
SATB2	2390	chr2:200032326-20003458	pro	200032326	200034582	chr2	-0.37
C2orf47	1425	chr2:200526649-20052706	pro	200526649	200527069	chr2	-0.55
TYW5	1735	chr2:200530386-20053049	pro	200530386	200530492	chr2	-0.68
AOX1	1458	chr2:201157344-20115768	pro	201157344	201157689	chr2	-0.48
BZW1	1887	chr2:201387070-20138730	pro	201387070	201387304	chr2	-0.62
PPIL3	1526	chr2:201460378-20146075	pro	201460378	201460759	chr2	-0.76
NIF3L1	1230	chr2:201463244-20146392	pro	201463244	201463921	chr2	-0.61
CFLAR-AS1	460	chr2:201730748-20173169	pro	201730748	201731692	chr2	-0.55
TMEM237	958	chr2:202214347-20221556	pro	202214347	202215560	chr2	-0.25
ALS2	1462	chr2:202352618-20235273	pro	202352618	202352738	chr2	-0.71
SUMO1	1718	chr2:202809699-20281000	pro	202809699	202810001	chr2	-0.32
CARF	2026	chr2:203483053-20348326	pro	203483053	203483263	chr2	-0.60
NBEAL1	1052	chr2:203588764-20358903	pro	203588764	203589031	chr2	-0.33
CYP20A1	530	chr2:203810555-20381120	pro	203810555	203811201	chr2	-0.31
CYP20A1	1980	chr2:203813004-20381377	pro	203813004	203813772	chr2	-0.27
ABI2	2167	chr2:203902906-20390384	pro	203902906	203903840	chr2	-0.86
RAPH1	1476	chr2:204105837-20410782	pro	204105837	204107820	chr2	-0.40
CD28	112	chr2:204279210-20427945	pro	204279210	204279450	chr2	-0.88
CD28	360	chr2:204279627-20427997	pro	204279627	204279977	chr2	-0.97
CD28	1544	chr2:204280114-20428185	pro	204280114	204281859	chr2	-0.99
NDUFS1	1379	chr2:206730642-20673092	pro	206730642	206730928	chr2	-0.29
ZDBF2	1696	chr2:206848308-20685107	pro	206848308	206851076	chr2	-0.40
CREB1	1376	chr2:208101361-20810160	pro	208101361	208101606	chr2	-0.53
METTL21A	1546	chr2:208196196-20819659	pro	208196196	208196596	chr2	-0.47
CCNYL1	1852	chr2:208286181-20828654	pro	208286181	208286540	chr2	-0.61
ATIC	1532	chr2:215885970-21588693	pro	215885970	215886938	chr2	-0.50
MREG	977	chr2:216585047-21658618	pro	216585047	216586183	chr2	-0.31
MREG	351	chr2:216586671-21658721	pro	216586671	216587215	chr2	-0.27
TMEM169	772	chr2:216654956-21665625	pro	216654956	216656251	chr2	-0.54
TMBIM1	1494	chr2:218862669-21886539	pro	218862669	218865390	chr2	-0.78
TMBIM1	368	chr2:218865604-21886618	pro	218865604	218866180	chr2	-0.64
PNKD	1955	chr2:218893884-21889449	pro	218893884	218894494	chr2	-0.63
ANKZF1	1266	chr2:219803928-21980430	pro	219803928	219804307	chr2	-0.25
STK16	3202	chr2:219819871-21982342	pro	219819871	219823421	chr2	-0.29

DNPEP	1010	chr2:219961614-21996221	pro	219961614	219962218	chr2	-0.26
CHPF	1539	chr2:220114426-22011462	pro	220114426	220114624	chr2	-0.49
EPHA4	1657	chr2:222146732-22214709	pro	222146732	222147090	chr2	-0.73
ACSL3	667	chr2:223432907-22343370	pro	223432907	223433707	chr2	-0.31
ACSL3	1617	chr2:223434636-22343654	pro	223434636	223436546	chr2	-0.28
WDFY1	1319	chr2:224516466-22451748	pro	224516466	224517488	chr2	-0.35
SERPINE2	246	chr2:224611197-22461151	pro	224611197	224611515	chr2	-0.34
CUL3	909	chr2:225143244-22514414	pro	225143244	225144146	chr2	-0.56
CUL3	1744	chr2:225144351-22514470	pro	225144351	225144708	chr2	-0.33
DOCK10	777	chr2:225516999-22552149	pro	225516999	225521499	chr2	-0.41
MIR4439	1926	chr2:225581164-22558198	pro	225581164	225581989	chr2	-0.90
RHBDD1	1913	chr2:227406211-22740779	pro	227406211	227407791	chr2	-0.86
PSMD1	482	chr2:231629213-23162946	pro	231629213	231629464	chr2	-0.71
MIR4777	166	chr2:231935419-23193557	pro	231935419	231935573	chr2	-0.29
MIR1244-1	341	chr2:232286496-23228671	pro	232286496	232286718	chr2	-0.50
DGKD	1854	chr2:233928490-23393099	pro	233928490	233930998	chr2	-0.51
DGKD	2650	chr2:233957960-23395981	pro	233957960	233959817	chr2	-0.73
ARL4C	2752	chr2:235065419-23506994	pro	235065419	235069941	chr2	-0.43
COPS8	1772	chr2:237660496-23766069	pro	237660496	237660691	chr2	-0.79
KLHL30	316	chr2:238712285-23871254	pro	238712285	238712547	chr2	-0.85
DUSP28	414	chr2:241147108-24114834	pro	241147108	241148348	chr2	-0.29
RAB10	1338	chr2:26108600-26109188	pro	26108600	26109188	chr2	-0.72
HADHA	2222	chr2:26318530-26319223	pro	26318530	26319223	chr2	-0.51
CENPA	1898	chr2:26863981-26864588	pro	26863981	26864588	chr2	-0.81
TMEM214	651	chr2:27108496-27108754	pro	27108496	27108754	chr2	-0.68
EMILIN1	1061	chr2:27153797-27153957	pro	27153797	27153957	chr2	-0.70
ATRAID	2076	chr2:27285916-27286737	pro	27285916	27286737	chr2	-0.80
SLC30A3	1676	chr2:27337080-27338496	pro	27337080	27338496	chr2	-0.87
TRIM54	2159	chr2:27356469-27356813	pro	27356469	27356813	chr2	-0.85
GTF3C2	1140	chr2:27434172-27434921	pro	27434172	27434921	chr2	-0.52
GPN1	434	chr2:27704281-27704886	pro	27704281	27704886	chr2	-0.34
SUPT7L	1394	chr2:27741429-27741782	pro	27741429	27741782	chr2	-0.68
TRMT61B	1874	chr2:28944494-28945118	pro	28944494	28945118	chr2	-0.36
YPEL5	2662	chr2:30224368-30227459	pro	30224368	30227459	chr2	-0.66
LCLAT1	429	chr2:30522890-30523504	pro	30522890	30523504	chr2	-0.50
GALNT14	1856	chr2:31213182-31213299	pro	31213182	31213299	chr2	-0.88
GALNT14	1474	chr2:31213418-31213826	pro	31213418	31213826	chr2	-0.77
CAPN14	1980	chr2:31295167-31296626	pro	31295167	31296626	chr2	-0.63
XDH	1893	chr2:31492812-31493206	pro	31492812	31493206	chr2	-0.72
SLC30A6	911	chr2:32243142-32243860	pro	32243142	32243860	chr2	-0.42
RNASEH1-AS1	1992	chr2:3585717-3585968	pro	3585717	3585968	chr2	-0.92
LOC100288911	2434	chr2:36433280-36434289	pro	36433280	36434289	chr2	-0.98
CRIM1	2035	chr2:36437680-36440134	pro	36437680	36440134	chr2	-0.99
HEATR5B	1758	chr2:37163156-37163307	pro	37163156	37163307	chr2	-0.70
CEBPZOS	2007	chr2:37278764-37279526	pro	37278764	37279526	chr2	-0.36
PRKD3	3268	chr2:37392413-37396503	pro	37392413	37396503	chr2	-0.59
PRKD3	1146	chr2:37396677-37401066	pro	37396677	37401066	chr2	-0.54
QPCT	786	chr2:37424305-37424634	pro	37424305	37424634	chr2	-0.63
QPCT	1630	chr2:37426526-37427245	pro	37426526	37427245	chr2	-0.50
HNRNPLL	1527	chr2:38681576-38682734	pro	38681576	38682734	chr2	-0.74
THUMPD2	2095	chr2:39861872-39862158	pro	39861872	39862158	chr2	-0.43
SLC8A1-AS1	3186	chr2:40000053-40002872	pro	40000053	40002872	chr2	-1.00
MTA3	830	chr2:42646674-42649042	pro	42646674	42649042	chr2	-0.33
PLEKHH2	370	chr2:43717344-43717799	pro	43717344	43717799	chr2	-0.97
SRBD1	396	chr2:45692066-45692601	pro	45692066	45692601	chr2	-0.27

RHOQ	1882	chr2:46621396-46621580	pro	46621396	46621580	chr2	-0.83
LINC01249	2068	chr2:4679192-4680047	pro	4679192	4680047	chr2	-0.95
TTC7A	1814	chr2:46997526-46999643	pro	46997526	46999643	chr2	-0.32
MSH6	1886	chr2:47861470-47862207	pro	47861470	47862207	chr2	-0.73
MSH6	1117	chr2:47862438-47862776	pro	47862438	47862776	chr2	-0.31
MSH6	863	chr2:47865326-47865592	pro	47865326	47865592	chr2	-0.55
FOXN2	1050	chr2:48393656-48394840	pro	48393656	48394840	chr2	-0.32
EML6	1606	chr2:54805803-54808713	pro	54805803	54808713	chr2	-0.55
MIR4426	452	chr2:55315155-55315352	pro	55315155	55315352	chr2	-0.72
PNPT1	1146	chr2:55773188-55773620	pro	55773188	55773620	chr2	-0.39
VRK2	1206	chr2:58125588-58126561	pro	58125588	58126561	chr2	-0.64
LOC400940	72	chr2:6039225-6039751	pro	6039225	6039751	chr2	-0.93
SNORA70B	3366	chr2:61499000-61503765	pro	61499000	61503765	chr2	-0.47
VPS54	871	chr2:64098232-64099462	pro	64098232	64099462	chr2	-0.26
PELI1	2886	chr2:64220199-64224249	pro	64220199	64224249	chr2	-0.29
PELI1	862	chr2:64225255-64226689	pro	64225255	64226689	chr2	-0.41
LOC100507006	210	chr2:64308404-64310093	pro	64308404	64310093	chr2	-0.28
LOC400958	1394	chr2:65009331-65014053	pro	65009331	65014053	chr2	-0.27
LOC400958	1976	chr2:65014439-65015684	pro	65014439	65015684	chr2	-0.77
SLC1A4	924	chr2:65067692-65068625	pro	65067692	65068625	chr2	-0.26
MEIS1	246	chr2:66514457-66518103	pro	66514457	66518103	chr2	-0.99
ETAA1	1636	chr2:67479352-67479807	pro	67479352	67479807	chr2	-0.67
LOC101927701	166	chr2:67906287-67906441	pro	67906287	67906441	chr2	-0.73
APLF	1110	chr2:68548536-68550073	pro	68548536	68550073	chr2	-0.48
LOC100133985	684	chr2:70206458-70206814	pro	70206458	70206814	chr2	-0.57
LOC100133985	1318	chr2:70207086-70207453	pro	70207086	70207453	chr2	-0.73
LOC100133985	2564	chr2:70207919-70209112	pro	70207919	70209112	chr2	-0.80
C2orf42	426	chr2:70271777-70272386	pro	70271777	70272386	chr2	-0.35
SNRPG	2211	chr2:70371755-70372571	pro	70371755	70372571	chr2	-0.35
ATP6V1B1-AS1	988	chr2:71027262-71029262	pro	71027262	71029262	chr2	-0.70
MCEE	2030	chr2:71208792-71208952	pro	71208792	71208952	chr2	-0.69
MPHOSPH10	1981	chr2:71212786-71213076	pro	71212786	71213076	chr2	-0.49
PAIP2B	894	chr2:71305985-71307711	pro	71305985	71307711	chr2	-0.99
PAIP2B	558	chr2:71308153-71308448	pro	71308153	71308448	chr2	-0.97
DUSP11	312	chr2:73860893-73861315	pro	73860893	73861315	chr2	-0.60
DGUOK	1781	chr2:74009137-74009345	pro	74009137	74009345	chr2	-0.60
DGUOK-AS1	1962	chr2:74059898-74060325	pro	74059898	74060325	chr2	-0.84
TET3	825	chr2:74066265-74069461	pro	74066265	74069461	chr2	-0.33
MOB1A	1932	chr2:74257407-74257738	pro	74257407	74257738	chr2	-0.51
MOB1A	1860	chr2:74261182-74261546	pro	74261182	74261546	chr2	-0.79
DCTN1	200	chr2:74472795-74473048	pro	74472795	74473048	chr2	-0.36
C2orf81	1856	chr2:74499954-74500463	pro	74499954	74500463	chr2	-0.98
WDR54	1380	chr2:74500574-74501450	pro	74500574	74501450	chr2	-0.95
WDR54	1174	chr2:74503489-74503642	pro	74503489	74503642	chr2	-0.89
INO80B-WBP1	2249	chr2:74533048-74533766	pro	74533048	74533766	chr2	-0.85
HK2	520	chr2:74913706-74913909	pro	74913706	74913909	chr2	-0.62
LOC101929551	71	chr2:7956712-7957622	pro	7956712	7957622	chr2	-0.49
CAPG	1772	chr2:85489466-85489655	pro	85489466	85489655	chr2	-0.59
CAPG	634	chr2:85490416-85490980	pro	85490416	85490980	chr2	-0.65
POLR1A	1976	chr2:86184661-86184967	pro	86184661	86184967	chr2	-0.65
IMMT	1038	chr2:86277327-86277557	pro	86277327	86277557	chr2	-0.76
MRPL35	1773	chr2:86281580-86282098	pro	86281580	86282098	chr2	-0.63
MRPS5	1495	chr2:95149612-95150362	pro	95149612	95150362	chr2	-0.38
FAHD2A	971	chr2:95432992-95433298	pro	95432992	95433298	chr2	-0.49
CNNM4	2018	chr2:96790563-96794202	pro	96790563	96794202	chr2	-0.31

ZAP70	192	chr2:97696224-97696317	pro	97696224	97696317	chr2	-0.67
UNC50	1742	chr2:98593142-98593287	pro	98593142	98593287	chr2	-0.63
SPTLC3	788	chr20:12938110-12938718	pro	12938110	12938718	chr20	-0.46
SNRPB2	319	chr20:16658022-16658556	pro	16658022	16658556	chr20	-0.46
DSTN	1746	chr20:17499286-17501402	pro	17499286	17501402	chr20	-0.48
POLR3F	1163	chr20:18397124-18397266	pro	18397124	18397266	chr20	-0.42
CRNKL1	1328	chr20:19979707-19979909	pro	19979707	19979909	chr20	-0.72
STK35	626	chr20:2029421-2030379	pro	2029421	2030379	chr20	-0.31
C20orf96	60	chr20:218308-220412	pro	218308	220412	chr20	-0.30
SNRPB	1668	chr20:2397518-2398145	pro	2397518	2398145	chr20	-0.44
ZNF343	717	chr20:2438410-2438580	pro	2438410	2438580	chr20	-0.39
ZNF343	114	chr20:2452955-2453154	pro	2452955	2453154	chr20	-0.27
ZNF337	676	chr20:25626117-25626314	pro	25626117	25626314	chr20	-0.68
REM1	820	chr20:29525310-29526550	pro	29525310	29526550	chr20	-0.88
BCL2L1	1350	chr20:29775531-29775806	pro	29775531	29775806	chr20	-0.57
TM9SF4	224	chr20:30160669-30160818	pro	30160669	30160818	chr20	-0.51
KIF3B	816	chr20:30329495-30330364	pro	30329495	30330364	chr20	-0.27
C20orf203	924	chr20:30704267-30704470	pro	30704267	30704470	chr20	-0.87
COMMD7	1214	chr20:30796566-30796815	pro	30796566	30796815	chr20	-0.78
DNMT3B	696	chr20:30812672-30813637	pro	30812672	30813637	chr20	-0.27
TRIB3	568	chr20:308341-309066	pro	308341	309066	chr20	-0.64
FASTKD5	2374	chr20:3085773-3086544	pro	3085773	3086544	chr20	-0.42
TRIB3	1249	chr20:310753-311717	pro	310753	311717	chr20	-0.26
SNTA1	1892	chr20:31492231-31494705	pro	31492231	31494705	chr20	-0.85
SNTA1	2460	chr20:31497323-31498317	pro	31497323	31498317	chr20	-0.92
E2F1	1802	chr20:31735277-31736864	pro	31735277	31736864	chr20	-0.39
ZNF341	2282	chr20:31785074-31785943	pro	31785074	31785943	chr20	-0.74
RALY	2030	chr20:32043009-32043168	pro	32043009	32043168	chr20	-0.69
PIGU	768	chr20:32729370-32729665	pro	32729370	32729665	chr20	-0.54
C20orf194	480	chr20:3335714-3335947	pro	3335714	3335947	chr20	-0.67
CEP250	1042	chr20:33507442-33507914	pro	33507442	33507914	chr20	-0.48
FER1L4	412	chr20:33658141-33658832	pro	33658141	33658832	chr20	-0.89
RBM39	1882	chr20:33795353-33795755	pro	33795353	33795755	chr20	-0.30
PHF20	294	chr20:33822890-33823193	pro	33822890	33823193	chr20	-0.31
C20orf24	1122	chr20:34666372-34666483	pro	34666372	34666483	chr20	-0.69
C20orf24	1911	chr20:34669406-34669516	pro	34669406	34669516	chr20	-0.54
SLA2	1732	chr20:34706065-34706538	pro	34706065	34706538	chr20	-0.96
SLA2	291	chr20:34707450-34708036	pro	34707450	34708036	chr20	-0.97
NDRG3	1434	chr20:34806376-34806669	pro	34806376	34806669	chr20	-0.69
MROH8	1745	chr20:35243093-35243209	pro	35243093	35243209	chr20	-0.29
MANBAL	724	chr20:35350566-35350914	pro	35350566	35350914	chr20	-0.69
MANBAL	1542	chr20:35352592-35353419	pro	35352592	35353419	chr20	-0.79
SNORA71D	1760	chr20:36494177-36494414	pro	36494177	36494414	chr20	-0.32
SNHG11	219	chr20:36508406-36508576	pro	36508406	36508576	chr20	-0.38
AP5S1	1878	chr20:3747232-3747352	pro	3747232	3747352	chr20	-0.73
TBC1D20	1640	chr20:389126-389990	pro	389126	389990	chr20	-0.62
L3MBTL1	1810	chr20:41578103-41578493	pro	41578103	41578493	chr20	-0.58
MYBL2	1860	chr20:41726997-41727428	pro	41726997	41727428	chr20	-0.91
MYBL2	1684	chr20:41730482-41731031	pro	41730482	41731031	chr20	-0.32
GTSF1L	1354	chr20:41790033-41790786	pro	41790033	41790786	chr20	-0.87
FITM2	258	chr20:42373436-42373688	pro	42373436	42373688	chr20	-0.47
PKIG	634	chr20:42593089-42593311	pro	42593089	42593311	chr20	-0.57
PKIG	988	chr20:42643122-42644106	pro	42643122	42644106	chr20	-0.35
ADA	1480	chr20:42712106-42712515	pro	42712106	42712515	chr20	-0.85
PABPC1L	1728	chr20:42973692-42973995	pro	42973692	42973995	chr20	-0.29

PIGT	1908	chr20:43479961-43480094	pro	43479961	43480094	chr20	-0.64
UBE2C	1460	chr20:43876417-43876658	pro	43876417	43876658	chr20	-0.72
SLC12A5	600	chr20:44082631-44083636	pro	44082631	44083636	chr20	-0.67
TP53RK	568	chr20:44751867-44752637	pro	44751867	44752637	chr20	-0.35
LINC00494	132	chr20:46421864-46421993	pro	46421864	46421993	chr20	-0.79
LINC00494	675	chr20:46422364-46423106	pro	46422364	46423106	chr20	-0.76
PREX1	3988	chr20:46871090-46876591	pro	46871090	46876591	chr20	-0.98
PREX1	974	chr20:46878471-46879134	pro	46878471	46879134	chr20	-0.97
ARFGEF2	1110	chr20:46970249-46970892	pro	46970249	46970892	chr20	-0.75
CSNK2A1	1667	chr20:470548-471082	pro	470548	471082	chr20	-0.59
CSE1L	2016	chr20:47097645-47098763	pro	47097645	47098763	chr20	-0.26
SNORD12	243	chr20:47329540-47332198	pro	47329540	47332198	chr20	-0.31
SNORD12	2751	chr20:47332373-47334381	pro	47332373	47334381	chr20	-0.53
B4GALT5	620	chr20:47764025-47764870	pro	47764025	47764870	chr20	-0.27
SPATA2	1160	chr20:47966316-47966980	pro	47966316	47966980	chr20	-0.82
TRERNA1	568	chr20:48090276-48091736	pro	48090276	48091736	chr20	-0.31
PTPN1	1983	chr20:48562153-48562341	pro	48562153	48562341	chr20	-0.78
NFATC2	1336	chr20:49590276-49592384	pro	49590276	49592384	chr20	-0.48
NFATC2	508	chr20:49592808-49593539	pro	49592808	49593539	chr20	-0.36
PCNA	888	chr20:5054300-5054460	pro	5054300	5054460	chr20	-0.58
PFDN4	294	chr20:52257517-52257711	pro	52257517	52257711	chr20	-0.41
RTFDC1	2243	chr20:54474410-54475196	pro	54474410	54475196	chr20	-0.70
ZBP1	2330	chr20:55626286-55627129	pro	55626286	55627129	chr20	-0.96
ZBP1	1216	chr20:55627244-55628401	pro	55627244	55628401	chr20	-0.66
ZBP1	384	chr20:55628513-55628796	pro	55628513	55628796	chr20	-0.66
ZBP1	206	chr20:55629039-55629450	pro	55629039	55629450	chr20	-0.57
ZBP1	836	chr20:55629558-55630189	pro	55629558	55630189	chr20	-0.90
PMEPA1	217	chr20:55718704-55719882	pro	55718704	55719882	chr20	-0.99
SLMO2	2385	chr20:57047852-57049970	pro	57047852	57049970	chr20	-0.36
TRMT6	1634	chr20:5877520-5877621	pro	5877520	5877621	chr20	-0.67
CDH4	1207	chr20:59508847-59509307	pro	59508847	59509307	chr20	-0.98
TAF4	1478	chr20:60074989-60076492	pro	60074989	60076492	chr20	-0.29
LAMA5	1651	chr20:60373946-60374280	pro	60373946	60374280	chr20	-0.74
LAMA5	1047	chr20:60374392-60375042	pro	60374392	60375042	chr20	-0.52
SLCO4A1	1732	chr20:60744988-60746957	pro	60744988	60746957	chr20	-0.41
LINC00659	126	chr20:60878318-60878737	pro	60878318	60878737	chr20	-0.73
PTK6	1170	chr20:61640243-61640434	pro	61640243	61640434	chr20	-0.62
SRMS	1564	chr20:61647416-61648059	pro	61647416	61648059	chr20	-0.85
C20orf195	97	chr20:61654300-61655138	pro	61654300	61655138	chr20	-0.90
C20orf195	1489	chr20:61656092-61656518	pro	61656092	61656518	chr20	-0.38
SAMD10	1182	chr20:62079899-62080616	pro	62079899	62080616	chr20	-0.26
FAM110A	540	chr20:763947-764392	pro	763947	764392	chr20	-0.86
FAM110A	27	chr20:764601-764765	pro	764601	764765	chr20	-0.85
FAM110A	286	chr20:772804-773125	pro	772804	773125	chr20	-0.69
FAM110A	2151	chr20:774218-776584	pro	774218	776584	chr20	-0.77
TMX4	1868	chr20:7946197-7946854	pro	7946197	7946854	chr20	-0.26
PLCB1	1364	chr20:8061566-8062981	pro	8061566	8062981	chr20	-0.99
HSPA13	1572	chr21:14674721-14676894	pro	14674721	14676894	chr21	-0.36
SAMSN1	632	chr21:14839355-14840486	pro	14839355	14840486	chr21	-0.66
LINC01549	700	chr21:17731972-17732785	pro	17731972	17732785	chr21	-0.98
MIR155HG	1036	chr21:25856620-25858103	pro	25856620	25858103	chr21	-0.42
MIR155	350	chr21:25867077-25868547	pro	25867077	25868547	chr21	-0.65
TIAM1	1322	chr21:31853827-31855142	pro	31853827	31855142	chr21	-0.49
SCAF4	1358	chr21:32026611-32028709	pro	32026611	32028709	chr21	-0.49
HUNK	734	chr21:32166675-32166852	pro	32166675	32166852	chr21	-0.39

URB1	1382	chr21:32685619-3268598	pro	32685619	32685986	chr21	-0.65
IL10RB	2333	chr21:33561949-3356378	pro	33561949	33563785	chr21	-0.37
IFNAR1	2320	chr21:33620655-3362214	pro	33620655	33622148	chr21	-0.66
GART	1504	chr21:33834343-3383531	pro	33834343	33835317	chr21	-0.55
CHAF1B	259	chr21:36679185-3667941	pro	36679185	36679413	chr21	-0.31
DSCR3	1798	chr21:37559863-3755995	pro	37559863	37559950	chr21	-0.66
LINC00114	1484	chr21:39060672-3906189	pro	39060672	39061895	chr21	-0.41
ETS2	1496	chr21:39100301-3910194	pro	39100301	39101940	chr21	-0.28
BRWD1-AS1	431	chr21:39609470-3961039	pro	39609470	39610396	chr21	-0.47
BRWD1-AS1	2214	chr21:39610882-3961255	pro	39610882	39612550	chr21	-0.48
MX1	23	chr21:41725490-4172615	pro	41725490	41726156	chr21	-0.81
RIPK4	1036	chr21:42060408-42062301	pro	42060408	42062301	chr21	-0.98
C2CD2	2270	chr21:42216807-4221838	pro	42216807	42218389	chr21	-0.74
UMODL1	2234	chr21:42358005-4235873	pro	42358005	42358735	chr21	-0.75
UMODL1-AS1	119	chr21:42401248-4240194	pro	42401248	42401942	chr21	-0.38
ABCG1	318	chr21:42491826-42493271	pro	42491826	42493271	chr21	-0.70
ABCG1	447	chr21:42511615-4251215	pro	42511615	42512159	chr21	-0.92
ABCG1	1076	chr21:42513092-4251521	pro	42513092	42515213	chr21	-0.51
PDXK	2056	chr21:43960768-4396192	pro	43960768	43961927	chr21	-0.73
AGPAT3	1574	chr21:44107734-4410820	pro	44107734	44108202	chr21	-0.78
PFKL	1948	chr21:44542262-44542531	pro	44542262	44542531	chr21	-0.59
ITGB2	1464	chr21:45171528-4517190	pro	45171528	45171909	chr21	-0.82
ITGB2	930	chr21:45172082-4517242	pro	45172082	45172422	chr21	-0.79
ITGB2	2397	chr21:45175064-4517609	pro	45175064	45176094	chr21	-0.66
HSFY1P1	2352	chr22:15685406-1568661	pro	15685406	15686615	chr22	-0.66
IL17RA	2282	chr22:15947050-15949211	pro	15947050	15949211	chr22	-0.59
CECR5	1560	chr22:16018278-1601894	pro	16018278	16018943	chr22	-0.57
CECR1	1696	chr22:16077742-1607981	pro	16077742	16079817	chr22	-0.87
CECR1	218	chr22:16079921-1608059	pro	16079921	16080595	chr22	-0.32
LINC00528	1732	chr22:16641698-1664187	pro	16641698	16641874	chr22	-0.67
MICAL3	934	chr22:16888009-1688851	pro	16888009	16888510	chr22	-0.83
PEX26	2094	chr22:16938274-1693890	pro	16938274	16938906	chr22	-0.93
PEX26	1342	chr22:16941970-16942231	pro	16941970	16942231	chr22	-0.45
MRPL40	962	chr22:17800727-1780126	pro	17800727	17801265	chr22	-0.44
CDC45	993	chr22:17847854-1784882	pro	17847854	17848828	chr22	-0.35
TXNRD2	1862	chr22:18311238-18311518	pro	18311238	18311518	chr22	-0.49
MIR185	762	chr22:18399712-1840008	pro	18399712	18400085	chr22	-0.61
KLHL22	932	chr22:19181040-1918116	pro	19181040	19181163	chr22	-0.31
TUBA3FP	304	chr22:19698038-1969850	pro	19698038	19698507	chr22	-0.32
YDJC	1748	chr22:20312410-2031277	pro	20312410	20312774	chr22	-0.56
YDJC	623	chr22:20314890-2031503	pro	20314890	20315036	chr22	-0.82
VPREB1	242	chr22:20928679-2092923	pro	20928679	20929232	chr22	-0.26
MIR650	2476	chr22:21492238-2149334	pro	21492238	21493345	chr22	-0.78
MIR650	282	chr22:21494896-2149507	pro	21494896	21495075	chr22	-0.59
MIR650	756	chr22:21495804-2149624	pro	21495804	21496243	chr22	-0.71
IGLL5	1287	chr22:21557445-2155989	pro	21557445	21559897	chr22	-0.38
GNAZ	1526	chr22:21743999-2174438	pro	21743999	21744389	chr22	-0.79
VPREB3	1102	chr22:22427313-22428151	pro	22427313	22428151	chr22	-0.60
CHCHD10	1612	chr22:22441469-2244207	pro	22441469	22442074	chr22	-0.30
SPECC1L	1920	chr22:22998597-2299881	pro	22998597	22998812	chr22	-0.35
ADRBK2	2076	chr22:24292706-2429316	pro	24292706	24293166	chr22	-0.28
HPS4	1869	chr22:25203397-25204161	pro	25203397	25204161	chr22	-0.81
CRYBB1	520	chr22:25343297-2534364	pro	25343297	25343648	chr22	-0.82
CHEK2	1280	chr22:27466292-2746679	pro	27466292	27466793	chr22	-0.77
XBP1	1852	chr22:27527663-27529161	pro	27527663	27529161	chr22	-0.53

ZNRF3	838	chr22:27608672-2760916	pro	27608672	27609160	chr22	-0.34
OSM	1098	chr22:28991648-2899181	pro	28991648	28991816	chr22	-0.40
PES1	1650	chr22:29316228-2931632	pro	29316228	29316328	chr22	-0.39
PES1	485	chr22:29318310-2931851	pro	29318310	29318516	chr22	-0.52
PES1	1399	chr22:29331534-2933166	pro	29331534	29331668	chr22	-0.55
PES1	1052	chr22:29331769-2933212	pro	29331769	29332126	chr22	-0.47
MORC2-AS1	1033	chr22:29646541-2964798	pro	29646541	29647981	chr22	-0.99
MORC2	65	chr22:29693502-2969474	pro	29693502	29694744	chr22	-0.34
SFI1	1270	chr22:30220600-3022110	pro	30220600	30221109	chr22	-0.58
APOL6	935	chr22:34373226-3437364	pro	34373226	34373640	chr22	-0.57
APOL6	1661	chr22:34375433-3437662	pro	34375433	34376625	chr22	-0.68
RBFOX2	388	chr22:34566895-3456703	pro	34566895	34567032	chr22	-0.57
EIF3D	1896	chr22:35253244-3525341	pro	35253244	35253411	chr22	-0.68
IFT27	760	chr22:35500984-3550174	pro	35500984	35501744	chr22	-0.26
NCF4	1788	chr22:35584699-3558567	pro	35584699	35585672	chr22	-0.94
NCF4	232	chr22:35586580-3558690	pro	35586580	35586903	chr22	-0.59
CSF2RB	2360	chr22:35641464-3564249	pro	35641464	35642496	chr22	-0.92
TST	604	chr22:35744785-3574488	pro	35744785	35744886	chr22	-0.78
TST	210	chr22:35746065-3574669	pro	35746065	35746694	chr22	-0.32
LGALS1	828	chr22:36401569-3640320	pro	36401569	36403204	chr22	-0.29
ANKRD54	1320	chr22:36568895-3656906	pro	36568895	36569066	chr22	-0.68
MIR658	689	chr22:36570947-3657107	pro	36570947	36571079	chr22	-0.49
PICK1	2084	chr22:36780945-3678129	pro	36780945	36781299	chr22	-0.95
PICK1	352	chr22:36782662-3678304	pro	36782662	36783046	chr22	-0.46
CSNK1E	2518	chr22:37039080-3704260	pro	37039080	37042603	chr22	-0.26
CSNK1E	1646	chr22:37122694-3712296	pro	37122694	37122963	chr22	-0.85
JOSD1	2255	chr22:37423637-3742466	pro	37423637	37424665	chr22	-0.56
CBX6	1196	chr22:37599319-3759948	pro	37599319	37599482	chr22	-0.90
CBX6	1666	chr22:37599822-3759991	pro	37599822	37599918	chr22	-0.69
APOBEC3C	59	chr22:37740132-3774040	pro	37740132	37740406	chr22	-0.31
APOBEC3C	462	chr22:37740585-3774075	pro	37740585	37740759	chr22	-0.66
APOBEC3D	457	chr22:37747434-3774760	pro	37747434	37747604	chr22	-0.32
APOBEC3D	930	chr22:37747726-3774825	pro	37747726	37748257	chr22	-0.90
APOBEC3H	759	chr22:37823801-3782406	pro	37823801	37824065	chr22	-0.96
CBX7	1535	chr22:37876892-3787700	pro	37876892	37877006	chr22	-0.27
GRAP2	1855	chr22:38624825-3862552	pro	38624825	38625525	chr22	-0.90
GRAP2	200	chr22:38626709-3862695	pro	38626709	38626950	chr22	-0.87
GRAP2	317	chr22:38672637-3867352	pro	38672637	38673529	chr22	-0.93
CENPM	814	chr22:40666604-4066736	pro	40666604	40667363	chr22	-0.60
CENPM	1397	chr22:40667464-4066767	pro	40667464	40667670	chr22	-0.51
CENPM	1086	chr22:40673731-4067462	pro	40673731	40674628	chr22	-0.93
LINC00634	2386	chr22:40675215-4067628	pro	40675215	40676285	chr22	-0.84
LINC00634	28	chr22:40678015-4067820	pro	40678015	40678201	chr22	-0.54
LINC00634	340	chr22:40678353-4067859	pro	40678353	40678598	chr22	-0.58
WBP2NL	626	chr22:40725214-4072538	pro	40725214	40725386	chr22	-0.48
NDUFA6	1457	chr22:40814883-4081587	pro	40814883	40815871	chr22	-0.57
SERHL2	799	chr22:41278878-4127914	pro	41278878	41279144	chr22	-0.64
A4GALT	1550	chr22:41444472-4144606	pro	41444472	41446069	chr22	-0.26
A4GALT	504	chr22:41447044-4144760	pro	41447044	41447605	chr22	-0.51
BIK	960	chr22:41835600-4183587	pro	41835600	41835871	chr22	-0.61
TSPO	494	chr22:41877781-4187897	pro	41877781	41878976	chr22	-0.40
MIR4762	2018	chr22:44533004-4453309	pro	44533004	44533091	chr22	-0.29
CDPF1	870	chr22:45025174-4502628	pro	45025174	45026282	chr22	-0.25
DENND6B	1330	chr22:49098209-4909915	pro	49098209	49099152	chr22	-0.81
DENND6B	162	chr22:49099286-4910040	pro	49099286	49100409	chr22	-0.71

EMC3	1433	chr3:10002034-10002144	pro	10002034	10002144	chr3	-0.66
EMC3-AS1	1060	chr3:10004253-10005018	pro	10004253	10005018	chr3	-0.32
DCBLD2	732	chr3:100103536-10010437	pro	100103536	100104375	chr3	-0.99
TRMT10C	1738	chr3:102765053-10276515	pro	102765053	102765159	chr3	-0.72
RPL24	832	chr3:102888770-10288940	pro	102888770	102889403	chr3	-0.40
CEP97	2138	chr3:102923641-10292444	pro	102923641	102924446	chr3	-0.56
NXPE3	1373	chr3:102979217-10297947	pro	102979217	102979473	chr3	-0.95
NXPE3	1282	chr3:102981208-10298330	pro	102981208	102983305	chr3	-0.43
NFKBIZ	1585	chr3:103027674-10302820	pro	103027674	103028200	chr3	-0.79
LOC152225	2442	chr3:103139455-10314044	pro	103139455	103140446	chr3	-0.74
LOC152225	1695	chr3:103143851-10314432	pro	103143851	103144323	chr3	-0.81
SEC13	1505	chr3:10336083-10336359	pro	10336083	10336359	chr3	-0.44
MIR885	1400	chr3:10411687-10413606	pro	10411687	10413606	chr3	-0.67
BBX	721	chr3:108723088-10872441	pro	108723088	108724414	chr3	-0.33
LINC01215	1786	chr3:109328642-10932964	pro	109328642	109329641	chr3	-0.35
DZIP3	1679	chr3:109788124-10979057	pro	109788124	109790570	chr3	-0.30
TMPRSS7	544	chr3:113240335-11324088	pro	113240335	113240886	chr3	-0.82
C3orf52	1096	chr3:113287268-11329066	pro	113287268	113290663	chr3	-0.36
MIR567	984	chr3:113313255-11331344	pro	113313255	113313448	chr3	-0.67
MIR567	786	chr3:113314693-11331555	pro	113314693	113315552	chr3	-0.73
MIR567	1494	chr3:113315698-11331596	pro	113315698	113315962	chr3	-0.29
MIR567	2434	chr3:113316256-11331728	pro	113316256	113317284	chr3	-0.54
BTLA	1856	chr3:113698739-11369974	pro	113698739	113699744	chr3	-0.67
SLC35A5	1447	chr3:113764633-11376535	pro	113764633	113765353	chr3	-0.26
CCDC80	2018	chr3:113844386-11384501	pro	113844386	113845011	chr3	-0.56
CD200R1L	2252	chr3:114049425-11405005	pro	114049425	114050054	chr3	-0.46
CD200R1	1149	chr3:114175354-11417560	pro	114175354	114175604	chr3	-0.59
GRAMD1C	22	chr3:115098726-11509933	pro	115098726	115099331	chr3	-0.53
LOC101929754	2080	chr3:115650689-11565540	pro	115650689	115655407	chr3	-0.91
LOC101929754	1504	chr3:115655611-11565765	pro	115655611	115657652	chr3	-0.81
VGLL4	1844	chr3:11616981-11621444	pro	11616981	11621444	chr3	-0.27
ZBTB20-AS4	30	chr3:116301286-11630269	pro	116301286	116302690	chr3	-0.77
ARHGAP31	1610	chr3:120497344-12049769	pro	120497344	120497691	chr3	-0.82
TIMMDC1	2027	chr3:120701206-12070296	pro	120701206	120702960	chr3	-0.36
STXBP5L	1474	chr3:122110454-12211197	pro	122110454	122111971	chr3	-0.99
ILDR1	2224	chr3:123224729-12322735	pro	123224729	123227356	chr3	-0.46
CCDC58	1264	chr3:123583405-12358359	pro	123583405	123583595	chr3	-0.77
KPNA1	1886	chr3:123714549-12371463	pro	123714549	123714631	chr3	-0.38
PARP15	986	chr3:123777435-12377886	pro	123777435	123778869	chr3	-0.45
PARP15	1753	chr3:123818881-12381905	pro	123818881	123819053	chr3	-0.29
HSPBAP1	1522	chr3:123993453-12399421	pro	123993453	123994215	chr3	-0.77
TSEN2	1672	chr3:12502585-12502774	pro	12502585	12502774	chr3	-0.79
UMPS	2176	chr3:125933888-12593426	pro	125933888	125934267	chr3	-0.66
KLF15	1476	chr3:127556583-12755831	pro	127556583	127558316	chr3	-0.78
ZXDC	2532	chr3:127674272-12767556	pro	127674272	127675569	chr3	-0.40
RPL32	1252	chr3:12855542-12855853	pro	12855542	12855853	chr3	-0.44
RPL32	570	chr3:12856181-12856580	pro	12856181	12856580	chr3	-0.47
IQSEC1	465	chr3:12984487-12984839	pro	12984487	12984839	chr3	-0.90
RAB43	1276	chr3:130324655-13032526	pro	130324655	130325265	chr3	-0.56
CNBP	2175	chr3:130387178-13038817	pro	130387178	130388172	chr3	-0.42
H1FX	1628	chr3:130519380-13051949	pro	130519380	130519497	chr3	-0.30
IQSEC1	1768	chr3:13085841-13089858	pro	13085841	13089858	chr3	-0.76
IQSEC1	703	chr3:13090063-13090579	pro	13090063	13090579	chr3	-0.63
PIK3R4	1892	chr3:131949636-13195091	pro	131949636	131950919	chr3	-0.74
ACPP	715	chr3:133518676-13352055	pro	133518676	133520554	chr3	-0.91

ACKR4	128	chr3:133798594-1337992	pro	133798594	133799203	chr3	-0.85
CDV3	1570	chr3:134773437-1347736	pro	134773437	134773668	chr3	-0.74
RYK	1079	chr3:135450601-1354517	pro	135450601	135451793	chr3	-0.36
PCCB	754	chr3:137450960-1374512	pro	137450960	137451244	chr3	-0.86
DBR1	2063	chr3:139374239-1393745	pro	139374239	139374599	chr3	-0.75
DBR1	1428	chr3:139374800-1393753	pro	139374800	139375309	chr3	-0.78
CEP70	2050	chr3:139793513-1397942	pro	139793513	139794220	chr3	-0.94
CEP70	1410	chr3:139794329-1397946	pro	139794329	139794684	chr3	-0.90
COPB2	1874	chr3:140589124-1405895	pro	140589124	140589553	chr3	-0.51
LOC100507291	1151	chr3:140592173-1405927	pro	140592173	140592797	chr3	-0.76
XPC	3132	chr3:14190886-14193201	pro	14190886	14193201	chr3	-0.31
SLC6A6	1671	chr3:14417016-14417798	pro	14417016	14417798	chr3	-0.51
SLC9A9	1436	chr3:145051386-1450516	pro	145051386	145051615	chr3	-0.94
CCDC174	1801	chr3:14669450-14670664	pro	14669450	14670664	chr3	-0.58
HLTF-AS1	2090	chr3:150284621-1502848	pro	150284621	150284814	chr3	-0.80
HLTF-AS1	1334	chr3:150285167-1502857	pro	150285167	150285782	chr3	-0.49
LOC101928105	530	chr3:151939296-1519406	pro	151939296	151940687	chr3	-0.57
MED12L	1112	chr3:152287671-1522891	pro	152287671	152289101	chr3	-0.59
MED12L	2058	chr3:152289245-1522894	pro	152289245	152289420	chr3	-0.89
SH3BP5	1296	chr3:15346807-15348881	pro	15346807	15348881	chr3	-0.30
P2RY1	318	chr3:154034771-1540354	pro	154034771	154035440	chr3	-0.54
P2RY1	300	chr3:154035557-1540358	pro	154035557	154035890	chr3	-0.43
ARHGEF26	2134	chr3:155323555-1553243	pro	155323555	155324390	chr3	-0.90
DHX36	1922	chr3:155522506-1555236	pro	155522506	155523609	chr3	-0.51
SSR3	613	chr3:157755875-1577566	pro	157755875	157756687	chr3	-0.36
LXN	230	chr3:159873259-1598735	pro	159873259	159873553	chr3	-0.97
SMC4	1904	chr3:161597659-1615981	pro	161597659	161598100	chr3	-0.68
MIR16-2	321	chr3:161605460-1616056	pro	161605460	161605634	chr3	-0.38
PPM1L	1618	chr3:161956585-1619600	pro	161956585	161960028	chr3	-0.52
WDR49	191	chr3:168853833-1688545	pro	168853833	168854517	chr3	-0.84
GOLIM4	2574	chr3:169291264-1692958	pro	169291264	169295812	chr3	-0.53
MYNN	1052	chr3:170975448-1709761	pro	170975448	170976148	chr3	-0.84
MYNN	1934	chr3:170976294-1709770	pro	170976294	170977065	chr3	-0.87
LOC100128164	1456	chr3:171164322-1711671	pro	171164322	171167197	chr3	-0.29
GPR160	1918	chr3:171240197-1712404	pro	171240197	171240495	chr3	-0.31
PRKCI	1810	chr3:171424562-1714248	pro	171424562	171424882	chr3	-0.81
SKIL	1875	chr3:171555333-1715572	pro	171555333	171557249	chr3	-0.40
SKIL	1426	chr3:171560040-1715630	pro	171560040	171563020	chr3	-0.82
RPL22L1	2512	chr3:172067122-1720693	pro	172067122	172069335	chr3	-0.29
EIF5A2	1613	chr3:172106393-1721086	pro	172106393	172108621	chr3	-1.00
FNDC3B	322	chr3:173239606-1732399	pro	173239606	173239971	chr3	-0.55
FNDC3B	558	chr3:173241294-1732418	pro	173241294	173241893	chr3	-0.62
ECT2	2035	chr3:173952890-1739535	pro	173952890	173953516	chr3	-0.75
LINC00578	293	chr3:178642127-1786432	pro	178642127	178643263	chr3	-0.44
KCNMB2	484	chr3:179737161-1797373	pro	179737161	179737363	chr3	-0.73
ZNF639	1684	chr3:180525861-1805259	pro	180525861	180525994	chr3	-0.35
MRPL47	1484	chr3:180803531-1808037	pro	180803531	180803756	chr3	-0.47
NDUFB5	1859	chr3:180806484-1808077	pro	180806484	180807770	chr3	-0.75
USP13	1694	chr3:180854671-1808559	pro	180854671	180855968	chr3	-0.31
DNAJC19	894	chr3:182189021-1821891	pro	182189021	182189192	chr3	-0.62
SOX2	1906	chr3:182910222-1829107	pro	182910222	182910775	chr3	-0.62
SOX2	504	chr3:182911545-1829122	pro	182911545	182912254	chr3	-0.90
SOX2	137	chr3:182912372-1829127	pro	182912372	182912710	chr3	-0.96
SOX2	1120	chr3:182913443-1829136	pro	182913443	182913606	chr3	-0.76
SOX2	2026	chr3:182914204-1829146	pro	182914204	182914657	chr3	-0.82

SATB1	152	chr3:18454706-18455530	pro	18454706	18455530	chr3	-0.94
SATB1	1744	chr3:18456504-18457525	pro	18456504	18457525	chr3	-0.87
KLHL6-AS1	680	chr3:184747679-18474939	pro	184747679	184749393	chr3	-0.69
KLHL6-AS1	1235	chr3:184749585-18475131	pro	184749585	184751317	chr3	-0.80
ABCC5-AS1	1934	chr3:185208389-18520911	pro	185208389	185209115	chr3	-0.56
DVL3	1904	chr3:185353822-18535432	pro	185353822	185354322	chr3	-0.82
ALG3	1214	chr3:185448135-18544834	pro	185448135	185448345	chr3	-0.47
POLR2H	1798	chr3:185564950-18556557	pro	185564950	185565575	chr3	-0.37
EPHB3	542	chr3:185761574-18576190	pro	185761574	185761902	chr3	-0.92
MAP3K13	2098	chr3:186480975-18648167	pro	186480975	186481672	chr3	-0.88
MAP3K13	523	chr3:186482463-18648333	pro	186482463	186483335	chr3	-0.83
MAP3K13	516	chr3:186483518-18648435	pro	186483518	186484357	chr3	-0.97
MAP3K13	273	chr3:186563093-18656341	pro	186563093	186563417	chr3	-0.81
MAP3K13	869	chr3:186563577-18656521	pro	186563577	186565217	chr3	-0.77
TMEM41A	274	chr3:186699645-18669998	pro	186699645	186699983	chr3	-0.69
AHSG	1679	chr3:187814684-18781575	pro	187814684	187815758	chr3	-0.54
ST6GAL1	1700	chr3:188219300-18822201	pro	188219300	188222016	chr3	-0.55
FLJ42393	1146	chr3:189379988-18938035	pro	189379988	189380351	chr3	-0.30
LPP	686	chr3:189413654-18941454	pro	189413654	189414547	chr3	-0.75
LPP	1790	chr3:189414804-18941560	pro	189414804	189415604	chr3	-0.65
IL1RAP	544	chr3:191713630-19171434	pro	191713630	191714345	chr3	-0.64
IL1RAP	579	chr3:191714528-19171569	pro	191714528	191715694	chr3	-0.96
CCDC50	166	chr3:192529058-19252974	pro	192529058	192529742	chr3	-0.97
UTS2B	397	chr3:192530141-19253269	pro	192530141	192532693	chr3	-0.99
OPA1	1625	chr3:194795194-19479530	pro	194795194	194795308	chr3	-0.48
OPA1	1972	chr3:194795420-19479577	pro	194795420	194795777	chr3	-0.42
LOC100505920	334	chr3:195406398-19540651	pro	195406398	195406514	chr3	-0.66
XXYLT1-AS2	1463	chr3:196349507-19635319	pro	196349507	196353195	chr3	-0.29
PPP1R2	3462	chr3:196745237-19675086	pro	196745237	196750867	chr3	-0.67
DLG1	444	chr3:198394281-19839563	pro	198394281	198395632	chr3	-0.54
MIR4797	304	chr3:198504849-19850497	pro	198504849	198504975	chr3	-0.57
KAT2B	1050	chr3:20054621-20056332	pro	20054621	20056332	chr3	-0.27
UBE2E2	1288	chr3:23220232-23221916	pro	23220232	23221916	chr3	-0.55
UBE2E1	1647	chr3:23823513-23827065	pro	23823513	23827065	chr3	-0.37
NGLY1	1502	chr3:25803613-25806451	pro	25803613	25806451	chr3	-0.40
SLC4A7	2090	chr3:27498711-27498941	pro	27498711	27498941	chr3	-0.44
AZI2	1668	chr3:28362787-28365120	pro	28362787	28365120	chr3	-0.32
TGFBR2	1314	chr3:30620300-30623065	pro	30620300	30623065	chr3	-0.38
TGFBR2	4337	chr3:30624713-30629953	pro	30624713	30629953	chr3	-0.48
CMTM6	2238	chr3:32516858-32517482	pro	32516858	32517482	chr3	-0.63
CRTAP	1602	chr3:33131689-33132419	pro	33131689	33132419	chr3	-0.64
PDCD6IP	2115	chr3:33816705-33817657	pro	33816705	33817657	chr3	-0.57
ARPP21	390	chr3:35658034-35658891	pro	35658034	35658891	chr3	-0.70
MIR128-2	1556	chr3:35762362-35762690	pro	35762362	35762690	chr3	-0.81
OXSR1	1936	chr3:38183325-38184604	pro	38183325	38184604	chr3	-0.65
WDR48	1328	chr3:39069537-39070139	pro	39069537	39070139	chr3	-0.52
SNORA62	988	chr3:39426485-39426634	pro	39426485	39426634	chr3	-0.61
TRAK1	832	chr3:42164249-42165547	pro	42164249	42165547	chr3	-0.67
TRAK1	1074	chr3:42177595-42177881	pro	42177595	42177881	chr3	-0.60
VIPR1	1238	chr3:42506475-42507589	pro	42506475	42507589	chr3	-0.93
SEC22C	1162	chr3:42596555-42598168	pro	42596555	42598168	chr3	-0.25
ZNF197-AS1	193	chr3:44640729-44641473	pro	44640729	44641473	chr3	-0.35
ITPR1	2020	chr3:4510161-4513940	pro	4510161	4513940	chr3	-0.30
NBEAL2	1411	chr3:46994576-46994954	pro	46994576	46994954	chr3	-0.46
CCDC12	102	chr3:46997988-46998815	pro	46997988	46998815	chr3	-0.51

KIF9-AS1	1766	chr3:47182118-47183138	pro	47182118	47183138	chr3	-0.78
PTPN23	1786	chr3:47395577-47395838	pro	47395577	47395838	chr3	-0.85
SCAP	574	chr3:47492933-47493116	pro	47492933	47493116	chr3	-0.30
ELP6	1763	chr3:47528083-47528799	pro	47528083	47528799	chr3	-0.53
SMARCC1	2346	chr3:47795481-47796648	pro	47795481	47796648	chr3	-0.37
CAMP	740	chr3:48238918-48239283	pro	48238918	48239283	chr3	-0.53
CAMP	1009	chr3:48239477-48242221	pro	48239477	48242221	chr3	-0.55
ZNF589	2212	chr3:48259572-48260047	pro	48259572	48260047	chr3	-0.47
NME6	1079	chr3:48316210-48317336	pro	48316210	48317336	chr3	-0.38
FBXW12	584	chr3:48388686-48389906	pro	48388686	48389906	chr3	-0.55
CCDC51	1162	chr3:48454967-48455776	pro	48454967	48455776	chr3	-0.35
TMA7	1460	chr3:48457858-48458439	pro	48457858	48458439	chr3	-0.54
PFKFB4	1229	chr3:48570216-48570706	pro	48570216	48570706	chr3	-0.39
PFKFB4	1778	chr3:48570859-48571162	pro	48570859	48571162	chr3	-0.58
CELSR3-AS1	614	chr3:48676741-48676896	pro	48676741	48676896	chr3	-0.30
USP4	2213	chr3:49354492-49355014	pro	49354492	49355014	chr3	-0.57
APEH	1643	chr3:49684715-49684875	pro	49684715	49684875	chr3	-0.73
MIR5193	124	chr3:49817320-49820292	pro	49817320	49820292	chr3	-0.81
MON1A	1014	chr3:49943091-49943837	pro	49943091	49943837	chr3	-0.56
RBM5	276	chr3:50100885-50101252	pro	50100885	50101252	chr3	-0.25
GNAI2	576	chr3:50238476-50238616	pro	50238476	50238616	chr3	-0.57
GNAI2	230	chr3:50242760-50243201	pro	50242760	50243201	chr3	-0.51
GNAI2	1112	chr3:50247397-50247562	pro	50247397	50247562	chr3	-0.75
C3orf18	634	chr3:50582500-50583157	pro	50582500	50583157	chr3	-0.55
ARL8B	258	chr3:5138551-5138789	pro	5138551	5138789	chr3	-0.54
RBM15B	1082	chr3:51402610-51402701	pro	51402610	51402701	chr3	-0.35
RAD54L2	1282	chr3:51549302-51549403	pro	51549302	51549403	chr3	-0.40
RRP9	1495	chr3:51949432-51949574	pro	51949432	51949574	chr3	-0.29
TLR9	204	chr3:52234819-52236029	pro	52234819	52236029	chr3	-0.50
TWF2	1376	chr3:52249036-52250164	pro	52249036	52250164	chr3	-0.57
WDR82	988	chr3:52288471-52288905	pro	52288471	52288905	chr3	-0.30
GLYCTK	681	chr3:52295943-52296443	pro	52295943	52296443	chr3	-0.27
GLT8D1	1809	chr3:52716442-52717456	pro	52716442	52717456	chr3	-0.61
PRKCD	1881	chr3:53171324-53172962	pro	53171324	53172962	chr3	-0.69
CCDC66	1981	chr3:56568143-56568263	pro	56568143	56568263	chr3	-0.79
FAM208A	2294	chr3:56688316-56691448	pro	56688316	56691448	chr3	-0.54
ARHGEF3	1176	chr3:56808765-56810954	pro	56808765	56810954	chr3	-0.56
ARHGEF3	1338	chr3:56924048-56924355	pro	56924048	56924355	chr3	-0.91
ARHGEF3	128	chr3:56924483-56926854	pro	56924483	56926854	chr3	-0.43
ARHGEF3	2419	chr3:56926970-56928948	pro	56926970	56928948	chr3	-0.78
IL17RD	408	chr3:57174767-57174936	pro	57174767	57174936	chr3	-0.51
DNAH12	442	chr3:57505224-57505883	pro	57505224	57505883	chr3	-0.72
FLNB	369	chr3:57968668-57968926	pro	57968668	57968926	chr3	-0.38
KCTD6	1954	chr3:58453314-58456318	pro	58453314	58456318	chr3	-0.50
KCTD6	1642	chr3:58456445-58458531	pro	58456445	58458531	chr3	-0.91
PTPRG	1000	chr3:61521214-61521350	pro	61521214	61521350	chr3	-0.71
CADPS	2607	chr3:62832640-62834354	pro	62832640	62834354	chr3	-0.92
CADPS	236	chr3:62836173-62836508	pro	62836173	62836508	chr3	-0.48
PRICKLE2	981	chr3:64183499-64186883	pro	64183499	64186883	chr3	-0.86
LRIG1	3609	chr3:66627035-66632819	pro	66627035	66632819	chr3	-0.99
LRIG1	1162	chr3:66634447-66634948	pro	66634447	66634948	chr3	-0.55
KBTBD8	1498	chr3:67131912-67133916	pro	67131912	67133916	chr3	-0.41
UBA3	1486	chr3:69213373-69214028	pro	69213373	69214028	chr3	-0.45
ARL6IP5	1224	chr3:69214419-69216690	pro	69214419	69216690	chr3	-0.42
FOXP1	1280	chr3:71194350-71196617	pro	71194350	71196617	chr3	-0.26

RYBP	1046	chr3:72576179-72578658	pro	72576179	72578658	chr3	-0.37
SHQ1	1832	chr3:72978412-72978500	pro	72978412	72978500	chr3	-0.67
LMCD1-AS1	594	chr3:8517346-8518154	pro	8517346	8518154	chr3	-0.91
LMCD1	1942	chr3:8519139-8521728	pro	8519139	8521728	chr3	-0.90
CHMP2B	2010	chr3:87360974-87361250	pro	87360974	87361250	chr3	-0.60
C3orf38	1217	chr3:88280180-88280550	pro	88280180	88280550	chr3	-0.64
THUMPD3	1079	chr3:9380637-9380953	pro	9380637	9380953	chr3	-0.44
DHFRL1	1981	chr3:95266634-95266844	pro	95266634	95266844	chr3	-0.53
CLDND1	1978	chr3:99722551-99722694	pro	99722551	99722694	chr3	-0.68
GPR15	656	chr3:99732030-99736145	pro	99732030	99736145	chr3	-0.98
CPOX	1018	chr3:99793643-99794613	pro	99793643	99794613	chr3	-0.48
EIF4E	2101	chr4:100066766-1000675	pro	100066766	100067564	chr4	-0.53
DAPP1	712	chr4:100955712-1009568	pro	100955712	100956867	chr4	-0.38
UBE2D3	2048	chr4:104006221-1040086	pro	104006221	104008666	chr4	-0.33
BDH2	224	chr4:104240606-1042407	pro	104240606	104240790	chr4	-0.46
AIMP1	1100	chr4:107455031-1074551	pro	107455031	107455197	chr4	-0.82
TBCK	1935	chr4:107459126-1074593	pro	107459126	107459364	chr4	-0.68
GIMD1	2044	chr4:107510021-1075101	pro	107510021	107510150	chr4	-0.60
PAPSS1	1638	chr4:108861694-1088633	pro	108861694	108863319	chr4	-0.27
LOC101929595	1340	chr4:109073981-1090741	pro	109073981	109074146	chr4	-0.83
HADH	3338	chr4:109131582-1091357	pro	109131582	109135729	chr4	-0.37
LEF1-AS1	1618	chr4:109313995-1093146	pro	109313995	109314688	chr4	-0.97
RPL34	2174	chr4:109763147-1097635	pro	109763147	109763594	chr4	-0.67
C4orf32	1819	chr4:113286704-11328893	pro	113286704	113288934	chr4	-0.71
AP1AR	1361	chr4:113372914-11337449	pro	113372914	113374492	chr4	-0.46
TIFA	2712	chr4:113428020-11343042	pro	113428020	113430420	chr4	-0.50
ALPK1	191	chr4:113437140-11343913	pro	113437140	113439134	chr4	-0.70
NEUROG2	2001	chr4:113658738-11365882	pro	113658738	113658820	chr4	-0.46
LARP7	1062	chr4:113778860-11377938	pro	113778860	113779384	chr4	-0.50
LOC101929741	1685	chr4:119824013-11982450	pro	119824013	119824505	chr4	-0.64
SYNPO2	66	chr4:119990875-11999183	pro	119990875	119991838	chr4	-0.62
C4orf3	738	chr4:120442027-1204422	pro	120442027	120442280	chr4	-0.73
EXOSC9	1830	chr4:122939983-1229401	pro	122939983	122940198	chr4	-0.75
BBS7	1206	chr4:123009604-1230101	pro	123009604	123010188	chr4	-0.48
CETN4P	363	chr4:123872373-1238730	pro	123872373	123873029	chr4	-0.29
PLK4	1428	chr4:129019808-1290202	pro	129019808	129020265	chr4	-0.65
PLK4	2042	chr4:129023708-1290240	pro	129023708	129024072	chr4	-0.80
MAEA	259	chr4:1292777-1293165	pro	1292777	1293165	chr4	-0.91
MAEA	166	chr4:1293305-1293488	pro	1293305	1293488	chr4	-0.87
MAEA	1628	chr4:1295100-1295311	pro	1295100	1295311	chr4	-0.42
JADE1	1189	chr4:129953214-1299540	pro	129953214	129954060	chr4	-0.28
JADE1	2258	chr4:129954271-1299551	pro	129954271	129955141	chr4	-0.90
C4orf33	830	chr4:130234338-1302374	pro	130234338	130237462	chr4	-0.34
ELF2	629	chr4:140225145-1402261	pro	140225145	140226149	chr4	-0.25
NDUFC1	1256	chr4:140444335-1404444	pro	140444335	140444490	chr4	-0.61
TBC1D9	1014	chr4:141895335-1418964	pro	141895335	141896481	chr4	-0.93
TBC1D9	520	chr4:141896937-1418979	pro	141896937	141897948	chr4	-0.40
GAB1	972	chr4:144476159-1444767	pro	144476159	144476760	chr4	-0.51
GAB1	1520	chr4:144478036-1444798	pro	144478036	144479869	chr4	-0.95
ABCE1	1138	chr4:146237382-1462375	pro	146237382	146237551	chr4	-0.56
SMAD1	830	chr4:146620917-1466222	pro	146620917	146622223	chr4	-0.31
SMAD1-AS2	549	chr4:146640323-1466457	pro	146640323	146645743	chr4	-0.26
LSM6	302	chr4:147315706-1473162	pro	147315706	147316257	chr4	-0.32
SNORD73A	1766	chr4:152242596-1522427	pro	152242596	152242729	chr4	-0.58
FBXL5	2144	chr4:15262519-15265460	pro	15262519	15265460	chr4	-0.56

FAM200B	1891	chr4:15289999-15291115	pro	15289999	15291115	chr4	-0.62
LOC100996286	102	chr4:153241185-15324185	pro	153241185	153241855	chr4	-0.39
MIR4453	1356	chr4:153677032-15367973	pro	153677032	153679735	chr4	-0.26
TMEM154	1694	chr4:153816247-15382190	pro	153816247	153821900	chr4	-0.49
CD38	571	chr4:15387975-15388939	pro	15387975	15388939	chr4	-0.77
CD38	3701	chr4:15389948-15395510	pro	15389948	15395510	chr4	-0.57
ARFIP1	2005	chr4:153922207-15392287	pro	153922207	153922879	chr4	-0.67
KIAA0922	1269	chr4:154604612-15460674	pro	154604612	154606742	chr4	-0.25
MAP9	1208	chr4:156515625-15651710	pro	156515625	156517102	chr4	-0.99
TAPT1	2183	chr4:15833515-15836639	pro	15833515	15836639	chr4	-0.56
TAPT1-AS1	1213	chr4:15838289-15838901	pro	15838289	15838901	chr4	-0.36
FAM198B	3376	chr4:159308374-15931120	pro	159308374	159311209	chr4	-0.91
FAM198B	638	chr4:159311863-15931319	pro	159311863	159313197	chr4	-0.78
FAM198B	548	chr4:159313313-15931508	pro	159313313	159315088	chr4	-0.94
TMEM144	1132	chr4:159349644-15934979	pro	159349644	159349793	chr4	-0.79
TMA16	902	chr4:164633971-16463446	pro	164633971	164634468	chr4	-0.63
GPM6A	882	chr4:177159719-17716019	pro	177159719	177160190	chr4	-0.78
GPM6A	74	chr4:177160344-17716117	pro	177160344	177161179	chr4	-0.61
WDR17	347	chr4:177223337-17722392	pro	177223337	177223925	chr4	-0.50
SPCS3	1571	chr4:177476383-17747663	pro	177476383	177476639	chr4	-0.89
CDKN2AIP	1876	chr4:184603450-18460586	pro	184603450	184605865	chr4	-0.29
LOC728175	1345	chr4:185513211-18551372	pro	185513211	185513727	chr4	-0.49
LOC102723766	1281	chr4:185540200-18554327	pro	185540200	185543270	chr4	-0.52
IRF2	2341	chr4:185634448-18563567	pro	185634448	185635674	chr4	-0.45
ACSL1	2369	chr4:185981433-18598235	pro	185981433	185982353	chr4	-0.84
MIR3945	136	chr4:186008774-18601001	pro	186008774	186010013	chr4	-0.33
ANKRD37	2619	chr4:186556506-18655839	pro	186556506	186558396	chr4	-0.63
UFSP2	2170	chr4:186581741-18658218	pro	186581741	186582186	chr4	-0.77
WHSC1	1078	chr4:1871006-1871138	pro	1871006	1871138	chr4	-0.72
TLR3	198	chr4:187226477-18722773	pro	187226477	187227730	chr4	-0.51
HAUS3	2447	chr4:2209386-2213036	pro	2209386	2213036	chr4	-0.33
DHX15	2016	chr4:24192254-24194279	pro	24192254	24194279	chr4	-0.26
DHX15	854	chr4:24196002-24196269	pro	24196002	24196269	chr4	-0.85
RNF4	1251	chr4:2439220-2439462	pro	2439220	2439462	chr4	-0.62
SEPSECS	1194	chr4:24769944-24770271	pro	24769944	24770271	chr4	-0.48
PI4K2B	502	chr4:24843963-24844533	pro	24843963	24844533	chr4	-0.38
ZCCHC4	2000	chr4:24921062-24921921	pro	24921062	24921921	chr4	-0.51
ZCCHC4	358	chr4:24922987-24923281	pro	24922987	24923281	chr4	-0.57
TBC1D19	484	chr4:26193625-26194690	pro	26193625	26194690	chr4	-0.34
TBC1D19	886	chr4:26195088-26195969	pro	26195088	26195969	chr4	-0.47
STIM2	4812	chr4:26473153-26479291	pro	26473153	26479291	chr4	-0.42
SH3BP2	353	chr4:2783388-2784802	pro	2783388	2784802	chr4	-0.70
SH3BP2	1389	chr4:2785070-2785192	pro	2785070	2785192	chr4	-0.69
DOK7	980	chr4:3456983-3457114	pro	3456983	3457114	chr4	-0.68
RELL1	1976	chr4:37362118-37362718	pro	37362118	37362718	chr4	-0.69
PGM2	1233	chr4:37503185-37503701	pro	37503185	37503701	chr4	-0.31
RHOH	1654	chr4:39867139-39867601	pro	39867139	39867601	chr4	-0.70
RBM47	832	chr4:40210779-40213052	pro	40210779	40213052	chr4	-0.76
RBM47	810	chr4:40213334-40213783	pro	40213334	40213783	chr4	-0.92
APBB2	1172	chr4:40552674-40552843	pro	40552674	40552843	chr4	-0.77
APBB2	1836	chr4:40555619-40555985	pro	40555619	40555985	chr4	-0.88
APBB2	1518	chr4:40909004-40910744	pro	40909004	40910744	chr4	-0.79
UCHL1-AS1	463	chr4:40952534-40953544	pro	40952534	40953544	chr4	-0.27
SLC30A9	1997	chr4:41689177-41689373	pro	41689177	41689373	chr4	-0.74
ATP8A1	2256	chr4:42350235-42353013	pro	42350235	42353013	chr4	-0.42

COMMD8	1387	chr4:47161381-47162261	pro	47161381	47162261	chr4	-0.85
LOC101927157	2317	chr4:47608187-47609179	pro	47608187	47609179	chr4	-0.36
ZNF721	583	chr4:482226-482528	pro	482226	482528	chr4	-0.36
MSX1	542	chr4:4911679-4911822	pro	4911679	4911822	chr4	-0.65
SGCB	1348	chr4:52596923-52598864	pro	52596923	52598864	chr4	-0.54
DANCR	966	chr4:53271676-53273144	pro	53271676	53273144	chr4	-0.32
SCFD2	2059	chr4:53928523-53929595	pro	53928523	53929595	chr4	-0.96
LOC100506444	343	chr4:54256839-54257495	pro	54256839	54257495	chr4	-0.94
TMEM165	2133	chr4:55954408-55954998	pro	55954408	55954998	chr4	-0.94
TMEM165	2909	chr4:55958791-55960699	pro	55958791	55960699	chr4	-0.26
EXOC1	422	chr4:56413897-56414404	pro	56413897	56414404	chr4	-0.32
AASDH	1220	chr4:56947001-56947422	pro	56947001	56947422	chr4	-0.51
PPAT	2232	chr4:56993955-56994702	pro	56993955	56994702	chr4	-0.46
POLR2B	1788	chr4:57541557-57541746	pro	57541557	57541746	chr4	-0.52
LOC285484	987	chr4:6254296-6254398	pro	6254296	6254398	chr4	-0.84
MRFAP1	2217	chr4:6694090-6695780	pro	6694090	6695780	chr4	-0.28
LOC93622	1658	chr4:6727255-6729500	pro	6727255	6729500	chr4	-0.52
MRFAP1L1	1290	chr4:6760416-6762021	pro	6760416	6762021	chr4	-0.65
MRFAP1L1	574	chr4:6762733-6763430	pro	6762733	6763430	chr4	-0.48
CENPC	807	chr4:68094064-68095254	pro	68094064	68095254	chr4	-0.29
STAP1	1962	chr4:68104822-68105334	pro	68104822	68105334	chr4	-0.91
UBA6	1846	chr4:68247417-68247859	pro	68247417	68247859	chr4	-0.60
KIAA0232	796	chr4:6834364-6834759	pro	6834364	6834759	chr4	-0.52
FLJ36777	920	chr4:7154975-7155193	pro	7154975	7155193	chr4	-0.37
FLJ36777	280	chr4:7156153-7156415	pro	7156153	7156415	chr4	-0.66
IGJ	1334	chr4:71751882-71753211	pro	71751882	71753211	chr4	-0.32
RUFY3	2044	chr4:71820804-71821136	pro	71820804	71821136	chr4	-0.29
ANKRD17	2044	chr4:74309479-74310002	pro	74309479	74310002	chr4	-0.79
RASSF6	2158	chr4:74699816-74706173	pro	74699816	74706173	chr4	-0.61
RASSF6	2060	chr4:74707078-74707465	pro	74707078	74707465	chr4	-0.96
MTHFD2L	1926	chr4:75244477-75244759	pro	75244477	75244759	chr4	-0.56
RCHY1	1797	chr4:76655230-76655424	pro	76655230	76655424	chr4	-0.71
USO1	1104	chr4:76866611-76868638	pro	76866611	76868638	chr4	-0.37
USO1	2640	chr4:76870475-76872260	pro	76870475	76872260	chr4	-0.72
PPEF2	790	chr4:77041818-77042015	pro	77041818	77042015	chr4	-0.49
CNOT6L	3376	chr4:78953547-78958836	pro	78953547	78958836	chr4	-0.50
CNOT6L	2098	chr4:78960585-78962746	pro	78960585	78962746	chr4	-0.27
MRPL1	1419	chr4:79003862-79004632	pro	79003862	79004632	chr4	-0.45
BMP2K	2300	chr4:79917045-79920664	pro	79917045	79920664	chr4	-0.35
PRDM8	2	chr4:81325333-81325554	pro	81325333	81325554	chr4	-0.64
BMP3	1615	chr4:82169257-82169797	pro	82169257	82169797	chr4	-0.64
HNRNPD	2014	chr4:83515719-83516658	pro	83515719	83516658	chr4	-0.85
ENOPH1	1784	chr4:83572361-83572518	pro	83572361	83572518	chr4	-0.74
SEC31A	1740	chr4:84029040-84030200	pro	84029040	84030200	chr4	-0.51
SEC31A	1322	chr4:84032705-84032854	pro	84032705	84032854	chr4	-0.58
THAP9-AS1	1750	chr4:84042478-84043210	pro	84042478	84043210	chr4	-0.84
LIN54	1248	chr4:84148934-84150594	pro	84148934	84150594	chr4	-0.33
PLAC8	2121	chr4:84252464-84253166	pro	84252464	84253166	chr4	-0.75
COQ2	1328	chr4:84422981-84424546	pro	84422981	84424546	chr4	-0.29
ACOX3	878	chr4:8492433-8492514	pro	8492433	8492514	chr4	-0.48
ARHGAP24	2086	chr4:86920835-86921085	pro	86920835	86921085	chr4	-0.64
ARHGAP24	1310	chr4:86966651-86966866	pro	86966651	86966866	chr4	-0.50
LOC100506746	616	chr4:88073799-88075022	pro	88073799	88075022	chr4	-0.30
AFF1	1614	chr4:88147536-88150045	pro	88147536	88150045	chr4	-0.27
PPM1K	1808	chr4:89426594-89427037	pro	89426594	89427037	chr4	-0.74

PYURF	460	chr4:89664039-89664832	pro	89664039	89664832	chr4	-0.61
TMEM175	1532	chr4:913772-915512	pro	913772	915512	chr4	-0.29
C5orf30	1874	chr5:102623385-10262504	pro	102623385	102625044	chr5	-0.29
LOC100506688	134	chr5:1050262-1050381	pro	1050262	1050381	chr5	-0.36
ANKRD33B	1702	chr5:10615625-10615840	pro	10615625	10615840	chr5	-0.29
ANKRD33B	1661	chr5:10617688-10620502	pro	10617688	10620502	chr5	-0.59
EPB41L4A-AS1	6	chr5:111523957-11152427	pro	111523957	111524270	chr5	-0.63
EPB41L4A	1131	chr5:111781726-11178183	pro	111781726	111781832	chr5	-0.54
CCDC112	704	chr5:114659122-11465924	pro	114659122	114659241	chr5	-0.53
AP3S1	2380	chr5:115206124-11520966	pro	115206124	115209669	chr5	-0.55
DTWD2	873	chr5:118350750-11835178	pro	118350750	118351784	chr5	-0.27
TNFAIP8	4946	chr5:118695589-11870783	pro	118695589	118707838	chr5	-0.35
PRR16	232	chr5:119827562-11982771	pro	119827562	119827714	chr5	-0.66
PRR16	444	chr5:119828118-11982851	pro	119828118	119828511	chr5	-0.97
SNX24	819	chr5:122209623-12221013	pro	122209623	122210131	chr5	-0.26
PHAX	1534	chr5:125965772-12596630	pro	125965772	125966305	chr5	-0.79
LMNB1	1002	chr5:126139096-12613932	pro	126139096	126139325	chr5	-0.60
LYRM7	1660	chr5:130536116-13053621	pro	130536116	130536211	chr5	-0.66
C5orf56	2078	chr5:131776168-13177671	pro	131776168	131776713	chr5	-0.94
IRF1	1819	chr5:131851313-13185377	pro	131851313	131853777	chr5	-0.27
KIF3A	1566	chr5:132099464-13209974	pro	132099464	132099745	chr5	-0.61
ZCCHC10	428	chr5:132390332-13239087	pro	132390332	132390872	chr5	-0.26
CDKL3	811	chr5:133731433-13373151	pro	133731433	133731517	chr5	-0.44
SAR1B	1298	chr5:133994849-13399541	pro	133994849	133995418	chr5	-0.62
PCBD2	1662	chr5:134270030-13427071	pro	134270030	134270710	chr5	-0.30
TERT	1525	chr5:1345866-1347408	pro	1345866	1347408	chr5	-0.66
TERT	1045	chr5:1348433-1349981	pro	1348433	1349981	chr5	-0.34
KLHL3	780	chr5:137098022-13709977	pro	137098022	137099773	chr5	-0.94
CDC23	1256	chr5:137575483-13757586	pro	137575483	137575868	chr5	-0.59
SNORA74A	2294	chr5:138638811-13864133	pro	138638811	138641332	chr5	-0.35
SNORA74A	167	chr5:138641892-13864250	pro	138641892	138642506	chr5	-0.80
SNORA74A	1716	chr5:138643931-13864423	pro	138643931	138644232	chr5	-0.85
PAIP2	2014	chr5:138707677-13870839	pro	138707677	138708390	chr5	-0.48
SLC23A1	415	chr5:138747226-13874748	pro	138747226	138747480	chr5	-0.69
SLC23A1	1984	chr5:138748227-13874961	pro	138748227	138749617	chr5	-0.29
PURA	2348	chr5:139475520-13947695	pro	139475520	139476955	chr5	-0.92
HBEGF	1495	chr5:139703920-13970583	pro	139703920	139705834	chr5	-0.73
HBEGF	1275	chr5:139706600-13970869	pro	139706600	139708694	chr5	-0.38
TAF7	1492	chr5:140678922-14067916	pro	140678922	140679166	chr5	-0.72
TAF7	852	chr5:140679311-14068005	pro	140679311	140680056	chr5	-0.55
PCDHGA4	350	chr5:140714332-14071451	pro	140714332	140714517	chr5	-0.69
PCDHGB2	230	chr5:140719733-14072049	pro	140719733	140720498	chr5	-0.94
PCDHGA5	1586	chr5:140721977-14072301	pro	140721977	140723010	chr5	-0.98
PCDHGC3	406	chr5:140835053-14083563	pro	140835053	140835638	chr5	-0.46
PCDHGC4	1166	chr5:140842846-14084466	pro	140842846	140844669	chr5	-0.48
LOC100505658	74	chr5:140917882-14091808	pro	140917882	140918089	chr5	-0.37
HDAC3	2076	chr5:140994445-14099462	pro	140994445	140994620	chr5	-0.39
HDAC3	1729	chr5:140994782-14099497	pro	140994782	140994976	chr5	-0.48
KIAA0141	1054	chr5:141282383-14128264	pro	141282383	141282644	chr5	-0.70
PCDH12	2130	chr5:141320697-14132118	pro	141320697	141321188	chr5	-0.56
RNF14	541	chr5:141326457-14132779	pro	141326457	141327793	chr5	-0.92
TRIO	1018	chr5:14195414-14196207	pro	14195414	14196207	chr5	-0.92
TRIO	1726	chr5:14198198-14198910	pro	14198198	14198910	chr5	-0.96
NR3C1	523	chr5:142795227-14279635	pro	142795227	142796359	chr5	-0.58
NR3C1	1476	chr5:142796531-14279696	pro	142796531	142796960	chr5	-0.69

YIPF5	1698	chr5:143528736-14352881	pro	143528736	143528813	chr5	-0.70
LARS	1907	chr5:145540365-14554079	pro	145540365	145540797	chr5	-0.71
RBM27	1847	chr5:145564935-14556546	pro	145564935	145565467	chr5	-0.27
JAKMIP2	1817	chr5:147139217-14714235	pro	147139217	147142357	chr5	-0.93
JAKMIP2	198	chr5:147142676-14714292	pro	147142676	147142929	chr5	-0.89
ADRB2	4887	chr5:148186388-14819608	pro	148186388	148196082	chr5	-0.86
GRPEL2	2516	chr5:148706744-14870862	pro	148706744	148708624	chr5	-0.70
TCOF1	1274	chr5:149718517-14971881	pro	149718517	149718818	chr5	-0.60
CD74	564	chr5:149772738-14977377	pro	149772738	149773773	chr5	-0.43
RPS14	536	chr5:149809996-14981010	pro	149809996	149810101	chr5	-0.38
LOC102546298	1486	chr5:149846444-14984802	pro	149846444	149848024	chr5	-0.56
ANXA6	107	chr5:150500529-15050207	pro	150500529	150502077	chr5	-0.80
ANXA6	967	chr5:150502234-15050252	pro	150502234	150502520	chr5	-0.85
CCDC69	1433	chr5:150584912-15058565	pro	150584912	150585650	chr5	-0.67
GM2A	1484	chr5:150611163-15061147	pro	150611163	150611477	chr5	-0.66
GM2A	730	chr5:150611639-15061251	pro	150611639	150612510	chr5	-0.32
FAM114A2	1528	chr5:153397014-15339731	pro	153397014	153397310	chr5	-0.76
HAVCR2	144	chr5:156468150-15646978	pro	156468150	156469789	chr5	-0.82
THG1L	489	chr5:157089059-15709176	pro	157089059	157091763	chr5	-0.28
CLINT1	644	chr5:157219371-15721944	pro	157219371	157219441	chr5	-0.58
CLINT1	1179	chr5:157219791-15722009	pro	157219791	157220091	chr5	-0.88
CLINT1	2082	chr5:157220198-15722148	pro	157220198	157221489	chr5	-0.47
RNF145	1802	chr5:158571225-15857165	pro	158571225	158571659	chr5	-0.63
LOC285626	1039	chr5:158691307-15869297	pro	158691307	158692975	chr5	-0.35
TTC1	120	chr5:159368481-15936864	pro	159368481	159368648	chr5	-0.48
TTC1	1454	chr5:159369964-15937031	pro	159369964	159370311	chr5	-0.34
TTC1	1874	chr5:159370498-15937061	pro	159370498	159370619	chr5	-0.42
PTTG1	1296	chr5:159778885-15978130	pro	159778885	159781302	chr5	-0.39
PTTG1	2190	chr5:159781645-15978572	pro	159781645	159785723	chr5	-0.29
GABRB2	2288	chr5:160904096-16090674	pro	160904096	160906744	chr5	-0.54
GABRB2	580	chr5:160906875-16090738	pro	160906875	160907382	chr5	-0.40
GABRB2	98	chr5:160907527-16090769	pro	160907527	160907693	chr5	-0.92
CCNG1	1761	chr5:162798686-16279914	pro	162798686	162799144	chr5	-0.40
ZNF622	1743	chr5:16520060-16521214	pro	16520060	16521214	chr5	-0.44
LCP2	61	chr5:169656906-16965777	pro	169656906	169657772	chr5	-0.95
LINC01366	10	chr5:169690421-16969154	pro	169690421	169691546	chr5	-0.68
MYO10	311	chr5:16988990-16989160	pro	16988990	16989160	chr5	-0.45
RPL26L1	1199	chr5:172320112-17232037	pro	172320112	172320374	chr5	-0.62
ATP6V0E1	1882	chr5:172344901-17234560	pro	172344901	172345600	chr5	-0.51
LINC01484	892	chr5:173106636-17310678	pro	173106636	173106783	chr5	-0.80
LINC01485	662	chr5:173149209-17315057	pro	173149209	173150571	chr5	-0.38
FAF2	1438	chr5:175809167-17580962	pro	175809167	175809628	chr5	-0.49
CDHR2	472	chr5:175900751-17590253	pro	175900751	175902538	chr5	-0.28
ZNF346	1126	chr5:176381078-17638127	pro	176381078	176381275	chr5	-0.51
ZNF346	2206	chr5:176384216-17638480	pro	176384216	176384800	chr5	-0.36
FGFR4	1416	chr5:176444710-17644541	pro	176444710	176445415	chr5	-0.83
FGFR4	486	chr5:176445814-17644617	pro	176445814	176446170	chr5	-0.60
PRELID1	1982	chr5:176665169-17666553	pro	176665169	176665530	chr5	-0.44
MXD3	2578	chr5:176668642-17666999	pro	176668642	176669998	chr5	-0.46
TMED9	1394	chr5:176952926-17695349	pro	176952926	176953499	chr5	-0.62
NHP2	1070	chr5:177514437-17751483	pro	177514437	177514839	chr5	-0.81
RUFY1	2032	chr5:178911766-17891262	pro	178911766	178912629	chr5	-0.63
CANX	1460	chr5:179056888-17905725	pro	179056888	179057259	chr5	-0.34
MGAT4B	1314	chr5:179163710-17916388	pro	179163710	179163881	chr5	-0.71
C5orf45	1216	chr5:179217058-17921740	pro	179217058	179217403	chr5	-0.61

CNOT6	778	chr5:179853171-17985331	pro	179853171	179853318	chr5	-0.59
MGAT1	1654	chr5:180160001-18016199	pro	180160001	180161999	chr5	-0.27
MGAT1	1986	chr5:180165337-18016565	pro	180165337	180165652	chr5	-0.51
HEIH	1950	chr5:180193106-18019324	pro	180193106	180193243	chr5	-0.71
MIR8089	1498	chr5:180403692-18040548	pro	180403692	180405483	chr5	-0.81
TRIM7	1732	chr5:180558689-18055892	pro	180558689	180558920	chr5	-0.75
BRIX1	2258	chr5:34953442-34954227	pro	34953442	34954227	chr5	-0.45
NADK2	1879	chr5:36273521-36277221	pro	36273521	36277221	chr5	-0.42
CARD6	433	chr5:40876622-40878576	pro	40876622	40878576	chr5	-0.66
ZNF131	678	chr5:43156017-43156144	pro	43156017	43156144	chr5	-0.48
LOC100506674	783	chr5:44843170-44844568	pro	44843170	44844568	chr5	-0.27
LOC102467147	1628	chr5:55810947-55812504	pro	55810947	55812504	chr5	-0.50
SETD9	1322	chr5:56239402-56239638	pro	56239402	56239638	chr5	-0.64
GAPT	1424	chr5:57824415-57824606	pro	57824415	57824606	chr5	-0.41
DEPDC1B	1830	chr5:60029606-60030234	pro	60029606	60030234	chr5	-0.73
DIMT1	989	chr5:61736308-61736642	pro	61736308	61736642	chr5	-0.62
IPO11	1741	chr5:61745949-61746189	pro	61745949	61746189	chr5	-0.63
PPWD1	1583	chr5:64896301-64896505	pro	64896301	64896505	chr5	-0.73
MAST4	876	chr5:66335883-66338274	pro	66335883	66338274	chr5	-0.27
CD180	1272	chr5:66529497-66529796	pro	66529497	66529796	chr5	-0.66
LOC102467655	615	chr5:67520763-67520923	pro	67520763	67520923	chr5	-0.51
TNPO1	351	chr5:72179042-72179624	pro	72179042	72179624	chr5	-0.51
HEXB	778	chr5:73969511-73972137	pro	73969511	73972137	chr5	-0.61
ENC1	110	chr5:73972431-73973801	pro	73972431	73973801	chr5	-0.81
ENC1	979	chr5:73973920-73974050	pro	73973920	73974050	chr5	-0.63
COL4A3BP	1356	chr5:74843559-74846276	pro	74843559	74846276	chr5	-0.43
IQGAP2	2029	chr5:75735212-75738514	pro	75735212	75738514	chr5	-0.85
IQGAP2	331	chr5:75878262-75880376	pro	75878262	75880376	chr5	-0.96
IQGAP2	1106	chr5:75938373-75940764	pro	75938373	75940764	chr5	-0.96
SCAMP1	1314	chr5:77690519-77691017	pro	77690519	77691017	chr5	-0.49
ARSB	35	chr5:78317046-78318068	pro	78317046	78318068	chr5	-0.37
HOMER1	1317	chr5:78843034-78845164	pro	78843034	78845164	chr5	-0.45
MTX3	1575	chr5:79320015-79322523	pro	79320015	79322523	chr5	-0.74
MTX3	568	chr5:79322855-79323968	pro	79322855	79323968	chr5	-0.62
SERINC5	1277	chr5:79588700-79589170	pro	79588700	79589170	chr5	-0.33
MSH3	1178	chr5:79984362-79985726	pro	79984362	79985726	chr5	-0.35
SSBP2	3638	chr5:81077066-81081313	pro	81077066	81081313	chr5	-0.72
RPS23	1676	chr5:81608229-81608402	pro	81608229	81608402	chr5	-0.59
ATP6AP1L	2	chr5:81610802-81611273	pro	81610802	81611273	chr5	-0.71
MIR3607	1164	chr5:85950529-85951278	pro	85950529	85951278	chr5	-0.52
TMEM161B	1919	chr5:87598451-87598615	pro	87598451	87598615	chr5	-0.62
TMEM161B-AS1	1857	chr5:87602207-87602683	pro	87602207	87602683	chr5	-0.49
CETN3	1762	chr5:89739472-89739724	pro	89739472	89739724	chr5	-0.77
POLR3G	1400	chr5:89807651-89808022	pro	89807651	89808022	chr5	-0.53
LUCAT1	26	chr5:90645849-90646050	pro	90645849	90646050	chr5	-0.38
MCTP1	230	chr5:94442852-94443341	pro	94442852	94443341	chr5	-0.72
RFESD	1102	chr5:95008378-95010503	pro	95008378	95010503	chr5	-0.46
ERAP1	2700	chr5:96177325-96179282	pro	96177325	96179282	chr5	-0.43
LNPEP	3833	chr5:96321759-96325727	pro	96321759	96325727	chr5	-0.35
LIX1	1954	chr5:96502190-96502454	pro	96502190	96502454	chr5	-0.94
RGMB-AS1	1752	chr5:98134258-98135615	pro	98134258	98135615	chr5	-0.27
RGMB-AS1	108	chr5:98136132-98137028	pro	98136132	98137028	chr5	-0.66
RGMB-AS1	2228	chr5:98138072-98139761	pro	98138072	98139761	chr5	-0.48
FAM174A	962	chr5:99898000-99898119	pro	99898000	99898119	chr5	-0.41
USP45	1076	chr6:100070706-10007139	pro	100070706	100071395	chr6	-0.50

PRDM1	1094	chr6:106638755-10664082	pro	106638755	106640828	chr6	-0.50
PRDM1	1206	chr6:106641012-10664317	pro	106641012	106643173	chr6	-0.62
RTN4IP1	2651	chr6:107180505-10718232	pro	107180505	107182325	chr6	-0.33
QRSL1	1913	chr6:107185849-10718624	pro	107185849	107186241	chr6	-0.84
PDSS2	1821	chr6:107885171-10788613	pro	107885171	107886131	chr6	-0.37
PAK1IP1	2028	chr6:10805117-10805283	pro	10805117	10805283	chr6	-0.78
SESN1	1397	chr6:109519635-10952237	pro	109519635	109522375	chr6	-0.32
ZBTB24	2130	chr6:109907874-10991013	pro	109907874	109910135	chr6	-0.27
FIG4	2068	chr6:110120878-11012149	pro	110120878	110121491	chr6	-0.50
WASF1	2178	chr6:110604590-11060685	pro	110604590	110606854	chr6	-0.50
RPF2	1642	chr6:111411444-11141166	pro	111411444	111411664	chr6	-0.79
TRAF3IP2	1088	chr6:111994125-11199421	pro	111994125	111994212	chr6	-0.67
SMIM13	1981	chr6:11203769-11204693	pro	11203769	11204693	chr6	-0.70
FYN	2611	chr6:112187264-11219201	pro	112187264	112192014	chr6	-0.98
FYN	1846	chr6:112298682-11230032	pro	112298682	112300323	chr6	-0.72
LOC101927686	2006	chr6:114079840-11408011	pro	114079840	114080113	chr6	-0.88
MARCKS	770	chr6:114283794-11428510	pro	114283794	114285103	chr6	-0.81
MARCKS	600	chr6:114285662-11428597	pro	114285662	114285974	chr6	-0.71
NT5DC1	880	chr6:116527097-11652852	pro	116527097	116528524	chr6	-0.29
NT5DC1	1523	chr6:116529132-11653129	pro	116529132	116531294	chr6	-0.45
TSPYL4	1290	chr6:116683181-11668330	pro	116683181	116683307	chr6	-0.55
DSE	1050	chr6:116707939-11671010	pro	116707939	116710108	chr6	-0.44
NUS1	1896	chr6:118104466-11810594	pro	118104466	118105941	chr6	-0.41
MAN1A1	3277	chr6:119713114-11971870	pro	119713114	119718700	chr6	-0.65
TBC1D32	482	chr6:121697429-12169822	pro	121697429	121698227	chr6	-0.86
NCOA7-AS1	587	chr6:126181042-12618118	pro	126181042	126181180	chr6	-0.53
TRMT11	1750	chr6:126350859-12635117	pro	126350859	126351176	chr6	-0.67
EPB41L2	1607	chr6:131423777-13142532	pro	131423777	131425321	chr6	-0.55
AKAP7	966	chr6:131612936-13161497	pro	131612936	131614976	chr6	-0.90
MED23	508	chr6:131991281-13199188	pro	131991281	131991880	chr6	-0.32
ENPP3	50	chr6:131999704-13200066	pro	131999704	132000665	chr6	-0.75
ENPP3	918	chr6:132000932-13200117	pro	132000932	132001171	chr6	-0.63
VNN2	630	chr6:133121095-13312184	pro	133121095	133121845	chr6	-0.36
LOC100130357	758	chr6:13403708-13405404	pro	13403708	13405404	chr6	-0.95
TBPL1	598	chr6:134314003-13431480	pro	134314003	134314802	chr6	-0.39
TBPL1	2022	chr6:134316515-13431951	pro	134316515	134319514	chr6	-0.35
SGK1	6	chr6:134680813-13468095	pro	134680813	134680955	chr6	-0.65
LINC01010	1379	chr6:134798813-13479952	pro	134798813	134799521	chr6	-0.61
LINC01010	408	chr6:134799981-13480029	pro	134799981	134800295	chr6	-0.75
MYB	1150	chr6:135542704-13554328	pro	135542704	135543283	chr6	-0.38
SIRT5	1152	chr6:13683845-13684131	pro	13683845	13684131	chr6	-0.72
IFNGR1	1770	chr6:137579111-13758187	pro	137579111	137581870	chr6	-0.28
LOC100507406	2440	chr6:138098933-13809992	pro	138098933	138099924	chr6	-0.76
LOC100130476	2136	chr6:138231067-13823533	pro	138231067	138235332	chr6	-0.54
NHSL1	112	chr6:138861427-13886289	pro	138861427	138862893	chr6	-0.86
CCDC28A	1450	chr6:139134819-13913497	pro	139134819	139134978	chr6	-0.90
LOC100507557	1956	chr6:146179553-14617976	pro	146179553	146179766	chr6	-0.92
UST	736	chr6:149108928-14910952	pro	149108928	149109524	chr6	-0.57
KATNA1	2134	chr6:150008945-15001005	pro	150008945	150010055	chr6	-0.80
KATNA1	2282	chr6:150013211-15001462	pro	150013211	150014620	chr6	-0.89
AKAP12	1270	chr6:151687018-15168715	pro	151687018	151687158	chr6	-0.45
FBXO5	2698	chr6:153341892-15334450	pro	153341892	153344503	chr6	-0.46
JARID2	864	chr6:15357118-15358738	pro	15357118	15358738	chr6	-0.46
EZR	472	chr6:159160690-15916114	pro	159160690	159161143	chr6	-0.33
WTAP	1861	chr6:160066053-16006626	pro	160066053	160066261	chr6	-0.72

MRPL18	1742	chr6:160132932-16013351	pro	160132932	160133511	chr6	-0.68
AGPAT4	678	chr6:161614229-16161461	pro	161614229	161614611	chr6	-0.69
AGPAT4	201	chr6:161615195-16161540	pro	161615195	161615403	chr6	-0.33
PACRG	140	chr6:163067805-16306821	pro	163067805	163068219	chr6	-0.49
PACRG	194	chr6:163069007-16306936	pro	163069007	163069362	chr6	-0.40
SFT2D1	1693	chr6:166674027-16667455	pro	166674027	166674551	chr6	-0.42
MPC1	1554	chr6:166714470-16671540	pro	166714470	166715405	chr6	-0.41
RNASET2	3304	chr6:167285295-16728823	pro	167285295	167288234	chr6	-0.52
CCR6	1626	chr6:167445242-16744857	pro	167445242	167448579	chr6	-0.27
CCR6	560	chr6:167454081-16745725	pro	167454081	167457259	chr6	-0.63
CCR6	1642	chr6:167457540-16745820	pro	167457540	167458205	chr6	-0.93
RNF144B	623	chr6:18494414-18495456	pro	18494414	18495456	chr6	-0.42
ID4	3566	chr6:19947441-19950848	pro	19947441	19950848	chr6	-0.99
SOX4	486	chr6:21701127-21701801	pro	21701127	21701801	chr6	-0.28
SOX4	2891	chr6:21703923-21705759	pro	21703923	21705759	chr6	-0.87
DUSP22	933	chr6:235301-236945	pro	235301	236945	chr6	-0.36
DUSP22	3952	chr6:237799-244217	pro	237799	244217	chr6	-0.71
ALDH5A1	1983	chr6:24600898-24601484	pro	24600898	24601484	chr6	-0.61
FAM65B	3401	chr6:25038423-25043295	pro	25038423	25043295	chr6	-0.30
CMAHP	18	chr6:25245711-25247524	pro	25245711	25247524	chr6	-0.44
LRRC16A	2072	chr6:25385172-25385953	pro	25385172	25385953	chr6	-0.86
LRRC16A	973	chr6:25386106-25387216	pro	25386106	25387216	chr6	-0.43
HIST1H3A	353	chr6:26128099-26128587	pro	26128099	26128587	chr6	-0.76
HIST1H2AB	857	chr6:26141955-26143311	pro	26141955	26143311	chr6	-0.55
HIST1H2BB	290	chr6:26151276-26151871	pro	26151276	26151871	chr6	-0.35
HIST1H4C	495	chr6:26211374-26211944	pro	26211374	26211944	chr6	-0.38
HIST1H2BC	1334	chr6:26230316-26231240	pro	26230316	26231240	chr6	-0.30
HIST1H4D	926	chr6:26298079-26298342	pro	26298079	26298342	chr6	-0.86
HIST1H4E	956	chr6:26311039-26312749	pro	26311039	26312749	chr6	-0.59
HIST1H2BG	1936	chr6:26322774-26323057	pro	26322774	26323057	chr6	-0.50
HIST1H2AE	1324	chr6:26326290-26326611	pro	26326290	26326611	chr6	-0.65
HIST1H2AE	2924	chr6:26326908-26329192	pro	26326908	26329192	chr6	-0.87
HIST1H2BH	1798	chr6:26361514-26361794	pro	26361514	26361794	chr6	-0.95
HIST1H2BI	1452	chr6:26381927-26383342	pro	26381927	26383342	chr6	-0.39
BTN3A2	620	chr6:26472190-26473297	pro	26472190	26473297	chr6	-0.67
BTN3A2	1232	chr6:26473440-26475752	pro	26473440	26475752	chr6	-0.77
BTN2A2	567	chr6:26491308-26492658	pro	26491308	26492658	chr6	-0.92
BTN3A1	1100	chr6:26509946-26513137	pro	26509946	26513137	chr6	-0.79
BTN2A3P	95	chr6:26529269-26530113	pro	26529269	26530113	chr6	-0.59
BTN3A3	448	chr6:26547862-26550390	pro	26547862	26550390	chr6	-0.60
BTN2A1	1312	chr6:26567263-26567582	pro	26567263	26567582	chr6	-0.94
BTN1A1	1175	chr6:26610018-26611276	pro	26610018	26611276	chr6	-0.55
HMGN4	1582	chr6:26647764-26648499	pro	26647764	26648499	chr6	-0.77
MYLK4	896	chr6:2695156-2695359	pro	2695156	2695359	chr6	-0.81
HIST1H2BJ	1862	chr6:27206012-27207372	pro	27206012	27207372	chr6	-0.41
HIST1H4I	1760	chr6:27213034-27213578	pro	27213034	27213578	chr6	-0.93
HIST1H4I	704	chr6:27213805-27214920	pro	27213805	27214920	chr6	-0.59
MIR3143	706	chr6:27223892-27224284	pro	27223892	27224284	chr6	-0.79
MIR3143	1662	chr6:27224768-27225320	pro	27224768	27225320	chr6	-0.69
POM121L2	580	chr6:27388230-27388910	pro	27388230	27388910	chr6	-0.54
LINC01012	1438	chr6:27771227-27771322	pro	27771227	27771322	chr6	-0.79
HIST1H2BL	1580	chr6:27881798-27882419	pro	27881798	27882419	chr6	-0.92
HIST1H2AJ	1912	chr6:27888462-27888710	pro	27888462	27888710	chr6	-0.94
HIST1H2BM	932	chr6:27891594-27891871	pro	27891594	27891871	chr6	-0.33
HIST1H2BM	1460	chr6:27892059-27892460	pro	27892059	27892460	chr6	-0.78

HIST1H4J	1264	chr6:27900790-27901497	pro	27900790	27901497	chr6	-0.30
HIST1H4K	412	chr6:27907482-27907910	pro	27907482	27907910	chr6	-0.36
HIST1H2AL	1696	chr6:27938403-27940372	pro	27938403	27940372	chr6	-0.99
HIST1H3I	1221	chr6:27946679-27947035	pro	27946679	27947035	chr6	-0.61
OR2B6	434	chr6:28032942-28033917	pro	28032942	28033917	chr6	-0.86
SERPINB9P1	117	chr6:2821478-2822244	pro	2821478	2822244	chr6	-0.44
SERPINB9P1	1651	chr6:2823180-2823610	pro	2823180	2823610	chr6	-0.95
LOC101927730	34	chr6:2828959-2829414	pro	2828959	2829414	chr6	-0.87
LOC101927730	1268	chr6:2829583-2831393	pro	2829583	2831393	chr6	-0.91
ZKSCAN4	1186	chr6:28326466-28327125	pro	28326466	28327125	chr6	-0.46
SERPINB9	2990	chr6:2844198-2846914	pro	2844198	2846914	chr6	-0.37
HTATSF1P2	1814	chr6:2970842-2972795	pro	2970842	2972795	chr6	-0.47
IRF4	1744	chr6:334423-335565	pro	334423	335565	chr6	-0.91
SYNGAP1	828	chr6:33494177-33495814	pro	33494177	33495814	chr6	-0.25
IRF4	532	chr6:335897-336515	pro	335897	336515	chr6	-0.46
LINC00336	866	chr6:33668147-33668308	pro	33668147	33668308	chr6	-0.41
LINC00336	268	chr6:33669173-33669550	pro	33669173	33669550	chr6	-0.26
IRF4	2304	chr6:338579-339505	pro	338579	339505	chr6	-0.83
LEMD2	340	chr6:33865037-33865412	pro	33865037	33865412	chr6	-0.52
GRM4	1594	chr6:34223213-34223759	pro	34223213	34223759	chr6	-0.96
PACSIN1	548	chr6:34540919-34541613	pro	34540919	34541613	chr6	-0.83
PACSIN1	836	chr6:34542007-34543293	pro	34542007	34543293	chr6	-0.97
PACSIN1	2694	chr6:34543561-34545456	pro	34543561	34545456	chr6	-0.95
SNRPC	558	chr6:34832204-34832377	pro	34832204	34832377	chr6	-0.45
TAF11	1173	chr6:34962597-34962709	pro	34962597	34962709	chr6	-0.70
ANKS1A	1864	chr6:34966800-34966955	pro	34966800	34966955	chr6	-0.57
DEF6	316	chr6:35373073-35373440	pro	35373073	35373440	chr6	-0.53
FANCE	890	chr6:35528474-35529535	pro	35528474	35529535	chr6	-0.25
MIR7111	1884	chr6:35548075-35548216	pro	35548075	35548216	chr6	-0.29
FKBP5	610	chr6:35804025-35805871	pro	35804025	35805871	chr6	-0.29
FKBP5	1746	chr6:35805978-35806189	pro	35805978	35806189	chr6	-0.46
LOC285847	708	chr6:35811836-35812151	pro	35811836	35812151	chr6	-0.84
PNPLA1	1154	chr6:36317531-36318006	pro	36317531	36318006	chr6	-0.47
KCTD20	1126	chr6:36516988-36517799	pro	36516988	36517799	chr6	-0.42
STK38	486	chr6:36623343-36624082	pro	36623343	36624082	chr6	-0.26
SRSF3	1935	chr6:36667522-36668740	pro	36667522	36668740	chr6	-0.70
FGD2	1088	chr6:37079900-37080724	pro	37079900	37080724	chr6	-0.81
FGD2	320	chr6:37080869-37081290	pro	37080869	37081290	chr6	-0.90
CMTR1	1917	chr6:37510708-37510894	pro	37510708	37510894	chr6	-0.58
CCDC167	1740	chr6:37573623-37574252	pro	37573623	37574252	chr6	-0.70
GLO1	1434	chr6:38777380-38777613	pro	38777380	38777613	chr6	-0.62
GLO1	304	chr6:38779085-38779383	pro	38779085	38779383	chr6	-0.42
PRPF4B	2013	chr6:3964057-3965049	pro	3964057	3965049	chr6	-0.27
APOBEC2	938	chr6:41127654-41128302	pro	41127654	41128302	chr6	-0.65
APOBEC2	2071	chr6:41130601-41131373	pro	41130601	41131373	chr6	-0.95
TREML2	257	chr6:41275372-41277922	pro	41275372	41277922	chr6	-0.51
NCR2	1826	chr6:41409582-41409773	pro	41409582	41409773	chr6	-0.37
TFEB	2936	chr6:41804455-41809908	pro	41804455	41809908	chr6	-0.48
CCND3	2574	chr6:42013282-42016698	pro	42013282	42016698	chr6	-0.58
CCND3	1998	chr6:42120829-42124394	pro	42120829	42124394	chr6	-0.51
TRERF1	1125	chr6:42525449-42527837	pro	42525449	42527837	chr6	-0.35
TRERF1	1594	chr6:42529037-42529686	pro	42529037	42529686	chr6	-0.30
ATP6V0CP3	866	chr6:42802034-42802815	pro	42802034	42802815	chr6	-0.30
TBCC	2665	chr6:42823790-42825264	pro	42823790	42825264	chr6	-0.76
PTCRA	124	chr6:42991393-42992262	pro	42991393	42992262	chr6	-0.57

PTK7	334	chr6:43151411-43151884	pro	43151411	43151884	chr6	-0.27
ZNF318	1175	chr6:43446274-43446396	pro	43446274	43446396	chr6	-0.67
ZNF318	2118	chr6:43446948-43447608	pro	43446948	43447608	chr6	-0.70
MAD2L1BP	1614	chr6:43706654-43707086	pro	43706654	43707086	chr6	-0.85
C6orf223	1270	chr6:44077262-44077907	pro	44077262	44077907	chr6	-0.30
SLC29A1	984	chr6:44294047-44294420	pro	44294047	44294420	chr6	-0.46
SLC29A1	2304	chr6:44301309-44301978	pro	44301309	44301978	chr6	-0.50
RUNX2	642	chr6:45498789-45499075	pro	45498789	45499075	chr6	-0.56
RUNX2	2190	chr6:45499953-45501007	pro	45499953	45501007	chr6	-0.90
TNFRSF21	1746	chr6:47383276-47384516	pro	47383276	47384516	chr6	-0.94
TNFRSF21	338	chr6:47385802-47386158	pro	47385802	47386158	chr6	-0.77
CD2AP	1073	chr6:47551631-47553187	pro	47551631	47553187	chr6	-0.50
OPN5	1282	chr6:47856315-47856584	pro	47856315	47856584	chr6	-0.62
MCM3	1361	chr6:52257852-52260146	pro	52257852	52260146	chr6	-0.37
PAQR8	2000	chr6:52332784-52332983	pro	52332784	52332983	chr6	-0.65
EFHC1	1314	chr6:52391480-52391796	pro	52391480	52391796	chr6	-0.88
EFHC1	890	chr6:52391923-52392202	pro	52391923	52392202	chr6	-0.80
EFHC1	835	chr6:52394534-52394660	pro	52394534	52394660	chr6	-0.58
TRAM2	1434	chr6:52547125-52549650	pro	52547125	52549650	chr6	-0.62
LOC730101	2028	chr6:52637329-52641040	pro	52637329	52641040	chr6	-0.76
ICK	968	chr6:53032897-53034288	pro	53032897	53034288	chr6	-0.56
ICK	731	chr6:53034727-53035855	pro	53034727	53035855	chr6	-0.42
FBXO9	333	chr6:53037302-53037540	pro	53037302	53037540	chr6	-0.51
FBXO9	1872	chr6:53040028-53040145	pro	53040028	53040145	chr6	-0.50
RPS16P5	895	chr6:53310893-53311645	pro	53310893	53311645	chr6	-0.61
RPS16P5	1637	chr6:53311787-53312235	pro	53311787	53312235	chr6	-0.55
DST	276	chr6:56824808-56825091	pro	56824808	56825091	chr6	-0.81
KIAA1586	1802	chr6:57020925-57021682	pro	57020925	57021682	chr6	-0.65
ZNF451	2307	chr6:57064431-57065755	pro	57064431	57065755	chr6	-0.47
EXOC2	1380	chr6:635915-637609	pro	635915	637609	chr6	-0.27
PHF3	702	chr6:64402438-64403487	pro	64402438	64403487	chr6	-0.28
SMAP1	610	chr6:71434900-71436224	pro	71434900	71436224	chr6	-0.28
MTO1	1686	chr6:74229761-74229960	pro	74229761	74229960	chr6	-0.28
EEF1A1	2202	chr6:74285071-74285478	pro	74285071	74285478	chr6	-0.42
LOC100506804	2154	chr6:76052732-76054473	pro	76052732	76054473	chr6	-0.85
TXNDC5	990	chr6:7853538-7855103	pro	7853538	7855103	chr6	-0.26
TXNDC5	2210	chr6:7856178-7860335	pro	7856178	7860335	chr6	-0.64
HMGN3-AS1	1751	chr6:79998196-79998518	pro	79998196	79998518	chr6	-0.68
HMGN3-AS1	1179	chr6:79998843-79999015	pro	79998843	79999015	chr6	-0.52
BLOC1S5	1566	chr6:8007933-8008227	pro	8007933	8008227	chr6	-0.91
LCA5	771	chr6:80302619-80303571	pro	80302619	80303571	chr6	-0.99
LCA5	841	chr6:80304122-80305292	pro	80304122	80305292	chr6	-0.99
EEF1E1-BLOC1	2198	chr6:8045367-8045892	pro	8045367	8045892	chr6	-0.56
EEF1E1-BLOC1	1784	chr6:8045999-8046089	pro	8045999	8046089	chr6	-0.35
BCKDHB	1232	chr6:80874005-80874582	pro	80874005	80874582	chr6	-0.48
UBE3D	1923	chr6:83830183-83830499	pro	83830183	83830499	chr6	-0.74
DOPEY1	376	chr6:83833499-83833953	pro	83833499	83833953	chr6	-0.51
SNX14	1728	chr6:86358537-86359148	pro	86358537	86359148	chr6	-0.68
SYNCRIP	1978	chr6:86405813-86406006	pro	86405813	86406006	chr6	-0.45
SYNCRIP	1550	chr6:86406215-86406462	pro	86406215	86406462	chr6	-0.73
SYNCRIP	1236	chr6:86406594-86406710	pro	86406594	86406710	chr6	-0.56
SNHG5	1204	chr6:86445472-86447276	pro	86445472	86447276	chr6	-0.28
SLC35A1	1505	chr6:88239856-88241874	pro	88239856	88241874	chr6	-0.26
RARS2	1847	chr6:88354516-88354698	pro	88354516	88354698	chr6	-0.74
UBE2J1	1150	chr6:90119946-90121031	pro	90119946	90121031	chr6	-0.47

MAP3K7	2086	chr6:91350761-91352550	pro	91350761	91352550	chr6	-0.31
NDUFAF4	1448	chr6:97450580-97451500	pro	97450580	97451500	chr6	-0.48
FBXL4	302	chr6:99502706-99503107	pro	99502706	99503107	chr6	-0.43
PNISR	2048	chr6:99981643-99982308	pro	99981643	99982308	chr6	-0.44
AP1S1	259	chr7:100584057-10058423	pro	100584057	100584233	chr7	-0.40
NAT16	2058	chr7:100612160-10061251	pro	100612160	100612513	chr7	-0.67
CUX1	2190	chr7:101243353-10124407	pro	101243353	101244072	chr7	-0.57
MIR4285	1708	chr7:101720498-10172226	pro	101720498	101722261	chr7	-0.36
MIR4285	1686	chr7:101724212-10172533	pro	101724212	101725337	chr7	-0.43
SRPK2	1640	chr7:104695059-10469518	pro	104695059	104695181	chr7	-0.61
SYPL1	2390	chr7:105542280-10554316	pro	105542280	105543161	chr7	-0.43
CCDC71L	260	chr7:106088953-10608930	pro	106088953	106089308	chr7	-0.37
PRKAR2B	3979	chr7:106473089-10647969	pro	106473089	106479693	chr7	-0.96
THAP5	1674	chr7:107994950-10799596	pro	107994950	107995969	chr7	-0.75
GPER1	1626	chr7:1091173-1091512	pro	1091173	1091512	chr7	-0.86
GPER1	1274	chr7:1091634-1091753	pro	1091634	1091753	chr7	-0.89
PHF14	2137	chr7:10981982-10982336	pro	10981982	10982336	chr7	-0.38
IFRD1	578	chr7:111848924-11185078	pro	111848924	111850789	chr7	-0.35
IFRD1	1954	chr7:111881252-11188135	pro	111881252	111881352	chr7	-0.58
LOC101927021	759	chr7:1167660-1167750	pro	1167660	1167750	chr7	-0.44
ING3	1962	chr7:120379828-12038019	pro	120379828	120380199	chr7	-0.62
ARL4A	588	chr7:12693719-12694325	pro	12693719	12694325	chr7	-0.99
AHCYL2	519	chr7:128795491-12879594	pro	128795491	128795943	chr7	-0.26
CEP41	1466	chr7:129866598-12986704	pro	129866598	129867046	chr7	-0.62
MEST	142	chr7:129913024-12991319	pro	129913024	129913191	chr7	-0.26
CHCHD3	1667	chr7:132415650-13241575	pro	132415650	132415752	chr7	-0.37
CHCHD3	1366	chr7:132415932-13241607	pro	132415932	132416071	chr7	-0.39
BPGM	1919	chr7:133983708-13398427	pro	133983708	133984270	chr7	-0.82
NUP205	1584	chr7:134891347-13489188	pro	134891347	134891885	chr7	-0.76
CREB3L2	2272	chr7:137333442-13733679	pro	137333442	137336791	chr7	-0.99
MRPS33	1847	chr7:140359037-14035916	pro	140359037	140359165	chr7	-0.71
SSBP1	1590	chr7:141086408-14108652	pro	141086408	141086520	chr7	-0.54
PRSS2	0	chr7:142178543-14217900	pro	142178543	142179008	chr7	-0.96
PRSS2	734	chr7:142179339-14217968	pro	142179339	142179681	chr7	-0.94
TMEM139	936	chr7:142690757-14269159	pro	142690757	142691594	chr7	-0.74
EZH2	2341	chr7:148208630-14820975	pro	148208630	148209756	chr7	-0.29
EZH2	1538	chr7:148213840-14821398	pro	148213840	148213985	chr7	-0.70
ZNF775	1658	chr7:149705586-14970577	pro	149705586	149705774	chr7	-0.59
FABP5P3	578	chr7:151765436-15176554	pro	151765436	151765544	chr7	-0.72
LMBR1	1410	chr7:156380003-15638014	pro	156380003	156380146	chr7	-0.54
DNAJB6	2280	chr7:156819367-15682101	pro	156819367	156821014	chr7	-0.91
PSMG3	772	chr7:1575133-1575634	pro	1575133	1575634	chr7	-0.31
WDR60	757	chr7:158341101-15834144	pro	158341101	158341441	chr7	-0.29
HDAC9	330	chr7:18514007-18516180	pro	18514007	18516180	chr7	-0.43
RPL23P8	1754	chr7:20835021-20835367	pro	20835021	20835367	chr7	-0.93
CDCA7L	877	chr7:21952158-21953732	pro	21952158	21953732	chr7	-0.36
RAPGEF5	1927	chr7:22359570-22362692	pro	22359570	22362692	chr7	-0.65
LOC100506178	22	chr7:22569249-22569756	pro	22569249	22569756	chr7	-0.86
SNORD93	277	chr7:22862106-22862852	pro	22862106	22862852	chr7	-0.50
FAM126A	2840	chr7:23015442-23019471	pro	23015442	23019471	chr7	-0.65
FAM126A	640	chr7:23020507-23021364	pro	23020507	23021364	chr7	-0.47
SNX8	1982	chr7:2318184-2319124	pro	2318184	2319124	chr7	-0.50
NUPL2	839	chr7:23186958-23187304	pro	23186958	23187304	chr7	-0.72
RPS2P32	242	chr7:23496011-23496565	pro	23496011	23496565	chr7	-0.28
RPS2P32	992	chr7:23497188-23497855	pro	23497188	23497855	chr7	-0.43

CCDC126	1847	chr7:23601554-23601796	pro	23601554	23601796	chr7	-0.76
LOC100507642	350	chr7:244380-244519	pro	244380	244519	chr7	-0.27
LFNG	203	chr7:2518794-2518988	pro	2518794	2518988	chr7	-0.62
MIR4648	2018	chr7:2535063-2535437	pro	2535063	2535437	chr7	-0.53
HOXA7	1030	chr7:27161373-27162210	pro	27161373	27162210	chr7	-0.65
JAZF1	1688	chr7:28187048-28190253	pro	28187048	28190253	chr7	-0.70
CREB5	1466	chr7:28303877-28304120	pro	28303877	28304120	chr7	-0.55
GNA12	1280	chr7:2848860-2849551	pro	2848860	2849551	chr7	-0.83
PLEKHA8	2754	chr7:30035007-30039502	pro	30035007	30039502	chr7	-0.41
NOD1	1588	chr7:30483042-30483619	pro	30483042	30483619	chr7	-0.91
GARS	1129	chr7:30599489-30599661	pro	30599489	30599661	chr7	-0.79
BBS9	1722	chr7:33137249-33137547	pro	33137249	33137547	chr7	-0.62
TBX20	1610	chr7:35257084-35260169	pro	35257084	35260169	chr7	-0.97
LOC100506725	1244	chr7:35721102-35721551	pro	35721102	35721551	chr7	-0.90
LOC100506725	34	chr7:35722145-35723063	pro	35722145	35723063	chr7	-0.90
VPS41	1289	chr7:38913989-38914085	pro	38913989	38914085	chr7	-0.33
COA1	1907	chr7:43733534-43733984	pro	43733534	43733984	chr7	-0.56
AEBP1	938	chr7:44111103-44111742	pro	44111103	44111742	chr7	-0.81
H2AFV	2004	chr7:44856126-44856381	pro	44856126	44856381	chr7	-0.89
MIR4657	1902	chr7:44885924-44886119	pro	44885924	44886119	chr7	-0.89
MIR4657	654	chr7:44886220-44890935	pro	44886220	44890935	chr7	-0.60
CCM2	1155	chr7:45004347-45005079	pro	45004347	45005079	chr7	-0.69
SNORA5B	2178	chr7:45114075-45114730	pro	45114075	45114730	chr7	-0.49
TBRG4	1499	chr7:45116209-45116537	pro	45116209	45116537	chr7	-0.33
VOPP1	1616	chr7:55609107-55609514	pro	55609107	55609514	chr7	-0.35
PSPH	1368	chr7:56085223-56085566	pro	56085223	56085566	chr7	-0.31
AIMP2	956	chr7:6016209-6016516	pro	6016209	6016516	chr7	-0.34
USP42	2144	chr7:6113072-6113365	pro	6113072	6113365	chr7	-0.68
ZNF736	1533	chr7:63412517-63413917	pro	63412517	63413917	chr7	-0.32
FAM220A	1493	chr7:6356299-6356919	pro	6356299	6356919	chr7	-0.58
ZNF680	1938	chr7:63658606-63659398	pro	63658606	63659398	chr7	-0.93
RAC1	1794	chr7:6378728-6378984	pro	6378728	6378984	chr7	-0.73
RAC1	1312	chr7:6379142-6379533	pro	6379142	6379533	chr7	-0.44
ZNF138	1571	chr7:63893342-63894200	pro	63893342	63894200	chr7	-0.74
ZNF273	1482	chr7:64002186-64002886	pro	64002186	64002886	chr7	-0.84
DAGLB	1132	chr7:6455232-6455368	pro	6455232	6455368	chr7	-0.75
KDELR2	550	chr7:6490862-6490986	pro	6490862	6490986	chr7	-0.73
KCTD7	1930	chr7:65731839-65734625	pro	65731839	65734625	chr7	-0.48
ZDHHC4	961	chr7:6582215-6583039	pro	6582215	6583039	chr7	-0.69
ZDHHC4	1046	chr7:6584540-6584727	pro	6584540	6584727	chr7	-0.89
TMEM248	1862	chr7:66025381-66025616	pro	66025381	66025616	chr7	-0.43
ZNF12	1578	chr7:6711389-6711639	pro	6711389	6711639	chr7	-0.52
TBL2	1874	chr7:72628991-72629162	pro	72628991	72629162	chr7	-0.34
ABHD11-AS1	6	chr7:72787257-72787422	pro	72787257	72787422	chr7	-0.57
WBSCR27	317	chr7:72894984-72895234	pro	72894984	72895234	chr7	-0.79
RFC2	901	chr7:73307534-73307716	pro	73307534	73307716	chr7	-0.50
WBSCR16	1306	chr7:74126264-74126433	pro	74126264	74126433	chr7	-0.35
HIP1	2168	chr7:75208142-75208647	pro	75208142	75208647	chr7	-0.50
HSPB1	1837	chr7:75771479-75771815	pro	75771479	75771815	chr7	-0.63
PHTF2	420	chr7:77306896-77307029	pro	77306896	77307029	chr7	-0.34
PHTF2	12	chr7:77307210-77307531	pro	77307210	77307531	chr7	-0.46
PCLO	532	chr7:82630428-82630903	pro	82630428	82630903	chr7	-0.97
CROT	1080	chr7:86813889-86814043	pro	86813889	86814043	chr7	-0.52
GET4	1142	chr7:881148-882001	pro	881148	882001	chr7	-0.65
CDK6	2308	chr7:92297450-92300269	pro	92297450	92300269	chr7	-0.58

ADAP1	1738	chr7:928718-928862	pro	928718	928862	chr7	-0.61
ADAP1	778	chr7:962124-962573	pro	962124	962573	chr7	-0.95
ACN9	14	chr7:96583760-96583892	pro	96583760	96583892	chr7	-0.60
ACN9	284	chr7:96584000-96584249	pro	96584000	96584249	chr7	-0.26
TECPR1	2045	chr7:97717408-97717502	pro	97717408	97717502	chr7	-0.80
NPTX2	1827	chr7:98086194-98086524	pro	98086194	98086524	chr7	-0.40
COX19	264	chr7:981851-982200	pro	981851	982200	chr7	-0.50
TMEM130	916	chr7:98306432-98306619	pro	98306432	98306619	chr7	-0.37
MIR3609	847	chr7:98316054-98316668	pro	98316054	98316668	chr7	-0.78
MBLAC1	1799	chr7:99560289-99560621	pro	99560289	99560621	chr7	-0.32
PVRIG	628	chr7:99654054-99654302	pro	99654054	99654302	chr7	-0.83
VPS13B	1465	chr8:100093108-1000932	pro	100093108	100093298	chr8	-0.42
VPS13B	1460	chr8:100095812-1000964	pro	100095812	100096444	chr8	-0.47
POLR2K	1306	chr8:101233233-1012334	pro	101233233	101233406	chr8	-0.79
LOC101927221	1818	chr8:103322598-1033227	pro	103322598	103322745	chr8	-0.59
UBR5	1581	chr8:103495531-10349581	pro	103495531	103495819	chr8	-0.75
FZD6	210	chr8:104379200-1043800	pro	104379200	104380053	chr8	-0.60
FZD6	1323	chr8:104380672-1043824	pro	104380672	104382442	chr8	-0.94
LOC101929229	408	chr8:10735006-10735697	pro	10735006	10735697	chr8	-0.31
OXR1	1362	chr8:107739741-1077414	pro	107739741	107741404	chr8	-0.98
ENY2	1613	chr8:110417090-11041758	pro	110417090	110417588	chr8	-0.74
XKR6	3568	chr8:11090889-11094547	pro	11090889	11094547	chr8	-0.72
XKR6	759	chr8:11096563-11097527	pro	11096563	11097527	chr8	-0.70
MTMR9	536	chr8:11178444-11179301	pro	11178444	11179301	chr8	-0.36
FAM167A	1740	chr8:11358557-11361334	pro	11358557	11361334	chr8	-0.57
FAM167A	1147	chr8:11362721-11362945	pro	11362721	11362945	chr8	-0.65
BLK	2248	chr8:11387206-11395145	pro	11387206	11395145	chr8	-0.38
NEIL2	864	chr8:11663385-11664047	pro	11663385	11664047	chr8	-0.77
TRPS1	1199	chr8:116747131-1167492	pro	116747131	116749299	chr8	-0.37
FDFT1	1517	chr8:11695682-11696340	pro	11695682	11696340	chr8	-0.77
TAF2	1248	chr8:120912898-12091311	pro	120912898	120913118	chr8	-0.45
LONRF1	1634	chr8:12657900-12660096	pro	12657900	12660096	chr8	-0.56
CASC19	600	chr8:128278071-1282788	pro	128278071	128278836	chr8	-0.91
MIR1204	1616	chr8:128878596-12887941	pro	128878596	128879413	chr8	-0.45
MIR1207	673	chr8:129129486-1291303	pro	129129486	129130324	chr8	-0.26
FAM49B	1191	chr8:131019513-1310207	pro	131019513	131020705	chr8	-0.49
MIR5194	325	chr8:131089787-1310906	pro	131089787	131090627	chr8	-0.64
MIR7848	39	chr8:134127728-1341283	pro	134127728	134128366	chr8	-0.93
TRAPPC9	1932	chr8:141535046-1415351	pro	141535046	141535178	chr8	-0.40
CHRAC1	1945	chr8:141588524-1415887	pro	141588524	141588742	chr8	-0.43
CHRAC1	1368	chr8:141589019-1415894	pro	141589019	141589402	chr8	-0.30
ZNF623	1094	chr8:144788120-1447883	pro	144788120	144788340	chr8	-0.51
PLEC	533	chr8:145085901-1450866	pro	145085901	145086657	chr8	-0.27
SPATC1	85	chr8:145158396-1451585	pro	145158396	145158570	chr8	-0.40
ZNF34	1539	chr8:145981786-1459822	pro	145981786	145982204	chr8	-0.39
MSR1	212	chr8:16094270-16094650	pro	16094270	16094650	chr8	-0.75
FGF20	997	chr8:16902607-16903491	pro	16902607	16903491	chr8	-0.26
MICU3	1043	chr8:16929644-16930674	pro	16929644	16930674	chr8	-0.38
ZDHHC2	754	chr8:17057054-17057850	pro	17057054	17057850	chr8	-0.30
ZDHHC2	1630	chr8:17059130-17060542	pro	17059130	17060542	chr8	-0.65
VPS37A	2010	chr8:17150625-17150936	pro	17150625	17150936	chr8	-0.68
ZNF596	705	chr8:173170-173336	pro	173170	173336	chr8	-0.29
MTUS1	182	chr8:17599081-17599608	pro	17599081	17599608	chr8	-0.78
PCM1	732	chr8:17823462-17824362	pro	17823462	17824362	chr8	-0.40
ATP6V1B2	188	chr8:20098573-20099014	pro	20098573	20099014	chr8	-0.28

XPO7	1743	chr8:21833749-21835985	pro	21833749	21835985	chr8	-0.44
FAM160B2	460	chr8:22002008-22002387	pro	22002008	22002387	chr8	-0.72
REEP4	461	chr8:22055466-22056244	pro	22055466	22056244	chr8	-0.32
SLC39A14	1552	chr8:22282494-22282597	pro	22282494	22282597	chr8	-0.62
CCAR2	422	chr8:22517326-22518007	pro	22517326	22518007	chr8	-0.33
RHOBTB2	519	chr8:22912202-22912832	pro	22912202	22912832	chr8	-0.39
TNFRSF10B	610	chr8:22983113-22983399	pro	22983113	22983399	chr8	-0.69
TNFRSF10D	1386	chr8:23075698-23076506	pro	23075698	23076506	chr8	-0.38
TNFRSF10A	1455	chr8:23136819-23137523	pro	23136819	23137523	chr8	-0.28
LOC389641	1730	chr8:23139929-23140888	pro	23139929	23140888	chr8	-0.48
CHMP7	1482	chr8:23155539-23155686	pro	23155539	23155686	chr8	-0.74
CHMP7	642	chr8:23155914-23156991	pro	23155914	23156991	chr8	-0.54
CHMP7	1386	chr8:23157148-23159811	pro	23157148	23159811	chr8	-0.28
R3HCC1	436	chr8:23200746-23201478	pro	23200746	23201478	chr8	-0.60
ENTPD4	3474	chr8:23364775-23370657	pro	23364775	23370657	chr8	-0.38
SLC25A37	484	chr8:23441480-23442164	pro	23441480	23442164	chr8	-0.33
SLC25A37	1580	chr8:23443155-23444617	pro	23443155	23444617	chr8	-0.34
KCTD9	1820	chr8:25369013-25371151	pro	25369013	25371151	chr8	-0.31
CDCA2	1284	chr8:25373107-25374317	pro	25373107	25374317	chr8	-0.33
PPP2R2A	713	chr8:26205731-26208991	pro	26205731	26208991	chr8	-0.34
BNIP3L	464	chr8:26295615-26296334	pro	26295615	26296334	chr8	-0.46
BNIP3L	1265	chr8:26297207-26298199	pro	26297207	26298199	chr8	-0.28
DPYSL2	1597	chr8:26488717-26490601	pro	26488717	26490601	chr8	-0.26
DPYSL2	1750	chr8:26492636-26494536	pro	26492636	26494536	chr8	-0.28
TRIM35	2414	chr8:27221486-27223190	pro	27221486	27223190	chr8	-0.69
PTK2B	580	chr8:27224968-27226021	pro	27224968	27226021	chr8	-0.40
PTK2B	460	chr8:27238040-27238863	pro	27238040	27238863	chr8	-0.41
ESCO2	960	chr8:27688221-27689651	pro	27688221	27689651	chr8	-0.44
PBK	1478	chr8:27749165-27750944	pro	27749165	27750944	chr8	-0.29
PBK	442	chr8:27751302-27752647	pro	27751302	27752647	chr8	-0.30
PBK	2127	chr8:27753429-27753889	pro	27753429	27753889	chr8	-0.86
NUGGC	662	chr8:27994720-27998571	pro	27994720	27998571	chr8	-0.35
NUGGC	1688	chr8:27998911-27999080	pro	27998911	27999080	chr8	-0.81
ELP3	934	chr8:28005520-28005617	pro	28005520	28005617	chr8	-0.63
ELP3	758	chr8:28006665-28007856	pro	28006665	28007856	chr8	-0.31
ELP3	1966	chr8:28008327-28008609	pro	28008327	28008609	chr8	-0.78
PNOC	1966	chr8:28249434-28250797	pro	28249434	28250797	chr8	-0.96
PNOC	582	chr8:28251255-28254073	pro	28251255	28254073	chr8	-0.35
ZNF395	598	chr8:28299984-28301004	pro	28299984	28301004	chr8	-0.43
ZNF395	1988	chr8:28301776-28301993	pro	28301776	28301993	chr8	-0.70
FBXO16	160	chr8:28403115-28404713	pro	28403115	28404713	chr8	-0.42
FZD3	908	chr8:28405968-28407495	pro	28405968	28407495	chr8	-0.33
FZD3	1685	chr8:28408308-28410342	pro	28408308	28410342	chr8	-0.63
INTS9	1645	chr8:28800081-28803333	pro	28800081	28803333	chr8	-0.54
HMBOX1	1397	chr8:28804730-28806348	pro	28804730	28806348	chr8	-0.57
KIF13B	920	chr8:29175287-29175934	pro	29175287	29175934	chr8	-0.26
SARAF	1635	chr8:30058143-30059119	pro	30058143	30059119	chr8	-0.27
SARAF	440	chr8:30060374-30061037	pro	30060374	30061037	chr8	-0.42
DCTN6	1160	chr8:30133906-30135122	pro	30133906	30135122	chr8	-0.32
GTF2E2	1852	chr8:30633141-30633715	pro	30633141	30633715	chr8	-0.32
GTF2E2	761	chr8:30636009-30636073	pro	30636009	30636073	chr8	-0.27
PPP2CB	1462	chr8:30788326-30788538	pro	30788326	30788538	chr8	-0.57
PPP2CB	288	chr8:30790081-30790283	pro	30790081	30790283	chr8	-0.74
PURG	1028	chr8:31010948-31012655	pro	31010948	31012655	chr8	-0.26
FUT10	285	chr8:33450398-33450584	pro	33450398	33450584	chr8	-0.39

TTI2	1706	chr8:33488375-33488704	pro	33488375	33488704	chr8	-0.71
RNF122	1726	chr8:33541962-33542962	pro	33541962	33542962	chr8	-0.55
RAB11FIP1	905	chr8:37877000-37877158	pro	37877000	37877158	chr8	-0.84
ASH2L	1552	chr8:38083596-38084439	pro	38083596	38084439	chr8	-0.62
BAG4	2446	chr8:38150313-38151319	pro	38150313	38151319	chr8	-0.48
FGFR1	1412	chr8:38441882-38444333	pro	38441882	38444333	chr8	-0.67
FGFR1	140	chr8:38445536-38445765	pro	38445536	38445765	chr8	-0.89
ADAM9	1608	chr8:38974231-38976304	pro	38974231	38976304	chr8	-0.58
IDO1	137	chr8:39890565-39890677	pro	39890565	39890677	chr8	-0.75
MIR486-1	2162	chr8:41639084-41639608	pro	41639084	41639608	chr8	-0.37
SMIM19	1584	chr8:42513426-42514314	pro	42513426	42514314	chr8	-0.41
CHRNA6	528	chr8:42741583-42743534	pro	42741583	42743534	chr8	-0.69
FNTA	1389	chr8:43029146-43029272	pro	43029146	43029272	chr8	-0.77
PRKDC	1620	chr8:49033511-49033842	pro	49033511	49033842	chr8	-0.65
UBE2V2	1336	chr8:49084665-49085100	pro	49084665	49085100	chr8	-0.38
RB1CC1	2018	chr8:53791242-53791954	pro	53791242	53791954	chr8	-0.74
LINC00968	43	chr8:57634081-57635877	pro	57634081	57635877	chr8	-0.39
LINC01301	1266	chr8:61487615-61487717	pro	61487615	61487717	chr8	-0.29
LOC100130298	906	chr8:62041412-62042501	pro	62041412	62042501	chr8	-0.78
MCPH1	1137	chr8:6252096-6253218	pro	6252096	6253218	chr8	-0.34
ASPH	2169	chr8:62786004-62789166	pro	62786004	62789166	chr8	-0.78
GGH	1296	chr8:64112072-64113664	pro	64112072	64113664	chr8	-0.48
YTHDF3-AS1	992	chr8:64241902-64243225	pro	64241902	64243225	chr8	-0.27
YTHDF3	1830	chr8:64245764-64246125	pro	64245764	64246125	chr8	-0.36
AGPAT5	1697	chr8:6554056-6555906	pro	6554056	6555906	chr8	-0.36
MTFR1	1462	chr8:66720604-66721201	pro	66720604	66721201	chr8	-0.67
GS1-24F4.2	2130	chr8:6676969-6679740	pro	6676969	6679740	chr8	-0.93
GS1-24F4.2	362	chr8:6679946-6680298	pro	6679946	6680298	chr8	-0.42
XKR5	224	chr8:6680554-6681047	pro	6680554	6681047	chr8	-0.80
SNORD87	94	chr8:67996076-67998413	pro	67996076	67998413	chr8	-0.35
SNHG6	1578	chr8:68001473-68002348	pro	68001473	68002348	chr8	-0.69
TCF24	354	chr8:68037661-68037808	pro	68037661	68037808	chr8	-0.89
LOC286190	1090	chr8:71684379-71684530	pro	71684379	71684530	chr8	-0.64
TCEB1	1378	chr8:75045071-75045569	pro	75045071	75045569	chr8	-0.39
TMEM70	1346	chr8:75052195-75052356	pro	75052195	75052356	chr8	-0.41
TMEM70	1744	chr8:75052548-75052799	pro	75052548	75052799	chr8	-0.55
PEX2	2057	chr8:78072903-78073143	pro	78072903	78073143	chr8	-0.54
MRPS28	1851	chr8:81103132-81103290	pro	81103132	81103290	chr8	-0.68
PAG1	3146	chr8:82181050-82186373	pro	82181050	82186373	chr8	-0.63
PAG1	434	chr8:82186999-82187584	pro	82186999	82187584	chr8	-0.33
SNX16	2696	chr8:82912859-82915902	pro	82912859	82915902	chr8	-0.34
CLDN23	266	chr8:8597260-8597421	pro	8597260	8597421	chr8	-0.36
CLDN23	1900	chr8:8598159-8599789	pro	8598159	8599789	chr8	-0.89
E2F5	2329	chr8:86273550-86275532	pro	86273550	86275532	chr8	-0.25
C8orf59	1524	chr8:86320329-86322528	pro	86320329	86322528	chr8	-0.52
WWP1	715	chr8:87423107-87423679	pro	87423107	87423679	chr8	-0.46
ERI1	327	chr8:8897105-8897685	pro	8897105	8897685	chr8	-0.98
ERI1	1064	chr8:8898213-8899358	pro	8898213	8899358	chr8	-0.95
NBN	376	chr8:91066189-91066715	pro	91066189	91066715	chr8	-0.70
TMEM64	4535	chr8:91719154-91726396	pro	91719154	91726396	chr8	-0.28
TMEM55A	1329	chr8:92119952-92122150	pro	92119952	92122150	chr8	-0.76
TMEM55A	456	chr8:92122380-92123291	pro	92122380	92123291	chr8	-0.47
OTUD6B	1628	chr8:92153149-92153303	pro	92153149	92153303	chr8	-0.63
TNKS	528	chr8:9450023-9450628	pro	9450023	9450628	chr8	-0.40
TNKS	1961	chr8:9451420-9454210	pro	9451420	9454210	chr8	-0.38

FAM92A1	634	chr8:94782468-94782621	pro	94782468	94782621	chr8	-0.46
RBM12B-AS1	2001	chr8:94819060-94819966	pro	94819060	94819966	chr8	-0.77
TMEM67	437	chr8:94835425-94836193	pro	94835425	94836193	chr8	-0.28
MIR3150B	1334	chr8:96154923-96156546	pro	96154923	96156546	chr8	-0.31
MTDH	1396	chr8:98723906-98724465	pro	98723906	98724465	chr8	-0.74
SNORA72	696	chr8:99124049-99124588	pro	99124049	99124588	chr8	-0.68
SNORA72	1474	chr8:99124928-99125263	pro	99124928	99125263	chr8	-0.48
POP1	1124	chr8:99200313-99200418	pro	99200313	99200418	chr8	-0.39
ALG2	1976	chr9:101021633-10102255	pro	101021633	101022550	chr9	-0.64
SEC61B	2020	chr9:101025701-10102712	pro	101025701	101027120	chr9	-0.83
LOC101928438	956	chr9:101620468-10162160	pro	101620468	101621603	chr9	-0.25
STX17	1260	chr9:101709911-10171007	pro	101709911	101710078	chr9	-0.31
DMRT2	472	chr9:1039604-1040140	pro	1039604	1040140	chr9	-0.98
DMRT2	388	chr9:1040461-1041550	pro	1040461	1041550	chr9	-0.98
NIPSNAP3B	1347	chr9:106566862-10656837	pro	106566862	106568372	chr9	-0.39
LOC286367	1424	chr9:106574538-10657551	pro	106574538	106575518	chr9	-0.58
ABCA1	2332	chr9:106727445-10672858	pro	106727445	106728588	chr9	-0.40
SLC44A1	1973	chr9:107044517-10704496	pro	107044517	107044965	chr9	-0.60
RAD23B	1768	chr9:109083376-10908375	pro	109083376	109083759	chr9	-0.80
TMEM245	576	chr9:110922330-11092291	pro	110922330	110922913	chr9	-0.57
PTPN3	1580	chr9:111218124-11121848	pro	111218124	111218484	chr9	-0.82
PTPN3	220	chr9:111218823-11122138	pro	111218823	111221385	chr9	-0.93
ZFP37	692	chr9:114857784-11485861	pro	114857784	114858615	chr9	-0.99
RGS3	1856	chr9:115384248-11538541	pro	115384248	115385416	chr9	-0.31
ZNF618	828	chr9:115679145-11567927	pro	115679145	115679275	chr9	-0.34
AKNA	1808	chr9:116194083-11619531	pro	116194083	116195313	chr9	-0.59
AKNA	720	chr9:116195579-11619599	pro	116195579	116195993	chr9	-0.77
C9orf91	1502	chr9:116411907-11641214	pro	116411907	116412141	chr9	-0.46
TNFSF8	1846	chr9:116734490-11673459	pro	116734490	116734594	chr9	-0.53
TLR4	2055	chr9:119508271-11950838	pro	119508271	119508383	chr9	-0.39
CDK5RAP2	1738	chr9:122380455-12238060	pro	122380455	122380609	chr9	-0.41
FBXW2	2022	chr9:122593455-12259362	pro	122593455	122593625	chr9	-0.69
LOC100288842	1231	chr9:122596767-12259688	pro	122596767	122596883	chr9	-0.54
PHF19	1642	chr9:122677157-12267841	pro	122677157	122678414	chr9	-0.27
PHF19	1535	chr9:122695030-12269589	pro	122695030	122695892	chr9	-0.69
TRAF1	60	chr9:122726851-12273101	pro	122726851	122731017	chr9	-0.62
TRAF1	1192	chr9:122732305-12273262	pro	122732305	122732624	chr9	-0.81
GGTA1P	1510	chr9:123300548-12330068	pro	123300548	123300689	chr9	-0.44
TTLL11	1660	chr9:123897252-12389748	pro	123897252	123897480	chr9	-0.42
MIR600	124	chr9:124913775-12491396	pro	124913775	124913961	chr9	-0.68
DENND1A	1926	chr9:125728931-12573169	pro	125728931	125731692	chr9	-0.52
NEK6	1028	chr9:126058492-12605885	pro	126058492	126058859	chr9	-0.84
NEK6	152	chr9:126093835-12609400	pro	126093835	126094000	chr9	-0.78
RPL35	1688	chr9:126665601-12666589	pro	126665601	126665899	chr9	-0.57
GOLGA1	2023	chr9:126741062-12674130	pro	126741062	126741308	chr9	-0.84
PPP6C	2056	chr9:126989877-12699009	pro	126989877	126990092	chr9	-0.25
NRON	1342	chr9:128213436-12821445	pro	128213436	128214455	chr9	-0.86
ZBTB34	1471	chr9:128663340-12866513	pro	128663340	128665130	chr9	-0.30
ZNF79	1556	chr9:129227968-12922808	pro	129227968	129228087	chr9	-0.73
SNORA65	32	chr9:129250451-12925096	pro	129250451	129250961	chr9	-0.69
TOR2A	358	chr9:129537605-12953801	pro	129537605	129538012	chr9	-0.62
SH2D3C	310	chr9:129580401-12958196	pro	129580401	129581960	chr9	-0.44
SH2D3C	1500	chr9:129582185-12958255	pro	129582185	129582554	chr9	-0.91
MIR3960	2468	chr9:129584812-12958611	pro	129584812	129586117	chr9	-0.67
ST6GALNAC6	1037	chr9:129702686-12970288	pro	129702686	129702884	chr9	-0.55

ST6GALNAC6	1514	chr9:129703042-12970348	pro	129703042	129703483	chr9	-0.78
ST6GALNAC6	374	chr9:129705367-12970878	pro	129705367	129708782	chr9	-0.37
ST6GALNAC4	564	chr9:129719377-12972000	pro	129719377	129720003	chr9	-0.32
ST6GALNAC4	1416	chr9:129720211-12972087	pro	129720211	129720873	chr9	-0.96
FAM102A	2782	chr9:129784534-12978629	pro	129784534	129786299	chr9	-0.48
PTGES2	2232	chr9:129927376-12992873	pro	129927376	129928736	chr9	-0.28
SET	1090	chr9:130484580-13048474	pro	130484580	130484747	chr9	-0.61
SET	1441	chr9:130489658-13049011	pro	130489658	130490116	chr9	-0.67
CCBL1	1780	chr9:130682183-13068260	pro	130682183	130682609	chr9	-0.53
PHYHD1	83	chr9:130722522-13072330	pro	130722522	130723300	chr9	-0.54
IER5L	586	chr9:130980855-13098104	pro	130980855	130981042	chr9	-0.45
NTMT1	1138	chr9:131409734-13140995	pro	131409734	131409955	chr9	-0.42
NTMT1	2079	chr9:131412857-13141326	pro	131412857	131413265	chr9	-0.31
NTMT1	1670	chr9:131426459-13142670	pro	131426459	131426705	chr9	-0.53
FNBP1	2346	chr9:131847072-13184820	pro	131847072	131848208	chr9	-0.46
GPR107	1570	chr9:131853909-13185455	pro	131853909	131854558	chr9	-0.79
TSC1	1744	chr9:134806834-13480936	pro	134806834	134809362	chr9	-0.44
GTF3C5	1093	chr9:134894636-13489494	pro	134894636	134894942	chr9	-0.30
GTF3C5	1355	chr9:134897164-13489731	pro	134897164	134897310	chr9	-0.53
RALGDS	224	chr9:134995982-13499630	pro	134995982	134996301	chr9	-0.89
SURF1	1348	chr9:135211798-13521187	pro	135211798	135211871	chr9	-0.29
REXO4	1212	chr9:135274181-13527447	pro	135274181	135274471	chr9	-0.85
ADAMTS13	1406	chr9:135275266-13527580	pro	135275266	135275801	chr9	-0.81
CACFD1	1139	chr9:135315489-13531660	pro	135315489	135316601	chr9	-0.49
CACFD1	2050	chr9:135316849-13531706	pro	135316849	135317064	chr9	-0.90
VAV2	1322	chr9:135845511-13584638	pro	135845511	135846380	chr9	-0.79
RXRA	625	chr9:136438723-13643902	pro	136438723	136439023	chr9	-0.39
FCN1	194	chr9:136949017-13694985	pro	136949017	136949852	chr9	-0.83
CAMSAP1	1062	chr9:137937185-13793834	pro	137937185	137938342	chr9	-0.41
CAMSAP1	1844	chr9:137940500-13794084	pro	137940500	137940841	chr9	-0.50
UBAC1	568	chr9:137993198-13799403	pro	137993198	137994034	chr9	-0.25
QSOX2	438	chr9:138277741-13827815	pro	138277741	138278150	chr9	-0.27
PMPCA	1582	chr9:138423040-13842348	pro	138423040	138423484	chr9	-0.40
TMEM141	652	chr9:138804810-13880507	pro	138804810	138805077	chr9	-0.27
CCDC183	454	chr9:138810025-13881028	pro	138810025	138810286	chr9	-0.86
CCDC183	28	chr9:138810476-13881079	pro	138810476	138810799	chr9	-0.73
C8G	184	chr9:138959252-13895941	pro	138959252	138959416	chr9	-0.53
TUBB4B	2052	chr9:139253397-13925356	pro	139253397	139253560	chr9	-0.87
ARRDC1-AS1	1546	chr9:139631156-13963135	pro	139631156	139631356	chr9	-0.59
NFIB	1916	chr9:14301261-14302999	pro	14301261	14302999	chr9	-0.96
NFIB	471	chr9:14303387-14303763	pro	14303387	14303763	chr9	-0.96
CCDC171	1612	chr9:15544263-15545152	pro	15544263	15545152	chr9	-0.27
HAUS6	1674	chr9:19091189-19091343	pro	19091189	19091343	chr9	-0.54
CDKN2B	1736	chr9:21997456-21997695	pro	21997456	21997695	chr9	-0.93
DOCK8	1656	chr9:263937-265467	pro	263937	265467	chr9	-0.37
NDUFB6	2034	chr9:32561053-32561244	pro	32561053	32561244	chr9	-0.64
NFX1	1975	chr9:33282165-33282617	pro	33282165	33282617	chr9	-0.40
AQP3	1096	chr9:33435554-33437519	pro	33435554	33437519	chr9	-0.36
NOL6	936	chr9:33464695-33465061	pro	33464695	33465061	chr9	-0.40
ZBTB5	1655	chr9:37456835-37457291	pro	37456835	37457291	chr9	-0.26
EXOSC3	2152	chr9:37772727-37773150	pro	37772727	37773150	chr9	-0.42
EXOSC3	1576	chr9:37773394-37773635	pro	37773394	37773635	chr9	-0.52
EXOSC3	869	chr9:37775662-37776256	pro	37775662	37776256	chr9	-0.36
DCAF10	1558	chr9:37788921-37789063	pro	37788921	37789063	chr9	-0.80
DCAF10	602	chr9:37789854-37790041	pro	37789854	37790041	chr9	-0.76

ERMP1	1898	chr9:5821030-5821339	pro	5821030	5821339	chr9	-0.30
LINC01506	972	chr9:70352218-70352401	pro	70352218	70352401	chr9	-0.55
SMC5	1659	chr9:72065137-72065573	pro	72065137	72065573	chr9	-0.44
C9orf85	1832	chr9:73717639-73718508	pro	73717639	73718508	chr9	-0.79
C9orf40	1740	chr9:76755759-76756006	pro	76755759	76756006	chr9	-0.82
C9orf41-AS1	761	chr9:76757807-76759115	pro	76757807	76759115	chr9	-0.43
RFK	1494	chr9:78197613-78197926	pro	78197613	78197926	chr9	-0.81
GCNT1	2393	chr9:78279810-78281556	pro	78279810	78281556	chr9	-0.98
VPS13A-AS1	2026	chr9:78984585-78984775	pro	78984585	78984775	chr9	-0.60
CEP78	1441	chr9:80042000-80042502	pro	80042000	80042502	chr9	-0.63
NAA35	516	chr9:87745132-87745588	pro	87745132	87745588	chr9	-0.28
SECISBP2	1690	chr9:91125159-91125388	pro	91125159	91125388	chr9	-0.82
GADD45G	1278	chr9:91407946-91408989	pro	91407946	91408989	chr9	-0.79
GADD45G	497	chr9:91409195-91409303	pro	91409195	91409303	chr9	-0.81
SYK	1247	chr9:92602428-92602642	pro	92602428	92602642	chr9	-0.34
MIR3651	954	chr9:94093304-94094089	pro	94093304	94094089	chr9	-0.67
ZNF484	2194	chr9:94677656-94678241	pro	94677656	94678241	chr9	-0.79
ZNF484	1610	chr9:94678352-94678712	pro	94678352	94678712	chr9	-0.83
SUSD3	379	chr9:94860211-94860611	pro	94860211	94860611	chr9	-0.33
C9orf89	2476	chr9:94895291-94896298	pro	94895291	94896298	chr9	-0.56
NINJ1	1381	chr9:94934954-94935068	pro	94934954	94935068	chr9	-0.26
PCAT7	1126	chr9:96355873-96356167	pro	96355873	96356167	chr9	-0.69
MIR2278	2073	chr9:96609870-96610112	pro	96609870	96610112	chr9	-0.47
LINC00476	2044	chr9:97680021-97680228	pro	97680021	97680228	chr9	-0.82
ZNF367	1808	chr9:98221532-98223063	pro	98221532	98223063	chr9	-0.38
ZNF782	1966	chr9:98654182-98654307	pro	98654182	98654307	chr9	-0.83
C9orf156	1234	chr9:99724723-99727092	pro	99724723	99727092	chr9	-0.28
HEMGN	2847	chr9:99736652-99738646	pro	99736652	99738646	chr9	-0.96
HEMGN	26	chr9:99739744-99741197	pro	99739744	99741197	chr9	-0.91
TRIM14	1734	chr9:99922897-99923483	pro	99922897	99923483	chr9	-0.77
XKRX	2934	chrX:100066435-1000688	pro	100066435	100068804	chrX	-0.98
XKRX	506	chrX:100069278-1000708	pro	100069278	100070819	chrX	-0.43
CENPI	226	chrX:100241170-1002412	pro	100241170	100241283	chrX	-0.77
TIMM8A	1630	chrX:100488497-1004889	pro	100488497	100488971	chrX	-0.54
BTK	2058	chrX:100525570-1005260	pro	100525570	100526049	chrX	-0.32
BTK	416	chrX:100527971-1005285	pro	100527971	100528597	chrX	-0.52
CLCN4	944	chrX:10083899-10084181	pro	10083899	10084181	chrX	-0.35
LINC00630	610	chrX:101910068-1019102	pro	101910068	101910211	chrX	-0.53
TCEAL8	356	chrX:102396825-1023974	pro	102396825	102397442	chrX	-0.32
MORF4L2	1684	chrX:102826377-1028270	pro	102826377	102827060	chrX	-0.58
MORF4L2	821	chrX:102830493-1028306	pro	102830493	102830633	chrX	-0.65
ZCCHC18	1212	chrX:103242517-1032428	pro	103242517	103242803	chrX	-0.92
ZCCHC18	563	chrX:103242932-1032436	pro	103242932	103243686	chrX	-0.49
ZCCHC18	1227	chrX:103244874-1032453	pro	103244874	103245324	chrX	-0.61
LOC286437	1700	chrX:103253760-1032547	pro	103253760	103254789	chrX	-0.80
SLC25A53	1374	chrX:103286937-1032870	pro	103286937	103287044	chrX	-0.77
CXorf57	1408	chrX:105741943-1057445	pro	105741943	105744500	chrX	-0.99
TBC1D8B	274	chrX:105932122-1059335	pro	105932122	105933574	chrX	-0.93
MORC4	282	chrX:106130253-1061305	pro	106130253	106130570	chrX	-0.46
RBM41	314	chrX:106248772-1062492	pro	106248772	106249283	chrX	-0.27
NUP62CL	705	chrX:106334867-1063363	pro	106334867	106336375	chrX	-0.98
PRPS1	548	chrX:106757359-1067581	pro	106757359	106758162	chrX	-0.26
TSC22D3	1410	chrX:106848199-1068485	pro	106848199	106848518	chrX	-0.80
ACSL4	1720	chrX:108864607-1088653	pro	108864607	108865389	chrX	-0.93
HCCS	1360	chrX:11040528-11040844	pro	11040528	11040844	chrX	-0.54

HCCS	2388	chrX:11041249-11042180	pro	11041249	11042180	chrX	-0.50
LHFPL1	377	chrX:111808809-11181050	pro	111808809	111810501	chrX	-0.99
SLC25A43	1893	chrX:118419137-11841921	pro	118419137	118419217	chrX	-0.75
NKRF	2106	chrX:118621588-11862194	pro	118621588	118621949	chrX	-0.29
SNORA69	52	chrX:118805457-11880560	pro	118805457	118805600	chrX	-0.59
SNORA69	618	chrX:118805945-11880624	pro	118805945	118806243	chrX	-0.38
SNORA69	1412	chrX:118806552-11880722	pro	118806552	118807223	chrX	-0.42
RPL39	1208	chrX:118810619-11881109	pro	118810619	118811096	chrX	-0.58
NDUFA1	2320	chrX:118887077-11888780	pro	118887077	118887804	chrX	-0.87
RNF113A	1343	chrX:118890814-11889151	pro	118890814	118891512	chrX	-0.57
NKAPP1	189	chrX:119263201-11926347	pro	119263201	119263477	chrX	-0.51
C1GALT1C1	1488	chrX:119646248-11964684	pro	119646248	119646844	chrX	-0.39
TLR7	459	chrX:12793837-12797325	pro	12793837	12797325	chrX	-0.85
SASH3	2071	chrX:128739244-1287397	pro	128739244	128739758	chrX	-0.27
ENOX2	325	chrX:129865182-1298654	pro	129865182	129865412	chrX	-0.37
MBNL3	5166	chrX:131442884-1314501	pro	131442884	131450140	chrX	-0.33
MMGT1	1908	chrX:134881771-1348820	pro	134881771	134882014	chrX	-0.58
TRAPPC2	2020	chrX:13659091-13662221	pro	13659091	13662221	chrX	-0.26
GEMIN8	1718	chrX:13954866-13957611	pro	13954866	13957611	chrX	-0.43
AFF2	933	chrX:147388101-1473896	pro	147388101	147389693	chrX	-0.30
FANCB	1669	chrX:14799289-14799585	pro	14799289	14799585	chrX	-0.80
FANCB	928	chrX:14799791-14800565	pro	14799791	14800565	chrX	-0.61
TMEM185A	1743	chrX:148519569-1485196	pro	148519569	148519697	chrX	-0.80
MTM1	450	chrX:149487086-1494874	pro	149487086	149487423	chrX	-0.46
MTM1	2236	chrX:149488230-1494916	pro	149488230	149491649	chrX	-0.76
MTMR1	2648	chrX:149613178-1496171	pro	149613178	149617171	chrX	-0.38
VMA21	1812	chrX:150317441-1503188	pro	150317441	150318810	chrX	-0.56
ZNF275	1806	chrX:152253742-1522554	pro	152253742	152255483	chrX	-0.51
AVPR2	1700	chrX:152819346-1528196	pro	152819346	152819610	chrX	-0.39
DKC1	2198	chrX:153646089-1536467	pro	153646089	153646727	chrX	-0.65
BRCC3	1620	chrX:153954298-1539547	pro	153954298	153954718	chrX	-0.54
RAB39B	223	chrX:154147100-1541474	pro	154147100	154147482	chrX	-0.46
GRPR	2646	chrX:16053182-16054797	pro	16053182	16054797	chrX	-0.99
RBBP7	1340	chrX:16798757-16800836	pro	16798757	16800836	chrX	-0.40
SCML2	1882	chrX:18280627-18281141	pro	18280627	18281141	chrX	-0.87
PDHA1	1956	chrX:19273743-19274029	pro	19273743	19274029	chrX	-0.75
EIF2S3	1964	chrX:23984884-23985012	pro	23984884	23985012	chrX	-0.54
PDK3	2088	chrX:24390684-24391668	pro	24390684	24391668	chrX	-0.84
PDK3	1871	chrX:24393766-24396504	pro	24393766	24396504	chrX	-0.40
POLA1	2615	chrX:24623810-24625388	pro	24623810	24625388	chrX	-0.27
GK	1806	chrX:30582831-30583572	pro	30582831	30583572	chrX	-0.84
DMD	1992	chrX:31191308-31194599	pro	31191308	31194599	chrX	-0.92
DMD	280	chrX:31195110-31195343	pro	31195110	31195343	chrX	-0.45
CYBB	34	chrX:37523809-37524682	pro	37523809	37524682	chrX	-0.38
CYBB	1746	chrX:37524993-37526924	pro	37524993	37526924	chrX	-0.54
DYNLT3	668	chrX:37592399-37592605	pro	37592399	37592605	chrX	-0.65
RPGR	1436	chrX:38069614-38070977	pro	38069614	38070977	chrX	-0.68
RPGR	392	chrX:38071920-38072327	pro	38071920	38072327	chrX	-0.43
MID1IP1	804	chrX:38545878-38546985	pro	38545878	38546985	chrX	-0.98
MID1IP1-AS1	503	chrX:38547185-38547969	pro	38547185	38547969	chrX	-0.97
MID1IP1-AS1	3258	chrX:38549836-38552841	pro	38549836	38552841	chrX	-0.95
NYX	1753	chrX:41189585-41190221	pro	41189585	41190221	chrX	-0.77
NYX	2156	chrX:41193202-41194422	pro	41193202	41194422	chrX	-0.46
GPR82	280	chrX:41467681-41468459	pro	41467681	41468459	chrX	-0.52
CASK	2077	chrX:41664771-41665539	pro	41664771	41665539	chrX	-0.66

MAOA	624	chrX:43398362-43398586	pro	43398362	43398586	chrX	-0.42
FUNDC1	1578	chrX:44285535-44285642	pro	44285535	44285642	chrX	-0.60
CFP	84	chrX:47374158-47374637	pro	47374158	47374637	chrX	-0.68
UXT	524	chrX:47403716-47404380	pro	47403716	47404380	chrX	-0.35
SLC38A5	1758	chrX:48210969-48212692	pro	48210969	48212692	chrX	-0.35
SLC38A5	422	chrX:48212888-48213445	pro	48212888	48213445	chrX	-0.86
FTSJ1	1103	chrX:48218161-48218337	pro	48218161	48218337	chrX	-0.73
EBP	596	chrX:48264056-48264963	pro	48264056	48264963	chrX	-0.34
TBC1D25	1201	chrX:48283385-48285053	pro	48283385	48285053	chrX	-0.45
PQBP1	1138	chrX:48641601-48642111	pro	48641601	48642111	chrX	-0.62
SLC35A2	1982	chrX:48656092-48656231	pro	48656092	48656231	chrX	-0.50
PIM2	994	chrX:48661443-48663261	pro	48661443	48663261	chrX	-0.44
OTUD5	2482	chrX:48701099-48705049	pro	48701099	48705049	chrX	-0.80
WDR45	1101	chrX:48843682-48844124	pro	48843682	48844124	chrX	-0.58
PPP1R3F	1861	chrX:49013960-49016258	pro	49013960	49016258	chrX	-0.40
GSPT2	1577	chrX:51503894-51505700	pro	51503894	51505700	chrX	-0.55
MAGED1	1020	chrX:51563496-51564333	pro	51563496	51564333	chrX	-0.38
MAGED1	1720	chrX:51651399-51652032	pro	51651399	51652032	chrX	-0.50
FAM156A	1062	chrX:53040003-53040624	pro	53040003	53040624	chrX	-0.40
KANTR	1538	chrX:53141519-53141681	pro	53141519	53141681	chrX	-0.68
FAM120C	548	chrX:54226821-54227155	pro	54226821	54227155	chrX	-0.27
LINC01420	950	chrX:56771336-56771647	pro	56771336	56771647	chrX	-0.48
SPIN2B	632	chrX:57165050-57165643	pro	57165050	57165643	chrX	-0.46
FAAH2	790	chrX:57330104-57331145	pro	57330104	57331145	chrX	-0.97
MSN	436	chrX:64803613-64803984	pro	64803613	64803984	chrX	-0.41
EDA2R	478	chrX:65774758-65775523	pro	65774758	65775523	chrX	-0.95
YIPF6	1286	chrX:67636583-67636685	pro	67636583	67636685	chrX	-0.36
FAM155B	2858	chrX:68642365-68646956	pro	68642365	68646956	chrX	-0.99
IGBP1	1632	chrX:69271280-69272067	pro	69271280	69272067	chrX	-0.45
KIF4A	2018	chrX:69427187-69430054	pro	69427187	69430054	chrX	-0.40
TAF1	1971	chrX:70504586-70504980	pro	70504586	70504980	chrX	-0.64
STS	42	chrX:7146445-7148580	pro	7146445	7148580	chrX	-0.91
STS	2622	chrX:7148888-7151297	pro	7148888	7151297	chrX	-0.99
CHIC1	1418	chrX:72701025-72701228	pro	72701025	72701228	chrX	-0.31
RLIM	1010	chrX:73752013-73752380	pro	73752013	73752380	chrX	-0.25
CYSLTR1	1794	chrX:77467734-77468367	pro	77467734	77468367	chrX	-0.92
CYSLTR1	490	chrX:77468503-77470205	pro	77468503	77470205	chrX	-0.69
P2RY10	3550	chrX:78089375-78092692	pro	78089375	78092692	chrX	-0.51
PNPLA4	1560	chrX:7853844-7853988	pro	7853844	7853988	chrX	-0.41
HIAT1	3137	chr1:100279420-1002796	intra_enh	100279420	100279606	chr1	-0.62
HIAT1	4132	chr1:100280401-10028061	intra_enh	100280401	100280615	chr1	-0.55
HIAT1	8762	chr1:100284743-1002855	intra_enh	100284743	100285532	chr1	-0.90
CDC14A	48116	chr1:100638544-1006389	intra_enh	100638544	100638907	chr1	-0.87
LOC102606465	2706	chr1:101266423-1012669	intra_enh	101266423	101266964	chr1	-0.76
NTNG1	107327	chr1:107590997-1075921	intra_enh	107590997	107592189	chr1	-0.91
NTNG1	133701	chr1:107617901-1076180	intra_enh	107617901	107618033	chr1	-0.52
VAV3	237124	chr1:107794998-1077960	intra_enh	107794998	107796054	chr1	-0.63
VAV3	50602	chr1:108083136-1080833	intra_enh	108083136	108083368	chr1	-0.26
MIR7852	92888	chr1:108147877-1081490	intra_enh	108147877	108149080	chr1	-0.49
MIR7852	67798	chr1:108173088-1081740	intra_enh	108173088	108174047	chr1	-0.40
C1orf127	15973	chr1:10948551-10948867	intra_enh	10948551	10948867	chr1	-0.68
KIAA1324	7468	chr1:109538055-1095382	intra_enh	109538055	109538266	chr1	-0.64
AHCYL1	5408	chr1:110334015-11033461	intra_enh	110334015	110334616	chr1	-0.84
AHCYL1	8098	chr1:110356030-11035635	intra_enh	110356030	110356350	chr1	-0.29
UBL4B	10114	chr1:110446256-11044668	intra_enh	110446256	110446685	chr1	-0.85

LAMTOR5	4956	chr1:110756928-11075712	intra_enh	110756928	110757124	chr1	-0.54
CEPT1	7112	chr1:111476562-11147675	intra_enh	111476562	111476755	chr1	-0.85
SLC16A1	3933	chr1:113296151-11329639	intra_enh	113296151	113296399	chr1	-0.65
SLC16A1	3100	chr1:113296958-11329725	intra_enh	113296958	113297258	chr1	-0.69
PHTF1	21834	chr1:114124796-11412547	intra_enh	114124796	114125473	chr1	-0.60
TRIM33	43347	chr1:114811545-11481236	intra_enh	114811545	114812369	chr1	-0.62
CSDE1	5308	chr1:115096821-11509695	intra_enh	115096821	115096950	chr1	-0.61
CSDE1	4634	chr1:115097311-11509781	intra_enh	115097311	115097810	chr1	-0.76
NGF	26997	chr1:115655054-11565571	intra_enh	115655054	115655712	chr1	-0.98
LOC101928977	29296	chr1:116350512-11635092	intra_enh	116350512	116350920	chr1	-0.60
LOC101929023	36395	chr1:116859297-11685943	intra_enh	116859297	116859437	chr1	-0.37
TTF2	2610	chr1:117407025-11740713	intra_enh	117407025	117407135	chr1	-0.78
TTF2	3040	chr1:117407463-11740755	intra_enh	117407463	117407557	chr1	-0.63
LOC102724659	6916	chr1:11755209-11755487	intra_enh	11755209	11755487	chr1	-0.69
LOC102724659	4156	chr1:11766345-11766495	intra_enh	11766345	11766495	chr1	-0.93
TBX15	70702	chr1:119262692-11926330	intra_enh	119262692	119263309	chr1	-0.86
TBX15	18932	chr1:119314573-11931496	intra_enh	119314573	119314968	chr1	-0.73
REG4	2246	chr1:120153428-12015353	intra_enh	120153428	120153531	chr1	-0.39
EMBP1	32956	chr1:120995311-12099546	intra_enh	120995311	120995464	chr1	-0.70
SNORA59A	26280	chr1:12463546-12463666	intra_enh	12463546	12463666	chr1	-0.64
NBPF12	57353	chr1:143247504-14324769	intra_enh	143247504	143247690	chr1	-0.29
PDE4DIP	28657	chr1:143677663-14367780	intra_enh	143677663	143677803	chr1	-0.77
PDE4DIP	7256	chr1:143715367-14371608	intra_enh	143715367	143716080	chr1	-0.78
PDE4DIP	17776	chr1:143726066-14372642	intra_enh	143726066	143726422	chr1	-0.66
HFE2	11092	chr1:144113153-14411375	intra_enh	144113153	144113755	chr1	-0.70
TXNIP	7784	chr1:144157379-14415777	intra_enh	144157379	144157776	chr1	-0.84
TXNIP	11718	chr1:144161309-14416171	intra_enh	144161309	144161715	chr1	-0.29
TXNIP	13062	chr1:144162816-14416289	intra_enh	144162816	144162897	chr1	-0.48
LIX1L	2440	chr1:144190791-14419093	intra_enh	144190791	144190933	chr1	-0.82
POLR3C	4084	chr1:144317875-14431844	intra_enh	144317875	144318441	chr1	-0.95
PRKAB2	2348	chr1:145108128-14510876	intra_enh	145108128	145108761	chr1	-0.77
FMO5	21318	chr1:145142430-14514264	intra_enh	145142430	145142642	chr1	-0.82
BCL9	8528	chr1:145471186-14547154	intra_enh	145471186	145471545	chr1	-0.95
LOC101927468	32528	chr1:146218419-14621856	intra_enh	146218419	146218568	chr1	-0.64
VPS45	13278	chr1:148319467-14831978	intra_enh	148319467	148319786	chr1	-0.97
VPS45	22836	chr1:148328718-14832965	intra_enh	148328718	148329651	chr1	-0.95
SSU72	16310	chr1:1483722-1483910	intra_enh	1483722	1483910	chr1	-0.88
ADAMTSL4-AS1	9574	chr1:148803907-14880424	intra_enh	148803907	148804249	chr1	-0.79
ADAMTSL4-AS1	4853	chr1:148808718-14880888	intra_enh	148808718	148808880	chr1	-0.39
ADAMTSL4-AS1	4415	chr1:148809162-14880931	intra_enh	148809162	148809312	chr1	-0.47
KAZN	141139	chr1:14938815-14939059	intra_enh	14938815	14939059	chr1	-0.76
KAZN	162430	chr1:14960428-14961132	intra_enh	14960428	14961132	chr1	-0.82
POGZ	3566	chr1:149684699-14968504	intra_enh	149684699	149685044	chr1	-0.83
S100A11	2482	chr1:150273548-15027375	intra_enh	150273548	150273759	chr1	-0.41
S100A13	3795	chr1:151862263-15186244	intra_enh	151862263	151862443	chr1	-0.57
GATAD2B	68166	chr1:152093651-15209416	intra_enh	152093651	152094168	chr1	-0.64
KCNN3	4210	chr1:153094695-15309480	intra_enh	153094695	153094809	chr1	-0.29
TMEM51	2815	chr1:15355411-15355847	intra_enh	15355411	15355847	chr1	-0.53
POU5F1P4	53006	chr1:153722437-15372276	intra_enh	153722437	153722763	chr1	-0.87
GON4L	48000	chr1:154045574-15404584	intra_enh	154045574	154045846	chr1	-0.90
GON4L	8952	chr1:154084600-15408491	intra_enh	154084600	154084917	chr1	-0.52
ARHGEF2	5715	chr1:154208763-15420898	intra_enh	154208763	154208987	chr1	-0.34
IQGAP3	19254	chr1:154789617-15478991	intra_enh	154789617	154789915	chr1	-0.73
EFHD2	69154	chr1:15539739-15539905	intra_enh	15539739	15539905	chr1	-0.34
EFHD2	47614	chr1:15561266-15561458	intra_enh	15561266	15561458	chr1	-0.89

FCRL4	17852	chr1:155816552-1558167	intra_enh	155816552	155816733	chr1	-0.52
CD5L	9712	chr1:156068491-1560686	intra_enh	156068491	156068602	chr1	-0.78
DDI2	2686	chr1:15819032-15819417	intra_enh	15819032	15819417	chr1	-0.35
COPA	3446	chr1:158583361-1585834	intra_enh	158583361	158583487	chr1	-0.30
SLAMF6	35700	chr1:158723736-15872421	intra_enh	158723736	158724216	chr1	-0.87
SLAMF6	35045	chr1:158724421-1587248	intra_enh	158724421	158724841	chr1	-0.59
CD84	10484	chr1:158805296-1588055	intra_enh	158805296	158805595	chr1	-0.66
SLAMF1	25344	chr1:158857988-1588587	intra_enh	158857988	158858777	chr1	-0.54
CD244	20134	chr1:159078935-1590794	intra_enh	159078935	159079429	chr1	-0.96
ATF6	6290	chr1:160008866-1600090	intra_enh	160008866	160009026	chr1	-0.83
UCK2	15360	chr1:164078494-1640789	intra_enh	164078494	164078933	chr1	-0.69
POU2F1	27355	chr1:165483895-1654843	intra_enh	165483895	165484307	chr1	-0.58
POU2F1	47668	chr1:165504294-1655045	intra_enh	165504294	165504535	chr1	-0.39
POU2F1	5531	chr1:165570326-1655705	intra_enh	165570326	165570544	chr1	-0.92
CREG1	10433	chr1:165779095-1657793	intra_enh	165779095	165779399	chr1	-0.93
CREG1	8592	chr1:165780798-1657813	intra_enh	165780798	165781379	chr1	-0.98
MPZL1	34045	chr1:165923668-1659238	intra_enh	165923668	165923862	chr1	-0.53
NECAP2	2323	chr1:16641969-16642181	intra_enh	16641969	16642181	chr1	-0.56
SELL	14204	chr1:167930271-1679305	intra_enh	167930271	167930566	chr1	-0.30
PRRC2C	3370	chr1:169724575-1697247	intra_enh	169724575	169724741	chr1	-0.70
DNM3OS	40426	chr1:170420906-17042114	intra_enh	170420906	170421142	chr1	-0.57
DNM3OS	40771	chr1:170421263-1704214	intra_enh	170421263	170421475	chr1	-0.68
C1orf105	44003	chr1:170612344-1706125	intra_enh	170612344	170612550	chr1	-0.88
KLHL20	2528	chr1:171953170-1719532	intra_enh	171953170	171953290	chr1	-0.55
CENPL	2804	chr1:172057012-1720571	intra_enh	172057012	172057168	chr1	-0.82
DARS2	3126	chr1:172063457-1720636	intra_enh	172063457	172063632	chr1	-0.93
LOC102724601	25050	chr1:172369929-1723700	intra_enh	172369929	172370067	chr1	-0.71
RABGAP1L	7104	chr1:172401612-1724029	intra_enh	172401612	172402945	chr1	-0.77
RABGAP1L	58700	chr1:172453726-1724540	intra_enh	172453726	172454022	chr1	-0.82
RABGAP1L	117632	chr1:172512490-1725131	intra_enh	172512490	172513122	chr1	-0.35
RABGAP1L	30824	chr1:173004610-1730050	intra_enh	173004610	173005053	chr1	-0.90
RABGAP1L	22550	chr1:173012671-1730135	intra_enh	173012671	173013540	chr1	-0.91
RABGAP1L	32497	chr1:173077447-1730778	intra_enh	173077447	173077851	chr1	-0.96
RABGAP1L	3972	chr1:173105876-1731064	intra_enh	173105876	173106472	chr1	-0.79
RABGAP1L	3465	chr1:173203647-1732043	intra_enh	173203647	173204335	chr1	-0.52
TNR	62668	chr1:173916309-1739171	intra_enh	173916309	173917108	chr1	-0.89
RFWD2	20472	chr1:174422373-1744226	intra_enh	174422373	174422691	chr1	-0.39
RFWD2	7316	chr1:174435477-1744358	intra_enh	174435477	174435899	chr1	-0.82
RFWD2	6719	chr1:174436148-1744364	intra_enh	174436148	174436422	chr1	-0.86
RFWD2	5410	chr1:174437251-1744379	intra_enh	174437251	174437938	chr1	-0.83
RASAL2-AS1	99079	chr1:176428592-1764290	intra_enh	176428592	176429070	chr1	-0.53
GNB1	46339	chr1:1766009-1766145	intra_enh	1766009	1766145	chr1	-0.31
RALGPS2	26012	chr1:176985911-17698792	intra_enh	176985911	176987921	chr1	-0.94
RALGPS2	71184	chr1:177031762-17703241	intra_enh	177031762	177032413	chr1	-0.98
GNB1	33530	chr1:1778775-1778996	intra_enh	1778775	1778996	chr1	-0.54
GNB1	29890	chr1:1782452-1782599	intra_enh	1782452	1782599	chr1	-0.30
GNB1	25412	chr1:1786902-1787105	intra_enh	1786902	1787105	chr1	-0.67
ACBD6	3008	chr1:178735526-1787357	intra_enh	178735526	178735750	chr1	-0.29
RGSL1	34351	chr1:180720105-1807203	intra_enh	180720105	180720353	chr1	-0.82
RGSL1	34832	chr1:180720583-1807208	intra_enh	180720583	180720837	chr1	-0.59
SHCBP1L	25148	chr1:181163436-18116461	intra_enh	181163436	181164619	chr1	-0.84
LAMC1	9902	chr1:181268923-18126931	intra_enh	181268923	181269312	chr1	-0.80
LAMC1	16760	chr1:181275781-1812761	intra_enh	181275781	181276171	chr1	-0.37
LAMC1	78904	chr1:181338043-1813381	intra_enh	181338043	181338196	chr1	-0.27
SMG7	25854	chr1:181733904-1817340	intra_enh	181733904	181734059	chr1	-0.92

SMG7	26230	chr1:181734248-18173446	intra_enh	181734248	181734469	chr1	-0.93
RGL1	106224	chr1:182146962-18214715	intra_enh	182146962	182147158	chr1	-0.86
COLGALT2	80702	chr1:182192726-18219284	intra_enh	182192726	182192843	chr1	-0.79
TRMT1L	2153	chr1:183390529-18339064	intra_enh	183390529	183390645	chr1	-0.80
BRINP3	100314	chr1:188612883-18861325	intra_enh	188612883	188613253	chr1	-0.92
RGS13	5403	chr1:190877140-19087744	intra_enh	190877140	190877446	chr1	-0.62
UCHL5	10179	chr1:191305931-19130614	intra_enh	191305931	191306147	chr1	-0.62
UCHL5	10560	chr1:191306315-19130652	intra_enh	191306315	191306526	chr1	-0.72
MIR4735	323010	chr1:194494928-19449552	intra_enh	194494928	194495521	chr1	-0.92
MIR4735	311033	chr1:194507118-19450728	intra_enh	194507118	194507284	chr1	-0.70
MIR4735	310671	chr1:194507484-19450764	intra_enh	194507484	194507642	chr1	-0.52
ZBTB41	18366	chr1:195417744-19541811	intra_enh	195417744	195418115	chr1	-0.83
ZBTB41	3757	chr1:195432434-19543264	intra_enh	195432434	195432644	chr1	-0.77
ZBTB41	3356	chr1:195432755-19543312	intra_enh	195432755	195433126	chr1	-0.80
DENND1B	13661	chr1:195997133-19599803	intra_enh	195997133	195998037	chr1	-0.59
NEK7	5430	chr1:196397851-19639846	intra_enh	196397851	196398468	chr1	-0.44
NEK7	10496	chr1:196402756-19640369	intra_enh	196402756	196403697	chr1	-0.57
NEK7	11523	chr1:196404077-19640442	intra_enh	196404077	196404429	chr1	-0.76
NEK7	42166	chr1:196434726-19643506	intra_enh	196434726	196435067	chr1	-0.90
ATP6V1G3	5792	chr1:196770554-19677125	intra_enh	196770554	196771259	chr1	-0.37
PTPRC	7980	chr1:196882670-19688272	intra_enh	196882670	196882729	chr1	-0.36
PTPRC	57542	chr1:196932108-19693241	intra_enh	196932108	196932415	chr1	-0.81
PTPRC	62667	chr1:196937000-19693777	intra_enh	196937000	196937774	chr1	-0.95
LINC01221	5532	chr1:197246252-19724645	intra_enh	197246252	197246451	chr1	-0.41
NR5A2	30100	chr1:198308427-19830892	intra_enh	198308427	198308921	chr1	-0.88
NR5A2	73061	chr1:198351433-19835183	intra_enh	198351433	198351837	chr1	-0.92
NR5A2	123174	chr1:198401570-19840192	intra_enh	198401570	198401927	chr1	-0.90
KIF21B	5902	chr1:199253308-19925379	intra_enh	199253308	199253792	chr1	-0.76
KIF21B	5160	chr1:199254068-19925451	intra_enh	199254068	199254515	chr1	-0.96
TMCO4	34837	chr1:19963977-19964345	intra_enh	19963977	19964345	chr1	-0.58
MIR5191	3246	chr1:199951795-19995223	intra_enh	199951795	199952230	chr1	-0.91
NAV1	17274	chr1:199992709-19999300	intra_enh	199992709	199993008	chr1	-0.92
KLHL12	3841	chr1:201158733-20115957	intra_enh	201158733	201159573	chr1	-0.71
OPTC	10534	chr1:201740321-20174053	intra_enh	201740321	201740531	chr1	-0.60
LINC00260	8414	chr1:201974579-20197490	intra_enh	201974579	201974901	chr1	-0.79
PLEKHA6	45739	chr1:202549852-20255003	intra_enh	202549852	202550030	chr1	-0.59
MFSD4	21958	chr1:203826616-20382676	intra_enh	203826616	203826767	chr1	-0.81
ELK4	6069	chr1:203862237-20386287	intra_enh	203862237	203862873	chr1	-0.36
NUCKS1	4492	chr1:203981403-20398160	intra_enh	203981403	203981604	chr1	-0.76
IL24	8652	chr1:205145933-20514619	intra_enh	205145933	205146190	chr1	-0.67
VWA5B1	32136	chr1:20522086-20522183	intra_enh	20522086	20522183	chr1	-0.78
HHAT	3129	chr1:208572232-20857255	intra_enh	208572232	208572550	chr1	-0.97
DDOST	5290	chr1:20865845-20865984	intra_enh	20865845	20865984	chr1	-0.89
DDOST	17238	chr1:20877744-20877980	intra_enh	20877744	20877980	chr1	-0.60
NEK2	3253	chr1:209912249-20991243	intra_enh	209912249	209912437	chr1	-0.85
NEK2	2808	chr1:209912704-20991287	intra_enh	209912704	209912873	chr1	-0.85
DTL	4446	chr1:210270957-21027118	intra_enh	210270957	210271184	chr1	-0.50
DTL	3948	chr1:210271378-21027175	intra_enh	210271378	210271757	chr1	-0.51
DTL	3344	chr1:210272123-21027222	intra_enh	210272123	210272222	chr1	-0.48
NSL1	2866	chr1:211028795-21102899	intra_enh	211028795	211028998	chr1	-0.73
EIF4G3	20748	chr1:21289509-21289923	intra_enh	21289509	21289923	chr1	-0.68
USH2A	105592	chr1:214768535-21476937	intra_enh	214768535	214769372	chr1	-0.91
ESRRG	49628	chr1:215267129-21526748	intra_enh	215267129	215267486	chr1	-0.81
ESRRG	49212	chr1:215267646-21526780	intra_enh	215267646	215267801	chr1	-0.81
GPATCH2	87906	chr1:215783074-21578325	intra_enh	215783074	215783250	chr1	-0.37

EPRS	2738	chr1:218283682-21828408	intra_enh	218283682	218284089	chr1	-0.75
USP48	21308	chr1:21960906-21961030	intra_enh	21960906	21961030	chr1	-0.91
USP48	18350	chr1:21963852-21963999	intra_enh	21963852	21963999	chr1	-0.50
USP48	18069	chr1:21964137-21964277	intra_enh	21964137	21964277	chr1	-0.36
FAM177B	4749	chr1:220972305-22097255	intra_enh	220972305	220972557	chr1	-0.75
TP53BP2	23012	chr1:222077177-22207739	intra_enh	222077177	222077396	chr1	-0.52
FBXO28	2477	chr1:222370695-22237107	intra_enh	222370695	222371079	chr1	-0.42
LOC101927164	16549	chr1:222490358-22249061	intra_enh	222490358	222490612	chr1	-0.95
WNT4	5192	chr1:22336756-22337073	intra_enh	22336756	22337073	chr1	-0.48
WNT4	4846	chr1:22337181-22337340	intra_enh	22337181	22337340	chr1	-0.75
LBR	111138	chr1:223793964-22379467	intra_enh	223793964	223794671	chr1	-0.98
ACBD3	26916	chr1:224413871-22441439	intra_enh	224413871	224414390	chr1	-0.94
ACBD3	26069	chr1:224414738-22441521	intra_enh	224414738	224415216	chr1	-0.89
ITPKB	23787	chr1:224969470-22496995	intra_enh	224969470	224969956	chr1	-0.79
ITPKB	22946	chr1:224970479-22497062	intra_enh	224970479	224970629	chr1	-0.81
PSEN2	13726	chr1:225138526-22513871	intra_enh	225138526	225138715	chr1	-0.31
GALNT2	36149	chr1:228305528-22830589	intra_enh	228305528	228305898	chr1	-0.58
GALNT2	65885	chr1:228335077-22833582	intra_enh	228335077	228335821	chr1	-0.77
TTC13	5546	chr1:229175611-22917578	intra_enh	229175611	229175782	chr1	-0.51
LINC01132	3212	chr1:232929419-23292982	intra_enh	232929419	232929825	chr1	-0.87
LOC101927851	2942	chr1:233163362-23316349	intra_enh	233163362	233163494	chr1	-0.70
LUZP1	49254	chr1:23318548-23318821	intra_enh	23318548	23318821	chr1	-0.84
ARID4B	67837	chr1:233489317-23348986	intra_enh	233489317	233489861	chr1	-0.83
ARID4B	51840	chr1:233505434-23350573	intra_enh	233505434	233505737	chr1	-0.56
MIR1537	10506	chr1:234071873-23407308	intra_enh	234071873	234073084	chr1	-0.81
MTR	2958	chr1:235028050-23502827	intra_enh	235028050	235028270	chr1	-0.57
LOC100130331	125166	chr1:235966873-23596698	intra_enh	235966873	235966988	chr1	-0.30
TCEA3	20455	chr1:23603246-23603540	intra_enh	23603246	23603540	chr1	-0.67
MDS2	3415	chr1:23829745-23829905	intra_enh	23829745	23829905	chr1	-0.93
MIR3123	221114	chr1:239141019-23914114	intra_enh	239141019	239141142	chr1	-0.76
WDR64	24146	chr1:239906119-23990657	intra_enh	239906119	239906577	chr1	-0.96
CEP170	18514	chr1:241466610-24146702	intra_enh	241466610	241467027	chr1	-0.91
KIF26B	519190	chr1:243903751-24390444	intra_enh	243903751	243904446	chr1	-0.52
GRHL3	18235	chr1:24540282-24540420	intra_enh	24540282	24540420	chr1	-0.80
RCAN3	13960	chr1:24726637-24728064	intra_enh	24726637	24728064	chr1	-0.98
RCAN3	19850	chr1:24733133-24733348	intra_enh	24733133	24733348	chr1	-0.46
ZNF683	8608	chr1:26563181-26563311	intra_enh	26563181	26563311	chr1	-0.48
SLC9A1	22878	chr1:27331220-27331441	intra_enh	27331220	27331441	chr1	-0.41
GPR3	34696	chr1:27626299-27626560	intra_enh	27626299	27626560	chr1	-0.49
GPR3	41222	chr1:27632881-27633031	intra_enh	27632881	27633031	chr1	-0.44
GPR3	47468	chr1:27639138-27639265	intra_enh	27639138	27639265	chr1	-0.85
WASF2	44627	chr1:27644276-27645002	intra_enh	27644276	27645002	chr1	-0.71
WASF2	38506	chr1:27650701-27650820	intra_enh	27650701	27650820	chr1	-0.64
WASF2	14749	chr1:27674448-27674586	intra_enh	27674448	27674586	chr1	-0.55
AHDC1	47478	chr1:27754963-27755264	intra_enh	27754963	27755264	chr1	-0.62
AHDC1	3572	chr1:27798921-27799118	intra_enh	27798921	27799118	chr1	-0.67
STX12	20501	chr1:27951653-27951905	intra_enh	27951653	27951905	chr1	-0.81
EYA3	32004	chr1:28255394-28256071	intra_enh	28255394	28256071	chr1	-0.57
EYA3	10301	chr1:28277338-28277532	intra_enh	28277338	28277532	chr1	-0.93
PHACTR4	20519	chr1:28616549-28616905	intra_enh	28616549	28616905	chr1	-0.57
YTHDF2	7470	chr1:28943397-28943620	intra_enh	28943397	28943620	chr1	-0.42
YTHDF2	9227	chr1:28945203-28945327	intra_enh	28945203	28945327	chr1	-0.70
YTHDF2	11558	chr1:28947314-28947878	intra_enh	28947314	28947878	chr1	-0.29
FABP3	24712	chr1:31593641-31593955	intra_enh	31593641	31593955	chr1	-0.36
PTP4A2	7006	chr1:32164428-32165275	intra_enh	32164428	32165275	chr1	-0.51

PTP4A2	8194	chr1:32165787-32166292	intra_enh	32165787	32166292	chr1	-0.53
KHDRBS1	5516	chr1:32257329-32257462	intra_enh	32257329	32257462	chr1	-0.70
LCK	6416	chr1:32495668-32496015	intra_enh	32495668	32496015	chr1	-0.77
LCK	7000	chr1:32505089-32505507	intra_enh	32505089	32505507	chr1	-0.77
MARCKSL1	15861	chr1:32558490-32558644	intra_enh	32558490	32558644	chr1	-0.44
RNF19B	11212	chr1:33191495-33192086	intra_enh	33191495	33192086	chr1	-0.90
ZMYM4	95925	chr1:35602832-35603326	intra_enh	35602832	35603326	chr1	-0.93
AGO3	3072	chr1:36172146-36172535	intra_enh	36172146	36172535	chr1	-0.65
TP73	21315	chr1:3625275-3626291	intra_enh	3625275	3626291	chr1	-0.91
TP73	22348	chr1:3626718-3626914	intra_enh	3626718	3626914	chr1	-0.81
TRAPPC3	19420	chr1:36413518-36413807	intra_enh	36413518	36413807	chr1	-0.55
MEAF6	6778	chr1:37746167-37746294	intra_enh	37746167	37746294	chr1	-0.38
RRAGC	11396	chr1:39086591-39086782	intra_enh	39086591	39086782	chr1	-0.65
AKIRIN1	5752	chr1:39235101-39235407	intra_enh	39235101	39235407	chr1	-0.70
MACF1	18402	chr1:39340756-39340896	intra_enh	39340756	39340896	chr1	-0.60
MACF1	99535	chr1:39421864-39422054	intra_enh	39421864	39422054	chr1	-0.95
MACF1	99950	chr1:39422209-39422538	intra_enh	39422209	39422538	chr1	-0.87
MACF1	108316	chr1:39430592-39430889	intra_enh	39430592	39430889	chr1	-0.34
KIAA0754	10796	chr1:39636775-39637157	intra_enh	39636775	39637157	chr1	-0.73
TRIT1	5854	chr1:40115679-40116142	intra_enh	40115679	40116142	chr1	-0.38
TRIT1	5084	chr1:40116619-40116740	intra_enh	40116619	40116740	chr1	-0.44
CAP1	3490	chr1:40282197-40282462	intra_enh	40282197	40282462	chr1	-0.52
RLF	25149	chr1:40424512-40425038	intra_enh	40424512	40425038	chr1	-0.88
SMAP2	5519	chr1:40618071-40618747	intra_enh	40618071	40618747	chr1	-0.36
KCNQ4	13564	chr1:41035677-41035990	intra_enh	41035677	41035990	chr1	-0.54
KCNQ4	25514	chr1:41047638-41047931	intra_enh	41047638	41047931	chr1	-0.55
YBX1	8842	chr1:42929331-42929658	intra_enh	42929331	42929658	chr1	-0.54
SLC2A1	21643	chr1:43218950-43219204	intra_enh	43218950	43219204	chr1	-0.86
TMEM53	2314	chr1:44910409-44910698	intra_enh	44910409	44910698	chr1	-0.58
KIF2C	24824	chr1:44953189-44953314	intra_enh	44953189	44953314	chr1	-0.48
KIF2C	24444	chr1:44953433-44953830	intra_enh	44953433	44953830	chr1	-0.60
KIF2C	18517	chr1:44959359-44959759	intra_enh	44959359	44959759	chr1	-0.40
UROD	21548	chr1:45271820-45272055	intra_enh	45271820	45272055	chr1	-0.74
UROD	39505	chr1:45289561-45290229	intra_enh	45289561	45290229	chr1	-0.65
MUTYH	52860	chr1:45631456-45631724	intra_enh	45631456	45631724	chr1	-0.92
PRDX1	4572	chr1:45755573-45755680	intra_enh	45755573	45755680	chr1	-0.66
MAST2	16996	chr1:46058702-46059031	intra_enh	46058702	46059031	chr1	-0.87
MAST2	19250	chr1:46060901-46061339	intra_enh	46060901	46061339	chr1	-0.39
MAST2	39152	chr1:46080935-46081110	intra_enh	46080935	46081110	chr1	-0.48
MAST2	39900	chr1:46081550-46081990	intra_enh	46081550	46081990	chr1	-0.59
MAST2	72415	chr1:46114207-46114363	intra_enh	46114207	46114363	chr1	-0.74
MAST2	122296	chr1:46163658-46164673	intra_enh	46163658	46164673	chr1	-0.77
PIK3R3	67151	chr1:46303666-46303968	intra_enh	46303666	46303968	chr1	-0.65
TSPAN1	4484	chr1:46417717-46417919	intra_enh	46417717	46417919	chr1	-0.55
TSPAN1	4794	chr1:46418066-46418191	intra_enh	46418066	46418191	chr1	-0.47
FOXD2-AS1	3212	chr1:47669629-47669746	intra_enh	47669629	47669746	chr1	-0.73
FOXD2-AS1	2874	chr1:47669867-47670186	intra_enh	47669867	47670186	chr1	-0.82
FAF1	235656	chr1:50962782-50962954	intra_enh	50962782	50962954	chr1	-0.34
FAF1	235212	chr1:50963147-50963476	intra_enh	50963147	50963476	chr1	-0.41
EPS15	11768	chr1:51671992-51672309	intra_enh	51671992	51672309	chr1	-0.84
EPS15	30468	chr1:51726947-51727285	intra_enh	51726947	51727285	chr1	-0.68
EPS15	9061	chr1:51747972-51749074	intra_enh	51747972	51749074	chr1	-0.71
NRD1	14442	chr1:52101744-52101973	intra_enh	52101744	52101973	chr1	-0.94
NRD1	14056	chr1:52102126-52102363	intra_enh	52102126	52102363	chr1	-0.90
RAB3B	34787	chr1:52194072-52194402	intra_enh	52194072	52194402	chr1	-0.96

BTF3L4	3130	chr1:52297536-52297613	intra_enh	52297536	52297613	chr1	-0.78
USP24	5808	chr1:55447600-55448039	intra_enh	55447600	55448039	chr1	-0.52
DAB1-AS1	209802	chr1:57888834-57889167	intra_enh	57888834	57889167	chr1	-0.98
LOC101926944	13373	chr1:59997583-59997779	intra_enh	59997583	59997779	chr1	-0.28
ANGPTL3	16008	chr1:62851425-62852078	intra_enh	62851425	62852078	chr1	-0.38
ATG4C	10043	chr1:63032289-63032525	intra_enh	63032289	63032525	chr1	-0.83
ATG4C	26506	chr1:63048785-63048954	intra_enh	63048785	63048954	chr1	-0.83
JAK1	104397	chr1:65100298-65100460	intra_enh	65100298	65100460	chr1	-0.74
JAK1	67768	chr1:65136929-65137087	intra_enh	65136929	65137087	chr1	-0.81
JAK1	32723	chr1:65171606-65172500	intra_enh	65171606	65172500	chr1	-0.58
JAK1	12344	chr1:65192281-65192582	intra_enh	65192281	65192582	chr1	-0.97
DNAJC6	57049	chr1:65445872-65445958	intra_enh	65445872	65445958	chr1	-0.28
DNAJC6	17679	chr1:65520398-65520888	intra_enh	65520398	65520888	chr1	-0.79
DNAJC6	19009	chr1:65566664-65566962	intra_enh	65566664	65566962	chr1	-0.76
LOC101927139	132889	chr1:66421758-66422000	intra_enh	66421758	66422000	chr1	-0.89
PDE4B	55684	chr1:66514623-66514766	intra_enh	66514623	66514766	chr1	-0.82
PDE4B	15150	chr1:66555063-66555392	intra_enh	66555063	66555392	chr1	-0.95
TCTEX1D1	12914	chr1:67003516-67003763	intra_enh	67003516	67003763	chr1	-0.82
MIER1	51274	chr1:67219727-67219844	intra_enh	67219727	67219844	chr1	-0.84
C1orf141	24574	chr1:67348507-67348830	intra_enh	67348507	67348830	chr1	-0.88
GADD45A	28420	chr1:67951432-67952299	intra_enh	67951432	67952299	chr1	-0.32
GADD45A	70270	chr1:67993640-67993791	intra_enh	67993640	67993791	chr1	-0.48
GNG12-AS1	71671	chr1:67998795-67998979	intra_enh	67998795	67998979	chr1	-0.48
DEPDC1-AS1	2578	chr1:68732218-68732518	intra_enh	68732218	68732518	chr1	-0.71
PIN1P1	114287	chr1:70271624-70272134	intra_enh	70271624	70272134	chr1	-0.97
VAMP3	18463	chr1:7735279-7735623	intra_enh	7735279	7735623	chr1	-0.69
AK5	6620	chr1:77527425-77527564	intra_enh	77527425	77527564	chr1	-0.56
ZZZ3	11782	chr1:77909067-77909232	intra_enh	77909067	77909232	chr1	-0.71
NEXN	40944	chr1:78085340-78086345	intra_enh	78085340	78086345	chr1	-0.58
FUBP1	27790	chr1:78189302-78189849	intra_enh	78189302	78189849	chr1	-0.89
LOC101927560	233706	chr1:83864984-83865239	intra_enh	83864984	83865239	chr1	-0.50
LOC101927560	218985	chr1:83879755-83879911	intra_enh	83879755	83879911	chr1	-0.56
LOC101927560	114055	chr1:83984507-83985019	intra_enh	83984507	83985019	chr1	-0.65
LOC102724552	51567	chr1:8458678-8459036	intra_enh	8458678	8459036	chr1	-0.25
LOC102724552	90399	chr1:8497611-8497767	intra_enh	8497611	8497767	chr1	-0.60
LOC102724552	91132	chr1:8498294-8498551	intra_enh	8498294	8498551	chr1	-0.76
LOC102724552	97400	chr1:8504307-8505072	intra_enh	8504307	8505072	chr1	-0.74
LOC102724552	107001	chr1:8514171-8514411	intra_enh	8514171	8514411	chr1	-0.95
LOC102724552	115230	chr1:8522459-8522581	intra_enh	8522459	8522581	chr1	-0.47
MCOLN2	3914	chr1:85231201-85231739	intra_enh	85231201	85231739	chr1	-0.87
LOC102724552	136234	chr1:8543285-8543764	intra_enh	8543285	8543764	chr1	-0.79
RERE	188079	chr1:8611879-8612535	intra_enh	8611879	8612535	chr1	-0.49
RERE	104838	chr1:8694851-8696045	intra_enh	8694851	8696045	chr1	-0.74
RERE	94591	chr1:8705435-8705955	intra_enh	8705435	8705955	chr1	-0.88
16-Sep	3027	chr1:87149424-87149914	intra_enh	87149424	87149914	chr1	-0.85
HS2ST1	18069	chr1:87170879-87171103	intra_enh	87170879	87171103	chr1	-0.78
HS2ST1	24172	chr1:87177043-87177145	intra_enh	87177043	87177145	chr1	-0.55
HS2ST1	50618	chr1:87203441-87203638	intra_enh	87203441	87203638	chr1	-0.82
HS2ST1	51231	chr1:87203807-87204499	intra_enh	87203807	87204499	chr1	-0.99
LINC01140	104318	chr1:87263249-87264184	intra_enh	87263249	87264184	chr1	-0.85
LINC01140	83738	chr1:87284234-87284357	intra_enh	87284234	87284357	chr1	-0.32
LINC01140	64116	chr1:87303487-87304348	intra_enh	87303487	87304348	chr1	-0.90
LINC01140	38003	chr1:87329970-87330092	intra_enh	87329970	87330092	chr1	-0.29
LRRC8C	37132	chr1:89907932-89908791	intra_enh	89907932	89908791	chr1	-0.84
LRRC8C	61139	chr1:89932039-89932699	intra_enh	89932039	89932699	chr1	-0.94

SLC2A7	15450	chr1:8993371-8993712	intra_enh	8993371	8993712	chr1	-0.82
SLC2A7	10138	chr1:8998759-8998949	intra_enh	8998759	8998949	chr1	-0.77
ZNF644	2731	chr1:91256806-91257040	intra_enh	91256806	91257040	chr1	-0.54
ZNF644	2257	chr1:91257248-91257546	intra_enh	91257248	91257546	chr1	-0.29
CDC7	3897	chr1:91742720-91743578	intra_enh	91742720	91743578	chr1	-0.63
SNORA66	18140	chr1:93096878-93097127	intra_enh	93096878	93097127	chr1	-0.30
FAM69A	6086	chr1:93120948-93121817	intra_enh	93120948	93121817	chr1	-0.84
FAM69A	26880	chr1:93141690-93142661	intra_enh	93141690	93142661	chr1	-0.97
LOC100131564	16679	chr1:93566946-93567608	intra_enh	93566946	93567608	chr1	-0.74
BCAR3	13930	chr1:93933590-93934235	intra_enh	93933590	93934235	chr1	-0.94
LINC01057	27704	chr1:95030654-95030789	intra_enh	95030654	95030789	chr1	-0.76
LINC01057	27375	chr1:95030989-95031113	intra_enh	95030989	95031113	chr1	-0.72
CNN3	51834	chr1:95112035-95112200	intra_enh	95112035	95112200	chr1	-0.64
CNN3	41994	chr1:95121811-95122106	intra_enh	95121811	95122106	chr1	-0.37
TMEM56	3571	chr1:95333993-95334469	intra_enh	95333993	95334469	chr1	-0.91
DPYD-AS2	334962	chr1:97699723-97700481	intra_enh	97699723	97700481	chr1	-0.96
CLSTN1	30638	chr1:9776425-9776576	intra_enh	9776425	9776576	chr1	-0.39
DPYD-AS2	52196	chr1:98086463-98088057	intra_enh	98086463	98088057	chr1	-0.71
CTNNBIP1	39182	chr1:9853655-9853788	intra_enh	9853655	9853788	chr1	-0.83
NMNAT1	7886	chr1:9933745-9934172	intra_enh	9933745	9934172	chr1	-0.59
ABCC2	63252	chr10:101595544-1015956	intra_enh	101595544	101595648	chr10	-0.76
DNMBP	4624	chr10:101754860-1017552	intra_enh	101754860	101755224	chr10	-0.68
CPN1	35922	chr10:101795516-1017959	intra_enh	101795516	101795905	chr10	-0.91
FBXW4	12383	chr10:103432153-1034325	intra_enh	103432153	103432549	chr10	-0.60
KCNIP2	59940	chr10:103653498-1036537	intra_enh	103653498	103653717	chr10	-0.59
KCNIP2	63037	chr10:103656597-1036568	intra_enh	103656597	103656813	chr10	-0.73
GBF1	35583	chr10:104030540-1040311	intra_enh	104030540	104031114	chr10	-0.40
SUFU	7642	chr10:104261218-1042614	intra_enh	104261218	104261481	chr10	-0.68
NT5C2	13898	chr10:104929093-1049292	intra_enh	104929093	104929220	chr10	-0.68
NT5C2	10382	chr10:104932350-1049329	intra_enh	104932350	104932995	chr10	-0.69
NT5C2	9522	chr10:104933376-1049336	intra_enh	104933376	104933687	chr10	-0.53
CALHM3	6804	chr10:105235720-1052358	intra_enh	105235720	105235864	chr10	-0.51
NEURL1	5106	chr10:105248449-1052492	intra_enh	105248449	105249212	chr10	-0.94
SH3PXD2A	21654	chr10:105583387-1055836	intra_enh	105583387	105583613	chr10	-0.68
GSTO2	16281	chr10:106041075-1060412	intra_enh	106041075	106041239	chr10	-0.52
XPNPEP1	39000	chr10:111634216-1116343	intra_enh	111634216	111634387	chr10	-0.41
ADD3	9337	chr10:111746124-1117466	intra_enh	111746124	111746630	chr10	-0.56
ADD3-AS1	50052	chr10:111807976-1118083	intra_enh	111807976	111808387	chr10	-0.30
ADD3-AS1	51677	chr10:111809681-1118099	intra_enh	111809681	111809933	chr10	-0.61
ADD3-AS1	59339	chr10:111817398-1118175	intra_enh	111817398	111817540	chr10	-0.45
SMC3	4875	chr10:112321839-1123227	intra_enh	112321839	112322787	chr10	-0.26
CELF2	14378	chr10:11232486-11232755	intra_enh	11232486	11232755	chr10	-0.80
RBM20	3558	chr10:112397625-1123977	intra_enh	112397625	112397779	chr10	-0.87
RBM20	4004	chr10:112398031-1123982	intra_enh	112398031	112398265	chr10	-0.72
RBM20	10273	chr10:112404287-1124045	intra_enh	112404287	112404547	chr10	-0.68
PDCD4-AS1	40764	chr10:112579781-1125799	intra_enh	112579781	112579996	chr10	-0.68
BBIP1	3440	chr10:112665169-1126653	intra_enh	112665169	112665318	chr10	-0.83
SHOC2	6560	chr10:112675769-1126759	intra_enh	112675769	112675930	chr10	-0.72
CELF2	80084	chr10:11326957-11327208	intra_enh	11326957	11327208	chr10	-0.84
CELF2	80422	chr10:11327314-11327527	intra_enh	11327314	11327527	chr10	-0.66
CELF2-AS1	86164	chr10:11340428-11340605	intra_enh	11340428	11340605	chr10	-0.88
CELF2-AS1	82742	chr10:11343755-11344120	intra_enh	11343755	11344120	chr10	-0.87
MIR2110	42724	chr10:115881152-1158812	intra_enh	115881152	115881257	chr10	-0.54
USP6NL	16654	chr10:11597556-11597709	intra_enh	11597556	11597709	chr10	-0.59
ABLIM1	31956	chr10:116244543-1162448	intra_enh	116244543	116244897	chr10	-0.94

ABLIM1	25811	chr10:116250547-1162511	intra_enh	116250547	116251183	chr10	-0.77
USP6NL	23334	chr10:11637566-11637674	intra_enh	11637566	11637674	chr10	-0.41
GRK5	76300	chr10:121033380-1210335	intra_enh	121033380	121033591	chr10	-0.87
MIR4681	48996	chr10:121078293-1210786	intra_enh	121078293	121078660	chr10	-0.61
MIR4681	47660	chr10:121174998-1211752	intra_enh	121174998	121175266	chr10	-0.62
INPP5F	35315	chr10:121533324-1215335	intra_enh	121533324	121533562	chr10	-0.44
NUDT5	46905	chr10:12324972-12325138	intra_enh	12324972	12325138	chr10	-0.82
ATE1	47032	chr10:123630331-1236307	intra_enh	123630331	123630740	chr10	-0.88
CAMK1D	40056	chr10:12471394-12471894	intra_enh	12471394	12471894	chr10	-0.67
LHPP	108416	chr10:126248695-1262487	intra_enh	126248695	126248796	chr10	-0.70
PRPF18	202203	chr10:13870877-13871417	intra_enh	13870877	13871417	chr10	-0.72
FAM107B	26215	chr10:14627913-14628045	intra_enh	14627913	14628045	chr10	-0.51
FAM107B	25849	chr10:14628214-14628476	intra_enh	14628214	14628476	chr10	-0.28
ADARB2-AS1	85640	chr10:1473141-1473228	intra_enh	1473141	1473228	chr10	-0.57
FAM107B	51483	chr10:14805267-14805571	intra_enh	14805267	14805571	chr10	-0.73
ADARB2-AS1	21994	chr10:1580755-1580880	intra_enh	1580755	1580880	chr10	-0.78
PTER	4062	chr10:16522911-16523106	intra_enh	16522911	16523106	chr10	-0.36
RSU1	18064	chr10:16917387-16917660	intra_enh	16917387	16917660	chr10	-0.59
SLC39A12-AS1	20429	chr10:18318904-18319234	intra_enh	18318904	18319234	chr10	-0.82
PLXDC2	187734	chr10:20332985-20333235	intra_enh	20332985	20333235	chr10	-0.75
NEBL	51514	chr10:21277617-21278487	intra_enh	21277617	21278487	chr10	-0.66
SPAG6	25018	chr10:22699245-22699547	intra_enh	22699245	22699547	chr10	-0.92
PIP4K2A	120616	chr10:22922610-22923177	intra_enh	22922610	22923177	chr10	-0.97
PIP4K2A	117170	chr10:22926271-22926410	intra_enh	22926271	22926410	chr10	-0.77
PIP4K2A	9284	chr10:23034149-23034303	intra_enh	23034149	23034303	chr10	-0.48
ZMYND11	44726	chr10:260602-260713	intra_enh	260602	260713	chr10	-0.64
APBB1IP	20300	chr10:26787395-26787745	intra_enh	26787395	26787745	chr10	-0.95
ABI1	81448	chr10:27108498-27108651	intra_enh	27108498	27108651	chr10	-0.70
ABI1	40676	chr10:27149200-27149491	intra_enh	27149200	27149491	chr10	-0.50
ABI1	5729	chr10:27184210-27184376	intra_enh	27184210	27184376	chr10	-0.61
LOC102031319	6089	chr10:32682210-32682560	intra_enh	32682210	32682560	chr10	-0.82
EPC1	10960	chr10:32696661-32696882	intra_enh	32696661	32696882	chr10	-0.29
EPC1	10604	chr10:32697018-32697239	intra_enh	32697018	32697239	chr10	-0.48
ITGB1	6770	chr10:33271104-33271419	intra_enh	33271104	33271419	chr10	-0.90
ITGB1	8234	chr10:33272242-33273209	intra_enh	33272242	33273209	chr10	-0.90
PARD3	177160	chr10:34966702-34967497	intra_enh	34966702	34967497	chr10	-0.93
CCNY	64032	chr10:35729763-35729913	intra_enh	35729763	35729913	chr10	-0.82
CCNY	125876	chr10:35791581-35791783	intra_enh	35791581	35791783	chr10	-0.53
GJD4	50537	chr10:35883469-35884141	intra_enh	35883469	35884141	chr10	-0.79
ZNF248	2434	chr10:38184031-38184242	intra_enh	38184031	38184242	chr10	-0.53
ZNF33A	28054	chr10:38367562-38367711	intra_enh	38367562	38367711	chr10	-0.71
CSGALNACT2	6634	chr10:42960203-42960862	intra_enh	42960203	42960862	chr10	-0.96
RASGEF1A	24478	chr10:43020633-43020798	intra_enh	43020633	43020798	chr10	-0.25
9-Mar	21498	chr10:45372201-45372492	intra_enh	45372201	45372492	chr10	-0.67
ZFAND4	14448	chr10:45473685-45473792	intra_enh	45473685	45473792	chr10	-0.45
WDFY4	31665	chr10:49595137-49595237	intra_enh	49595137	49595237	chr10	-0.69
VSTM4	38612	chr10:49954704-49955241	intra_enh	49954704	49955241	chr10	-0.86
SGMS1	172248	chr10:51881437-51881554	intra_enh	51881437	51881554	chr10	-0.37
PRKG1-AS1	97184	chr10:53646357-53647062	intra_enh	53646357	53647062	chr10	-0.89
PRKG1-AS1	96520	chr10:53647208-53647539	intra_enh	53647208	53647539	chr10	-0.94
NET1	2998	chr10:5475445-5475582	intra_enh	5475445	5475582	chr10	-0.85
IL15RA	36342	chr10:6096052-6096944	intra_enh	6096052	6096944	chr10	-0.62
CCDC6	72637	chr10:61263482-61264084	intra_enh	61263482	61264084	chr10	-0.72
CCDC6	53594	chr10:61282708-61282944	intra_enh	61282708	61282944	chr10	-0.67
ANK3	69536	chr10:61640201-61640432	intra_enh	61640201	61640432	chr10	-0.37

ANK3	123431	chr10:61695721-61696697	intra_enh	61695721	61696697	chr10	-0.43
RHOBTB1	16897	chr10:62390653-62391221	intra_enh	62390653	62391221	chr10	-0.91
MIR3155B	13296	chr10:6247399-6247656	intra_enh	6247399	6247656	chr10	-0.56
C10orf107	89564	chr10:63182203-63182372	intra_enh	63182203	63182372	chr10	-0.89
ARID5B	5203	chr10:63336166-63336276	intra_enh	63336166	63336276	chr10	-0.72
MIR548AV	34638	chr10:63370810-63372047	intra_enh	63370810	63372047	chr10	-0.60
MIR548AV	32854	chr10:63372744-63373681	intra_enh	63372744	63373681	chr10	-0.58
MIR548AV	31561	chr10:63374362-63374648	intra_enh	63374362	63374648	chr10	-0.86
MIR548AV	14564	chr10:63391429-63391574	intra_enh	63391429	63391574	chr10	-0.26
MIR548AV	5716	chr10:63399929-63400772	intra_enh	63399929	63400772	chr10	-0.61
MIR548AV	13074	chr10:63419056-63419225	intra_enh	63419056	63419225	chr10	-0.87
MIR548AV	13780	chr10:63419645-63420048	intra_enh	63419645	63420048	chr10	-0.73
ARID5B	27764	chr10:63450915-63451504	intra_enh	63450915	63451504	chr10	-0.31
ARID5B	10348	chr10:63468233-63469018	intra_enh	63468233	63469018	chr10	-0.29
ARID5B	5433	chr10:63473298-63473784	intra_enh	63473298	63473784	chr10	-0.59
ARID5B	4069	chr10:63474616-63475194	intra_enh	63474616	63475194	chr10	-0.59
RTKN2	4098	chr10:63694414-63694647	intra_enh	63694414	63694647	chr10	-0.57
RTKN2	3457	chr10:63694960-63695382	intra_enh	63694960	63695382	chr10	-0.58
ZNF365	69189	chr10:63880548-63881498	intra_enh	63880548	63881498	chr10	-0.95
ZNF365	73928	chr10:64024050-64024231	intra_enh	64024050	64024231	chr10	-0.53
JMJD1C	49069	chr10:64649769-64650073	intra_enh	64649769	64650073	chr10	-0.38
JMJD1C	32602	chr10:64666355-64666420	intra_enh	64666355	64666420	chr10	-0.70
JMJD1C	26325	chr10:64672472-64672858	intra_enh	64672472	64672858	chr10	-0.66
JMJD1C	24948	chr10:64673976-64674107	intra_enh	64673976	64674107	chr10	-0.31
JMJD1C	13677	chr10:64685217-64685409	intra_enh	64685217	64685409	chr10	-0.61
JMJD1C	4447	chr10:64703166-64703708	intra_enh	64703166	64703708	chr10	-0.28
JMJD1C-AS1	43648	chr10:64851223-64851468	intra_enh	64851223	64851468	chr10	-0.35
TET1	65170	chr10:70055120-70055464	intra_enh	70055120	70055464	chr10	-0.93
HK1	30426	chr10:70778931-70779138	intra_enh	70778931	70779138	chr10	-0.28
COL13A1	44068	chr10:71275593-71275839	intra_enh	71275593	71275839	chr10	-0.81
COL13A1	46909	chr10:71278485-71278629	intra_enh	71278485	71278629	chr10	-0.73
AIFM2	25340	chr10:71537312-71537399	intra_enh	71537312	71537399	chr10	-0.41
PPA1	11961	chr10:71651037-71651433	intra_enh	71651037	71651433	chr10	-0.63
PALD1	9971	chr10:71918448-71918630	intra_enh	71918448	71918630	chr10	-0.28
PALD1	10664	chr10:71918762-71919703	intra_enh	71918762	71919703	chr10	-0.50
MIR6797	28978	chr10:73067705-73068626	intra_enh	73067705	73068626	chr10	-0.86
C10orf105	52196	chr10:73097213-73097562	intra_enh	73097213	73097562	chr10	-0.29
CDH23	6021	chr10:73231428-73231678	intra_enh	73231428	73231678	chr10	-0.94
SPOCK2	12470	chr10:73505949-73506187	intra_enh	73505949	73506187	chr10	-0.92
SPOCK2	18382	chr10:73536622-73537735	intra_enh	73536622	73537735	chr10	-0.87
ASCC1	5796	chr10:73652618-73652769	intra_enh	73652618	73652769	chr10	-0.34
ASCC1	11032	chr10:73657881-73657979	intra_enh	73657881	73657979	chr10	-0.62
ANXA7	8292	chr10:74835486-74835626	intra_enh	74835486	74835626	chr10	-0.71
PPP3CB	5671	chr10:74931356-74931562	intra_enh	74931356	74931562	chr10	-0.85
VCL	9276	chr10:75437078-75437225	intra_enh	75437078	75437225	chr10	-0.91
ADK	12620	chr10:75593203-75593934	intra_enh	75593203	75593934	chr10	-0.92
ADK	51760	chr10:75657808-75658217	intra_enh	75657808	75658217	chr10	-0.49
KAT6B	8846	chr10:76264991-76265053	intra_enh	76264991	76265053	chr10	-0.64
KAT6B	25890	chr10:76281499-76282632	intra_enh	76281499	76282632	chr10	-0.52
VDAC2	43511	chr10:76596291-76596519	intra_enh	76596291	76596519	chr10	-0.61
KCNMA1	14652	chr10:79052751-79053114	intra_enh	79052751	79053114	chr10	-0.75
DLG5	90054	chr10:79266015-79266586	intra_enh	79266015	79266586	chr10	-0.65
RPS24	13856	chr10:79477305-79477450	intra_enh	79477305	79477450	chr10	-0.75
FAM213A	8230	chr10:82171573-82171996	intra_enh	82171573	82171996	chr10	-0.56
TSPAN14	15167	chr10:82218931-82219435	intra_enh	82218931	82219435	chr10	-0.40

CCSER2	2322	chr10:86080593-86080698	intra_enh	86080593	86080698	chr10	-0.50
CCSER2	2729	chr10:86080837-86081269	intra_enh	86080837	86081269	chr10	-0.78
MIR346	2861	chr10:88011567-88011763	intra_enh	88011567	88011763	chr10	-0.29
PTEN	10594	chr10:89622997-89624538	intra_enh	89622997	89624538	chr10	-0.91
RNLS	291165	chr10:90041826-90041968	intra_enh	90041826	90041968	chr10	-0.84
RNLS	250558	chr10:90082232-90082777	intra_enh	90082232	90082777	chr10	-0.93
RNLS	238153	chr10:90094821-90094997	intra_enh	90094821	90094997	chr10	-0.67
RNLS	169818	chr10:90163159-90163329	intra_enh	90163159	90163329	chr10	-0.76
LIPM	22578	chr10:90574891-90575197	intra_enh	90574891	90575197	chr10	-0.46
ACTA2-AS1	3027	chr10:90685351-90685543	intra_enh	90685351	90685543	chr10	-0.55
LIPA	8766	chr10:90992821-90992938	intra_enh	90992821	90992938	chr10	-0.69
LIPA	8568	chr10:90993040-90993115	intra_enh	90993040	90993115	chr10	-0.68
KIF20B	4596	chr10:91455854-91455989	intra_enh	91455854	91455989	chr10	-0.50
PCGF5	27556	chr10:92939873-92940735	intra_enh	92939873	92940735	chr10	-0.77
PCGF5	11108	chr10:92958436-92959119	intra_enh	92958436	92959119	chr10	-0.90
PCGF5	5242	chr10:92964413-92964874	intra_enh	92964413	92964874	chr10	-0.91
HECTD2	20251	chr10:93139606-93139932	intra_enh	93139606	93139932	chr10	-0.56
BTAF1	2422	chr10:93676038-93676235	intra_enh	93676038	93676235	chr10	-0.73
CPEB3	61618	chr10:93931176-93931621	intra_enh	93931176	93931621	chr10	-0.81
EXOC6	53648	chr10:94651760-94651943	intra_enh	94651760	94651943	chr10	-0.60
MYOF	54574	chr10:95177325-95177656	intra_enh	95177325	95177656	chr10	-0.44
PDLIM1	31914	chr10:97072709-97072912	intra_enh	97072709	97072912	chr10	-0.59
PDLIM1	32278	chr10:97073027-97073321	intra_enh	97073027	97073321	chr10	-0.92
C10orf131	66120	chr10:97591334-97591845	intra_enh	97591334	97591845	chr10	-0.87
C10orf131	42376	chr10:97615258-97615409	intra_enh	97615258	97615409	chr10	-0.90
CC2D2B	36092	chr10:97713373-97714115	intra_enh	97713373	97714115	chr10	-0.90
CC2D2B	11958	chr10:97737531-97738225	intra_enh	97737531	97738225	chr10	-0.71
LCOR	2440	chr10:98585069-98585210	intra_enh	98585069	98585210	chr10	-0.79
LCOR	2986	chr10:98585339-98586034	intra_enh	98585339	98586034	chr10	-0.88
C10orf12	43040	chr10:98773885-98774256	intra_enh	98773885	98774256	chr10	-0.87
MMS19	3234	chr10:99244792-99245452	intra_enh	99244792	99245452	chr10	-0.39
ARHGAP42	53986	chr11:100117409-1001177	intra_enh	100117409	100117795	chr11	-0.80
SBF2	208304	chr11:10063988-10064064	intra_enh	10063988	10064064	chr11	-0.40
MIR3920	5459	chr11:100901076-1009015	intra_enh	100901076	100901534	chr11	-0.95
BIRC2	14348	chr11:101737550-1017377	intra_enh	101737550	101737774	chr11	-0.50
TMEM123	31408	chr11:101797015-1017981	intra_enh	101797015	101798140	chr11	-0.85
TMEM123	29836	chr11:101798897-1017994	intra_enh	101798897	101799404	chr11	-0.61
TMEM123	26834	chr11:101802045-1018022	intra_enh	101802045	101802259	chr11	-0.74
DCUN1D5	21717	chr11:102446112-1024467	intra_enh	102446112	102446762	chr11	-0.75
CAND1.11	58305	chr11:10344582-10344896	intra_enh	10344582	10344896	chr11	-0.30
CUL5	16970	chr11:107401490-1074016	intra_enh	107401490	107401681	chr11	-0.30
NPAT	47018	chr11:107551226-1075518	intra_enh	107551226	107551890	chr11	-0.88
RDX	10278	chr11:109662197-1096625	intra_enh	109662197	109662544	chr11	-0.92
RDX	8922	chr11:109663447-1096640	intra_enh	109663447	109664006	chr11	-0.94
USP28	35382	chr11:113216027-1132162	intra_enh	113216027	113216214	chr11	-0.57
ZBTB16	112332	chr11:113548496-1135491	intra_enh	113548496	113549161	chr11	-0.48
NNMT	116403	chr11:113555264-1135554	intra_enh	113555264	113555418	chr11	-0.33
NNMT	101037	chr11:113570536-1135708	intra_enh	113570536	113570878	chr11	-0.91
CADM1	284568	chr11:114595474-1145962	intra_enh	114595474	114596295	chr11	-0.50
CADM1	283968	chr11:114596406-1145965	intra_enh	114596406	114596563	chr11	-0.50
CADM1	86453	chr11:114793912-1147940	intra_enh	114793912	114794086	chr11	-0.85
CADM1	50096	chr11:114829999-1148307	intra_enh	114829999	114830712	chr11	-0.99
CADM1	35206	chr11:114845005-1148454	intra_enh	114845005	114845488	chr11	-0.97
APOA1	78690	chr11:116292077-1162923	intra_enh	116292077	116292398	chr11	-0.96
APOA1	79668	chr11:116293023-1162934	intra_enh	116293023	116293409	chr11	-0.36

APOA1	120900	chr11:116333980-1163349	intra_enh	116333980	116334916	chr11	-0.80
APOA1	124661	chr11:116338022-1163383	intra_enh	116338022	116338396	chr11	-0.82
SIK3	118036	chr11:116356033-1163565	intra_enh	116356033	116356579	chr11	-0.40
SIK3	116832	chr11:116357406-1163576	intra_enh	116357406	116357614	chr11	-0.58
SIK3	116368	chr11:116357893-1163580	intra_enh	116357893	116358056	chr11	-0.37
SIK3	21065	chr11:116453024-1164535	intra_enh	116453024	116453530	chr11	-0.76
IL10RA	5915	chr11:117368091-1173683	intra_enh	117368091	117368367	chr11	-0.81
AMICA1	6726	chr11:117582174-1175829	intra_enh	117582174	117582941	chr11	-0.86
KMT2A	3352	chr11:117815682-1178158	intra_enh	117815682	117815850	chr11	-0.66
KMT2A	3688	chr11:117816041-1178161	intra_enh	117816041	117816163	chr11	-0.73
KMT2A	3934	chr11:117816289-1178164	intra_enh	117816289	117816408	chr11	-0.62
ARCN1	3376	chr11:117951541-1179518	intra_enh	117951541	117951831	chr11	-0.88
DDX6	4107	chr11:118162565-1181629	intra_enh	118162565	118162957	chr11	-0.31
USP47	8170	chr11:11827629-11827799	intra_enh	11827629	11827799	chr11	-0.61
MIR4492	3692	chr11:118282884-1182829	intra_enh	118282884	118282984	chr11	-0.44
CBL	31486	chr11:118613563-1186137	intra_enh	118613563	118613798	chr11	-0.96
CBL	33384	chr11:118615405-1186157	intra_enh	118615405	118615751	chr11	-0.92
CBL	37950	chr11:118619975-1186203	intra_enh	118619975	118620312	chr11	-0.84
CBL	42464	chr11:118624204-1186251	intra_enh	118624204	118625111	chr11	-0.98
MIR6756	51356	chr11:118637492-1186376	intra_enh	118637492	118637661	chr11	-0.51
MIR6756	50666	chr11:118638213-1186383	intra_enh	118638213	118638320	chr11	-0.55
MIR6756	49717	chr11:118638429-1186400	intra_enh	118638429	118640001	chr11	-0.63
USP2	6416	chr11:118746287-1187467	intra_enh	118746287	118746750	chr11	-0.70
THY1	17788	chr11:118817135-1188173	intra_enh	118817135	118817353	chr11	-0.90
PVRL1	34934	chr11:119069662-1190697	intra_enh	119069662	119069761	chr11	-0.30
ARHGEF12	7659	chr11:119720208-1197207	intra_enh	119720208	119720762	chr11	-0.73
CRTAM	82062	chr11:122131860-1221329	intra_enh	122131860	122132945	chr11	-0.86
ST3GAL4	11061	chr11:125767414-1257675	intra_enh	125767414	125767504	chr11	-0.52
ST3GAL4	34980	chr11:125816201-1258163	intra_enh	125816201	125816332	chr11	-0.68
LOC101929517	18548	chr11:127919608-1279199	intra_enh	127919608	127919979	chr11	-0.62
BARX2	60289	chr11:128811149-1288116	intra_enh	128811149	128811609	chr11	-0.96
LINC00167	9884	chr11:129367390-1293682	intra_enh	129367390	129368298	chr11	-0.82
LINC00167	3916	chr11:129373705-1293739	intra_enh	129373705	129373919	chr11	-0.27
LINC00167	3072	chr11:129374594-1293747	intra_enh	129374594	129374719	chr11	-0.72
APLP2	6778	chr11:129452313-1294525	intra_enh	129452313	129452586	chr11	-0.50
APLP2	12237	chr11:129457825-1294579	intra_enh	129457825	129457993	chr11	-0.73
ST14	27518	chr11:129507308-1295074	intra_enh	129507308	129507436	chr11	-0.29
ST14	22362	chr11:129556762-1295577	intra_enh	129556762	129557741	chr11	-0.31
ZBTB44	45180	chr11:129644548-1296447	intra_enh	129644548	129644727	chr11	-0.73
C11orf39	5576	chr11:131044128-1310443	intra_enh	131044128	131044344	chr11	-0.79
VPS26B	3951	chr11:133603653-1336037	intra_enh	133603653	133603789	chr11	-0.83
FAR1	2457	chr11:13648923-13649551	intra_enh	13648923	13649551	chr11	-0.57
FAR1	4082	chr11:13650747-13650976	intra_enh	13650747	13650976	chr11	-0.81
RRAS2	155868	chr11:14180596-14180885	intra_enh	14180596	14180885	chr11	-0.70
RRAS2	120955	chr11:14215474-14215832	intra_enh	14215474	14215832	chr11	-0.74
PSMA1	34746	chr11:14533205-14533422	intra_enh	14533205	14533422	chr11	-0.82
C11orf58	3778	chr11:16720423-16720576	intra_enh	16720423	16720576	chr11	-0.55
PLEKHA7	67746	chr11:16924669-16924919	intra_enh	16924669	16924919	chr11	-0.38
LSP1	11216	chr11:1859859-1860028	intra_enh	1859859	1860028	chr11	-0.74
LSP1	11493	chr11:1860140-1860302	intra_enh	1860140	1860302	chr11	-0.78
IGSF22	5516	chr11:18709534-18710206	intra_enh	18709534	18710206	chr11	-0.75
NAV2-AS5	56762	chr11:19428474-19428706	intra_enh	19428474	19428706	chr11	-0.92
NAV2	62769	chr11:19937757-19938057	intra_enh	19937757	19938057	chr11	-0.72
NAV2	53160	chr11:19947316-19947715	intra_enh	19947316	19947715	chr11	-0.77
NAV2	43532	chr11:19957099-19957189	intra_enh	19957099	19957189	chr11	-0.33

SLC22A18AS	9966	chr11:2891354-2892083	intra_enh	2891354	2892083	chr11	-0.84
ARL14EP	5993	chr11:30306505-30307921	intra_enh	30306505	30307921	chr11	-0.86
EIF3M	2874	chr11:32564505-32565018	intra_enh	32564505	32565018	chr11	-0.31
CAPRIN1	4298	chr11:34033794-34034411	intra_enh	34033794	34034411	chr11	-0.32
CAPRIN1	4828	chr11:34034581-34034684	intra_enh	34034581	34034684	chr11	-0.30
CD44	43552	chr11:35160374-35160715	intra_enh	35160374	35160715	chr11	-0.76
SLC1A2	84998	chr11:35312581-35312788	intra_enh	35312581	35312788	chr11	-0.36
TRIM44	17929	chr11:35658699-35659015	intra_enh	35658699	35659015	chr11	-0.85
TRIM44	20788	chr11:35661095-35662336	intra_enh	35661095	35662336	chr11	-0.93
TRIM44	59200	chr11:35699977-35700280	intra_enh	35699977	35700280	chr11	-0.73
MIR4687	5762	chr11:3839423-3839832	intra_enh	3839423	3839832	chr11	-0.43
MIR4687	32230	chr11:3865963-3866228	intra_enh	3865963	3866228	chr11	-0.59
RRM1	4922	chr11:4077354-4077487	intra_enh	4077354	4077487	chr11	-0.73
LRRC4C	149810	chr11:41287852-41288051	intra_enh	41287852	41288051	chr11	-0.75
API5	2359	chr11:43292356-43292522	intra_enh	43292356	43292522	chr11	-0.45
CD82	3448	chr11:44546988-44547341	intra_enh	44546988	44547341	chr11	-0.58
GYLTL1B	16608	chr11:45917213-45917606	intra_enh	45917213	45917606	chr11	-0.45
HARBI1	5072	chr11:46590148-46590416	intra_enh	46590148	46590416	chr11	-0.29
C11orf49	63137	chr11:46977505-46978397	intra_enh	46977505	46978397	chr11	-0.96
ARFGAP2	72405	chr11:47082577-47083117	intra_enh	47082577	47083117	chr11	-0.87
DDB2	5567	chr11:47198451-47198819	intra_enh	47198451	47198819	chr11	-0.93
PTPRJ	67667	chr11:48026006-48026696	intra_enh	48026006	48026696	chr11	-0.28
PTPRJ	94197	chr11:48052501-48053261	intra_enh	48052501	48053261	chr11	-0.27
LMNTD2	11562	chr11:539123-539312	intra_enh	539123	539312	chr11	-0.54
CTNND1	38930	chr11:57324678-57324799	intra_enh	57324678	57324799	chr11	-0.43
CTNND1	39338	chr11:57324991-57325301	intra_enh	57324991	57325301	chr11	-0.88
LPXN	8084	chr11:58091650-58092115	intra_enh	58091650	58092115	chr11	-0.58
LPXN	7080	chr11:58092734-58093039	intra_enh	58092734	58093039	chr11	-0.33
LOC283194	48652	chr11:58533766-58533933	intra_enh	58533766	58533933	chr11	-0.74
MS4A13	13260	chr11:60052389-60053050	intra_enh	60052389	60053050	chr11	-0.95
MS4A8	15174	chr11:60208299-60208598	intra_enh	60208299	60208598	chr11	-0.85
TMEM109	5220	chr11:60442973-60443358	intra_enh	60442973	60443358	chr11	-0.43
VPS37C	19408	chr11:60665954-60666213	intra_enh	60665954	60666213	chr11	-0.36
DDB1	2984	chr11:60860138-60860351	intra_enh	60860138	60860351	chr11	-0.41
DDB1	3354	chr11:60860550-60860679	intra_enh	60860550	60860679	chr11	-0.71
SDHAF2	2196	chr11:60956225-60956510	intra_enh	60956225	60956510	chr11	-0.52
SDHAF2	2591	chr11:60956688-60956838	intra_enh	60956688	60956838	chr11	-0.60
AHNAK	7629	chr11:62063202-62063356	intra_enh	62063202	62063356	chr11	-0.34
MARK2	22654	chr11:63389739-63390078	intra_enh	63389739	63390078	chr11	-0.30
MARK2	22009	chr11:63390438-63390668	intra_enh	63390438	63390668	chr11	-0.61
FLRT1	3126	chr11:63624743-63624876	intra_enh	63624743	63624876	chr11	-0.57
KCNK7	7237	chr11:65127149-65127413	intra_enh	65127149	65127413	chr11	-0.94
PACS1	44302	chr11:65638387-65639014	intra_enh	65638387	65639014	chr11	-0.42
PACS1	55248	chr11:65649501-65649790	intra_enh	65649501	65649790	chr11	-0.61
PACS1	61904	chr11:65655959-65656644	intra_enh	65655959	65656644	chr11	-0.35
PACS1	67300	chr11:65661454-65661943	intra_enh	65661454	65661943	chr11	-0.78
PACS1	68146	chr11:65662363-65662724	intra_enh	65662363	65662724	chr11	-0.38
C11orf80	48050	chr11:66316677-66316988	intra_enh	66316677	66316988	chr11	-0.51
RCE1	27543	chr11:66339733-66340097	intra_enh	66339733	66340097	chr11	-0.97
SYT12	8045	chr11:66555276-66555594	intra_enh	66555276	66555594	chr11	-0.63
KDM2A	26849	chr11:66736983-66737479	intra_enh	66736983	66737479	chr11	-0.72
PPP6R3	20126	chr11:67964549-67964720	intra_enh	67964549	67964720	chr11	-0.39
SHANK2	23674	chr11:70589685-70589947	intra_enh	70589685	70589947	chr11	-0.90
FLJ42102	4573	chr11:70807312-70807638	intra_enh	70807312	70807638	chr11	-0.94
FLJ42102	2885	chr11:70809099-70809227	intra_enh	70809099	70809227	chr11	-0.86

EPS8L2	17490	chr11:713536-713679	intra_enh	713536	713679	chr11	-0.76
LOC100128494	22654	chr11:71425357-71425918	intra_enh	71425357	71425918	chr11	-0.54
MIR3165	2748	chr11:71458194-71458302	intra_enh	71458194	71458302	chr11	-0.48
ATG16L2	137748	chr11:72340660-72341031	intra_enh	72340660	72341031	chr11	-0.26
ATG16L2	138421	chr11:72341423-72341615	intra_enh	72341423	72341615	chr11	-0.27
FAM168A	59306	chr11:72927409-72927743	intra_enh	72927409	72927743	chr11	-0.88
LOC100506258	42562	chr11:7400879-7401282	intra_enh	7400879	7401282	chr11	-0.93
UVRAG	11672	chr11:75215195-75215866	intra_enh	75215195	75215866	chr11	-0.57
WNT11	81481	chr11:75513689-75513793	intra_enh	75513689	75513793	chr11	-0.83
LOC100506127	2766	chr11:75772699-75772864	intra_enh	75772699	75772864	chr11	-0.87
KCTD21-AS1	4110	chr11:77532512-77532681	intra_enh	77532512	77532681	chr11	-0.90
USP35	35438	chr11:77612832-77613053	intra_enh	77612832	77613053	chr11	-0.91
USP35	39322	chr11:77616483-77617168	intra_enh	77616483	77617168	chr11	-0.94
LOC101928865	8949	chr11:77827361-77827597	intra_enh	77827361	77827597	chr11	-0.73
DDIAS	26018	chr11:82316192-82316613	intra_enh	82316192	82316613	chr11	-0.61
RAB30	27563	chr11:82395353-82396041	intra_enh	82395353	82396041	chr11	-0.64
PCF11	16982	chr11:82562706-82562827	intra_enh	82562706	82562827	chr11	-0.70
DLG2	249860	chr11:83955016-83956764	intra_enh	83955016	83956764	chr11	-0.73
DLG2	175579	chr11:84136383-84136687	intra_enh	84136383	84136687	chr11	-0.80
DLG2	175124	chr11:84136895-84137085	intra_enh	84136895	84137085	chr11	-0.77
DLG2	200518	chr11:84512313-84512952	intra_enh	84512313	84512952	chr11	-0.98
DLG2	241486	chr11:84774267-84774684	intra_enh	84774267	84774684	chr11	-0.95
TMEM135	268644	chr11:86695064-86695287	intra_enh	86695064	86695287	chr11	-0.93
ST5	21807	chr11:8810860-8811670	intra_enh	8810860	8811670	chr11	-0.75
AP2A2	2210	chr11:917904-918132	intra_enh	917904	918132	chr11	-0.60
DENND5A	56180	chr11:9187016-9187524	intra_enh	9187016	9187524	chr11	-0.81
DENND5A	4061	chr11:9239192-9239586	intra_enh	9239192	9239586	chr11	-0.91
MED17	3295	chr11:93160262-93160432	intra_enh	93160262	93160432	chr11	-0.57
IPO7	13102	chr11:9375791-9375900	intra_enh	9375791	9375900	chr11	-0.76
PIWIL4	35560	chr11:93975366-93975994	intra_enh	93975366	93975994	chr11	-0.84
MIR1260B	143573	chr11:95570649-95570701	intra_enh	95570649	95570701	chr11	-0.55
MIR1260B	143215	chr11:95570872-95571194	intra_enh	95570872	95571194	chr11	-0.65
WEE1	4591	chr11:9557320-9557478	intra_enh	9557320	9557478	chr11	-0.67
WEE1	4999	chr11:9557677-9557937	intra_enh	9557677	9557937	chr11	-0.50
MIR1260B	128488	chr11:95585320-95586201	intra_enh	95585320	95586201	chr11	-0.80
MIR1260B	120984	chr11:95592985-95593542	intra_enh	95592985	95593542	chr11	-0.53
SWAP70	10286	chr11:9652325-9652642	intra_enh	9652325	9652642	chr11	-0.26
SWAP70	33635	chr11:9675743-9675923	intra_enh	9675743	9675923	chr11	-0.53
SWAP70	34948	chr11:9676986-9677305	intra_enh	9676986	9677305	chr11	-0.72
SWAP70	38045	chr11:9679947-9680539	intra_enh	9679947	9680539	chr11	-0.53
SBF2-AS1	40117	chr11:9696208-9696386	intra_enh	9696208	9696386	chr11	-0.42
SBF2-AS1	39860	chr11:9696489-9696620	intra_enh	9696489	9696620	chr11	-0.58
SBF2-AS1	39524	chr11:9696829-9696950	intra_enh	9696829	9696950	chr11	-0.69
SBF2-AS1	9454	chr11:9726901-9727018	intra_enh	9726901	9727018	chr11	-0.38
LOC101928008	36698	chr11:9780465-9780667	intra_enh	9780465	9780667	chr11	-0.90
MYBPC1	21442	chr12:100534059-1005345	intra_enh	100534059	100534500	chr12	-0.84
SYCP3	41246	chr12:100698532-1006987	intra_enh	100698532	100698723	chr12	-0.88
GNPTAB	5768	chr12:100742816-1007432	intra_enh	100742816	100743201	chr12	-0.90
DRAM1	40718	chr12:100835898-1008360	intra_enh	100835898	100836007	chr12	-0.69
CLEC9A	21609	chr12:10096062-10096240	intra_enh	10096062	10096240	chr12	-0.89
CHST11	33842	chr12:103408490-1034088	intra_enh	103408490	103408835	chr12	-0.70
MIR3922	10482	chr12:103498919-1034991	intra_enh	103498919	103499196	chr12	-0.88
MIR3922	7496	chr12:103501970-1035021	intra_enh	103501970	103502117	chr12	-0.73
MIR3922	149328	chr12:103658787-1036589	intra_enh	103658787	103658949	chr12	-0.79
ALDH1L2	31510	chr12:103970885-1039710	intra_enh	103970885	103971039	chr12	-0.75

ALDH1L2	11378	chr12:103990950-1039912	intra_enh	103990950	103991239	chr12	-0.79
RIC8B	21137	chr12:105671309-1056714	intra_enh	105671309	105671473	chr12	-0.55
SART3	4659	chr12:107474363-1074749	intra_enh	107474363	107474911	chr12	-0.77
CORO1C	23588	chr12:107597205-1075974	intra_enh	107597205	107597427	chr12	-0.85
CORO1C	13098	chr12:107607332-1076082	intra_enh	107607332	107608280	chr12	-0.78
CORO1C	12226	chr12:107632784-1076334	intra_enh	107632784	107633475	chr12	-0.96
DAO	50044	chr12:107847791-1078482	intra_enh	107847791	107848265	chr12	-0.93
ANKRD13A	8811	chr12:108930140-1089307	intra_enh	108930140	108930714	chr12	-0.89
C12orf76	17469	chr12:108972231-1089725	intra_enh	108972231	108972599	chr12	-0.58
IFT81	75306	chr12:109121437-1091222	intra_enh	109121437	109122218	chr12	-0.97
ATP2A2	5068	chr12:109208422-1092085	intra_enh	109208422	109208541	chr12	-0.87
ARPC3	6122	chr12:109378598-1093788	intra_enh	109378598	109378846	chr12	-0.90
PPTC7	20012	chr12:109485353-1094855	intra_enh	109485353	109485518	chr12	-0.65
PPTC7	19172	chr12:109486117-1094864	intra_enh	109486117	109486434	chr12	-0.60
TCTN1	22596	chr12:109558762-1095590	intra_enh	109558762	109559017	chr12	-0.71
SH2B3	4094	chr12:110352768-1103531	intra_enh	110352768	110353140	chr12	-0.86
DTX1	27020	chr12:112006996-1120071	intra_enh	112006996	112007131	chr12	-0.44
RASAL1	13424	chr12:112044297-1120444	intra_enh	112044297	112044430	chr12	-0.80
IQCD	7618	chr12:112135515-1121358	intra_enh	112135515	112135812	chr12	-0.77
IQCD	6952	chr12:112136253-1121364	intra_enh	112136253	112136407	chr12	-0.57
TPCN1	8594	chr12:112151961-1121524	intra_enh	112151961	112152474	chr12	-0.67
MIR620	46488	chr12:115117145-1151175	intra_enh	115117145	115117516	chr12	-0.39
FBXW8	11455	chr12:115844537-1158446	intra_enh	115844537	115844657	chr12	-0.77
LINC01252	6264	chr12:11598396-11598591	intra_enh	11598396	11598591	chr12	-0.91
PEBP1	46244	chr12:117104407-1171045	intra_enh	117104407	117104585	chr12	-0.29
TAOK3	42810	chr12:117251920-1172527	intra_enh	117251920	117252728	chr12	-0.79
TAOK3	42114	chr12:117252874-1172531	intra_enh	117252874	117253166	chr12	-0.52
ETV6	72919	chr12:11766858-11767088	intra_enh	11766858	11767088	chr12	-0.86
ERC1	175278	chr12:1182386-1182517	intra_enh	1182386	1182517	chr12	-0.37
BCL2L14	192457	chr12:11922598-11922776	intra_enh	11922598	11922776	chr12	-0.57
BCL2L14	192216	chr12:11922901-11922956	intra_enh	11922901	11922956	chr12	-0.61
BCL2L14	188542	chr12:11925989-11927216	intra_enh	11925989	11927216	chr12	-0.79
CABP1	3533	chr12:119569106-1195692	intra_enh	119569106	119569212	chr12	-0.50
CABP1	3236	chr12:119569365-1195695	intra_enh	119569365	119569548	chr12	-0.49
UNC119B	3456	chr12:119635967-1196361	intra_enh	119635967	119636184	chr12	-0.89
SPPL3	56078	chr12:119769882-1197710	intra_enh	119769882	119771038	chr12	-0.27
SPPL3	54271	chr12:119772113-1197724	intra_enh	119772113	119772421	chr12	-0.56
RNF34	2282	chr12:120324530-1203246	intra_enh	120324530	120324639	chr12	-0.49
WDR66	8576	chr12:120849306-1208495	intra_enh	120849306	120849534	chr12	-0.40
WDR66	20884	chr12:120861678-1208617	intra_enh	120861678	120861779	chr12	-0.43
BCL7A	43058	chr12:120900980-1209013	intra_enh	120900980	120901387	chr12	-0.46
KNTC1	84007	chr12:121661657-1216618	intra_enh	121661657	121661877	chr12	-0.88
LOC100507091	23034	chr12:122108669-1221090	intra_enh	122108669	122109027	chr12	-0.63
TMED2	3072	chr12:122638032-1226381	intra_enh	122638032	122638167	chr12	-0.90
ZNF664-FAM10	136946	chr12:123160546-1231607	intra_enh	123160546	123160773	chr12	-0.64
SCARB1	7528	chr12:123906785-1239071	intra_enh	123906785	123907104	chr12	-0.91
THRIL	14199	chr12:124063585-1240638	intra_enh	124063585	124063861	chr12	-0.44
ERC1	234523	chr12:1241528-1241866	intra_enh	1241528	1241866	chr12	-0.94
TMEM132B	112045	chr12:124488890-1244894	intra_enh	124488890	124489428	chr12	-0.97
TMEM132B	114425	chr12:124491407-1244916	intra_enh	124491407	124491671	chr12	-0.95
DUSP16	24192	chr12:12582365-12582682	intra_enh	12582365	12582682	chr12	-0.70
DUSP16	10960	chr12:12595688-12595823	intra_enh	12595688	12595823	chr12	-0.72
LINC00942	194328	chr12:1285287-1285889	intra_enh	1285287	1285889	chr12	-0.93
MIR614	6352	chr12:12953388-12953964	intra_enh	12953388	12953964	chr12	-0.89
GPR133	41424	chr12:130045519-1300461	intra_enh	130045519	130046137	chr12	-0.96

GRIN2B	189432	chr12:13834751-1383496	intra_enh	13834751	13834966	chr12	-0.95
LINC00942	54002	chr12:1425794-1426035	intra_enh	1425794	1426035	chr12	-0.58
ATF7IP	4166	chr12:14433267-1443359	intra_enh	14433267	14433593	chr12	-0.97
ATF7IP	5378	chr12:14434539-1443474	intra_enh	14434539	14434745	chr12	-0.93
ATF7IP	6058	chr12:14434988-1443565	intra_enh	14434988	14435656	chr12	-0.92
ATF7IP	7460	chr12:14436658-1443678	intra_enh	14436658	14436789	chr12	-0.86
ATF7IP	31613	chr12:14460807-1446094	intra_enh	14460807	14460947	chr12	-0.83
PLBD1	10307	chr12:14622308-1462242	intra_enh	14622308	14622422	chr12	-0.88
PTPRO	19980	chr12:15570471-1557065	intra_enh	15570471	15570656	chr12	-0.65
ADIPOR2	2204	chr12:1672586-1672834	intra_enh	1672586	1672834	chr12	-0.29
ADIPOR2	50774	chr12:1721077-1721483	intra_enh	1721077	1721483	chr12	-0.41
CACNA1C-AS4	39431	chr12:2163229-2163725	intra_enh	2163229	2163725	chr12	-0.84
CACNA1C-AS4	13362	chr12:2189373-2189718	intra_enh	2189373	2189718	chr12	-0.86
CACNA1C-IT3	19558	chr12:2229521-2229767	intra_enh	2229521	2229767	chr12	-0.35
SOX5	48312	chr12:23580410-2358059	intra_enh	23580410	23580595	chr12	-0.80
C12orf77	2638	chr12:25038866-2503913	intra_enh	25038866	25039137	chr12	-0.78
LRMP	9552	chr12:25105830-2510616	intra_enh	25105830	25106166	chr12	-0.61
ITPR2	118895	chr12:26758444-2675856	intra_enh	26758444	26758562	chr12	-0.39
ITPR2	100908	chr12:26776185-2677679	intra_enh	26776185	26776796	chr12	-0.55
ITPR2	100433	chr12:26776902-2677702	intra_enh	26776902	26777028	chr12	-0.29
ITPR2	63807	chr12:26813373-2681380	intra_enh	26813373	26813809	chr12	-0.94
ITPR2	15814	chr12:26861470-2686169	intra_enh	26861470	26861697	chr12	-0.73
PPFIBP1	11720	chr12:27579906-2758015	intra_enh	27579906	27580155	chr12	-0.94
PPFIBP1	14260	chr12:27582277-2758286	intra_enh	27582277	27582864	chr12	-0.95
FAR2	16046	chr12:29209116-2920937	intra_enh	29209116	29209379	chr12	-0.91
DENND5B-AS1	64887	chr12:31569032-3156943	intra_enh	31569032	31569438	chr12	-0.83
DENND5B-AS1	64362	chr12:31569592-3156992	intra_enh	31569592	31569928	chr12	-0.85
DENND5B-AS1	63686	chr12:31570230-3157064	intra_enh	31570230	31570641	chr12	-0.89
TSPAN9	101986	chr12:3158065-3159468	intra_enh	3158065	3159468	chr12	-0.46
DENND5B	9632	chr12:31644653-3164505	intra_enh	31644653	31645050	chr12	-0.71
DENND5B	12318	chr12:31647311-3164776	intra_enh	31647311	31647765	chr12	-0.79
METTL20	23047	chr12:31726782-3172706	intra_enh	31726782	31727060	chr12	-0.89
AMN1	4331	chr12:31768792-3176929	intra_enh	31768792	31769298	chr12	-0.52
BICD1	3926	chr12:32155255-3215549	intra_enh	32155255	32155496	chr12	-0.43
BICD1	7061	chr12:32158448-3215857	intra_enh	32158448	32158574	chr12	-0.75
BICD1	20405	chr12:32171702-3217200	intra_enh	32171702	32172008	chr12	-0.72
BICD1	26398	chr12:32177632-3217806	intra_enh	32177632	32178065	chr12	-0.26
BICD1	30304	chr12:32181584-3218192	intra_enh	32181584	32181924	chr12	-0.93
BICD1	107342	chr12:32258706-3225887	intra_enh	32258706	32258879	chr12	-0.93
BICD1	159850	chr12:32311187-32311413	intra_enh	32311187	32311413	chr12	-0.91
BICD1	192078	chr12:32343283-3234377	intra_enh	32343283	32343773	chr12	-0.39
FGD4	31064	chr12:32577168-3257757	intra_enh	32577168	32577573	chr12	-0.73
C12orf40	2967	chr12:38309018-3830939	intra_enh	38309018	38309392	chr12	-0.88
LRRK2	39160	chr12:38944156-3894431	intra_enh	38944156	38944319	chr12	-0.92
CNTN1	130968	chr12:39241498-3924158	intra_enh	39241498	39241587	chr12	-0.77
PDZRN4	72880	chr12:40190467-4019090	intra_enh	40190467	40190904	chr12	-0.95
PUS7L	5082	chr12:42433497-4243399	intra_enh	42433497	42433994	chr12	-0.71
TMEM117	459034	chr12:42974780-4297514	intra_enh	42974780	42975147	chr12	-0.53
NELL2	256686	chr12:43298976-4329907	intra_enh	43298976	43299077	chr12	-0.84
NELL2	256071	chr12:43299342-4329994	intra_enh	43299342	43299940	chr12	-0.53
NELL2	154984	chr12:43400387-4340106	intra_enh	43400387	43401068	chr12	-0.89
NELL2	153763	chr12:43401888-4340201	intra_enh	43401888	43402010	chr12	-0.64
SCAF11	6207	chr12:44664201-4466472	intra_enh	44664201	44664721	chr12	-0.42
SCAF11	4132	chr12:44666396-4466667	intra_enh	44666396	44666676	chr12	-0.48
HDAC7	16601	chr12:46483195-4648366	intra_enh	46483195	46483663	chr12	-0.28

VDR	36446	chr12:46548571-46548701	intra_enh	46548571	46548701	chr12	-0.91
FMNL3	16742	chr12:48370649-48370794	intra_enh	48370649	48370794	chr12	-0.65
FMNL3	16226	chr12:48371146-48371331	intra_enh	48371146	48371331	chr12	-0.79
FMNL3	4328	chr12:48383072-48383199	intra_enh	48383072	48383199	chr12	-0.83
TMBIM6	2612	chr12:48424395-48424544	intra_enh	48424395	48424544	chr12	-0.44
TMBIM6	8952	chr12:48430734-48430886	intra_enh	48430734	48430886	chr12	-0.43
RACGAP1	2418	chr12:48702814-48703499	intra_enh	48702814	48703499	chr12	-0.46
ASIC1	3036	chr12:48750502-48750693	intra_enh	48750502	48750693	chr12	-0.28
LIMA1	8994	chr12:48893523-48894001	intra_enh	48893523	48894001	chr12	-0.97
DIP2B	12720	chr12:49197445-49198064	intra_enh	49197445	49198064	chr12	-0.63
DIP2B	120520	chr12:49305235-49305873	intra_enh	49305235	49305873	chr12	-0.77
SMAGP	22192	chr12:49972536-49972788	intra_enh	49972536	49972788	chr12	-0.68
CELA1	22126	chr12:50048765-50048947	intra_enh	50048765	50048947	chr12	-0.46
ACVR1B	17838	chr12:50651071-50651465	intra_enh	50651071	50651465	chr12	-0.51
SP1	6819	chr12:52067398-52067628	intra_enh	52067398	52067628	chr12	-0.34
HOXC6	2405	chr12:52705810-52706300	intra_enh	52705810	52706300	chr12	-0.76
RAB5B	8690	chr12:54662512-54662989	intra_enh	54662512	54662989	chr12	-0.50
BAZ2A	3363	chr12:55306898-55307140	intra_enh	55306898	55307140	chr12	-0.68
SDR9C7	2700	chr12:55611637-55611876	intra_enh	55611637	55611876	chr12	-0.60
MON2	2614	chr12:61149400-61149552	intra_enh	61149400	61149552	chr12	-0.40
PPM1H	31520	chr12:61583159-61583666	intra_enh	61583159	61583666	chr12	-0.93
RASSF3	12004	chr12:63302444-63302681	intra_enh	63302444	63302681	chr12	-0.95
RASSF3	12912	chr12:63303259-63303681	intra_enh	63303259	63303681	chr12	-0.83
RASSF3	13524	chr12:63304016-63304147	intra_enh	63304016	63304147	chr12	-0.81
RASSF3	63446	chr12:63353652-63354355	intra_enh	63353652	63354355	chr12	-0.77
RASSF3	66734	chr12:63357215-63357370	intra_enh	63357215	63357370	chr12	-0.79
LEMD3	5136	chr12:63854614-63854889	intra_enh	63854614	63854889	chr12	-0.48
LEMD3	36424	chr12:63885548-63886531	intra_enh	63885548	63886531	chr12	-0.70
LEMD3	39988	chr12:63888953-63890256	intra_enh	63888953	63890256	chr12	-0.73
LOC100129940	36074	chr12:64598085-64598492	intra_enh	64598085	64598492	chr12	-0.75
NCAPD2	3014	chr12:6476488-6476656	intra_enh	6476488	6476656	chr12	-0.82
IRAK3	7853	chr12:64876876-64877318	intra_enh	64876876	64877318	chr12	-0.92
IRAK3	28381	chr12:64897545-64897705	intra_enh	64897545	64897705	chr12	-0.74
GRIP1	130129	chr12:65228757-65229369	intra_enh	65228757	65229369	chr12	-0.89
GRIP1	101790	chr12:65257099-65257706	intra_enh	65257099	65257706	chr12	-0.96
GRIP1	89840	chr12:65269155-65269550	intra_enh	65269155	65269550	chr12	-0.88
GRIP1	52419	chr12:65306513-65307033	intra_enh	65306513	65307033	chr12	-0.97
CAND1	4829	chr12:65954049-65954261	intra_enh	65954049	65954261	chr12	-0.30
IFNG-AS1	22568	chr12:66646872-66646972	intra_enh	66646872	66646972	chr12	-0.46
SNORA70G	5673	chr12:67312609-67313581	intra_enh	67312609	67313581	chr12	-0.54
SNORA70G	8984	chr12:67316208-67316604	intra_enh	67316208	67316604	chr12	-0.87
MDM2	5718	chr12:67494691-67494870	intra_enh	67494691	67494870	chr12	-0.36
CPM	50132	chr12:67562971-67563257	intra_enh	67562971	67563257	chr12	-0.91
CPM	36119	chr12:67576689-67577565	intra_enh	67576689	67577565	chr12	-0.93
LRRC10	36040	chr12:68327101-68327399	intra_enh	68327101	68327399	chr12	-0.57
LPCAT3	10380	chr12:6985566-6985881	intra_enh	6985566	6985881	chr12	-0.88
TMEM19	7440	chr12:70373398-70373769	intra_enh	70373398	70373769	chr12	-0.67
TRHDE-AS1	250792	chr12:71203641-71205054	intra_enh	71203641	71205054	chr12	-0.53
OSBPL8	5198	chr12:75472404-75472639	intra_enh	75472404	75472639	chr12	-0.72
CSRP2	11927	chr12:75784938-75785112	intra_enh	75784938	75785112	chr12	-0.50
E2F7	5140	chr12:75978210-75978493	intra_enh	75978210	75978493	chr12	-0.30
NAV3	94526	chr12:76843659-76843790	intra_enh	76843659	76843790	chr12	-0.41
NAV3	168636	chr12:76917735-76917934	intra_enh	76917735	76917934	chr12	-0.34
SYT1	24112	chr12:77806546-77806833	intra_enh	77806546	77806833	chr12	-0.83
PTPRQ	41108	chr12:79403044-79403683	intra_enh	79403044	79403683	chr12	-0.97

FOXJ2	4400	chr12:8080991-8081056	intra_enh	8080991	8081056	chr12	-0.26
FOXJ2	4680	chr12:8081182-8081425	intra_enh	8081182	8081425	chr12	-0.65
TMTC2	2769	chr12:81607469-8160819	intra_enh	81607469	81608197	chr12	-0.64
IQSEC3	28731	chr12:85405-85661	intra_enh	85405	85661	chr12	-0.83
IQSEC3	29246	chr12:85810-86285	intra_enh	85810	86285	chr12	-0.86
RIMKLB	6540	chr12:8731621-8732535	intra_enh	8731621	8732535	chr12	-0.58
RIMKLB	2896	chr12:8738696-8739036	intra_enh	8738696	8739036	chr12	-0.66
RIMKLB	2468	chr12:8739138-8739451	intra_enh	8739138	8739451	chr12	-0.62
C12orf79	111156	chr12:90948331-9094859	intra_enh	90948331	90948597	chr12	-0.65
C12orf79	110774	chr12:90948709-9094898	intra_enh	90948709	90948982	chr12	-0.51
C12orf79	92112	chr12:90967382-9096763	intra_enh	90967382	90967633	chr12	-0.93
C12orf79	9027	chr12:91050494-9105069	intra_enh	91050494	91050692	chr12	-0.31
PLEKHG7	33142	chr12:91687237-9168783	intra_enh	91687237	91687835	chr12	-0.95
PLEKHG7	74033	chr12:91728324-9172853	intra_enh	91728324	91728530	chr12	-0.79
LOC102724933	75995	chr12:92016222-9201633	intra_enh	92016222	92016332	chr12	-0.45
LOC101928731	109896	chr12:92765483-9276576	intra_enh	92765483	92765768	chr12	-0.48
CEP83	54272	chr12:93323294-9332395	intra_enh	93323294	93323954	chr12	-0.79
TMCC3	5852	chr12:93539754-9354006	intra_enh	93539754	93540067	chr12	-0.43
TMCC3	5854	chr12:93562455-9356277	intra_enh	93562455	93562776	chr12	-0.65
RAD52	9132	chr12:938194-938369	intra_enh	938194	938369	chr12	-0.38
FGD6	14617	chr12:94120589-9412092	intra_enh	94120589	94120921	chr12	-0.95
VEZT	2982	chr12:94138417-9413885	intra_enh	94138417	94138850	chr12	-0.79
NTN4	59042	chr12:94649559-9464969	intra_enh	94649559	94649694	chr12	-0.77
NTN4	58784	chr12:94649809-9464996	intra_enh	94649809	94649960	chr12	-0.76
ELK3	2536	chr12:95114825-95114918	intra_enh	95114825	95114918	chr12	-0.62
ELK3	14242	chr12:95126441-9512671	intra_enh	95126441	95126715	chr12	-0.74
ELK3	19614	chr12:95131859-9513204	intra_enh	95131859	95132041	chr12	-0.64
ELK3	101334	chr12:95213361-9521397	intra_enh	95213361	95213978	chr12	-0.56
ELK3	102220	chr12:95214215-9521489	intra_enh	95214215	95214898	chr12	-0.92
CDK17	65138	chr12:95253194-9525352	intra_enh	95253194	95253525	chr12	-0.85
CDK17	52678	chr12:95265607-9526603	intra_enh	95265607	95266034	chr12	-0.93
NEDD1	4072	chr12:95829361-9582953	intra_enh	95829361	95829530	chr12	-0.37
TMPO-AS1	6270	chr12:97440325-9744048	intra_enh	97440325	97440487	chr12	-0.83
TMPO-AS1	6555	chr12:97440626-9744075	intra_enh	97440626	97440756	chr12	-0.71
CLECL1	8704	chr12:9768078-9768838	intra_enh	9768078	9768838	chr12	-0.98
CLECL1	8016	chr12:9768953-9769340	intra_enh	9768953	9769340	chr12	-0.94
CLECL1	7465	chr12:9769443-9769951	intra_enh	9769443	9769951	chr12	-0.89
CLECL1	6650	chr12:9770154-9770869	intra_enh	9770154	9770869	chr12	-0.97
LOC101928937	6738	chr12:98017771-9801823	intra_enh	98017771	98018237	chr12	-0.94
ANKS1B	15016	chr12:98087961-9808807	intra_enh	98087961	98088072	chr12	-0.76
ANKS1B	127376	chr12:98199889-9820086	intra_enh	98199889	98200864	chr12	-0.94
ANKS1B	190600	chr12:98263481-9826371	intra_enh	98263481	98263718	chr12	-0.90
FAM71C	120050	chr12:98685629-9868578	intra_enh	98685629	98685788	chr12	-0.59
FGF14	47466	chr13:101319475-101319	intra_enh	101319475	101319585	chr13	-0.70
UPF3A	18090	chr13:114046894-114047	intra_enh	114046894	114047247	chr13	-0.89
ZMYM2	8847	chr13:19439418-1944022	intra_enh	19439418	19440220	chr13	-0.83
ZMYM2	25808	chr13:19456571-1945698	intra_enh	19456571	19456988	chr13	-0.51
ZMYM2	26220	chr13:19457099-1945728	intra_enh	19457099	19457284	chr13	-0.52
MICU2	24143	chr13:21052080-2105234	intra_enh	21052080	21052346	chr13	-0.37
C1QTNF9B-AS1	94123	chr13:23266564-2326724	intra_enh	23266564	23267242	chr13	-0.92
C1QTNF9B-AS1	77213	chr13:23283494-2328413	intra_enh	23283494	23284132	chr13	-0.94
C1QTNF9B-AS1	43270	chr13:23317473-2331804	intra_enh	23317473	23318040	chr13	-0.76
C1QTNF9B-AS1	42666	chr13:23318160-2331856	intra_enh	23318160	23318561	chr13	-0.94
MTMR6	5668	chr13:24753913-2475415	intra_enh	24753913	24754159	chr13	-0.53
MTMR6	2470	chr13:24757182-2475728	intra_enh	24757182	24757287	chr13	-0.83

SHISA2	312870	chr13:25210263-25210392	intra_enh	25210263	25210392	chr13	-0.60
USP12	7593	chr13:26636331-26636551	intra_enh	26636331	26636551	chr13	-0.71
PAN3-AS1	129876	chr13:27740564-27741812	intra_enh	27740564	27741812	chr13	-0.95
FLT1	71914	chr13:27895119-27895586	intra_enh	27895119	27895586	chr13	-0.65
MTUS2	59338	chr13:28841045-28841831	intra_enh	28841045	28841831	chr13	-0.61
UBL3	32299	chr13:29290351-29290691	intra_enh	29290351	29290691	chr13	-0.85
ALOX5AP	7146	chr13:30192500-30193019	intra_enh	30192500	30193019	chr13	-0.90
FRY-AS1	5043	chr13:31508483-31509155	intra_enh	31508483	31509155	chr13	-0.44
N4BP2L2	7714	chr13:32003135-32003301	intra_enh	32003135	32003301	chr13	-0.27
N4BP2L2	7142	chr13:32003521-32004060	intra_enh	32003521	32004060	chr13	-0.26
N4BP2L2	3700	chr13:32007165-32007299	intra_enh	32007165	32007299	chr13	-0.76
PDS5B	4009	chr13:32062367-32062775	intra_enh	32062367	32062775	chr13	-0.90
PDS5B	53112	chr13:32111618-32111729	intra_enh	32111618	32111729	chr13	-0.71
PDS5B	61745	chr13:32120053-32120561	intra_enh	32120053	32120561	chr13	-0.76
PDS5B	64330	chr13:32122801-32122983	intra_enh	32122801	32122983	chr13	-0.65
LINC00423	100183	chr13:32283513-32283701	intra_enh	32283513	32283701	chr13	-0.62
LINC00423	72438	chr13:32311154-32311550	intra_enh	32311154	32311550	chr13	-0.84
STARD13	128534	chr13:33020158-33020718	intra_enh	33020158	33020718	chr13	-0.94
RFXAP	4642	chr13:36295861-36296099	intra_enh	36295861	36296099	chr13	-0.87
ALG5	25584	chr13:36445482-36446358	intra_enh	36445482	36446358	chr13	-0.95
POSTN	116868	chr13:37187706-37187993	intra_enh	37187706	37187993	chr13	-0.82
LHFP	150916	chr13:38924126-38924753	intra_enh	38924126	38924753	chr13	-0.89
LHFP	12298	chr13:39062362-39063753	intra_enh	39062362	39063753	chr13	-0.98
MRPS31	7561	chr13:40235743-40235831	intra_enh	40235743	40235831	chr13	-0.81
ELF1	17222	chr13:40437071-40437320	intra_enh	40437071	40437320	chr13	-0.30
ELF1	13952	chr13:40440103-40440828	intra_enh	40440103	40440828	chr13	-0.29
ELF1	8894	chr13:40463126-40463497	intra_enh	40463126	40463497	chr13	-0.34
ELF1	16077	chr13:40470295-40470695	intra_enh	40470295	40470695	chr13	-0.49
VWA8	149297	chr13:41283842-41284008	intra_enh	41283842	41284008	chr13	-0.40
AKAP11	4638	chr13:41748702-41749149	intra_enh	41748702	41749149	chr13	-0.78
AKAP11	5562	chr13:41749498-41750201	intra_enh	41749498	41750201	chr13	-0.37
DNAJC15	26252	chr13:42521168-42522057	intra_enh	42521168	42522057	chr13	-0.35
SMIM2-AS1	6976	chr13:43589458-43589861	intra_enh	43589458	43589861	chr13	-0.86
TSC22D1-AS1	3394	chr13:44044343-44044928	intra_enh	44044343	44044928	chr13	-0.80
TPT1-AS1	26173	chr13:44839431-44839871	intra_enh	44839431	44839871	chr13	-0.68
CPB2	3080	chr13:45573984-45574281	intra_enh	45573984	45574281	chr13	-0.76
LCP1	21381	chr13:45632882-45633276	intra_enh	45632882	45633276	chr13	-0.38
LRCH1	13274	chr13:46038377-46038762	intra_enh	46038377	46038762	chr13	-0.59
LRCH1	30094	chr13:46054978-46055802	intra_enh	46054978	46055802	chr13	-0.94
LRCH1	65728	chr13:46090959-46091088	intra_enh	46090959	46091088	chr13	-0.60
LRCH1	77641	chr13:46102853-46103021	intra_enh	46102853	46103021	chr13	-0.64
LRCH1	109746	chr13:46134868-46135217	intra_enh	46134868	46135217	chr13	-0.87
CAB39L	35960	chr13:48837663-48837770	intra_enh	48837663	48837770	chr13	-0.37
CAB39L	30778	chr13:48842510-48843286	intra_enh	48842510	48843286	chr13	-0.59
CAB39L	2792	chr13:48888548-48888812	intra_enh	48888548	48888812	chr13	-0.83
CAB39L	4487	chr13:48889998-48890752	intra_enh	48889998	48890752	chr13	-0.84
SETDB2	3167	chr13:48926612-48927098	intra_enh	48926612	48927098	chr13	-0.35
KPNA3	3260	chr13:49261665-49261931	intra_enh	49261665	49261931	chr13	-0.65
KPNA3	2908	chr13:49262041-49262258	intra_enh	49262041	49262258	chr13	-0.59
TRIM13	3326	chr13:49472330-49472605	intra_enh	49472330	49472605	chr13	-0.44
DLEU1	8485	chr13:49545755-49545883	intra_enh	49545755	49545883	chr13	-0.75
ST13P4	76856	chr13:49720933-49721087	intra_enh	49720933	49721087	chr13	-0.62
ST13P4	85952	chr13:49730024-49730188	intra_enh	49730024	49730188	chr13	-0.80
DLEU1-AS1	171934	chr13:49827564-49827740	intra_enh	49827564	49827740	chr13	-0.31
DLEU1-AS1	156597	chr13:49842922-49843056	intra_enh	49842922	49843056	chr13	-0.41

DLEU1-AS1	12788	chr13:49986639-49986957	intra_enh	49986639	49986957	chr13	-0.88
RNASEH2B	11171	chr13:50370421-50370865	intra_enh	50370421	50370865	chr13	-0.83
FAM124A	16696	chr13:50710931-50711400	intra_enh	50710931	50711400	chr13	-0.81
FAM124A	31366	chr13:50725251-50726422	intra_enh	50725251	50726422	chr13	-0.85
DHRS12	19920	chr13:51296001-51296440	intra_enh	51296001	51296440	chr13	-0.84
LINC00282	10432	chr13:51306760-51306952	intra_enh	51306760	51306952	chr13	-0.53
CKAP2	2313	chr13:51930317-51930521	intra_enh	51930317	51930521	chr13	-0.69
DIAPH3-AS1	143131	chr13:59341406-59342036	intra_enh	59341406	59342036	chr13	-0.79
DIAPH3-AS1	139242	chr13:59345525-59345694	intra_enh	59345525	59345694	chr13	-0.68
LINC00376	20778	chr13:62779396-62779505	intra_enh	62779396	62779505	chr13	-0.52
PCDH9-AS3	7200	chr13:66442243-66442397	intra_enh	66442243	66442397	chr13	-0.67
DACH1	256224	chr13:71082643-71083574	intra_enh	71082643	71083574	chr13	-0.96
DIS3	3528	chr13:72257711-72257880	intra_enh	72257711	72257880	chr13	-0.71
KLF12	231151	chr13:73374754-73375080	intra_enh	73374754	73375080	chr13	-0.78
KLF12	177457	chr13:73428521-73428701	intra_enh	73428521	73428701	chr13	-0.64
KLF12	145518	chr13:73460481-73460618	intra_enh	73460481	73460618	chr13	-0.56
KLF12	139982	chr13:73465963-73466209	intra_enh	73465963	73466209	chr13	-0.30
KLF12	58054	chr13:73547843-73548184	intra_enh	73547843	73548184	chr13	-0.71
KLF12	57497	chr13:73548423-73548719	intra_enh	73548423	73548719	chr13	-0.65
KLF12	56092	chr13:73549691-73550261	intra_enh	73549691	73550261	chr13	-0.90
TBC1D4	113706	chr13:74840359-74840732	intra_enh	74840359	74840732	chr13	-0.95
TBC1D4	110716	chr13:74843159-74843912	intra_enh	74843159	74843912	chr13	-0.98
TBC1D4	98512	chr13:74855485-74855994	intra_enh	74855485	74855994	chr13	-0.71
TBC1D4	86918	chr13:74867012-74867656	intra_enh	74867012	74867656	chr13	-0.97
SLAIN1	20337	chr13:77191231-77191475	intra_enh	77191231	77191475	chr13	-0.52
LINC00446	9298	chr13:77494211-77494421	intra_enh	77494211	77494421	chr13	-0.92
MIR548A2	79994	chr13:78663242-78663409	intra_enh	78663242	78663409	chr13	-0.70
RBM26	23370	chr13:78854614-78855362	intra_enh	78854614	78855362	chr13	-0.77
MIR4500HG	17158	chr13:87103836-87104288	intra_enh	87103836	87104288	chr13	-0.94
ABCC4	61772	chr13:94689832-94690027	intra_enh	94689832	94690027	chr13	-0.28
DOCK9	59092	chr13:98369145-98369352	intra_enh	98369145	98369352	chr13	-0.81
GPR18	27190	chr13:98681318-98681670	intra_enh	98681318	98681670	chr13	-0.39
GPR18	5796	chr13:98714359-98714602	intra_enh	98714359	98714602	chr13	-0.55
PPP2R5C	19204	chr14:101326615-1013267	intra_enh	101326615	101326761	chr14	-0.50
PPP2R5C	33786	chr14:101379525-1013798	intra_enh	101379525	101379830	chr14	-0.48
PPP2R5C	44571	chr14:101390371-1013905	intra_enh	101390371	101390555	chr14	-0.68
WDR20	40856	chr14:101716724-1017168	intra_enh	101716724	101716868	chr14	-0.48
MOK	20558	chr14:101756087-1017562	intra_enh	101756087	101756222	chr14	-0.39
TECPR2	5906	chr14:101904823-1019050	intra_enh	101904823	101905092	chr14	-0.92
RCOR1	14698	chr14:102143330-1021435	intra_enh	102143330	102143562	chr14	-0.94
AMN	13438	chr14:102471914-1024724	intra_enh	102471914	102472450	chr14	-0.78
EXOC3L4	8820	chr14:102644963-1026451	intra_enh	102644963	102645142	chr14	-0.78
MARK3	6913	chr14:102928269-1029284	intra_enh	102928269	102928461	chr14	-0.47
AHNAK2	9722	chr14:104505789-1045062	intra_enh	104505789	104506247	chr14	-0.34
JAG2	6188	chr14:104712233-1047125	intra_enh	104712233	104712555	chr14	-0.62
RNASE4	8887	chr14:20235508-20235814	intra_enh	20235508	20235814	chr14	-0.58
DAD1	21867	chr14:22105611-22106623	intra_enh	22105611	22106623	chr14	-0.57
DAD1	20858	chr14:22106804-22107448	intra_enh	22106804	22107448	chr14	-0.59
DAD1	20184	chr14:22107712-22107889	intra_enh	22107712	22107889	chr14	-0.84
DAD1	4336	chr14:22123471-22123825	intra_enh	22123471	22123825	chr14	-0.64
OXA1L	19928	chr14:22325332-22325664	intra_enh	22325332	22325664	chr14	-0.84
SLC7A7	24541	chr14:22330026-22330776	intra_enh	22330026	22330776	chr14	-0.90
PPP1R3E	3082	chr14:22838744-22838888	intra_enh	22838744	22838888	chr14	-0.82
STXBP6	185767	chr14:24403013-24403325	intra_enh	24403013	24403325	chr14	-0.96
STXBP6	23099	chr14:24565568-24566106	intra_enh	24565568	24566106	chr14	-0.97

LOC100506071	31770	chr14:30460379-30460694	intra_enh	30460379	30460694	chr14	-0.94
MIR624	30960	chr14:30522522-30522958	intra_enh	30522522	30522958	chr14	-0.88
AP4S1	57651	chr14:30622908-30623590	intra_enh	30622908	30623590	chr14	-0.41
ARHGAP5	25376	chr14:31641573-31641668	intra_enh	31641573	31641668	chr14	-0.58
NPAS3	35090	chr14:32512995-32513602	intra_enh	32512995	32513602	chr14	-0.98
NPAS3	41814	chr14:32519808-32520236	intra_enh	32519808	32520236	chr14	-0.98
SPTSSA	25700	chr14:33975351-33975688	intra_enh	33975351	33975688	chr14	-0.81
SRP54	2686	chr14:34524256-34524823	intra_enh	34524256	34524823	chr14	-0.51
KIAA0391	3733	chr14:34665153-34665329	intra_enh	34665153	34665329	chr14	-0.79
PSMA6	3616	chr14:34834777-34834998	intra_enh	34834777	34834998	chr14	-0.68
PSMA6	7660	chr14:34838826-34839037	intra_enh	34838826	34839037	chr14	-0.55
PSMA6	8639	chr14:34839659-34840163	intra_enh	34839659	34840163	chr14	-0.82
PSMA6	9539	chr14:34840485-34841137	intra_enh	34840485	34841137	chr14	-0.94
TRAPPC6B	2798	chr14:38706435-38706740	intra_enh	38706435	38706740	chr14	-0.55
KLHL28	3332	chr14:44497443-44497753	intra_enh	44497443	44497753	chr14	-0.57
FAM179B	6628	chr14:44507594-44507989	intra_enh	44507594	44507989	chr14	-0.78
LRR1	2638	chr14:49137729-49137874	intra_enh	49137729	49137874	chr14	-0.82
C14orf183	6804	chr14:49621858-49622759	intra_enh	49621858	49622759	chr14	-0.45
NIN	51769	chr14:50315742-50315900	intra_enh	50315742	50315900	chr14	-0.57
NIN	34655	chr14:50332563-50333307	intra_enh	50332563	50333307	chr14	-0.33
ABHD12B	29460	chr14:50437989-50438184	intra_enh	50437989	50438184	chr14	-0.85
TXNDC16	3124	chr14:52085771-52086086	intra_enh	52085771	52086086	chr14	-0.74
CDKN3	2568	chr14:53935758-53936221	intra_enh	53935758	53936221	chr14	-0.79
CNIH1	2940	chr14:53974823-53975092	intra_enh	53974823	53975092	chr14	-0.63
CNIH1	2578	chr14:53975195-53975446	intra_enh	53975195	53975446	chr14	-0.73
TBPL2	10382	chr14:54966506-54966763	intra_enh	54966506	54966763	chr14	-0.78
PSMA3	2288	chr14:57783345-57783780	intra_enh	57783345	57783780	chr14	-0.54
DAAM1	22656	chr14:58747445-58748131	intra_enh	58747445	58748131	chr14	-0.63
DAAM1	8434	chr14:58791274-58791679	intra_enh	58791274	58791679	chr14	-0.44
DAAM1	39766	chr14:58839484-58839867	intra_enh	58839484	58839867	chr14	-0.32
DAAM1	43556	chr14:58843389-58843543	intra_enh	58843389	58843543	chr14	-0.87
DAAM1	52746	chr14:58852519-58852794	intra_enh	58852519	58852794	chr14	-0.45
L3HYPDH	2975	chr14:59017792-59017910	intra_enh	59017792	59017910	chr14	-0.39
LRRC9	23202	chr14:59479289-59479480	intra_enh	59479289	59479480	chr14	-0.90
LRRC9	24024	chr14:59479868-59480544	intra_enh	59479868	59480544	chr14	-0.98
LRRC9	46302	chr14:59502423-59502544	intra_enh	59502423	59502544	chr14	-0.51
DHRS7	13398	chr14:59688442-59688690	intra_enh	59688442	59688690	chr14	-0.66
MNAT1	80974	chr14:60352115-60352254	intra_enh	60352115	60352254	chr14	-0.45
TRMT5	2141	chr14:60515335-60515483	intra_enh	60515335	60515483	chr14	-0.59
LOC101927780	94613	chr14:61011976-61012130	intra_enh	61011976	61012130	chr14	-0.71
LOC101927780	68428	chr14:61037972-61038504	intra_enh	61037972	61038504	chr14	-0.60
LOC101927780	58102	chr14:61048518-61048611	intra_enh	61048518	61048611	chr14	-0.67
LOC101927780	28608	chr14:61135479-61135984	intra_enh	61135479	61135984	chr14	-0.77
LOC101927780	36814	chr14:61143778-61144097	intra_enh	61143778	61144097	chr14	-0.44
HIF1A	52978	chr14:61178840-61178945	intra_enh	61178840	61178945	chr14	-0.73
HIF1A	5331	chr14:61239308-61239538	intra_enh	61239308	61239538	chr14	-0.51
HIF1A	5832	chr14:61239822-61240027	intra_enh	61239822	61240027	chr14	-0.39
HIF1A	6461	chr14:61240366-61240740	intra_enh	61240366	61240740	chr14	-0.55
HIF1A	13792	chr14:61247511-61248257	intra_enh	61247511	61248257	chr14	-0.39
HIF1A	14680	chr14:61248652-61248891	intra_enh	61248652	61248891	chr14	-0.38
PPP2R5E	69828	chr14:62974772-62974993	intra_enh	62974772	62974993	chr14	-0.73
PPP2R5E	69542	chr14:62975100-62975235	intra_enh	62975100	62975235	chr14	-0.41
SGPP1	22115	chr14:63242215-63242575	intra_enh	63242215	63242575	chr14	-0.29
SGPP1	20651	chr14:63243765-63243953	intra_enh	63243765	63243953	chr14	-0.64
SGPP1	17540	chr14:63246542-63247398	intra_enh	63246542	63247398	chr14	-0.31

SYNE2	6196	chr14:63395504-63395757	intra_enh	63395504	63395757	chr14	-0.34
SYNE2	12555	chr14:63401872-63402106	intra_enh	63401872	63402106	chr14	-0.65
SYNE2	18184	chr14:63407485-63407750	intra_enh	63407485	63407750	chr14	-0.79
SYNE2	86983	chr14:63476344-63476490	intra_enh	63476344	63476490	chr14	-0.50
SYNE2	21452	chr14:63773732-63774020	intra_enh	63773732	63774020	chr14	-0.79
ESR2	16672	chr14:63802708-63803039	intra_enh	63802708	63803039	chr14	-0.81
ZBTB25	3768	chr14:64036224-64036855	intra_enh	64036224	64036855	chr14	-0.77
FUT8	70284	chr14:65019114-65019853	intra_enh	65019114	65019853	chr14	-0.97
RDH12	2521	chr14:67240717-67241033	intra_enh	67240717	67241033	chr14	-0.74
RAD51B	142286	chr14:67498368-67498701	intra_enh	67498368	67498701	chr14	-0.52
RAD51B	432154	chr14:67788082-67788722	intra_enh	67788082	67788722	chr14	-0.65
RAD51B	441444	chr14:67797388-67797996	intra_enh	67797388	67797996	chr14	-0.76
RAD51B	452412	chr14:67808512-67808808	intra_enh	67808512	67808808	chr14	-0.74
RAD51B	453818	chr14:67809912-67810220	intra_enh	67809912	67810220	chr14	-0.63
RAD51B	454499	chr14:67810484-67811010	intra_enh	67810484	67811010	chr14	-0.71
ZFP36L1	451798	chr14:67878460-67878711	intra_enh	67878460	67878711	chr14	-0.92
ZFP36L1	425762	chr14:67904377-67904867	intra_enh	67904377	67904867	chr14	-0.76
ZFP36L1	424542	chr14:67905274-67906409	intra_enh	67905274	67906409	chr14	-0.84
ZFP36L1	419769	chr14:67910378-67910852	intra_enh	67910378	67910852	chr14	-0.88
ZFP36L1	393655	chr14:67936521-67936937	intra_enh	67936521	67936937	chr14	-0.83
ZFP36L1	317290	chr14:68012735-68013454	intra_enh	68012735	68013454	chr14	-0.56
ZFP36L1	273990	chr14:68056159-68056628	intra_enh	68056159	68056628	chr14	-0.68
KIAA0247	40434	chr14:69188350-69188641	intra_enh	69188350	69188641	chr14	-0.50
SRSF5	66504	chr14:69237029-69237124	intra_enh	69237029	69237124	chr14	-0.72
TTC9	27418	chr14:70205604-70205743	intra_enh	70205604	70205743	chr14	-0.51
SIPA1L1	4698	chr14:71128480-71128995	intra_enh	71128480	71128995	chr14	-0.91
PAPLN	3666	chr14:72777541-72777702	intra_enh	72777541	72777702	chr14	-0.81
PAPLN	10972	chr14:72784719-72785136	intra_enh	72784719	72785136	chr14	-0.79
PAPLN	66418	chr14:72840071-72840676	intra_enh	72840071	72840676	chr14	-0.52
NUMB	5830	chr14:72988922-72989499	intra_enh	72988922	72989499	chr14	-0.58
MIR4505	8592	chr14:73286502-73286719	intra_enh	73286502	73286719	chr14	-0.67
MIR4505	7930	chr14:73287201-73287342	intra_enh	73287201	73287342	chr14	-0.41
ELMSAN1	3264	chr14:73299845-73300192	intra_enh	73299845	73300192	chr14	-0.90
ENTPD5	23906	chr14:73531808-73531939	intra_enh	73531808	73531939	chr14	-0.58
YLPM1	29538	chr14:74329239-74329478	intra_enh	74329239	74329478	chr14	-0.56
JDP2	21739	chr14:74990182-74990472	intra_enh	74990182	74990472	chr14	-0.28
IFT43	8090	chr14:75529865-75530010	intra_enh	75529865	75530010	chr14	-0.82
GPATCH2L	36870	chr14:75727067-75727570	intra_enh	75727067	75727570	chr14	-0.74
GPATCH2L	40728	chr14:75731065-75731286	intra_enh	75731065	75731286	chr14	-0.36
LRRC74A	20141	chr14:76382392-76382842	intra_enh	76382392	76382842	chr14	-0.89
SPTLC2	27496	chr14:77125143-77125594	intra_enh	77125143	77125594	chr14	-0.62
TSHR	40818	chr14:80532345-80532531	intra_enh	80532345	80532531	chr14	-0.63
SNORA79	80246	chr14:80658581-80658791	intra_enh	80658581	80658791	chr14	-0.95
GTF2A1	3948	chr14:80753024-80753179	intra_enh	80753024	80753179	chr14	-0.67
SEL1L	3788	chr14:81065076-81067265	intra_enh	81065076	81067265	chr14	-0.92
FOXN3	99642	chr14:88853276-88853857	intra_enh	88853276	88853857	chr14	-0.73
FOXN3	85331	chr14:88867426-88868328	intra_enh	88867426	88868328	chr14	-0.78
FOXN3	35800	chr14:88917294-88917521	intra_enh	88917294	88917521	chr14	-0.96
FOXN3-AS1	27040	chr14:88980098-88980883	intra_enh	88980098	88980883	chr14	-0.69
RPS6KA5	51170	chr14:90545501-90545651	intra_enh	90545501	90545651	chr14	-0.73
SNORA11B	15948	chr14:90678267-90678672	intra_enh	90678267	90678672	chr14	-0.68
GPR68	24772	chr14:90814697-90814804	intra_enh	90814697	90814804	chr14	-0.70
GPR68	64125	chr14:90854049-90854157	intra_enh	90854049	90854157	chr14	-0.43
CCDC88C	55390	chr14:90898388-90898716	intra_enh	90898388	90898716	chr14	-0.90
CCDC88C	32912	chr14:90920842-90921219	intra_enh	90920842	90921219	chr14	-0.46

CCDC88C	5630	chr14:90948061-90948562	intra_enh	90948061	90948562	chr14	-0.59
SMEK1	17023	chr14:91029453-91029657	intra_enh	91029453	91029657	chr14	-0.34
SLC24A4	33307	chr14:91893087-91893335	intra_enh	91893087	91893335	chr14	-0.90
RIN3	37752	chr14:92087548-92087707	intra_enh	92087548	92087707	chr14	-0.49
LGMN	72658	chr14:92212039-92212245	intra_enh	92212039	92212245	chr14	-0.65
LGMN	67268	chr14:92217443-92217622	intra_enh	92217443	92217622	chr14	-0.78
ITPK1-AS1	33036	chr14:92570429-92570595	intra_enh	92570429	92570595	chr14	-0.70
FAM181A	12602	chr14:93476007-93476161	intra_enh	93476007	93476161	chr14	-0.34
MIR3173	5790	chr14:94679188-94680543	intra_enh	94679188	94680543	chr14	-0.79
DICER1	5794	chr14:94687618-94687819	intra_enh	94687618	94687819	chr14	-0.89
CLMN	32912	chr14:94822939-94823232	intra_enh	94822939	94823232	chr14	-0.93
CLMN	20237	chr14:94835634-94835888	intra_enh	94835634	94835888	chr14	-0.85
LINC00341	31899	chr14:94977967-94978191	intra_enh	94977967	94978191	chr14	-0.79
LINC00341	32318	chr14:94978307-94978688	intra_enh	94978307	94978688	chr14	-0.55
BDKRB2	12424	chr14:95752976-95753643	intra_enh	95752976	95753643	chr14	-0.75
PAPOLA	2418	chr14:96041146-96041598	intra_enh	96041146	96041598	chr14	-0.42
PAPOLA	6854	chr14:96045723-96045892	intra_enh	96045723	96045892	chr14	-0.74
PAPOLA	9902	chr14:96048581-96049131	intra_enh	96048581	96049131	chr14	-0.88
PAPOLA	12097	chr14:96050617-96051485	intra_enh	96050617	96051485	chr14	-0.85
PAPOLA	14615	chr14:96053409-96053729	intra_enh	96053409	96053729	chr14	-0.74
YY1	10802	chr14:99785557-99785756	intra_enh	99785557	99785756	chr14	-0.76
MIR6764	17619	chr14:99795626-99796028	intra_enh	99795626	99796028	chr14	-0.86
MIR6764	15662	chr14:99797593-99797976	intra_enh	99797593	99797976	chr14	-0.79
NIPA1	15312	chr15:20622456-20622676	intra_enh	20622456	20622676	chr15	-0.56
NIPA1	12358	chr15:20625420-20625619	intra_enh	20625420	20625619	chr15	-0.83
UBE3A	11392	chr15:23212682-23213595	intra_enh	23212682	23213595	chr15	-0.90
UBE3A	12788	chr15:23213869-23215200	intra_enh	23213869	23215200	chr15	-0.97
MIR4715	16332	chr15:23628686-23628782	intra_enh	23628686	23628782	chr15	-0.68
MIR4715	4316	chr15:23648994-23649770	intra_enh	23648994	23649770	chr15	-0.98
LOC100128714	36562	chr15:23735065-23735255	intra_enh	23735065	23735255	chr15	-0.75
NDNL2	59829	chr15:27409058-27409224	intra_enh	27409058	27409224	chr15	-0.83
TJP1	2975	chr15:27904558-27905388	intra_enh	27904558	27905388	chr15	-0.95
KLF13	70760	chr15:29476984-29477231	intra_enh	29476984	29477231	chr15	-0.33
CHRM5	297457	chr15:31750750-31751096	intra_enh	31750750	31751096	chr15	-0.97
AVEN	22834	chr15:32141324-32141536	intra_enh	32141324	32141536	chr15	-0.64
EIF2AK4	34387	chr15:38047889-38048117	intra_enh	38047889	38048117	chr15	-0.88
C15orf57	14410	chr15:38629768-38630508	intra_enh	38629768	38630508	chr15	-0.84
OIP5-AS1	24848	chr15:39338349-39338939	intra_enh	39338349	39338939	chr15	-0.48
RTF1	7291	chr15:39503614-39504152	intra_enh	39503614	39504152	chr15	-0.59
MAPKBP1	20962	chr15:39874746-39875022	intra_enh	39874746	39875022	chr15	-0.75
STARD9	44362	chr15:40699442-40699579	intra_enh	40699442	40699579	chr15	-0.37
PDIA3	2283	chr15:41828092-41828234	intra_enh	41828092	41828234	chr15	-0.26
PDIA3	4993	chr15:41830777-41830969	intra_enh	41830777	41830969	chr15	-0.39
PDIA3	5274	chr15:41831092-41831215	intra_enh	41831092	41831215	chr15	-0.29
SERF2	5118	chr15:41866130-41866295	intra_enh	41866130	41866295	chr15	-0.84
FRMD5	111396	chr15:42162404-42162677	intra_enh	42162404	42162677	chr15	-0.86
CASC4	2675	chr15:42370735-42371015	intra_enh	42370735	42371015	chr15	-0.70
CASC4	12040	chr15:42380148-42380333	intra_enh	42380148	42380333	chr15	-0.44
CASC4	21020	chr15:42389111-42389329	intra_enh	42389111	42389329	chr15	-0.93
EIF3J	9084	chr15:42625582-42625699	intra_enh	42625582	42625699	chr15	-0.42
PATL2	5807	chr15:42750500-42750642	intra_enh	42750500	42750642	chr15	-0.89
BLOC1S6	3724	chr15:43670120-43670743	intra_enh	43670120	43670743	chr15	-0.43
MYEF2	2402	chr15:46255364-46255532	intra_enh	46255364	46255532	chr15	-0.68
COPS2	7172	chr15:47227920-47228028	intra_enh	47227920	47228028	chr15	-0.49
FGF7	40030	chr15:47462449-47462824	intra_enh	47462449	47462824	chr15	-0.61

USP8	20230	chr15:48523941-48524248	intra_enh	48523941	48524248	chr15	-0.57
TMOD3	13834	chr15:49922866-49923033	intra_enh	49922866	49923033	chr15	-0.57
MAPK6	21208	chr15:50119669-50120151	intra_enh	50119669	50120151	chr15	-0.51
LOC100129973	3516	chr15:50262970-50263091	intra_enh	50262970	50263091	chr15	-0.64
GNB5	40533	chr15:50311171-50311611	intra_enh	50311171	50311611	chr15	-0.56
ARPP19	4087	chr15:50644345-50644493	intra_enh	50644345	50644493	chr15	-0.62
ARPP19	3424	chr15:50644868-50645295	intra_enh	50644868	50645295	chr15	-0.51
PRTG	61212	chr15:53761149-53761368	intra_enh	53761149	53761368	chr15	-0.52
PRTG	38930	chr15:53783306-53783773	intra_enh	53783306	53783773	chr15	-0.92
NEDD4	22613	chr15:53973956-53974062	intra_enh	53973956	53974062	chr15	-0.86
LINC00926	15583	chr15:55363970-55364572	intra_enh	55363970	55364572	chr15	-0.28
HSP90AB4P	64738	chr15:56708090-56708630	intra_enh	56708090	56708630	chr15	-0.29
HSP90AB4P	22005	chr15:56794960-56795246	intra_enh	56794960	56795246	chr15	-0.89
SLTM	8932	chr15:57004072-57004352	intra_enh	57004072	57004352	chr15	-0.80
LDHAL6B	30564	chr15:57316763-57316977	intra_enh	57316763	57316977	chr15	-0.59
MYO1E	39868	chr15:57412415-57412576	intra_enh	57412415	57412576	chr15	-0.36
MYO1E	38932	chr15:57413354-57413509	intra_enh	57413354	57413509	chr15	-0.53
LOC101928784	28596	chr15:58587100-58587428	intra_enh	58587100	58587428	chr15	-0.34
LOC100996876	235348	chr15:58996338-58996475	intra_enh	58996338	58996475	chr15	-0.78
RAB8B	3822	chr15:61272431-61272772	intra_enh	61272431	61272772	chr15	-0.31
USP3	2798	chr15:61586497-61586624	intra_enh	61586497	61586624	chr15	-0.67
USP3	6238	chr15:61589770-61590231	intra_enh	61589770	61590231	chr15	-0.72
DAPK2	54251	chr15:62070954-62071692	intra_enh	62070954	62071692	chr15	-0.80
FAM96A	3286	chr15:62169665-62170284	intra_enh	62169665	62170284	chr15	-0.45
SNX1	15350	chr15:62190383-62190586	intra_enh	62190383	62190586	chr15	-0.57
ZNF609	72706	chr15:62651234-62651518	intra_enh	62651234	62651518	chr15	-0.78
IGDCC3	6840	chr15:63464225-63464318	intra_enh	63464225	63464318	chr15	-0.35
IGDCC4	21734	chr15:63480670-63480791	intra_enh	63480670	63480791	chr15	-0.49
VWA9	27088	chr15:63663127-63663777	intra_enh	63663127	63663777	chr15	-0.39
SLC24A1	4287	chr15:63717946-63718072	intra_enh	63717946	63718072	chr15	-0.44
SLC24A1	3899	chr15:63718185-63718609	intra_enh	63718185	63718609	chr15	-0.44
DENND4A	18488	chr15:63852992-63853404	intra_enh	63852992	63853404	chr15	-0.71
DENND4A	15011	chr15:63856605-63856745	intra_enh	63856605	63856745	chr15	-0.43
RAB11A	12685	chr15:63961445-63961625	intra_enh	63961445	63961625	chr15	-0.38
RAB11A	32964	chr15:63981698-63981931	intra_enh	63981698	63981931	chr15	-0.53
RAB11A	33342	chr15:63982108-63982277	intra_enh	63982108	63982277	chr15	-0.56
RAB11A	34640	chr15:63983328-63983653	intra_enh	63983328	63983653	chr15	-0.88
RAB11A	85176	chr15:64033632-64034419	intra_enh	64033632	64034419	chr15	-0.59
MIR4311	75958	chr15:64195114-64196050	intra_enh	64195114	64196050	chr15	-0.46
AAGAB	41668	chr15:65375888-65376628	intra_enh	65375888	65376628	chr15	-0.78
IQCH-AS1	14711	chr15:65585556-65585754	intra_enh	65585556	65585754	chr15	-0.93
IQCH-AS1	14163	chr15:65586094-65586312	intra_enh	65586094	65586312	chr15	-0.90
SKOR1	31646	chr15:65867371-65867524	intra_enh	65867371	65867524	chr15	-0.81
CORO2B	9166	chr15:66667109-66667942	intra_enh	66667109	66667942	chr15	-0.90
CORO2B	17188	chr15:66728153-66728984	intra_enh	66728153	66728984	chr15	-0.91
CORO2B	43156	chr15:66754354-66754719	intra_enh	66754354	66754719	chr15	-0.76
LOC101929173	45352	chr15:69815800-69816768	intra_enh	69815800	69816768	chr15	-0.98
SENP8	56380	chr15:70137220-70137323	intra_enh	70137220	70137323	chr15	-0.51
PKM	3791	chr15:70305019-70305635	intra_enh	70305019	70305635	chr15	-0.33
ARIH1	2644	chr15:70556114-70556615	intra_enh	70556114	70556615	chr15	-0.48
BBS4	5984	chr15:70771441-70771672	intra_enh	70771441	70771672	chr15	-0.67
CD276	16014	chr15:71779630-71779747	intra_enh	71779630	71779747	chr15	-0.53
UBE2Q2	2826	chr15:73926221-73926307	intra_enh	73926221	73926307	chr15	-0.60
LOC101929439	33212	chr15:74227608-74227733	intra_enh	74227608	74227733	chr15	-0.41
LINC00597	37386	chr15:75267043-75267788	intra_enh	75267043	75267788	chr15	-0.37

TBC1D2B	27359	chr15:76129348-76130034	intra_enh	76129348	76130034	chr15	-0.68
ZFAND6	4142	chr15:78143618-78143779	intra_enh	78143618	78143779	chr15	-0.53
FAH	8112	chr15:78240348-78240447	intra_enh	78240348	78240447	chr15	-0.50
MIR549A	18098	chr15:78903241-78903503	intra_enh	78903241	78903503	chr15	-0.36
MESDC2	2774	chr15:79066200-79066800	intra_enh	79066200	79066800	chr15	-0.67
IL16	7501	chr15:79383730-79383888	intra_enh	79383730	79383888	chr15	-0.59
ZSCAN2	4520	chr15:82949711-82949834	intra_enh	82949711	82949834	chr15	-0.33
SEC11A	2608	chr15:83058022-83058155	intra_enh	83058022	83058155	chr15	-0.51
PDE8A	6298	chr15:83332165-83332848	intra_enh	83332165	83332848	chr15	-0.87
PDE8A	28596	chr15:83354590-83355018	intra_enh	83354590	83355018	chr15	-0.74
AKAP13	12666	chr15:83736990-83738042	intra_enh	83736990	83738042	chr15	-0.50
AKAP13	61312	chr15:83786025-83786300	intra_enh	83786025	83786300	chr15	-0.46
AKAP13	75577	chr15:83800214-83800640	intra_enh	83800214	83800640	chr15	-0.27
AKAP13	80520	chr15:83883509-83883820	intra_enh	83883509	83883820	chr15	-0.88
AKAP13	67189	chr15:84031316-84031430	intra_enh	84031316	84031430	chr15	-0.42
AEN	4537	chr15:86970010-86970124	intra_enh	86970010	86970124	chr15	-0.44
MESP1	10917	chr15:88084529-88084725	intra_enh	88084529	88084725	chr15	-0.50
AP3S2	3154	chr15:88235394-88235543	intra_enh	88235394	88235543	chr15	-0.83
ZNF710	32823	chr15:88378476-88378622	intra_enh	88378476	88378622	chr15	-0.70
PRC1	4942	chr15:89333835-89334053	intra_enh	89333835	89334053	chr15	-0.52
SV2B	154756	chr15:89599230-89599367	intra_enh	89599230	89599367	chr15	-0.50
SV2B	171603	chr15:89616066-89616224	intra_enh	89616066	89616224	chr15	-0.59
SLCO3A1	60184	chr15:90257785-90258463	intra_enh	90257785	90258463	chr15	-0.98
SLCO3A1	67760	chr15:90265560-90265841	intra_enh	90265560	90265841	chr15	-0.81
SLCO3A1	248221	chr15:90445949-90446373	intra_enh	90445949	90446373	chr15	-0.47
SLCO3A1	255601	chr15:90453222-90453860	intra_enh	90453222	90453860	chr15	-0.96
LOC100507217	4089	chr15:91231416-91231818	intra_enh	91231416	91231818	chr15	-0.62
MIR3175	13962	chr15:91262389-91262798	intra_enh	91262389	91262798	chr15	-0.53
LINC00924	14054	chr15:93791328-93791427	intra_enh	93791328	93791427	chr15	-0.88
SYNM	2686	chr15:97465431-97465557	intra_enh	97465431	97465557	chr15	-0.60
CERS3	83269	chr15:98818661-98818909	intra_enh	98818661	98818909	chr15	-0.85
LRRK1	36672	chr15:99313541-99313766	intra_enh	99313541	99313766	chr15	-0.42
LRRK1	61603	chr15:99338493-99338677	intra_enh	99338493	99338677	chr15	-0.67
LRRK1	61940	chr15:99338893-99338951	intra_enh	99338893	99338951	chr15	-0.52
CIITA	4458	chr16:10882653-10883370	intra_enh	10882653	10883370	chr16	-0.49
CLEC16A	9818	chr16:10955602-10955723	intra_enh	10955602	10955723	chr16	-0.50
CLEC16A	10132	chr16:10955891-10956062	intra_enh	10955891	10956062	chr16	-0.53
CLEC16A	37296	chr16:10983059-10983221	intra_enh	10983059	10983221	chr16	-0.48
SOCS1	150998	chr16:11106192-11106893	intra_enh	11106192	11106893	chr16	-0.27
LITAF	3744	chr16:11583925-11584048	intra_enh	11583925	11584048	chr16	-0.57
SNN	17426	chr16:11687025-11687404	intra_enh	11687025	11687404	chr16	-0.98
TXNDC11	26890	chr16:11716841-11717680	intra_enh	11716841	11717680	chr16	-0.78
TXNDC11	4524	chr16:11739285-11739968	intra_enh	11739285	11739968	chr16	-0.70
ZC3H7A	26800	chr16:11771654-11771977	intra_enh	11771654	11771977	chr16	-0.46
SNX29	2691	chr16:11980646-11980916	intra_enh	11980646	11980916	chr16	-0.43
SNX29	169388	chr16:12147377-12147580	intra_enh	12147377	12147580	chr16	-0.82
SNX29	279052	chr16:12256931-12257353	intra_enh	12256931	12257353	chr16	-0.69
SNX29	279568	chr16:12257498-12257819	intra_enh	12257498	12257819	chr16	-0.73
SNX29	320678	chr16:12298686-12298851	intra_enh	12298686	12298851	chr16	-0.60
SNX29	339450	chr16:12317467-12317612	intra_enh	12317467	12317612	chr16	-0.35
SNX29	360420	chr16:12338270-12338749	intra_enh	12338270	12338749	chr16	-0.36
SNX29	370858	chr16:12348794-12349102	intra_enh	12348794	12349102	chr16	-0.49
MIR4718	309404	chr16:12412182-12412366	intra_enh	12412182	12412366	chr16	-0.82
BFAR	25284	chr16:14659388-14659516	intra_enh	14659388	14659516	chr16	-0.69
MYH11	90776	chr16:15767544-15767681	intra_enh	15767544	15767681	chr16	-0.79

ABCC1	40896	chr16:15991716-15991943	intra_enh	15991716	15991943	chr16	-0.59
ABCC1	44976	chr16:15995646-15996175	intra_enh	15995646	15996175	chr16	-0.92
ABCC1	49052	chr16:15999784-16000188	intra_enh	15999784	16000188	chr16	-0.55
ABCC1	89486	chr16:16040358-16040482	intra_enh	16040358	16040482	chr16	-0.68
XYLT1	176110	chr16:17295847-17296412	intra_enh	17295847	17296412	chr16	-0.83
XYLT1	170622	chr16:17301438-17301797	intra_enh	17301438	17301797	chr16	-0.98
XYLT1	102938	chr16:17369244-17369361	intra_enh	17369244	17369361	chr16	-0.65
XYLT1	92910	chr16:17379127-17379533	intra_enh	17379127	17379533	chr16	-0.40
XYLT1	61614	chr16:17410391-17410860	intra_enh	17410391	17410860	chr16	-0.56
XYLT1	35834	chr16:17436336-17436477	intra_enh	17436336	17436477	chr16	-0.74
GDE1	28190	chr16:19412726-19412798	intra_enh	19412726	19412798	chr16	-0.64
LYRM1	3638	chr16:20822593-20823831	intra_enh	20822593	20823831	chr16	-0.38
METTL9	6672	chr16:21509206-21509535	intra_enh	21509206	21509535	chr16	-0.92
IGSF6	11574	chr16:21559753-21560074	intra_enh	21559753	21560074	chr16	-0.29
C16orf52	19686	chr16:21946534-21946751	intra_enh	21946534	21946751	chr16	-0.94
CDR2	16545	chr16:22276572-22277218	intra_enh	22276572	22277218	chr16	-0.58
SCNN1B	63640	chr16:23284435-23285026	intra_enh	23284435	23285026	chr16	-0.81
GGA2	7878	chr16:23421305-23421572	intra_enh	23421305	23421572	chr16	-0.53
DCTN5	10062	chr16:23569979-23570517	intra_enh	23569979	23570517	chr16	-0.95
PRKCB	7172	chr16:23761896-23762048	intra_enh	23761896	23762048	chr16	-0.81
PRKCB	7518	chr16:23762169-23762468	intra_enh	23762169	23762468	chr16	-0.77
PRKCB	45831	chr16:23800564-23800698	intra_enh	23800564	23800698	chr16	-0.57
PRKCB	178725	chr16:23933398-23933652	intra_enh	23933398	23933652	chr16	-0.70
PRKCB	184578	chr16:23939270-23939485	intra_enh	23939270	23939485	chr16	-0.87
CACNG3	182396	chr16:23991793-23992162	intra_enh	23991793	23992162	chr16	-0.67
ARHGAP17	34954	chr16:24898836-24899656	intra_enh	24898836	24899656	chr16	-0.54
NSMCE1	6872	chr16:27194373-27194599	intra_enh	27194373	27194599	chr16	-0.82
IL21R	2140	chr16:27348137-27348300	intra_enh	27348137	27348300	chr16	-0.82
XPO6	24122	chr16:28106347-28106890	intra_enh	28106347	28106890	chr16	-0.67
XPO6	23274	chr16:28107080-28107851	intra_enh	28107080	28107851	chr16	-0.55
RABEP2	15039	chr16:28828945-28829045	intra_enh	28828945	28829045	chr16	-0.62
MMP25-AS1	3956	chr16:3045313-3045518	intra_enh	3045313	3045518	chr16	-0.33
MIR4519	9082	chr16:30784969-30785158	intra_enh	30784969	30785158	chr16	-0.92
MIR4519	8576	chr16:30785436-30785705	intra_enh	30785436	30785705	chr16	-0.85
ZNF843	3672	chr16:31357964-31358392	intra_enh	31357964	31358392	chr16	-0.79
NLRC3	9659	chr16:3576905-3577225	intra_enh	3576905	3577225	chr16	-0.75
ADCY9	51017	chr16:4055055-4055287	intra_enh	4055055	4055287	chr16	-0.54
CDIP1	11500	chr16:4516899-4517045	intra_enh	4516899	4517045	chr16	-0.28
CDIP1	8880	chr16:4519028-4520155	intra_enh	4519028	4520155	chr16	-0.50
C16orf87	22286	chr16:45400156-45400424	intra_enh	45400156	45400424	chr16	-0.73
PHKB	62062	chr16:46114662-46114883	intra_enh	46114662	46114883	chr16	-0.63
PHKB	62482	chr16:46115032-46115352	intra_enh	46115032	46115352	chr16	-0.64
C16orf78	201428	chr16:48166573-48166898	intra_enh	48166573	48166898	chr16	-0.74
MIR6771	34815	chr16:48918761-48918921	intra_enh	48918761	48918921	chr16	-0.64
CHD9	9417	chr16:51655690-51656032	intra_enh	51655690	51656032	chr16	-0.93
CHD9	12672	chr16:51659007-51659224	intra_enh	51659007	51659224	chr16	-0.83
CHD9	47052	chr16:51693289-51693703	intra_enh	51693289	51693703	chr16	-0.91
RBL2	15578	chr16:52041063-52041794	intra_enh	52041063	52041794	chr16	-0.99
MIR138-2	31102	chr16:55418510-55419145	intra_enh	55418510	55419145	chr16	-0.99
MIR6863	5298	chr16:55490281-55490476	intra_enh	55490281	55490476	chr16	-0.84
CCDC102A	13224	chr16:56114666-56114843	intra_enh	56114666	56114843	chr16	-0.59
NDRG4	4831	chr16:57086624-57086806	intra_enh	57086624	57086806	chr16	-0.61
GOT2	4198	chr16:57321367-57321761	intra_enh	57321367	57321761	chr16	-0.55
TK2	9954	chr16:65131023-65131530	intra_enh	65131023	65131530	chr16	-0.41
CBFB	6416	chr16:65626774-65627157	intra_enh	65626774	65627157	chr16	-0.73

RANBP10	3790	chr16:66394023-6639451	intra_enh	66394023	66394510	chr16	-0.74
NFATC3	8742	chr16:66685245-6668577	intra_enh	66685245	66685774	chr16	-0.67
PRMT7	57542	chr16:66959973-6696014	intra_enh	66959973	66960142	chr16	-0.40
CDH1	20268	chr16:67348797-6734912	intra_enh	67348797	67349128	chr16	-0.97
IST1	5056	chr16:70491645-7049225	intra_enh	70491645	70492259	chr16	-0.38
PSMD7	2442	chr16:72890543-7289068	intra_enh	72890543	72890684	chr16	-0.81
GLG1	2650	chr16:73195815-7319597	intra_enh	73195815	73195973	chr16	-0.58
ZNRF1	13778	chr16:73604034-7360435	intra_enh	73604034	73604350	chr16	-0.73
BCAR1	51964	chr16:73911176-73911657	intra_enh	73911176	73911657	chr16	-0.77
CFDP1	53290	chr16:73971485-7397171	intra_enh	73971485	73971710	chr16	-0.77
CHST6	9948	chr16:74076381-7407657	intra_enh	74076381	74076578	chr16	-0.57
ADAT1	2156	chr16:74212490-7421264	intra_enh	74212490	74212643	chr16	-0.64
MPG	6601	chr16:74603-74935	intra_enh	74603	74935	chr16	-0.61
SYCE1L	100245	chr16:75890886-7589130	intra_enh	75890886	75891300	chr16	-0.97
MAF	638006	chr16:77553845-7755439	intra_enh	77553845	77554390	chr16	-0.83
CDYL2	93154	chr16:79302443-7930260	intra_enh	79302443	79302601	chr16	-0.57
CMIP	9616	chr16:80096030-8009611	intra_enh	80096030	80096111	chr16	-0.73
CMIP	9914	chr16:80096302-8009643	intra_enh	80096302	80096433	chr16	-0.61
MIR6504	2468	chr16:80199824-8020014	intra_enh	80199824	80200143	chr16	-0.48
PLCG2	16201	chr16:80386348-8038677	intra_enh	80386348	80386778	chr16	-0.31
PLCG2	48920	chr16:80419186-8041937	intra_enh	80419186	80419378	chr16	-0.35
PLCG2	94658	chr16:80464948-8046509	intra_enh	80464948	80465093	chr16	-0.80
PLCG2	95028	chr16:80465321-8046546	intra_enh	80465321	80465460	chr16	-0.81
CDH13	25344	chr16:81242824-8124366	intra_enh	81242824	81243660	chr16	-0.56
CDH13	27252	chr16:81244961-8124533	intra_enh	81244961	81245339	chr16	-0.62
SLC38A8	27386	chr16:82605774-8260598	intra_enh	82605774	82605982	chr16	-0.88
COTL1	8029	chr16:83201052-8320129	intra_enh	83201052	83201298	chr16	-0.65
USP10	54758	chr16:83345702-8334592	intra_enh	83345702	83345921	chr16	-0.46
KIAA0513	20250	chr16:83674376-8367476	intra_enh	83674376	83674760	chr16	-0.93
FAM92B	7458	chr16:83695983-8369633	intra_enh	83695983	83696332	chr16	-0.74
C16orf74	2287	chr16:84339827-8433997	intra_enh	84339827	84339979	chr16	-0.62
EMC8	9296	chr16:84381094-8438161	intra_enh	84381094	84381614	chr16	-0.92
KLHDC4	53091	chr16:86303820-8630419	intra_enh	86303820	86304198	chr16	-0.30
KLHDC4	42332	chr16:86314642-8631489	intra_enh	86314642	86314894	chr16	-0.56
KLHDC4	37706	chr16:86319295-8631949	intra_enh	86319295	86319493	chr16	-0.87
KLHDC4	3242	chr16:86360247-8636043	intra_enh	86360247	86360436	chr16	-0.46
LOC400553	54616	chr16:86637351-8663760	intra_enh	86637351	86637602	chr16	-0.57
LOC100129697	2960	chr16:87530742-8753123	intra_enh	87530742	87531231	chr16	-0.55
CBFA2T3	2412	chr16:87537462-8753758	intra_enh	87537462	87537582	chr16	-0.53
CBFA2T3	11448	chr16:87559223-8755989	intra_enh	87559223	87559894	chr16	-0.62
CBFA2T3	9648	chr16:87561259-8756145	intra_enh	87561259	87561456	chr16	-0.38
CBFA2T3	9164	chr16:87561633-8756205	intra_enh	87561633	87562052	chr16	-0.51
ANKRD11	3275	chr16:88081025-8808136	intra_enh	88081025	88081365	chr16	-0.75
YWHAE	22883	chr17:1227329-1227517	intra_enh	1227329	1227517	chr17	-0.49
YWHAE	9104	chr17:1241148-1241255	intra_enh	1241148	1241255	chr17	-0.29
CDRT15	40284	chr17:14040331-1404085	intra_enh	14040331	14040852	chr17	-0.91
RPA1	3368	chr17:1683332-1683448	intra_enh	1683332	1683448	chr17	-0.42
SMCR5	24850	chr17:17598658-1759877	intra_enh	17598658	17598778	chr17	-0.43
SREBF1	10409	chr17:17670576-1767070	intra_enh	17670576	17670706	chr17	-0.51
SREBF1	7590	chr17:17673387-1767353	intra_enh	17673387	17673532	chr17	-0.76
SREBF1	60605	chr17:17741442-1774186	intra_enh	17741442	17741868	chr17	-0.91
TOM1L2	12555	chr17:17803901-1780400	intra_enh	17803901	17804009	chr17	-0.69
EPN2	5416	chr17:19086373-1908702	intra_enh	19086373	19087023	chr17	-0.80
EPN2	6684	chr17:19087865-1908806	intra_enh	19087865	19088068	chr17	-0.92
EPN2-AS1	2350	chr17:19152291-1915274	intra_enh	19152291	19152746	chr17	-0.96

EPN2-AS1	10950	chr17:19161004-19161233	intra_enh	19161004	19161233	chr17	-0.59
SMG6	49760	chr17:1988353-1988779	intra_enh	1988353	1988779	chr17	-0.48
USP22	6772	chr17:20880083-20880261	intra_enh	20880083	20880261	chr17	-0.47
USP22	6280	chr17:20880503-20880826	intra_enh	20880503	20880826	chr17	-0.64
USP22	5899	chr17:20880968-20881122	intra_enh	20880968	20881122	chr17	-0.60
USP22	5590	chr17:20881276-20881433	intra_enh	20881276	20881433	chr17	-0.64
USP22	5250	chr17:20881559-20881830	intra_enh	20881559	20881830	chr17	-0.81
KSR1	34965	chr17:22858052-22858202	intra_enh	22858052	22858202	chr17	-0.86
NLK	55522	chr17:23449239-23449434	intra_enh	23449239	23449434	chr17	-0.80
SEZ6	23518	chr17:24333567-24333812	intra_enh	24333567	24333812	chr17	-0.50
TAOK1	56299	chr17:24798279-24798455	intra_enh	24798279	24798455	chr17	-0.89
CORO6	60728	chr17:25032958-25033633	intra_enh	25032958	25033633	chr17	-0.87
SSH2	44369	chr17:25068120-25068294	intra_enh	25068120	25068294	chr17	-0.74
SSH2	39785	chr17:25072442-25073140	intra_enh	25072442	25073140	chr17	-0.29
SSH2	34430	chr17:25077569-25078722	intra_enh	25077569	25078722	chr17	-0.75
SSH2	47314	chr17:25159624-25160157	intra_enh	25159624	25160157	chr17	-0.67
EFCAB5	46092	chr17:25234800-25235012	intra_enh	25234800	25235012	chr17	-0.69
TMIGD1	11710	chr17:25673397-25673567	intra_enh	25673397	25673567	chr17	-0.83
SH3GL1P2	22068	chr17:25953318-25953467	intra_enh	25953318	25953467	chr17	-0.41
SUZ12P1	23882	chr17:26084552-26084712	intra_enh	26084552	26084712	chr17	-0.50
CRLF3	18293	chr17:26157363-26157859	intra_enh	26157363	26157859	chr17	-0.58
CRLF3	17492	chr17:26158155-26158669	intra_enh	26158155	26158669	chr17	-0.66
CRLF3	14685	chr17:26161081-26161357	intra_enh	26161081	26161357	chr17	-0.84
CRLF3	12344	chr17:26163468-26163651	intra_enh	26163468	26163651	chr17	-0.62
EVI2B	6159	chr17:26658944-26659250	intra_enh	26658944	26659250	chr17	-0.41
RAP1GAP2	32345	chr17:2678748-2678902	intra_enh	2678748	2678902	chr17	-0.85
UTP6	18742	chr17:27234008-27234192	intra_enh	27234008	27234192	chr17	-0.68
LOC101927911	35267	chr17:2780606-2780740	intra_enh	2780606	2780740	chr17	-0.56
CDK5R1	68077	chr17:27906150-27906436	intra_enh	27906150	27906436	chr17	-0.92
TMEM98	9366	chr17:28288338-28288475	intra_enh	28288338	28288475	chr17	-0.49
AA06	217704	chr17:29102534-29102658	intra_enh	29102534	29102658	chr17	-0.60
RFFL	12404	chr17:30402216-30402719	intra_enh	30402216	30402719	chr17	-0.73
SLFN11	5665	chr17:30719057-30719281	intra_enh	30719057	30719281	chr17	-0.75
SLFN11	5346	chr17:30719420-30719556	intra_enh	30719420	30719556	chr17	-0.84
TAF15	2558	chr17:31163074-31163182	intra_enh	31163074	31163182	chr17	-0.40
MYO19	16234	chr17:31949038-31949331	intra_enh	31949038	31949331	chr17	-0.91
GGNBP2	4116	chr17:31978852-31979076	intra_enh	31978852	31979076	chr17	-0.59
GGNBP2	4916	chr17:31979639-31979890	intra_enh	31979639	31979890	chr17	-0.74
SRCIN1	21199	chr17:33994328-33994694	intra_enh	33994328	33994694	chr17	-0.65
SRCIN1	14280	chr17:34001254-34001606	intra_enh	34001254	34001606	chr17	-0.90
PCGF2	5432	chr17:34152461-34152842	intra_enh	34152461	34152842	chr17	-0.54
PLXDC1	33014	chr17:34528272-34528555	intra_enh	34528272	34528555	chr17	-0.77
STAC2	81082	chr17:34716376-34716919	intra_enh	34716376	34716919	chr17	-0.83
PGAP3	8368	chr17:35089293-35089670	intra_enh	35089293	35089670	chr17	-0.81
IKZF3	3082	chr17:35190746-35191425	intra_enh	35190746	35191425	chr17	-0.39
IKZF3	16782	chr17:35204371-35205200	intra_enh	35204371	35205200	chr17	-0.58
IKZF3	41192	chr17:35229113-35229280	intra_enh	35229113	35229280	chr17	-0.67
IKZF3	15996	chr17:35257035-35258909	intra_enh	35257035	35258909	chr17	-0.40
IKZF3	11800	chr17:35262068-35262268	intra_enh	35262068	35262268	chr17	-0.76
ZPBP2	2891	chr17:35280623-35281119	intra_enh	35280623	35281119	chr17	-0.70
HAP1	6592	chr17:37137749-37137914	intra_enh	37137749	37137914	chr17	-0.81
DNAJC7	21148	chr17:37401465-37401658	intra_enh	37401465	37401658	chr17	-0.78
DNAJC7	20252	chr17:37402378-37402539	intra_enh	37402378	37402539	chr17	-0.37
STAT5B	15545	chr17:37666325-37666485	intra_enh	37666325	37666485	chr17	-0.90
PTRF	8094	chr17:37820556-37820984	intra_enh	37820556	37820984	chr17	-0.44

EZH1	2272	chr17:38148254-38148397	intra_enh	38148254	38148397	chr17	-0.61
RUNDC1	4151	chr17:38390155-38390359	intra_enh	38390155	38390359	chr17	-0.78
ZZEF1	68437	chr17:3924451-3924679	intra_enh	3924451	3924679	chr17	-0.36
GPATCH8	3080	chr17:39932949-39933858	intra_enh	39932949	39933858	chr17	-0.52
ANKFY1	48436	chr17:4065375-4065537	intra_enh	4065375	4065537	chr17	-0.36
MAP3K14	21100	chr17:40729018-40729211	intra_enh	40729018	40729211	chr17	-0.83
KANSL1	56300	chr17:41569423-41569865	intra_enh	41569423	41569865	chr17	-0.86
KANSL1	55828	chr17:41569982-41570251	intra_enh	41569982	41570251	chr17	-0.93
KANSL1	45563	chr17:41580215-41580547	intra_enh	41580215	41580547	chr17	-0.42
KANSL1	44864	chr17:41580784-41581375	intra_enh	41580784	41581375	chr17	-0.35
KANSL1	4294	chr17:41621598-41621701	intra_enh	41621598	41621701	chr17	-0.35
LOC103021295	42397	chr17:4164217-4164453	intra_enh	4164217	4164453	chr17	-0.54
UBE2G1	31441	chr17:4185045-4185509	intra_enh	4185045	4185509	chr17	-0.35
UBE2G1	30996	chr17:4185642-4185802	intra_enh	4185642	4185802	chr17	-0.39
UBE2G1	27712	chr17:4188780-4189232	intra_enh	4188780	4189232	chr17	-0.75
UBE2G1	26316	chr17:4190121-4190684	intra_enh	4190121	4190684	chr17	-0.88
UBE2G1	22618	chr17:4193964-4194236	intra_enh	4193964	4194236	chr17	-0.70
UBE2G1	20704	chr17:4195588-4196439	intra_enh	4195588	4196439	chr17	-0.56
UBE2G1	13336	chr17:4203274-4203491	intra_enh	4203274	4203491	chr17	-0.87
UBE2G1	12308	chr17:4204066-4204753	intra_enh	4204066	4204753	chr17	-0.60
UBE2G1	9716	chr17:4206926-4207077	intra_enh	4206926	4207077	chr17	-0.66
UBE2G1	9358	chr17:4207266-4207455	intra_enh	4207266	4207455	chr17	-0.64
UBE2G1	9038	chr17:4207624-4207735	intra_enh	4207624	4207735	chr17	-0.66
UBE2G1	6526	chr17:4210142-4210243	intra_enh	4210142	4210243	chr17	-0.70
CDC27	5614	chr17:42615900-42616227	intra_enh	42615900	42616227	chr17	-0.58
CDC27	4754	chr17:42616428-42617419	intra_enh	42616428	42617419	chr17	-0.66
CDC27	3144	chr17:42618264-42618805	intra_enh	42618264	42618805	chr17	-0.51
CDC27	2362	chr17:42619013-42619620	intra_enh	42619013	42619620	chr17	-0.58
MYL4	9668	chr17:42651186-42651575	intra_enh	42651186	42651575	chr17	-0.52
ITGB3	32870	chr17:42718812-42719340	intra_enh	42718812	42719340	chr17	-0.42
KPNB1	8568	chr17:43092067-43092189	intra_enh	43092067	43092189	chr17	-0.43
KPNB1	9013	chr17:43092443-43092703	intra_enh	43092443	43092703	chr17	-0.39
GNGT2	5722	chr17:44648520-44648795	intra_enh	44648520	44648795	chr17	-0.47
FAM117A	20063	chr17:45176380-45176530	intra_enh	45176380	45176530	chr17	-0.38
FAM117A	11528	chr17:45184907-45185074	intra_enh	45184907	45185074	chr17	-0.72
FAM117A	10159	chr17:45186257-45186461	intra_enh	45186257	45186461	chr17	-0.54
SPAG9	16856	chr17:46462180-46462765	intra_enh	46462180	46462765	chr17	-0.67
MBTD1	28545	chr17:46663690-46664072	intra_enh	46663690	46664072	chr17	-0.82
MBTD1	20867	chr17:46671479-46671639	intra_enh	46671479	46671639	chr17	-0.87
LOC100130950	20106	chr17:5056130-5056285	intra_enh	5056130	5056285	chr17	-0.91
LOC100130950	20847	chr17:5056750-5057148	intra_enh	5056750	5057148	chr17	-0.96
SCIMP	7884	chr17:5070927-5071066	intra_enh	5070927	5071066	chr17	-0.64
SCIMP	7166	chr17:5071648-5071780	intra_enh	5071648	5071780	chr17	-0.68
SCIMP	2284	chr17:5076451-5076741	intra_enh	5076451	5076741	chr17	-0.30
ANKFN1	137193	chr17:51722862-51723192	intra_enh	51722862	51723192	chr17	-0.60
RABEP1	47882	chr17:5173946-5174377	intra_enh	5173946	5174377	chr17	-0.48
DGKE	4284	chr17:52270541-52270944	intra_enh	52270541	52270944	chr17	-0.63
LOC101927539	4354	chr17:53045011-53045241	intra_enh	53045011	53045241	chr17	-0.30
LOC101927539	21128	chr17:53061743-53062057	intra_enh	53061743	53062057	chr17	-0.89
DHX33	2568	chr17:5310350-5310722	intra_enh	5310350	5310722	chr17	-0.60
LOC101927539	63934	chr17:53104502-53104911	intra_enh	53104502	53104911	chr17	-0.75
MRPS23	17944	chr17:53300321-53300431	intra_enh	53300321	53300431	chr17	-0.68
BZRAP1-AS1	7604	chr17:53750088-53750320	intra_enh	53750088	53750320	chr17	-0.54
PRR11	4118	chr17:54591328-54592188	intra_enh	54591328	54592188	chr17	-0.76
PRR11	4800	chr17:54592323-54592556	intra_enh	54592323	54592556	chr17	-0.66

MIR4729	9891	chr17:54807943-54808287	intra_enh	54807943	54808287	chr17	-0.94
MIR4729	72087	chr17:54870192-54870430	intra_enh	54870192	54870430	chr17	-0.60
MIR4729	75065	chr17:54873207-54873371	intra_enh	54873207	54873371	chr17	-0.56
LINC01476	5322	chr17:54953598-54953758	intra_enh	54953598	54953758	chr17	-0.69
MIR21	57691	chr17:55215496-55215938	intra_enh	55215496	55215938	chr17	-0.89
MIR21	8137	chr17:55265119-55265423	intra_enh	55265119	55265423	chr17	-0.84
MAP3K3	2265	chr17:59055723-59055871	intra_enh	59055723	59055871	chr17	-0.73
MAP3K3	24030	chr17:59077520-59077604	intra_enh	59077520	59077604	chr17	-0.53
LOC729683	5359	chr17:59136728-59136846	intra_enh	59136728	59136846	chr17	-0.63
ICAM2	42701	chr17:59494217-59494637	intra_enh	59494217	59494637	chr17	-0.72
ERN1	3200	chr17:59557558-59558509	intra_enh	59557558	59558509	chr17	-0.97
MILR1	6098	chr17:59881716-59881881	intra_enh	59881716	59881881	chr17	-0.73
MIR6080	6281	chr17:60200990-60201124	intra_enh	60200990	60201124	chr17	-0.25
MIR6080	3105	chr17:60204107-60204359	intra_enh	60204107	60204359	chr17	-0.34
AMZ2P1	6176	chr17:60395919-60396060	intra_enh	60395919	60396060	chr17	-0.61
AMZ2P1	5124	chr17:60396912-60397173	intra_enh	60396912	60397173	chr17	-0.70
GNA13	36934	chr17:60445324-60445516	intra_enh	60445324	60445516	chr17	-0.42
GNA13	35506	chr17:60446597-60447099	intra_enh	60446597	60447099	chr17	-0.67
GNA13	34570	chr17:60447699-60447870	intra_enh	60447699	60447870	chr17	-0.78
GNA13	28152	chr17:60454125-60454280	intra_enh	60454125	60454280	chr17	-0.59
GNA13	23432	chr17:60458866-60458979	intra_enh	60458866	60458979	chr17	-0.68
GNA13	23104	chr17:60459158-60459342	intra_enh	60459158	60459342	chr17	-0.73
GNA13	21534	chr17:60460716-60460924	intra_enh	60460716	60460924	chr17	-0.80
GNA13	21092	chr17:60461176-60461347	intra_enh	60461176	60461347	chr17	-0.77
GNA13	17792	chr17:60464436-60464689	intra_enh	60464436	60464689	chr17	-0.38
GNA13	10008	chr17:60472149-60472542	intra_enh	60472149	60472542	chr17	-0.75
GNA13	7724	chr17:60474498-60474762	intra_enh	60474498	60474762	chr17	-0.54
GNA13	7211	chr17:60474864-60475422	intra_enh	60474864	60475422	chr17	-0.53
RGS9	17974	chr17:60581694-60582086	intra_enh	60581694	60582086	chr17	-0.92
PRKCA-AS1	21266	chr17:61864609-61864792	intra_enh	61864609	61864792	chr17	-0.64
MIR634	80300	chr17:62133274-62133426	intra_enh	62133274	62133426	chr17	-0.71
MIR634	80046	chr17:62133534-62133673	intra_enh	62133534	62133673	chr17	-0.59
MIR634	12200	chr17:62201234-62201666	intra_enh	62201234	62201666	chr17	-0.86
MIR634	10890	chr17:62202730-62202791	intra_enh	62202730	62202791	chr17	-0.56
CACNG1	37760	chr17:62508769-62508976	intra_enh	62508769	62508976	chr17	-0.92
MIR548AA2	19998	chr17:62877959-62878178	intra_enh	62877959	62878178	chr17	-0.67
MIR548AA2	4769	chr17:62893036-62893558	intra_enh	62893036	62893558	chr17	-0.98
AMZ2	5259	chr17:63760885-63761109	intra_enh	63760885	63761109	chr17	-0.68
MIR635	15333	chr17:63947398-63947836	intra_enh	63947398	63947836	chr17	-0.49
WIPI1	2968	chr17:63968100-63968331	intra_enh	63968100	63968331	chr17	-0.75
PRKAR1A	26294	chr17:63992950-63993491	intra_enh	63992950	63993491	chr17	-0.47
PRKAR1A	20183	chr17:63999252-63999410	intra_enh	63999252	63999410	chr17	-0.47
MIR4524B	5969	chr17:64601072-64601542	intra_enh	64601072	64601542	chr17	-0.94
MAP2K6	88774	chr17:65010851-65011561	intra_enh	65010851	65011561	chr17	-0.68
MAP2K6	89408	chr17:65011671-65012010	intra_enh	65011671	65012010	chr17	-0.30
LOC102723505	2798	chr17:67530570-67531266	intra_enh	67530570	67531266	chr17	-0.97
LINC01152	3318	chr17:67541572-67541839	intra_enh	67541572	67541839	chr17	-0.96
LINC00511	87536	chr17:68235688-68235796	intra_enh	68235688	68235796	chr17	-0.40
ARMC7	7499	chr17:70610104-70610250	intra_enh	70610104	70610250	chr17	-0.38
SLC25A19	47048	chr17:70843929-70844420	intra_enh	70843929	70844420	chr17	-0.96
SLC25A19	50110	chr17:70847185-70847287	intra_enh	70847185	70847287	chr17	-0.76
GRB2	55350	chr17:70857960-70858107	intra_enh	70857960	70858107	chr17	-0.70
GRB2	52422	chr17:70860889-70861035	intra_enh	70860889	70861035	chr17	-0.26
GRB2	45076	chr17:70868103-70868513	intra_enh	70868103	70868513	chr17	-0.81
GRB2	38655	chr17:70874609-70874849	intra_enh	70874609	70874849	chr17	-0.59

GRB2	36706	chr17:70876583-7087677	intra_enh	70876583	70876773	chr17	-0.76
MYO15B	21216	chr17:71074416-7107461	intra_enh	71074416	71074615	chr17	-0.94
MYO15B	16821	chr17:71078809-7107901	intra_enh	71078809	71079013	chr17	-0.46
ITGB4	13486	chr17:71245781-7124593	intra_enh	71245781	71245931	chr17	-0.31
FOXJ1	38818	chr17:71687452-7168813	intra_enh	71687452	71688137	chr17	-0.87
RNF157	48193	chr17:71699505-7170008	intra_enh	71699505	71700081	chr17	-0.68
METTL23	4808	chr17:72239023-7223960	intra_enh	72239023	72239604	chr17	-0.74
MFSD11	14562	chr17:72259499-7225997	intra_enh	72259499	72259977	chr17	-0.92
SEC14L1	14004	chr17:72662500-7266270	intra_enh	72662500	72662704	chr17	-0.84
SEC14L1	2886	chr17:72689611-72690394	intra_enh	72689611	72690394	chr17	-0.29
10-Sep	5710	chr17:72832818-7283298	intra_enh	72832818	72832981	chr17	-0.60
10-Sep	8492	chr17:72949514-7294991	intra_enh	72949514	72949915	chr17	-0.34
AFMID	6184	chr17:73701070-7370128	intra_enh	73701070	73701281	chr17	-0.76
PGS1	10234	chr17:73896375-7389667	intra_enh	73896375	73896676	chr17	-0.73
CYTH1	2753	chr17:74228598-7422875	intra_enh	74228598	74228752	chr17	-0.87
CYTH1	26142	chr17:74257531-7425761	intra_enh	74257531	74257610	chr17	-0.62
CYTH1	25642	chr17:74264099-7426465	intra_enh	74264099	74264658	chr17	-0.66
CYTH1	24971	chr17:74264902-7426519	intra_enh	74264902	74265196	chr17	-0.51
CYTH1	10167	chr17:74279663-7428004	intra_enh	74279663	74280043	chr17	-0.46
CYTH1	3378	chr17:74286479-7428680	intra_enh	74286479	74286806	chr17	-0.91
LOC101928855	41176	chr17:76435124-7643528	intra_enh	76435124	76435283	chr17	-0.90
FOXK2	4790	chr17:78075631-7807571	intra_enh	78075631	78075714	chr17	-0.36
FOXK2	16692	chr17:78087484-7808766	intra_enh	78087484	78087665	chr17	-0.32
FOXK2	24972	chr17:78095743-7809596	intra_enh	78095743	78095965	chr17	-0.73
FOXK2	25479	chr17:78096298-7809642	intra_enh	78096298	78096424	chr17	-0.35
ZNF750	45345	chr17:78436488-7843664	intra_enh	78436488	78436642	chr17	-0.53
B3GNTL1	84232	chr17:78518620-7851886	intra_enh	78518620	78518867	chr17	-0.43
B3GNTL1	82222	chr17:78520707-7852080	intra_enh	78520707	78520802	chr17	-0.75
B3GNTL1	81550	chr17:78521196-7852165	intra_enh	78521196	78521655	chr17	-0.76
CTC1	3768	chr17:8088257-8088482	intra_enh	8088257	8088482	chr17	-0.91
LOC100506371	45764	chr17:82755-82857	intra_enh	82755	82857	chr17	-0.48
MFSD6L	7932	chr17:8651242-8651405	intra_enh	8651242	8651405	chr17	-0.71
PIK3R6	11674	chr17:8699962-8700129	intra_enh	8699962	8700129	chr17	-0.81
PIK3R5	11399	chr17:8745103-8745219	intra_enh	8745103	8745219	chr17	-0.61
LOC101927410	125758	chr18:10777570-1077780	intra_enh	10777570	10777801	chr18	-0.67
LOC101927410	231730	chr18:10883368-1088394	intra_enh	10883368	10883948	chr18	-0.98
GNAL	30526	chr18:11710651-11711237	intra_enh	11710651	11711237	chr18	-0.90
GNAL	38492	chr18:11779792-11780132	intra_enh	11779792	11780132	chr18	-0.68
TUBB6	6620	chr18:12304332-1230542	intra_enh	12304332	12305420	chr18	-0.89
LOC100996324	3932	chr18:12735316-1273566	intra_enh	12735316	12735663	chr18	-0.30
PTPN2	29706	chr18:12844530-1284472	intra_enh	12844530	12844725	chr18	-0.74
PTPN2	20380	chr18:12853592-1285431	intra_enh	12853592	12854316	chr18	-0.86
PTPN2	16354	chr18:12857782-1285817	intra_enh	12857782	12858178	chr18	-0.78
PTPN2	6856	chr18:12867401-1286755	intra_enh	12867401	12867555	chr18	-0.45
MC2R	21698	chr18:13883677-1388400	intra_enh	13883677	13884000	chr18	-0.91
ROCK1	37257	chr18:16908481-1690862	intra_enh	16908481	16908625	chr18	-0.58
ROCK1	36674	chr18:16908726-1690954	intra_enh	16908726	16909545	chr18	-0.65
ROCK1	9402	chr18:16936299-1693651	intra_enh	16936299	16936516	chr18	-0.37
ESCO1	3596	chr18:17430891-1743130	intra_enh	17430891	17431301	chr18	-0.64
RBBP8	2780	chr18:18770528-1877070	intra_enh	18770528	18770705	chr18	-0.73
CABLES1	36294	chr18:19025898-1902626	intra_enh	19025898	19026261	chr18	-0.29
CABLES1	83554	chr18:19073270-1907340	intra_enh	19073270	19073409	chr18	-0.66
CABLES1	83896	chr18:19073553-1907381	intra_enh	19073553	19073810	chr18	-0.56
CABLES1	84760	chr18:19074101-1907499	intra_enh	19074101	19074991	chr18	-0.43
NPC1	2392	chr18:19418114-19418261	intra_enh	19418114	19418261	chr18	-0.61

LAMA3	10704	chr18:19696218-19696335	intra_enh	19696218	19696335	chr18	-0.75
LAMA3	6323	chr18:19700174-19701140	intra_enh	19700174	19701140	chr18	-0.76
TTC39C	58345	chr18:19768007-19768771	intra_enh	19768007	19768771	chr18	-0.95
TTC39C	5434	chr18:19832102-19832233	intra_enh	19832102	19832233	chr18	-0.78
SS18	4735	chr18:21919812-21919938	intra_enh	21919812	21919938	chr18	-0.88
PSMA8	38331	chr18:22005728-22006558	intra_enh	22005728	22006558	chr18	-0.99
TAF4B	45920	chr18:22014861-22014987	intra_enh	22014861	22014987	chr18	-0.83
TAF4B	41449	chr18:22019184-22019606	intra_enh	22019184	22019606	chr18	-0.97
TAF4B	25052	chr18:22085654-22086137	intra_enh	22085654	22086137	chr18	-0.83
TAF4B	25700	chr18:22086423-22086665	intra_enh	22086423	22086665	chr18	-0.87
TAF4B	26181	chr18:22086930-22087120	intra_enh	22086930	22087120	chr18	-0.92
TAF4B	26712	chr18:22087299-22087814	intra_enh	22087299	22087814	chr18	-0.97
TAF4B	30400	chr18:22091047-22091441	intra_enh	22091047	22091441	chr18	-0.77
TAF4B	35320	chr18:22095980-22096349	intra_enh	22095980	22096349	chr18	-0.83
AQP4	112972	chr18:22812427-22812945	intra_enh	22812427	22812945	chr18	-0.91
CDH2	96473	chr18:23914640-23915302	intra_enh	23914640	23915302	chr18	-0.95
NDC80	34052	chr18:2595505-2595615	intra_enh	2595505	2595615	chr18	-0.60
NDC80	34370	chr18:2595757-2595999	intra_enh	2595757	2595999	chr18	-0.79
SMCHD1	3689	chr18:2649426-2649720	intra_enh	2649426	2649720	chr18	-0.81
DSG2	2367	chr18:27334283-27334499	intra_enh	27334283	27334499	chr18	-0.87
KLHL14	58494	chr18:28548297-28548658	intra_enh	28548297	28548658	chr18	-0.67
CCDC178	238368	chr18:29035605-29035747	intra_enh	29035605	29035747	chr18	-0.49
CCDC178	207680	chr18:29066255-29066473	intra_enh	29066255	29066473	chr18	-0.81
LOC727896	11142	chr18:2947679-2947849	intra_enh	2947679	2947849	chr18	-0.79
LOC727896	16385	chr18:2952963-2953051	intra_enh	2952963	2953051	chr18	-0.56
LPIN2	31813	chr18:2969752-2970514	intra_enh	2969752	2970514	chr18	-0.43
NOL4	171746	chr18:29710774-29710883	intra_enh	29710774	29710883	chr18	-0.74
LPIN2	30460	chr18:2971157-2971814	intra_enh	2971157	2971814	chr18	-0.91
NOL4	130108	chr18:29752017-29752914	intra_enh	29752017	29752914	chr18	-0.68
NOL4	129324	chr18:29753043-29753457	intra_enh	29753043	29753457	chr18	-0.55
NOL4	9226	chr18:29873085-29873611	intra_enh	29873085	29873611	chr18	-0.52
DTNA	53786	chr18:30490352-30490459	intra_enh	30490352	30490459	chr18	-0.57
LPIN2	55912	chr18:3057725-3057991	intra_enh	3057725	3057991	chr18	-0.48
INO80C	3166	chr18:31328727-31328849	intra_enh	31328727	31328849	chr18	-0.76
MYOM1	45248	chr18:3164701-3165016	intra_enh	3164701	3165016	chr18	-0.54
TPGS2	135633	chr18:32798739-32798883	intra_enh	32798739	32798883	chr18	-0.90
TPGS2	136034	chr18:32799057-32799367	intra_enh	32799057	32799367	chr18	-0.78
DLGAP1-AS2	112977	chr18:3706592-3706830	intra_enh	3706592	3706830	chr18	-0.73
DLGAP1	118809	chr18:3716110-3716988	intra_enh	3716110	3716988	chr18	-0.47
SIGLEC15	49497	chr18:41708873-41709205	intra_enh	41708873	41709205	chr18	-0.34
RNF165	12336	chr18:42180475-42180566	intra_enh	42180475	42180566	chr18	-0.38
SMAD7	18138	chr18:44704913-44705164	intra_enh	44704913	44705164	chr18	-0.79
MIR4744	127628	chr18:44957434-44958094	intra_enh	44957434	44958094	chr18	-0.86
DYM	100914	chr18:45139836-45140492	intra_enh	45139836	45140492	chr18	-0.95
DYM	3692	chr18:45237270-45237501	intra_enh	45237270	45237501	chr18	-0.64
DYM	2751	chr18:45238276-45238378	intra_enh	45238276	45238378	chr18	-0.54
MEX3C	9446	chr18:46968440-46968767	intra_enh	46968440	46968767	chr18	-0.26
C18orf42	37764	chr18:5149224-5149759	intra_enh	5149224	5149759	chr18	-0.78
C18orf42	29181	chr18:5157904-5158246	intra_enh	5157904	5158246	chr18	-0.77
TXNL1	2967	chr18:52453817-52454085	intra_enh	52453817	52454085	chr18	-0.62
OACYLP	15172	chr18:54869043-54869202	intra_enh	54869043	54869202	chr18	-0.28
PIGN	4454	chr18:58000683-58000948	intra_enh	58000683	58000948	chr18	-0.85
PIGN	3520	chr18:58001547-58001954	intra_enh	58001547	58001954	chr18	-0.71
ZCCHC2	6835	chr18:58348322-58348620	intra_enh	58348322	58348620	chr18	-0.37
PHLPP1	224104	chr18:58757604-58757904	intra_enh	58757604	58757904	chr18	-0.75

BCL2	132210	chr18:59005325-59005443	intra_enh	59005325	59005443	chr18	-0.45
C18orf63	19010	chr18:70152988-70153207	intra_enh	70152988	70153207	chr18	-0.96
LOC100131655	3175	chr18:72659988-72660142	intra_enh	72659988	72660142	chr18	-0.61
MBP	31191	chr18:72889045-72889425	intra_enh	72889045	72889425	chr18	-0.68
ATP9B	104480	chr18:75034501-75035226	intra_enh	75034501	75035226	chr18	-0.89
ATP9B	113066	chr18:75043344-75043556	intra_enh	75043344	75043556	chr18	-0.73
NFATC1	153372	chr18:75103119-75103653	intra_enh	75103119	75103653	chr18	-0.88
NFATC1	77009	chr18:75338130-75338408	intra_enh	75338130	75338408	chr18	-0.30
RAB12	3992	chr18:8603352-8603517	intra_enh	8603352	8603517	chr18	-0.31
TWSG1	91520	chr18:9232901-9233588	intra_enh	9232901	9233588	chr18	-0.98
TXNDC2	56452	chr18:9819192-9819347	intra_enh	9819192	9819347	chr18	-0.84
VAPA	10805	chr18:9914669-9914849	intra_enh	9914669	9914849	chr18	-0.30
VAPA	13424	chr18:9917150-9917607	intra_enh	9917150	9917607	chr18	-0.40
PDE4A	2264	chr19:10400020-10400492	intra_enh	10400020	10400492	chr19	-0.81
ILF3	4078	chr19:10629767-10630261	intra_enh	10629767	10630261	chr19	-0.47
ILF3	9568	chr19:10635377-10635631	intra_enh	10635377	10635631	chr19	-0.71
MIR638	20984	chr19:10710853-10711272	intra_enh	10710853	10711272	chr19	-0.98
CARM1	2455	chr19:10845629-10845785	intra_enh	10845629	10845785	chr19	-0.65
SMARCA4	5958	chr19:10938545-10938984	intra_enh	10938545	10938984	chr19	-0.63
SMARCA4	10224	chr19:10942940-10943119	intra_enh	10942940	10943119	chr19	-0.76
LDLR	39161	chr19:11021819-11021931	intra_enh	11021819	11021931	chr19	-0.33
KANK2	4004	chr19:11162077-11162447	intra_enh	11162077	11162447	chr19	-0.53
ELOF1	4681	chr19:11526316-11526426	intra_enh	11526316	11526426	chr19	-0.85
ZNF791	2809	chr19:12585420-12585658	intra_enh	12585420	12585658	chr19	-0.49
GADD45GIP1	2405	chr19:12926574-12926752	intra_enh	12926574	12926752	chr19	-0.36
LYL1	3115	chr19:13077945-13078233	intra_enh	13077945	13078233	chr19	-0.48
IER2	127077	chr19:13249214-13249500	intra_enh	13249214	13249500	chr19	-0.27
CACNA1A	109519	chr19:13368669-13368841	intra_enh	13368669	13368841	chr19	-0.54
ASF1B	8344	chr19:14099972-14100221	intra_enh	14099972	14100221	chr19	-0.89
CLEC17A	20849	chr19:14575509-14575977	intra_enh	14575509	14575977	chr19	-0.94
CLEC17A	21327	chr19:14576131-14576311	intra_enh	14576131	14576311	chr19	-0.81
CLEC17A	21920	chr19:14576671-14576957	intra_enh	14576671	14576957	chr19	-0.95
RAB8A	5390	chr19:16088794-16088961	intra_enh	16088794	16088961	chr19	-0.65
RAB8A	7964	chr19:16091363-16091542	intra_enh	16091363	16091542	chr19	-0.62
EPS15L1	24002	chr19:16419698-16419945	intra_enh	16419698	16419945	chr19	-0.45
MED26	4620	chr19:16595312-16595479	intra_enh	16595312	16595479	chr19	-0.31
HAUS8	7684	chr19:17039549-17039771	intra_enh	17039549	17039771	chr19	-0.62
USHBP1	3877	chr19:17232565-17232769	intra_enh	17232565	17232769	chr19	-0.74
ABHD8	9540	chr19:17265616-17265869	intra_enh	17265616	17265869	chr19	-0.79
PLVAP	7014	chr19:17341875-17342374	intra_enh	17341875	17342374	chr19	-0.89
COLGALT1	24412	chr19:17551707-17552138	intra_enh	17551707	17552138	chr19	-0.46
ARRDC2	4288	chr19:17968602-17968701	intra_enh	17968602	17968701	chr19	-0.72
IL12RB1	2150	chr19:18060876-18061053	intra_enh	18060876	18061053	chr19	-0.43
IL12RB1	4394	chr19:18062875-18063542	intra_enh	18062875	18063542	chr19	-0.84
ISYNA1	40826	chr19:18450671-18451205	intra_enh	18450671	18451205	chr19	-0.76
TMEM161A	14758	chr19:19124953-19125183	intra_enh	19124953	19125183	chr19	-0.81
MEF2B	2073	chr19:19144107-19144235	intra_enh	19144107	19144235	chr19	-0.77
GATAD2A	9032	chr19:19366585-19366760	intra_enh	19366585	19366760	chr19	-0.90
ZNF101	2454	chr19:19642991-19643108	intra_enh	19642991	19643108	chr19	-0.77
DOT1L	3034	chr19:2117927-2118432	intra_enh	2117927	2118432	chr19	-0.93
MIR1227	10240	chr19:2174819-2174998	intra_enh	2174819	2174998	chr19	-0.63
GNG7	93005	chr19:2560391-2561091	intra_enh	2560391	2561091	chr19	-0.66
GNG7	89217	chr19:2564102-2564956	intra_enh	2564102	2564956	chr19	-0.54
GNG7	85692	chr19:2567892-2568215	intra_enh	2567892	2568215	chr19	-0.38
GNG7	70139	chr19:2583528-2583686	intra_enh	2583528	2583686	chr19	-0.31

GNG7	57067	chr19:2596616-2596742	intra_enh	2596616	2596742	chr19	-0.84
GNG7	3890	chr19:2649536-2650177	intra_enh	2649536	2650177	chr19	-0.63
LOC100420587	246466	chr19:33663908-33664044	intra_enh	33663908	33664044	chr19	-0.34
LOC100420587	137874	chr19:33772373-33772762	intra_enh	33772373	33772762	chr19	-0.68
LOC100420587	136349	chr19:33773969-33774217	intra_enh	33773969	33774217	chr19	-0.89
LOC100420587	107866	chr19:33802462-33802691	intra_enh	33802462	33802691	chr19	-0.88
LOC100420587	107466	chr19:33802841-33803111	intra_enh	33802841	33803111	chr19	-0.89
LOC100420587	96212	chr19:33813971-33814490	intra_enh	33813971	33814490	chr19	-0.67
POP4	4782	chr19:34793687-34793894	intra_enh	34793687	34793894	chr19	-0.47
CCNE1	3326	chr19:34997868-34998263	intra_enh	34997868	34998263	chr19	-0.26
URI1	2678	chr19:35127026-35128299	intra_enh	35127026	35128299	chr19	-0.59
URI1	24654	chr19:35149581-35149694	intra_enh	35149581	35149694	chr19	-0.32
ZNF536	168938	chr19:35723567-35724640	intra_enh	35723567	35724640	chr19	-0.98
TSHZ3	9083	chr19:36522804-36523090	intra_enh	36522804	36523090	chr19	-0.94
DPY19L3	16074	chr19:37604819-37605050	intra_enh	37604819	37605050	chr19	-0.56
LSM14A	6016	chr19:39360940-39361471	intra_enh	39360940	39361471	chr19	-0.35
KIAA0355	22624	chr19:39459596-39460241	intra_enh	39459596	39460241	chr19	-0.75
KIAA0355	54010	chr19:39491085-39491524	intra_enh	39491085	39491524	chr19	-0.89
GPI	49900	chr19:39497086-39498081	intra_enh	39497086	39498081	chr19	-0.84
HPN	2251	chr19:40220912-40221082	intra_enh	40220912	40221082	chr19	-0.51
SIPA1L3	3972	chr19:43093395-43093948	intra_enh	43093395	43093948	chr19	-0.36
SIPA1L3	16186	chr19:43105647-43106125	intra_enh	43105647	43106125	chr19	-0.30
SIPA1L3	20824	chr19:43110185-43110864	intra_enh	43110185	43110864	chr19	-0.34
SIPA1L3	44164	chr19:43133740-43133987	intra_enh	43133740	43133987	chr19	-0.47
SIPA1L3	52342	chr19:43141801-43142283	intra_enh	43141801	43142283	chr19	-0.50
SIPA1L3	52886	chr19:43142455-43142717	intra_enh	43142455	43142717	chr19	-0.74
SIPA1L3	66808	chr19:43156353-43156664	intra_enh	43156353	43156664	chr19	-0.68
SIPA1L3	67830	chr19:43156972-43158089	intra_enh	43156972	43158089	chr19	-0.52
SIPA1L3	70960	chr19:43160237-43161083	intra_enh	43160237	43161083	chr19	-0.78
SIPA1L3	80174	chr19:43169789-43169960	intra_enh	43169789	43169960	chr19	-0.43
SIPA1L3	102634	chr19:43192278-43192391	intra_enh	43192278	43192391	chr19	-0.34
DPF1	144020	chr19:43262400-43263019	intra_enh	43262400	43263019	chr19	-0.88
MAP4K1	34100	chr19:43766297-43766536	intra_enh	43766297	43766536	chr19	-0.82
PRX	3362	chr19:45607617-45607882	intra_enh	45607617	45607882	chr19	-0.70
BLVRB	3744	chr19:45659644-45659999	intra_enh	45659644	45659999	chr19	-0.96
EGLN2	6762	chr19:45989734-45990513	intra_enh	45989734	45990513	chr19	-0.95
CEACAM21	12412	chr19:46761902-46762015	intra_enh	46761902	46762015	chr19	-0.54
POU2F2	16816	chr19:47311149-47312151	intra_enh	47311149	47312151	chr19	-0.69
MIR4323	2530	chr19:47331976-47332095	intra_enh	47331976	47332095	chr19	-0.80
CXCL17	37974	chr19:47676840-47677061	intra_enh	47676840	47677061	chr19	-0.48
PLIN3	3914	chr19:4814779-4814952	intra_enh	4814779	4814952	chr19	-0.76
ZNF428	5018	chr19:48820827-48820916	intra_enh	48820827	48820916	chr19	-0.57
TOMM40	13917	chr19:50072290-50072508	intra_enh	50072290	50072508	chr19	-0.96
RELB	5634	chr19:50202121-50202239	intra_enh	50202121	50202239	chr19	-0.61
RELB	14418	chr19:50210852-50211076	intra_enh	50210852	50211076	chr19	-0.90
CLASRP	2372	chr19:50236405-50236610	intra_enh	50236405	50236610	chr19	-0.31
PPP1R37	25415	chr19:50313446-50313924	intra_enh	50313446	50313924	chr19	-0.29
NKPD1	29308	chr19:50325826-50326054	intra_enh	50325826	50326054	chr19	-0.84
ERCC1	3330	chr19:50615280-50615379	intra_enh	50615280	50615379	chr19	-0.65
VASP	7610	chr19:50709959-50710314	intra_enh	50709959	50710314	chr19	-0.29
VASP	36554	chr19:50738881-50739280	intra_enh	50738881	50739280	chr19	-0.57
OPA3	21902	chr19:50757806-50758315	intra_enh	50757806	50758315	chr19	-0.39
OPA3	20345	chr19:50759341-50759893	intra_enh	50759341	50759893	chr19	-0.66
GPR4	3656	chr19:50793323-50793978	intra_enh	50793323	50793978	chr19	-0.38
DMWD	6580	chr19:50994401-50994559	intra_enh	50994401	50994559	chr19	-0.49

PNMAL2	8103	chr19:51682783-51683031	intra_enh	51682783	51683031	chr19	-0.88
ARHGAP35	16742	chr19:52130193-52130834	intra_enh	52130193	52130834	chr19	-0.71
PTPRS	63856	chr19:5227845-5228072	intra_enh	5227845	5228072	chr19	-0.77
PTPRS	63525	chr19:5228236-5228342	intra_enh	5228236	5228342	chr19	-0.94
SAE1	2154	chr19:52327999-52328217	intra_enh	52327999	52328217	chr19	-0.59
PTPRS	47228	chr19:5244438-5244734	intra_enh	5244438	5244734	chr19	-0.96
DHX34	2280	chr19:52546594-52546717	intra_enh	52546594	52546717	chr19	-0.82
DHX34	2602	chr19:52546906-52547050	intra_enh	52546906	52547050	chr19	-0.80
DHX34	2884	chr19:52547169-52547351	intra_enh	52547169	52547351	chr19	-0.91
C19orf68	15429	chr19:53381061-53381317	intra_enh	53381061	53381317	chr19	-0.81
LMTK3	20461	chr19:53687684-53687910	intra_enh	53687684	53687910	chr19	-0.51
SULT2B1	13467	chr19:53784206-53784336	intra_enh	53784206	53784336	chr19	-0.59
CA11	3462	chr19:53844628-53844825	intra_enh	53844628	53844825	chr19	-0.30
RASIP1	2105	chr19:53933572-53933782	intra_enh	53933572	53933782	chr19	-0.39
FTL	5980	chr19:54166291-54166420	intra_enh	54166291	54166420	chr19	-0.48
SNRNP70	2214	chr19:54282338-54282507	intra_enh	54282338	54282507	chr19	-0.45
TRPM4	47560	chr19:54400189-54400582	intra_enh	54400189	54400582	chr19	-0.97
SLC17A7	5266	chr19:54631264-54631445	intra_enh	54631264	54631445	chr19	-0.53
ATF5	3063	chr19:55120508-55120906	intra_enh	55120508	55120906	chr19	-0.40
SAFB2	2353	chr19:5571504-5571666	intra_enh	5571504	5571666	chr19	-0.53
C19orf81	29914	chr19:55874277-55874576	intra_enh	55874277	55874576	chr19	-0.96
MIR935	4515	chr19:59172802-59172912	intra_enh	59172802	59172912	chr19	-0.47
TNNT1	14232	chr19:60338113-60338490	intra_enh	60338113	60338490	chr19	-0.92
TNNI3	2832	chr19:60363675-60363814	intra_enh	60363675	60363814	chr19	-0.79
NLRP11	18852	chr19:61058436-61059149	intra_enh	61058436	61059149	chr19	-0.89
A1BG-AS1	3372	chr19:63551537-63552010	intra_enh	63551537	63552010	chr19	-0.39
VAV1	27330	chr19:6750873-6751142	intra_enh	6750873	6751142	chr19	-0.54
INSR	110658	chr19:7133977-7134732	intra_enh	7133977	7134732	chr19	-0.62
INSR	50082	chr19:7194585-7195275	intra_enh	7194585	7195275	chr19	-0.99
ARHGEF18	12478	chr19:7378426-7378526	intra_enh	7378426	7378526	chr19	-0.61
ARHGEF18	13407	chr19:7379337-7379473	intra_enh	7379337	7379473	chr19	-0.54
EVI5L	12046	chr19:7829293-7829568	intra_enh	7829293	7829568	chr19	-0.40
RNU6-2	5575	chr19:849983-850131	intra_enh	849983	850131	chr19	-0.55
R3HDM4	6546	chr19:857639-857720	intra_enh	857639	857720	chr19	-0.55
CYS1	8588	chr2:10129323-10129482	intra_enh	10129323	10129482	chr2	-0.89
CYS1	7828	chr2:10130078-10130245	intra_enh	10130078	10130245	chr2	-0.76
MAP4K4	60184	chr2:101741022-101741028	intra_enh	101741022	101741283	chr2	-0.54
HPCAL1	5488	chr2:10382145-10382354	intra_enh	10382145	10382354	chr2	-0.80
LINC01159	66096	chr2:104921484-104921688	intra_enh	104921484	104921681	chr2	-0.84
NCK2	3071	chr2:105730833-105731200	intra_enh	105730833	105731209	chr2	-0.87
NCK2	5317	chr2:105733150-105733388	intra_enh	105733150	105733384	chr2	-0.88
NCK2	32646	chr2:105760545-105760644	intra_enh	105760545	105760647	chr2	-0.65
NCK2	43118	chr2:105770838-105771299	intra_enh	105770838	105771297	chr2	-0.73
NCK2	45115	chr2:105772880-105773255	intra_enh	105772880	105773250	chr2	-0.78
NCK2	23874	chr2:105810646-105810877	intra_enh	105810646	105810874	chr2	-0.91
LIMS1	2188	chr2:108601776-108602111	intra_enh	108601776	108602111	chr2	-0.39
CCDC138	9836	chr2:108759732-108759899	intra_enh	108759732	108759897	chr2	-0.30
ACOXL	15654	chr2:111222002-11122254	intra_enh	111222002	111222546	chr2	-0.82
ACOXL	16467	chr2:111222901-11122327	intra_enh	111222901	111223273	chr2	-0.81
ACOXL	79518	chr2:111286058-11128621	intra_enh	111286058	111286217	chr2	-0.43
LOC400997	175370	chr2:111414173-11141436	intra_enh	111414173	111414360	chr2	-0.89
LOC400997	121492	chr2:111468082-11146820	intra_enh	111468082	111468205	chr2	-0.53
LOC400997	121174	chr2:111468355-11146856	intra_enh	111468355	111468568	chr2	-0.69
LOC400997	43753	chr2:111545617-11154614	intra_enh	111545617	111546149	chr2	-0.86
BCL2L11	12417	chr2:111606725-11160802	intra_enh	111606725	111608029	chr2	-0.38

POLR1B	2836	chr2:113018551-11301928	intra_enh	113018551	113019285	chr2	-0.43
PAX8	5923	chr2:113746936-11374715	intra_enh	113746936	113747154	chr2	-0.28
ROCK2	4420	chr2:11397651-11397832	intra_enh	11397651	11397832	chr2	-0.36
ROCK2	3243	chr2:11398704-11399134	intra_enh	11398704	11399134	chr2	-0.66
ACTR3	29226	chr2:114334669-11433483	intra_enh	114334669	114334838	chr2	-0.88
ACTR3	4415	chr2:114359136-11435999	intra_enh	114359136	114359994	chr2	-0.61
LOC101060091	11011	chr2:114375423-11437667	intra_enh	114375423	114376679	chr2	-0.42
LOC101060091	32053	chr2:114396817-11439736	intra_enh	114396817	114397369	chr2	-0.53
LOC101060091	32985	chr2:114397969-11439808	intra_enh	114397969	114398081	chr2	-0.91
CCDC93	10856	chr2:118477270-11847743	intra_enh	118477270	118477438	chr2	-0.79
CCDC93	2268	chr2:118485796-11848608	intra_enh	118485796	118486087	chr2	-0.91
C2orf76	4722	chr2:119835799-11983621	intra_enh	119835799	119836212	chr2	-0.92
LOC100506457	3662	chr2:12068284-12068424	intra_enh	12068284	12068424	chr2	-0.69
LOC100506457	20274	chr2:12084881-12085050	intra_enh	12084881	12085050	chr2	-0.78
LOC100506457	43462	chr2:12107748-12108561	intra_enh	12107748	12108561	chr2	-0.57
TFCP2L1	3404	chr2:121755791-12175589	intra_enh	121755791	121755898	chr2	-0.39
MIR3681	213849	chr2:12470490-12470620	intra_enh	12470490	12470620	chr2	-0.28
BIN1	20170	chr2:127560971-12756143	intra_enh	127560971	127561438	chr2	-0.69
MYO7B	39998	chr2:128049704-12804998	intra_enh	128049704	128049983	chr2	-0.87
GPR17	24852	chr2:128094882-12809522	intra_enh	128094882	128095229	chr2	-0.82
SFT2D3	49020	chr2:128224010-12822416	intra_enh	128224010	128224163	chr2	-0.29
WDR33	6228	chr2:128278915-12827909	intra_enh	128278915	128279094	chr2	-0.66
POTEKP	12054	chr2:132058683-13205884	intra_enh	132058683	132058842	chr2	-0.54
POTEKP	9305	chr2:132061391-13206163	intra_enh	132061391	132061631	chr2	-0.73
POTEKP	8416	chr2:132061997-13206280	intra_enh	132061997	132062802	chr2	-0.65
MGAT5	154248	chr2:134882257-13488283	intra_enh	134882257	134882834	chr2	-0.66
CCNT2	24831	chr2:135417613-13541776	intra_enh	135417613	135417769	chr2	-0.78
RAB3GAP1	4687	chr2:135530763-13553121	intra_enh	135530763	135531219	chr2	-0.78
R3HDM1	2866	chr2:136007938-13600878	intra_enh	136007938	136008781	chr2	-0.64
R3HDM1	4284	chr2:136064032-13606525	intra_enh	136064032	136065259	chr2	-0.95
DARS	15018	chr2:136474621-13647486	intra_enh	136474621	136474863	chr2	-0.43
DARS	20326	chr2:136479787-13648031	intra_enh	136479787	136480314	chr2	-0.83
ARHGAP15	24300	chr2:143627588-14362774	intra_enh	143627588	143627748	chr2	-0.55
ARHGAP15	129424	chr2:143732677-14373290	intra_enh	143732677	143732907	chr2	-0.70
ARHGAP15	130398	chr2:143733684-14373384	intra_enh	143733684	143733848	chr2	-0.69
GTDC1	11708	chr2:144794745-14479498	intra_enh	144794745	144794984	chr2	-0.52
LINC01412	26434	chr2:145022242-14502243	intra_enh	145022242	145022435	chr2	-0.70
LINC01412	27088	chr2:145022871-14502311	intra_enh	145022871	145023114	chr2	-0.88
LINC01412	40526	chr2:145036353-14503650	intra_enh	145036353	145036506	chr2	-0.70
TEX41	11056	chr2:145152938-14515317	intra_enh	145152938	145153179	chr2	-0.34
TEX41	19040	chr2:145160750-14516133	intra_enh	145160750	145161333	chr2	-0.58
TEX41	34376	chr2:145176241-14517651	intra_enh	145176241	145176516	chr2	-0.31
TEX41	326487	chr2:145468451-14546852	intra_enh	145468451	145468527	chr2	-0.28
TEX41	331755	chr2:145473532-14547398	intra_enh	145473532	145473982	chr2	-0.83
EPC2	8544	chr2:149127313-14912783	intra_enh	149127313	149127832	chr2	-0.48
CYTIP	10128	chr2:157998666-15799877	intra_enh	157998666	157998779	chr2	-0.53
PKP4	31945	chr2:159053529-15905380	intra_enh	159053529	159053801	chr2	-0.96
DAPL1	155076	chr2:159204842-15920515	intra_enh	159204842	159205155	chr2	-0.81
ITGB6	55972	chr2:160708979-16070921	intra_enh	160708979	160709216	chr2	-0.91
LOC100505984	57002	chr2:160893464-16089384	intra_enh	160893464	160893843	chr2	-0.88
MIR4785	13469	chr2:160958710-16095963	intra_enh	160958710	160959632	chr2	-0.91
MIR4785	4229	chr2:160967893-16096892	intra_enh	160967893	160968929	chr2	-0.94
MIR4785	21406	chr2:160993974-16099411	intra_enh	160993974	160994118	chr2	-0.40
TANK	10346	chr2:161735338-16173572	intra_enh	161735338	161735723	chr2	-0.89
SNORA70F	50190	chr2:165302634-16530281	intra_enh	165302634	165302813	chr2	-0.89

SLC38A11	45104	chr2:165474783-16547557	intra_enh	165474783	165475573	chr2	-0.97
SCN1A	21190	chr2:166692641-16669275	intra_enh	166692641	166692756	chr2	-0.72
B3GALT1	194814	chr2:168577840-16857864	intra_enh	168577840	168578641	chr2	-0.91
LOC101929753	13988	chr2:170901660-17090176	intra_enh	170901660	170901765	chr2	-0.76
GORASP2	3822	chr2:171497046-17149715	intra_enh	171497046	171497159	chr2	-0.41
TLK1	14140	chr2:171711296-17171173	intra_enh	171711296	171711737	chr2	-0.76
TLK1	7382	chr2:171718071-17171847	intra_enh	171718071	171718478	chr2	-0.82
TLK1	2624	chr2:171728052-17172850	intra_enh	171728052	171728509	chr2	-0.67
DCAF17	96205	chr2:171902601-17190300	intra_enh	171902601	171903001	chr2	-0.79
DCAF17	92022	chr2:171906768-17190719	intra_enh	171906768	171907199	chr2	-0.70
DCAF17	89769	chr2:171908354-17191012	intra_enh	171908354	171910120	chr2	-0.73
DCAF17	86917	chr2:171911538-17191264	intra_enh	171911538	171912640	chr2	-0.46
DCAF17	44592	chr2:171954344-17195448	intra_enh	171954344	171954484	chr2	-0.77
DCAF17	40134	chr2:171958792-17195895	intra_enh	171958792	171958952	chr2	-0.61
DCAF17	28056	chr2:171970897-17197100	intra_enh	171970897	171971003	chr2	-0.56
SP3	22573	chr2:174514570-17451467	intra_enh	174514570	174514672	chr2	-0.40
SP3	12236	chr2:174524912-17452500	intra_enh	174524912	174525004	chr2	-0.76
SP3	5416	chr2:174531272-17453228	intra_enh	174531272	174532284	chr2	-0.73
GPR155	36486	chr2:175023465-17502368	intra_enh	175023465	175023687	chr2	-0.70
VSNL1	105890	chr2:17691061-17691290	intra_enh	17691061	17691290	chr2	-0.29
MIR6512	18818	chr2:177905569-17790577	intra_enh	177905569	177905778	chr2	-0.65
TTC30A	10781	chr2:178202656-17820278	intra_enh	178202656	178202786	chr2	-0.67
TTC30A	14364	chr2:178206206-17820640	intra_enh	178206206	178206403	chr2	-0.68
CCDC141	19130	chr2:179603786-17960401	intra_enh	179603786	179604017	chr2	-0.68
PPP1R1C	7283	chr2:182565796-18256635	intra_enh	182565796	182566358	chr2	-0.33
ZNF804A	135662	chr2:185306722-18530727	intra_enh	185306722	185307275	chr2	-0.76
ZC3H15	5178	chr2:187064242-18706436	intra_enh	187064242	187064369	chr2	-0.60
ZC3H15	5466	chr2:187064539-18706464	intra_enh	187064539	187064648	chr2	-0.72
ASNSD1	2322	chr2:190236632-19023674	intra_enh	190236632	190236747	chr2	-0.51
C2orf88	7510	chr2:190730675-19073077	intra_enh	190730675	190730778	chr2	-0.37
HIBCH	3230	chr2:190889703-19088986	intra_enh	190889703	190889868	chr2	-0.64
MFSD6	7562	chr2:190988796-19098897	intra_enh	190988796	190988976	chr2	-0.44
MFSD6	56960	chr2:191037969-19103859	intra_enh	191037969	191038598	chr2	-0.86
MFSD6	59772	chr2:191040841-19104135	intra_enh	191040841	191041352	chr2	-0.28
STK17B	12482	chr2:196732022-19673217	intra_enh	196732022	196732177	chr2	-0.90
LOC101927482	11224	chr2:196821636-19682190	intra_enh	196821636	196821900	chr2	-0.70
LOC101927482	10252	chr2:196843084-19684340	intra_enh	196843084	196843405	chr2	-0.68
LOC101927482	12796	chr2:196845722-19684585	intra_enh	196845722	196845854	chr2	-0.91
ANKRD44-IT1	164181	chr2:197710927-19771168	intra_enh	197710927	197711687	chr2	-0.63
ANKRD44-IT1	163406	chr2:197711925-19771223	intra_enh	197711925	197712238	chr2	-0.52
ANKRD44-IT1	156219	chr2:197718931-19771960	intra_enh	197718931	197719607	chr2	-0.74
ANKRD44-IT1	111080	chr2:197764323-19776449	intra_enh	197764323	197764493	chr2	-0.78
ANKRD44-IT1	110676	chr2:197764727-19776489	intra_enh	197764727	197764896	chr2	-0.56
ANKRD44-IT1	27973	chr2:197847388-19784764	intra_enh	197847388	197847642	chr2	-0.96
SF3B1	8378	chr2:197999582-19799969	intra_enh	197999582	197999695	chr2	-0.76
SF3B1	7670	chr2:198000296-19800039	intra_enh	198000296	198000395	chr2	-0.55
LOC101927619	60510	chr2:198887473-19888763	intra_enh	198887473	198887638	chr2	-0.83
LOC101927619	48382	chr2:198899331-19890003	intra_enh	198899331	198900037	chr2	-0.97
TTC32	4382	chr2:19960770-19960919	intra_enh	19960770	19960919	chr2	-0.73
SATB2	67420	chr2:199963525-19996376	intra_enh	199963525	199963764	chr2	-0.59
SATB2	5222	chr2:200025282-20002640	intra_enh	200025282	200026402	chr2	-0.38
FTCDNL1	72950	chr2:200351025-20035136	intra_enh	200351025	200351360	chr2	-0.86
SPATS2L	74916	chr2:200956644-20095702	intra_enh	200956644	200957021	chr2	-0.74
KCTD18	58378	chr2:201024534-20102478	intra_enh	201024534	201024786	chr2	-0.82
KCTD18	53975	chr2:201028910-20102921	intra_enh	201028910	201029216	chr2	-0.87

KCTD18	46380	chr2:201036560-20103675	intra_enh	201036560	201036756	chr2	-0.85
AOX1	31994	chr2:201190916-20119102	intra_enh	201190916	201191021	chr2	-0.69
AOX2P	7256	chr2:201275664-20127622	intra_enh	201275664	201276227	chr2	-0.58
AOX2P	10383	chr2:201279034-20127911	intra_enh	201279034	201279112	chr2	-0.68
TRAK2	37252	chr2:201986822-20198780	intra_enh	201986822	201987803	chr2	-0.84
MPP4	35312	chr2:202306764-20230718	intra_enh	202306764	202307183	chr2	-0.95
MPP4	35933	chr2:202307445-20230774	intra_enh	202307445	202307745	chr2	-0.77
SNORD70	4538	chr2:202844742-20284497	intra_enh	202844742	202844979	chr2	-0.78
SNORD70	3789	chr2:202845437-20284578	intra_enh	202845437	202845781	chr2	-0.81
SNORD70	3124	chr2:202846172-20284637	intra_enh	202846172	202846377	chr2	-0.82
BMPR2	4046	chr2:202953162-20295351	intra_enh	202953162	202953519	chr2	-0.97
BMPR2	8802	chr2:202957937-20295825	intra_enh	202957937	202958254	chr2	-0.90
FAM117B	34394	chr2:203242054-20324302	intra_enh	203242054	203243022	chr2	-0.36
ICA1L	78492	chr2:203323587-20332383	intra_enh	203323587	203323833	chr2	-0.79
NBEAL1	2314	chr2:203589997-20359032	intra_enh	203589997	203590322	chr2	-0.59
NBEAL1	3472	chr2:203591037-20359159	intra_enh	203591037	203591599	chr2	-0.50
GPR1	27417	chr2:206818311-20681855	intra_enh	206818311	206818555	chr2	-0.60
HS1BP3	18150	chr2:20696099-20696292	intra_enh	20696099	20696292	chr2	-0.83
GDF7	32884	chr2:20762568-20763007	intra_enh	20762568	20763007	chr2	-0.83
GDF7	70973	chr2:20800713-20801041	intra_enh	20800713	20801041	chr2	-0.96
C2orf43	78134	chr2:20807876-20808600	intra_enh	20807876	20808600	chr2	-0.84
CREB1	3283	chr2:208105988-20810629	intra_enh	208105988	208106298	chr2	-0.47
CREB1	3968	chr2:208106430-20810722	intra_enh	208106430	208107225	chr2	-0.72
CCNYL1	14874	chr2:208299142-20829962	intra_enh	208299142	208299622	chr2	-0.65
LOC101928103	92348	chr2:215475189-21547590	intra_enh	215475189	215475900	chr2	-0.88
LINC00607	11958	chr2:216404389-21640470	intra_enh	216404389	216404702	chr2	-0.92
LINC00607	2504	chr2:216413912-21641408	intra_enh	216413912	216414088	chr2	-0.88
TMEM169	2759	chr2:216657241-21665794	intra_enh	216657241	216657941	chr2	-0.89
LINC01280	3420	chr2:217176390-21717658	intra_enh	217176390	217176581	chr2	-0.47
IGFBP5	13066	chr2:217255384-21725552	intra_enh	217255384	217255520	chr2	-0.63
ARPC2	7698	chr2:218798028-21879809	intra_enh	218798028	218798095	chr2	-0.64
PNKD	2650	chr2:218845924-21884609	intra_enh	218845924	218846093	chr2	-0.48
TMBIM1	8742	chr2:218874192-21887434	intra_enh	218874192	218874341	chr2	-0.86
FARSB	2826	chr2:223226170-22322632	intra_enh	223226170	223226323	chr2	-0.58
ACSL3	49681	chr2:223483574-22348373	intra_enh	223483574	223483736	chr2	-0.87
AP1S3	36433	chr2:224374059-22437420	intra_enh	224374059	224374203	chr2	-0.50
AP1S3	7602	chr2:224402875-22440305	intra_enh	224402875	224403050	chr2	-0.75
CUL3	6760	chr2:225151526-22515167	intra_enh	225151526	225151671	chr2	-0.41
DOCK10	24541	chr2:225495093-22549587	intra_enh	225495093	225495877	chr2	-0.79
RHBDD1	81016	chr2:227489147-22749071	intra_enh	227489147	227490713	chr2	-0.93
TRIP12	10816	chr2:230483983-23048432	intra_enh	230483983	230484326	chr2	-0.28
SP140	32279	chr2:230830803-23083113	intra_enh	230830803	230831131	chr2	-0.36
SP100	23159	chr2:231012581-23101316	intra_enh	231012581	231013165	chr2	-0.73
SP100	24816	chr2:231014473-23101458	intra_enh	231014473	231014587	chr2	-0.32
CAB39	8291	chr2:231294444-23129515	intra_enh	231294444	231295150	chr2	-0.77
CAB39	9102	chr2:231295400-23129581	intra_enh	231295400	231295815	chr2	-0.81
DIS3L2	176254	chr2:232710439-23271114	intra_enh	232710439	232711140	chr2	-0.73
CHRND	6608	chr2:233105615-23310582	intra_enh	233105615	233105824	chr2	-0.78
INPP5D	42006	chr2:233674794-23367505	intra_enh	233674794	233675057	chr2	-0.47
ATG16L1	2302	chr2:233827157-23382735	intra_enh	233827157	233827355	chr2	-0.78
USP40	38642	chr2:234095895-23409603	intra_enh	234095895	234096033	chr2	-0.65
USP40	22567	chr2:234111955-23411212	intra_enh	234111955	234112123	chr2	-0.91
MIR6811	3962	chr2:238088163-23808838	intra_enh	238088163	238088385	chr2	-0.75
MIR6811	18751	chr2:238102752-23810337	intra_enh	238102752	238103374	chr2	-0.77
RAMP1	39162	chr2:238471725-23847244	intra_enh	238471725	238472447	chr2	-0.93

RAMP1	45666	chr2:238478494-23847868	intra_enh	238478494	238478687	chr2	-0.90
UBE2F	8632	chr2:238550725-23855088	intra_enh	238550725	238550884	chr2	-0.29
UBE2F	9004	chr2:238551083-23855127	intra_enh	238551083	238551270	chr2	-0.48
MIR4269	45790	chr2:239846109-23984649	intra_enh	239846109	239846496	chr2	-0.70
MIR4269	40748	chr2:239851283-23985140	intra_enh	239851283	239851404	chr2	-0.78
MIR4269	13691	chr2:239878253-23987854	intra_enh	239878253	239878549	chr2	-0.89
3-Sep	4110	chr2:241908024-24190809	intra_enh	241908024	241908092	chr2	-0.36
FAM228A	40022	chr2:24291303-24291690	intra_enh	24291303	24291690	chr2	-0.96
DNMT3A	46028	chr2:25464935-25465048	intra_enh	25464935	25465048	chr2	-0.41
DTNB	152031	chr2:25574235-25574895	intra_enh	25574235	25574895	chr2	-0.98
DTNB	8948	chr2:25740994-25741151	intra_enh	25740994	25741151	chr2	-0.50
ASXL2	83546	chr2:25871163-25871377	intra_enh	25871163	25871377	chr2	-0.79
RAB10	34460	chr2:26144632-26144753	intra_enh	26144632	26144753	chr2	-0.74
RAB10	34930	chr2:26144963-26145360	intra_enh	26144963	26145360	chr2	-0.69
SUPT7L	2108	chr2:27742272-27742369	intra_enh	27742272	27742369	chr2	-0.71
PPP1CB	3948	chr2:28831894-28832257	intra_enh	28831894	28832257	chr2	-0.54
PPP1CB	19051	chr2:28847022-28847336	intra_enh	28847022	28847336	chr2	-0.91
SPAST	16910	chr2:32158897-32159288	intra_enh	32158897	32159288	chr2	-0.82
BIRC6	3268	chr2:32438514-32439218	intra_enh	32438514	32439218	chr2	-0.25
LINC00486	13292	chr2:32917237-32917372	intra_enh	32917237	32917372	chr2	-0.68
LOC100271832	21430	chr2:32983981-32984551	intra_enh	32983981	32984551	chr2	-0.78
LOC100271832	17290	chr2:32988321-32988490	intra_enh	32988321	32988490	chr2	-0.69
LTBP1	5738	chr2:33020009-33020259	intra_enh	33020009	33020259	chr2	-0.82
LTBP1	4191	chr2:33029160-33030966	intra_enh	33029160	33030966	chr2	-0.33
LTBP1	91050	chr2:33116745-33117100	intra_enh	33116745	33117100	chr2	-0.51
LTBP1	91662	chr2:33117277-33117791	intra_enh	33117277	33117791	chr2	-0.78
LTBP1	61072	chr2:33151943-33152244	intra_enh	33151943	33152244	chr2	-0.84
LTBP1	59384	chr2:33153720-33153843	intra_enh	33153720	33153843	chr2	-0.86
RASGRP3	16600	chr2:33575773-33575915	intra_enh	33575773	33575915	chr2	-0.55
RASGRP3	16298	chr2:33576076-33576215	intra_enh	33576076	33576215	chr2	-0.45
RASGRP3	14742	chr2:33607068-33607304	intra_enh	33607068	33607304	chr2	-0.49
TRAPPC12	24094	chr2:3386310-3386783	intra_enh	3386310	3386783	chr2	-0.41
MYADML	56834	chr2:33863369-33863876	intra_enh	33863369	33863876	chr2	-0.97
CRIM1	105190	chr2:36541802-36542321	intra_enh	36541802	36542321	chr2	-0.96
NDUFAF7	31196	chr2:37343216-37343729	intra_enh	37343216	37343729	chr2	-0.51
PRKD3	11680	chr2:37385787-37386304	intra_enh	37385787	37386304	chr2	-0.28
PRKD3	11202	chr2:37386449-37386600	intra_enh	37386449	37386600	chr2	-0.38
QPCT	2908	chr2:37427954-37428373	intra_enh	37427954	37428373	chr2	-0.68
QPCT	13078	chr2:37438166-37438502	intra_enh	37438166	37438502	chr2	-0.94
HNRNPLL	21488	chr2:38662077-38662311	intra_enh	38662077	38662311	chr2	-0.45
MAP4K3	59764	chr2:39458098-39458289	intra_enh	39458098	39458289	chr2	-0.51
MAP4K3	59390	chr2:39458474-39458663	intra_enh	39458474	39458663	chr2	-0.56
MAP4K3	34000	chr2:39483841-39484075	intra_enh	39483841	39484075	chr2	-0.73
MAP4K3	28432	chr2:39489333-39489719	intra_enh	39489333	39489719	chr2	-0.52
LOC728730	93134	chr2:39610988-39611399	intra_enh	39610988	39611399	chr2	-0.68
SLC8A1	71246	chr2:40439482-40439923	intra_enh	40439482	40439923	chr2	-0.85
SLC8A1	22838	chr2:40569978-40570506	intra_enh	40569978	40570506	chr2	-0.80
SLC8A1	4932	chr2:40588078-40588218	intra_enh	40588078	40588218	chr2	-0.33
LOC102723824	13768	chr2:42264538-42264751	intra_enh	42264538	42264751	chr2	-0.89
MTA3	8081	chr2:42640518-42640696	intra_enh	42640518	42640696	chr2	-0.95
MTA3	31818	chr2:42680843-42681114	intra_enh	42680843	42681114	chr2	-0.62
LINC01126	6606	chr2:43314175-43314741	intra_enh	43314175	43314741	chr2	-0.70
THADA	169838	chr2:43506309-43507251	intra_enh	43506309	43507251	chr2	-0.53
THADA	169064	chr2:43507463-43507645	intra_enh	43507463	43507645	chr2	-0.63
THADA	134288	chr2:43542275-43542384	intra_enh	43542275	43542384	chr2	-0.72

PRKCE	12912	chr2:45745284-45745633	intra_enh	45745284	45745633	chr2	-0.56
PRKCE	258009	chr2:45990264-45990846	intra_enh	45990264	45990846	chr2	-0.43
FBXO11	21229	chr2:47948053-47948213	intra_enh	47948053	47948213	chr2	-0.81
FBXO11	3811	chr2:47972819-47973527	intra_enh	47972819	47973527	chr2	-0.86
FBXO11	5310	chr2:47974509-47974835	intra_enh	47974509	47974835	chr2	-0.68
FBXO11	6795	chr2:47976101-47976213	intra_enh	47976101	47976213	chr2	-0.29
FBXO11	6126	chr2:47980172-47980447	intra_enh	47980172	47980447	chr2	-0.62
FBXO11	5572	chr2:47980601-47981126	intra_enh	47980601	47981126	chr2	-0.44
FBXO11	3938	chr2:47982418-47982577	intra_enh	47982418	47982577	chr2	-0.73
FOXN2	5404	chr2:48400556-48400847	intra_enh	48400556	48400847	chr2	-0.84
FOXN2	13601	chr2:48408812-48408986	intra_enh	48408812	48408986	chr2	-0.51
FOXN2	29553	chr2:48424485-48425217	intra_enh	48424485	48425217	chr2	-0.64
FOXN2	38477	chr2:48433411-48434139	intra_enh	48433411	48434139	chr2	-0.85
FOXN2	42368	chr2:48437282-48438051	intra_enh	48437282	48438051	chr2	-0.42
PPP1R21	3770	chr2:48525055-48525305	intra_enh	48525055	48525305	chr2	-0.64
NRXN1	133222	chr2:50561473-50561768	intra_enh	50561473	50561768	chr2	-0.96
NRXN1	144643	chr2:50572883-50573199	intra_enh	50572883	50573199	chr2	-0.67
NRXN1	212064	chr2:50900644-50901583	intra_enh	50900644	50901583	chr2	-0.94
NRXN1	168824	chr2:50943932-50944776	intra_enh	50943932	50944776	chr2	-0.99
RPL23AP32	35366	chr2:54574418-54574574	intra_enh	54574418	54574574	chr2	-0.80
RPL23AP32	31860	chr2:54577888-54578115	intra_enh	54577888	54578115	chr2	-0.95
SPTBN1	4594	chr2:54643527-54643730	intra_enh	54643527	54643730	chr2	-0.84
SPTBN1	24705	chr2:54663324-54664154	intra_enh	54663324	54664154	chr2	-0.91
SPTBN1	38910	chr2:54677894-54677993	intra_enh	54677894	54677993	chr2	-0.84
EML6	34729	chr2:54840327-54840435	intra_enh	54840327	54840435	chr2	-0.72
EML6	35622	chr2:54840893-54841656	intra_enh	54840893	54841656	chr2	-0.67
EML6	113571	chr2:54919165-54919281	intra_enh	54919165	54919281	chr2	-0.87
RTN4	15735	chr2:55114002-55114188	intra_enh	55114002	55114188	chr2	-0.53
RTN4	3106	chr2:55126600-55126848	intra_enh	55126600	55126848	chr2	-0.85
RTN4	2498	chr2:55127037-55127628	intra_enh	55127037	55127628	chr2	-0.77
MIR4432	81660	chr2:60549644-60549845	intra_enh	60549644	60549845	chr2	-0.31
BCL11A	12158	chr2:60621772-60622188	intra_enh	60621772	60622188	chr2	-0.94
BCL11A	11062	chr2:60622994-60623159	intra_enh	60622994	60623159	chr2	-0.81
LINC01185	7726	chr2:60954089-60954366	intra_enh	60954089	60954366	chr2	-0.94
REL	6842	chr2:60968882-60969067	intra_enh	60968882	60969067	chr2	-0.25
REL	7234	chr2:60969238-60969495	intra_enh	60969238	60969495	chr2	-0.49
REL	9160	chr2:60970976-60971608	intra_enh	60970976	60971608	chr2	-0.35
SNORA70B	11244	chr2:61508941-61509579	intra_enh	61508941	61509579	chr2	-0.72
SNORA70B	15663	chr2:61513451-61513907	intra_enh	61513451	61513907	chr2	-0.74
USP34	23754	chr2:61527536-61527665	intra_enh	61527536	61527665	chr2	-0.81
USP34	23222	chr2:61527924-61528340	intra_enh	61527924	61528340	chr2	-0.67
USP34	16740	chr2:61534500-61534727	intra_enh	61534500	61534727	chr2	-0.86
USP34	12010	chr2:61539261-61539426	intra_enh	61539261	61539426	chr2	-0.47
USP34	9040	chr2:61542166-61542462	intra_enh	61542166	61542462	chr2	-0.75
COMMD1	105160	chr2:62091238-62091693	intra_enh	62091238	62091693	chr2	-0.86
WDPCP	79664	chr2:63438898-63439065	intra_enh	63438898	63439065	chr2	-0.88
WDPCP	79193	chr2:63439368-63439538	intra_enh	63439368	63439538	chr2	-0.95
PELI1	43017	chr2:64181667-64182519	intra_enh	64181667	64182519	chr2	-0.81
PELI1	40980	chr2:64183824-64184437	intra_enh	64183824	64184437	chr2	-0.89
PELI1	32202	chr2:64192779-64193036	intra_enh	64192779	64193036	chr2	-0.82
PELI1	13462	chr2:64211559-64211736	intra_enh	64211559	64211736	chr2	-0.81
PELI1	5461	chr2:64219427-64219871	intra_enh	64219427	64219871	chr2	-0.64
MIR4434	9072	chr2:64615108-64615335	intra_enh	64615108	64615335	chr2	-0.41
MIR4434	37068	chr2:64643002-64643434	intra_enh	64643002	64643434	chr2	-0.87
SPRED2	16290	chr2:65430002-65432290	intra_enh	65430002	65432290	chr2	-0.26

SPRED2	6212	chr2:65441197-65441252	intra_enh	65441197	65441252	chr2	-0.40
SPRED2	23308	chr2:65489492-65490212	intra_enh	65489492	65490212	chr2	-0.61
PNO1	42674	chr2:68280751-68281614	intra_enh	68280751	68281614	chr2	-0.82
PNO1	43512	chr2:68281729-68282310	intra_enh	68281729	68282310	chr2	-0.81
PPP3R1	27260	chr2:68305795-68305998	intra_enh	68305795	68305998	chr2	-0.68
CNRIP1	24387	chr2:68375992-68376610	intra_enh	68375992	68376610	chr2	-0.89
ARHGAP25	16996	chr2:68832355-68832468	intra_enh	68832355	68832468	chr2	-0.31
GMCL1	2683	chr2:69912916-69913090	intra_enh	69912916	69913090	chr2	-0.72
GMCL1	6694	chr2:69916563-69917464	intra_enh	69916563	69917464	chr2	-0.70
PCBP1-AS1	15776	chr2:70151720-70152032	intra_enh	70151720	70152032	chr2	-0.32
DGUOK	2752	chr2:74010062-74010362	intra_enh	74010062	74010362	chr2	-0.72
TET3	67093	chr2:74133923-74134339	intra_enh	74133923	74134339	chr2	-0.71
SLC4A5	17633	chr2:74377914-74378140	intra_enh	74377914	74378140	chr2	-0.85
DOK1	16916	chr2:74651776-74652092	intra_enh	74651776	74652092	chr2	-0.63
M1AP	28144	chr2:74700450-74700607	intra_enh	74700450	74700607	chr2	-0.49
M1AP	27840	chr2:74700712-74700952	intra_enh	74700712	74700952	chr2	-0.51
LOC100506274	7471	chr2:7486195-7486431	intra_enh	7486195	7486431	chr2	-0.76
LOC100506274	16918	chr2:7495470-7496050	intra_enh	7495470	7496050	chr2	-0.96
LINC00298	81935	chr2:8116264-8116398	intra_enh	8116264	8116398	chr2	-0.55
LINC00299	89321	chr2:8296612-8296746	intra_enh	8296612	8296746	chr2	-0.30
LINC00299	85809	chr2:8299958-8300424	intra_enh	8299958	8300424	chr2	-0.46
LINC00299	61415	chr2:8324342-8324828	intra_enh	8324342	8324828	chr2	-0.46
TRABD2A	34982	chr2:84926621-84927175	intra_enh	84926621	84927175	chr2	-0.94
POLR1A	2328	chr2:86184380-86184545	intra_enh	86184380	86184545	chr2	-0.63
MIR4779	18244	chr2:86255345-86255651	intra_enh	86255345	86255651	chr2	-0.88
MRPL35	26882	chr2:86306893-86307002	intra_enh	86306893	86307002	chr2	-0.53
EIF2AK3	25150	chr2:88682905-88683216	intra_enh	88682905	88683216	chr2	-0.65
EIF2AK3	18115	chr2:88689877-88690313	intra_enh	88689877	88690313	chr2	-0.62
EIF2AK3	16284	chr2:88691790-88692062	intra_enh	88691790	88692062	chr2	-0.47
EIF2AK3	8099	chr2:88700034-88700188	intra_enh	88700034	88700188	chr2	-0.86
ANKRD36BP2	4250	chr2:88850688-88850877	intra_enh	88850688	88850877	chr2	-0.79
KIDINS220	48125	chr2:8943026-8943636	intra_enh	8943026	8943636	chr2	-0.98
IAH1	3550	chr2:9535580-9535761	intra_enh	9535580	9535761	chr2	-0.44
IAH1	5094	chr2:9537065-9537364	intra_enh	9537065	9537364	chr2	-0.89
IAH1	5950	chr2:9537720-9538421	intra_enh	9537720	9538421	chr2	-0.91
ADAM17	17252	chr2:9595650-9596581	intra_enh	9595650	9596581	chr2	-0.48
ADAM17	3230	chr2:9609281-9610995	intra_enh	9609281	9610995	chr2	-0.35
STARD7-AS1	8666	chr2:96229092-96229336	intra_enh	96229092	96229336	chr2	-0.65
SNTG2	28726	chr2:965100-965455	intra_enh	965100	965455	chr2	-0.73
YWHAQ	34444	chr2:9654064-9654319	intra_enh	9654064	9654319	chr2	-0.54
FAM178B	23788	chr2:96992190-96992291	intra_enh	96992190	96992291	chr2	-0.48
ZAP70	16330	chr2:97679959-97680306	intra_enh	97679959	97680306	chr2	-0.53
INPP4A	38381	chr2:98466024-98466242	intra_enh	98466024	98466242	chr2	-0.65
LOC101927070	8186	chr2:98746525-98746690	intra_enh	98746525	98746690	chr2	-0.79
LOC101927070	65509	chr2:98820224-98820382	intra_enh	98820224	98820382	chr2	-0.57
TSGA10	75048	chr2:99049223-99049621	intra_enh	99049223	99049621	chr2	-0.70
REV1	150240	chr2:99622949-99623354	intra_enh	99622949	99623354	chr2	-0.34
REV1	152573	chr2:99625395-99625575	intra_enh	99625395	99625575	chr2	-0.67
REV1	217282	chr2:99689796-99690592	intra_enh	99689796	99690592	chr2	-0.50
REV1	283266	chr2:99756138-99756219	intra_enh	99756138	99756219	chr2	-0.81
AFF3	227430	chr2:99860750-99861345	intra_enh	99860750	99861345	chr2	-0.30
SLX4IP	2326	chr20:10365990-10366562	intra_enh	10365990	10366562	chr20	-0.66
SLX4IP	41122	chr20:10404967-10405177	intra_enh	10404967	10405177	chr20	-0.53
SIRPD	19962	chr20:1466332-1466433	intra_enh	1466332	1466433	chr20	-0.48
RIN2	185208	chr20:19629739-19630174	intra_enh	19629739	19630174	chr20	-0.58

RIN2	179669	chr20:19635430-19635560	intra_enh	19635430	19635560	chr20	-0.72
CFAP61	151456	chr20:20136485-20137002	intra_enh	20136485	20137002	chr20	-0.90
INSM1	33393	chr20:20263207-20263535	intra_enh	20263207	20263535	chr20	-0.54
STK35	22752	chr20:2052950-2053607	intra_enh	2052950	2053607	chr20	-0.52
TGM6	6254	chr20:2315648-2315965	intra_enh	2315648	2315965	chr20	-0.81
GINS1	31590	chr20:25367827-25367996	intra_enh	25367827	25367996	chr20	-0.69
COX4I2	36554	chr20:29725783-29726025	intra_enh	29725783	29726025	chr20	-0.68
BCL2L1	32317	chr20:29741926-29742076	intra_enh	29741926	29742076	chr20	-0.92
BCL2L1	8521	chr20:29765253-29766341	intra_enh	29765253	29766341	chr20	-0.51
BCL2L1	7358	chr20:29766888-29767031	intra_enh	29766888	29767031	chr20	-0.86
HCK	15502	chr20:30119085-30119220	intra_enh	30119085	30119220	chr20	-0.82
CBFA2T2	14076	chr20:31555454-31555873	intra_enh	31555454	31555873	chr20	-0.85
CBFA2T2	14728	chr20:31556149-31556483	intra_enh	31556149	31556483	chr20	-0.96
CBFA2T2	7163	chr20:31606146-31607188	intra_enh	31606146	31607188	chr20	-0.51
CBFA2T2	8470	chr20:31621915-31622684	intra_enh	31621915	31622684	chr20	-0.95
CBFA2T2	10986	chr20:31624771-31624862	intra_enh	31624771	31624862	chr20	-0.83
CBFA2T2	14332	chr20:31627657-31628666	intra_enh	31627657	31628666	chr20	-0.85
ZNF341-AS1	33020	chr20:31829344-31829747	intra_enh	31829344	31829747	chr20	-0.81
CHMP4B	9108	chr20:31871674-31872082	intra_enh	31871674	31872082	chr20	-0.91
CHMP4B	26350	chr20:31888895-31889346	intra_enh	31888895	31889346	chr20	-0.82
RALY-AS1	15332	chr20:32061114-32061217	intra_enh	32061114	32061217	chr20	-0.72
MIR4755	9528	chr20:32110059-32110165	intra_enh	32110059	32110165	chr20	-0.83
EIF2S2	3854	chr20:32159296-32160489	intra_enh	32159296	32160489	chr20	-0.48
CEP250	36657	chr20:33543178-33543408	intra_enh	33543178	33543408	chr20	-0.54
C20orf173	23413	chr20:33557430-33557536	intra_enh	33557430	33557536	chr20	-0.65
CPNE1	5513	chr20:33710653-33710865	intra_enh	33710653	33710865	chr20	-0.62
PHF20	24586	chr20:33847799-33848045	intra_enh	33847799	33848045	chr20	-0.31
CNBD2	24482	chr20:34044311-34044538	intra_enh	34044311	34044538	chr20	-0.89
EPB41L1	21590	chr20:34165520-34165747	intra_enh	34165520	34165747	chr20	-0.86
MYL9	15014	chr20:34618150-34618479	intra_enh	34618150	34618479	chr20	-0.47
DSN1	18889	chr20:34854453-34854613	intra_enh	34854453	34854613	chr20	-0.86
SOGA1	21912	chr20:34899693-34899862	intra_enh	34899693	34899862	chr20	-0.81
SAMHD1	53763	chr20:35067331-35067515	intra_enh	35067331	35067515	chr20	-0.73
MANBAL	6832	chr20:35358188-35358405	intra_enh	35358188	35358405	chr20	-0.82
GFRA4	41948	chr20:3550029-3550166	intra_enh	3550029	3550166	chr20	-0.63
CTNNBL1	51674	chr20:35807111-35807778	intra_enh	35807111	35807778	chr20	-0.59
RPRD1B	2944	chr20:36098236-36098373	intra_enh	36098236	36098373	chr20	-0.31
RPRD1B	3446	chr20:36098722-36098890	intra_enh	36098722	36098890	chr20	-0.49
LBP	7230	chr20:36415401-36415510	intra_enh	36415401	36415510	chr20	-0.71
PPP1R16B	31366	chr20:36898882-36899371	intra_enh	36898882	36899371	chr20	-0.94
PANK2	5990	chr20:3824278-3824626	intra_enh	3824278	3824626	chr20	-0.30
PANK2	9010	chr20:3827389-3827556	intra_enh	3827389	3827556	chr20	-0.82
PANK2	10574	chr20:3828748-3829323	intra_enh	3828748	3829323	chr20	-0.52
PANK2	11692	chr20:3829978-3830329	intra_enh	3829978	3830329	chr20	-0.69
PANK2	12216	chr20:3830607-3830749	intra_enh	3830607	3830749	chr20	-0.83
MIR103A2	10006	chr20:3836086-3836181	intra_enh	3836086	3836181	chr20	-0.64
TOP1	44064	chr20:39134869-39135006	intra_enh	39134869	39135006	chr20	-0.75
TOP1	49452	chr20:39140168-39140484	intra_enh	39140168	39140484	chr20	-0.56
LINC01433	20536	chr20:4101072-4101329	intra_enh	4101072	4101329	chr20	-0.38
MYBL2	9556	chr20:41738465-41738792	intra_enh	41738465	41738792	chr20	-0.91
MYBL2	13392	chr20:41742349-41742578	intra_enh	41742349	41742578	chr20	-0.71
PKIG	5981	chr20:42638534-42638708	intra_enh	42638534	42638708	chr20	-0.45
PKIG	11512	chr20:42656049-42656180	intra_enh	42656049	42656180	chr20	-0.65
YWHAB	10978	chr20:42958434-42958826	intra_enh	42958434	42958826	chr20	-0.82
TOMM34	4839	chr20:43017487-43017891	intra_enh	43017487	43017891	chr20	-0.88

EYA2	5722	chr20:44962099-44962682	intra_enh	44962099	44962682	chr20	-0.86
EYA2	76686	chr20:45033164-45033543	intra_enh	45033164	45033543	chr20	-0.86
EYA2	104286	chr20:45060874-45061035	intra_enh	45060874	45061035	chr20	-0.89
EYA2	108812	chr20:45065110-45065851	intra_enh	45065110	45065851	chr20	-0.92
NCOA3	10904	chr20:45574771-45575050	intra_enh	45574771	45575050	chr20	-0.31
NCOA3	11448	chr20:45575363-45575546	intra_enh	45575363	45575546	chr20	-0.54
NCOA3	35430	chr20:45599320-45599551	intra_enh	45599320	45599551	chr20	-0.59
NCOA3	38976	chr20:45602921-45603044	intra_enh	45602921	45603044	chr20	-0.48
NCOA3	58776	chr20:45622611-45622952	intra_enh	45622611	45622952	chr20	-0.65
NCOA3	61602	chr20:45625529-45625686	intra_enh	45625529	45625686	chr20	-0.49
NCOA3	62732	chr20:45626457-45627019	intra_enh	45626457	45627019	chr20	-0.73
NCOA3	118940	chr20:45682621-45683271	intra_enh	45682621	45683271	chr20	-0.69
SULF2	60706	chr20:45787393-45787626	intra_enh	45787393	45787626	chr20	-0.34
KCNB1	96823	chr20:47435674-47435856	intra_enh	47435674	47435856	chr20	-0.79
PTGIS	33542	chr20:47584431-47584714	intra_enh	47584431	47584714	chr20	-0.94
SLC23A2	82444	chr20:4847460-4847945	intra_enh	4847460	4847945	chr20	-0.47
PTPN1	6445	chr20:48566267-48567151	intra_enh	48566267	48567151	chr20	-0.77
PTPN1	13508	chr20:48573680-48573865	intra_enh	48573680	48573865	chr20	-0.58
PTPN1	29520	chr20:48589708-48589859	intra_enh	48589708	48589859	chr20	-0.91
PTPN1	31526	chr20:48591416-48592164	intra_enh	48591416	48592164	chr20	-0.62
PTPN1	33162	chr20:48593133-48593718	intra_enh	48593133	48593718	chr20	-0.99
PTPN1	36382	chr20:48596469-48596824	intra_enh	48596469	48596824	chr20	-0.30
FAM65C	12444	chr20:48674372-48674465	intra_enh	48674372	48674465	chr20	-0.72
BCAS4	23849	chr20:48868566-48868804	intra_enh	48868566	48868804	chr20	-0.38
BCAS4	42788	chr20:48886983-48888265	intra_enh	48886983	48888265	chr20	-0.69
BCAS4	55432	chr20:48900136-48900400	intra_enh	48900136	48900400	chr20	-0.84
BCAS4	56218	chr20:48900977-48901130	intra_enh	48900977	48901130	chr20	-0.66
ADNP	5896	chr20:48965359-48965905	intra_enh	48965359	48965905	chr20	-0.43
ADNP	6646	chr20:48966211-48966553	intra_enh	48966211	48966553	chr20	-0.30
ADNP-AS1	5515	chr20:48975291-48975531	intra_enh	48975291	48975531	chr20	-0.52
MIR3194	48406	chr20:49454409-49454624	intra_enh	49454409	49454624	chr20	-0.88
MIR3194	17564	chr20:49520149-49520824	intra_enh	49520149	49520824	chr20	-0.89
NFATC2	61424	chr20:49674145-49674260	intra_enh	49674145	49674260	chr20	-0.27
ATP9A	101430	chr20:49716728-49717043	intra_enh	49716728	49717043	chr20	-0.78
ZFP64	19010	chr20:50222712-50223133	intra_enh	50222712	50223133	chr20	-0.87
CDS2	18852	chr20:5074122-5074394	intra_enh	5074122	5074394	chr20	-0.62
TSHZ2	57764	chr20:51079956-51080276	intra_enh	51079956	51080276	chr20	-0.82
TSHZ2	62773	chr20:51084924-51085326	intra_enh	51084924	51085326	chr20	-0.80
TSHZ2	98532	chr20:51120585-51121184	intra_enh	51120585	51121184	chr20	-0.89
TSHZ2	99616	chr20:51135462-51135763	intra_enh	51135462	51135763	chr20	-0.81
TSHZ2	81990	chr20:51153056-51153419	intra_enh	51153056	51153419	chr20	-0.34
TSHZ2	63374	chr20:51171722-51171987	intra_enh	51171722	51171987	chr20	-0.86
GPCPD1	23884	chr20:5515558-5516019	intra_enh	5515558	5516019	chr20	-0.71
STX16-NPEPL1	4258	chr20:56663778-56664166	intra_enh	56663778	56664166	chr20	-0.61
STX16-NPEPL1	4804	chr20:56664351-56664686	intra_enh	56664351	56664686	chr20	-0.49
C20orf196	9832	chr20:5688814-5688935	intra_enh	5688814	5688935	chr20	-0.52
C20orf196	14005	chr20:5692983-5693111	intra_enh	5692983	5693111	chr20	-0.78
C20orf196	14454	chr20:5693322-5693669	intra_enh	5693322	5693669	chr20	-0.86
C20orf196	19015	chr20:5697945-5698169	intra_enh	5697945	5698169	chr20	-0.61
C20orf196	38300	chr20:5717257-5717426	intra_enh	5717257	5717426	chr20	-0.87
C20orf196	43868	chr20:5722673-5723148	intra_enh	5722673	5723148	chr20	-0.93
ZNF831	31514	chr20:57230907-57231056	intra_enh	57230907	57231056	chr20	-0.59
C20orf196	72296	chr20:5751217-5751460	intra_enh	5751217	5751460	chr20	-0.95
TAF4	25862	chr20:60048310-60048491	intra_enh	60048310	60048491	chr20	-0.41
SLCO4A1-AS1	11050	chr20:60757307-60757428	intra_enh	60757307	60757428	chr20	-0.68

DIDO1	2372	chr20:61030494-61030945	intra_enh	61030494	61030945	chr20	-0.35
LIME1	8754	chr20:61829485-61829847	intra_enh	61829485	61829847	chr20	-0.89
SLC2A4RG	7970	chr20:61849487-61849761	intra_enh	61849487	61849761	chr20	-0.44
HAO1	5143	chr20:7863698-7864204	intra_enh	7863698	7864204	chr20	-0.78
TMX4	2397	chr20:7945913-7946081	intra_enh	7945913	7946081	chr20	-0.49
PLCB1	173202	chr20:8234030-8234194	intra_enh	8234030	8234194	chr20	-0.68
PLCB1	289738	chr20:8350381-8350916	intra_enh	8350381	8350916	chr20	-0.93
PLCB1	293893	chr20:8354294-8355312	intra_enh	8354294	8355312	chr20	-0.93
PLCB1	387162	chr20:8447963-8448182	intra_enh	8447963	8448182	chr20	-0.90
PLCB1	392370	chr20:8452993-8453568	intra_enh	8452993	8453568	chr20	-0.89
PLCB4	467154	chr20:8530360-8530731	intra_enh	8530360	8530731	chr20	-0.95
SAMSN1	12047	chr21:14828435-14828575	intra_enh	14828435	14828575	chr21	-0.62
SAMSN1-AS1	14478	chr21:14861733-14862094	intra_enh	14861733	14862094	chr21	-0.73
SAMSN1	6691	chr21:14884229-14884341	intra_enh	14884229	14884341	chr21	-0.76
SAMSN1	19299	chr21:14896562-14897224	intra_enh	14896562	14897224	chr21	-0.66
LOC388813	24925	chr21:14912016-14912734	intra_enh	14912016	14912734	chr21	-0.91
USP25	3286	chr21:16027444-16027555	intra_enh	16027444	16027555	chr21	-0.47
APP	69932	chr21:26364578-26364718	intra_enh	26364578	26364718	chr21	-0.68
APP	69296	chr21:26365046-26365523	intra_enh	26365046	26365523	chr21	-0.25
USP16	2435	chr21:29321033-29321453	intra_enh	29321033	29321453	chr21	-0.85
CCT8	2504	chr21:29365413-29365558	intra_enh	29365413	29365558	chr21	-0.47
MAP3K7CL	5010	chr21:29419585-29419748	intra_enh	29419585	29419748	chr21	-0.71
TIAM1	231974	chr21:31620848-31621529	intra_enh	31620848	31621529	chr21	-0.60
TIAM1	51957	chr21:31801108-31801302	intra_enh	31801108	31801302	chr21	-0.82
TIAM1	51292	chr21:31801771-31801968	intra_enh	31801771	31801968	chr21	-0.90
SCAF4	15128	chr21:32011047-32011301	intra_enh	32011047	32011301	chr21	-0.78
URB1	3112	chr21:32683972-32684172	intra_enh	32683972	32684172	chr21	-0.69
SYNJ1	15792	chr21:33006106-33006555	intra_enh	33006106	33006555	chr21	-0.75
IFNAR1	4280	chr21:33623160-33623565	intra_enh	33623160	33623565	chr21	-0.79
IFNGR2	3584	chr21:33700562-33700746	intra_enh	33700562	33700746	chr21	-0.51
TMEM50B	38557	chr21:33735578-33735680	intra_enh	33735578	33735680	chr21	-0.74
TMEM50B	37779	chr21:33736126-33736688	intra_enh	33736126	33736688	chr21	-0.69
RUNX1-IT1	18629	chr21:35314597-35315333	intra_enh	35314597	35315333	chr21	-0.77
CBR1	7529	chr21:36371398-36371840	intra_enh	36371398	36371840	chr21	-0.33
MORC3	37630	chr21:36576620-36576832	intra_enh	36576620	36576832	chr21	-0.95
CLDN14	27178	chr21:36801349-36801523	intra_enh	36801349	36801523	chr21	-0.88
HLCS	106510	chr21:37154255-37154376	intra_enh	37154255	37154376	chr21	-0.80
HLCS	106186	chr21:37154557-37154722	intra_enh	37154557	37154722	chr21	-0.56
HLCS	3430	chr21:37271432-37271977	intra_enh	37271432	37271977	chr21	-0.60
DYRK1A	5162	chr21:37666769-37667011	intra_enh	37666769	37667011	chr21	-0.68
DYRK1A	5926	chr21:37667572-37667736	intra_enh	37667572	37667736	chr21	-0.58
LOC101928398	40158	chr21:39191153-39191828	intra_enh	39191153	39191828	chr21	-0.80
SH3BGR	9763	chr21:39755257-39755565	intra_enh	39755257	39755565	chr21	-0.81
PRDM15	45946	chr21:42110355-42110712	intra_enh	42110355	42110712	chr21	-0.75
C2CD2	2138	chr21:42221921-42222092	intra_enh	42221921	42222092	chr21	-0.42
UMODL1	3896	chr21:42360427-42360768	intra_enh	42360427	42360768	chr21	-0.91
UMODL1	2464	chr21:42361966-42362094	intra_enh	42361966	42362094	chr21	-0.33
ABCG1	26216	chr21:42539108-42539475	intra_enh	42539108	42539475	chr21	-0.77
TFF1	3516	chr21:42656137-42656260	intra_enh	42656137	42656260	chr21	-0.61
SLC37A1	4248	chr21:42796761-42797354	intra_enh	42796761	42797354	chr21	-0.60
SLC37A1	29354	chr21:42822023-42822304	intra_enh	42822023	42822304	chr21	-0.68
PKNOX1	41303	chr21:43308938-43309044	intra_enh	43308938	43309044	chr21	-0.68
LINC00322	6103	chr21:43570103-43570387	intra_enh	43570103	43570387	chr21	-0.34
TRPM2	2120	chr21:44599917-44600144	intra_enh	44599917	44600144	chr21	-0.61
ADARB1	17600	chr21:45336439-45336602	intra_enh	45336439	45336602	chr21	-0.90

ADARB1	48314	chr21:45366644-4536782	intra_enh	45366644	45367823	chr21	-0.69
ADARB1	49492	chr21:45368160-4536866	intra_enh	45368160	45368663	chr21	-0.94
XKR3	10863	chr22:15671409-1567203	intra_enh	15671409	15672033	chr22	-0.87
XKR3	2516	chr22:15679599-1568053	intra_enh	15679599	15680536	chr22	-0.94
CECR7	2817	chr22:15900224-1590032	intra_enh	15900224	15900326	chr22	-0.82
CECR5	3205	chr22:16016778-1601715	intra_enh	16016778	16017152	chr22	-0.46
CECR2	7302	chr22:16228084-1622819	intra_enh	16228084	16228196	chr22	-0.30
CECR2	24088	chr22:16360633-1636079	intra_enh	16360633	16360795	chr22	-0.68
CECR2	24492	chr22:16361018-1636121	intra_enh	16361018	16361218	chr22	-0.39
MICAL3	33002	chr22:16854235-1685441	intra_enh	16854235	16854412	chr22	-0.73
MICAL3	21823	chr22:16865378-1686562	intra_enh	16865378	16865628	chr22	-0.92
MICAL3	13828	chr22:16873154-1687384	intra_enh	16873154	16873843	chr22	-0.71
DGCR2	12990	chr22:17476884-1747707	intra_enh	17476884	17477071	chr22	-0.80
DGCR2	12486	chr22:17477204-1747775	intra_enh	17477204	17477759	chr22	-0.50
HIRA	69452	chr22:17729598-1772993	intra_enh	17729598	17729939	chr22	-0.59
HIRA	10992	chr22:17788063-1778839	intra_enh	17788063	17788394	chr22	-0.89
GNB1L	42008	chr22:18264389-1826455	intra_enh	18264389	18264550	chr22	-0.54
UBE2L3	15326	chr22:20267186-2026750	intra_enh	20267186	20267502	chr22	-0.44
YDJC	13213	chr22:20301029-2030122	intra_enh	20301029	20301225	chr22	-0.54
YPEL1	46332	chr22:20466158-2046664	intra_enh	20466158	20466649	chr22	-0.27
RAB36	12326	chr22:21829738-2182993	intra_enh	21829738	21829938	chr22	-0.51
BCR	28623	chr22:21881045-2188130	intra_enh	21881045	21881301	chr22	-0.56
SMARCB1	2382	chr22:22461463-2246159	intra_enh	22461463	22461598	chr22	-0.30
DERL3	12348	chr22:22498779-2249892	intra_enh	22498779	22498924	chr22	-0.52
CABIN1	17326	chr22:22754933-2275535	intra_enh	22754933	22755355	chr22	-0.83
SPECC1L	2626	chr22:22999220-2299959	intra_enh	22999220	22999599	chr22	-0.30
UPB1	12038	chr22:23233062-2323351	intra_enh	23233062	23233515	chr22	-0.44
MYO18B	85314	chr22:24382735-2438287	intra_enh	24382735	24382873	chr22	-0.78
SEZ6L	181490	chr22:24713895-2471400	intra_enh	24713895	24714002	chr22	-0.52
MIR1302-1	39181	chr22:25086315-2508648	intra_enh	25086315	25086483	chr22	-0.68
TFIP11	9151	chr22:25229209-2522936	intra_enh	25229209	25229365	chr22	-0.58
MIAT	3465	chr22:25386595-2538722	intra_enh	25386595	25387223	chr22	-0.79
PITPNB	4419	chr22:26640725-2664084	intra_enh	26640725	26640841	chr22	-0.61
PITPNB	3254	chr22:26641847-2664205	intra_enh	26641847	26642050	chr22	-0.75
XBP1	2430	chr22:27523938-2752432	intra_enh	27523938	27524322	chr22	-0.71
AP1B1	16652	chr22:28097868-2809797	intra_enh	28097868	28097971	chr22	-0.38
ZMAT5	18283	chr22:28474598-2847477	intra_enh	28474598	28474776	chr22	-0.94
TBC1D10A	16612	chr22:29036113-2903657	intra_enh	29036113	29036575	chr22	-0.33
LIMK2	9669	chr22:29947842-2994799	intra_enh	29947842	29947992	chr22	-0.51
EIF4ENIF1	11787	chr22:30203405-30204117	intra_enh	30203405	30204117	chr22	-0.73
MIR4764	119070	chr22:32043308-3204386	intra_enh	32043308	32043865	chr22	-0.94
MIR4764	55880	chr22:32218337-3221873	intra_enh	32218337	32218735	chr22	-0.39
MIR4764	83070	chr22:32245495-3224595	intra_enh	32245495	32245957	chr22	-0.59
MIR4764	83904	chr22:32246343-3224677	intra_enh	32246343	32246778	chr22	-0.89
MIR4764	139794	chr22:32302109-3230279	intra_enh	32302109	32302792	chr22	-0.56
MIR4764	140340	chr22:32302949-3230304	intra_enh	32302949	32303043	chr22	-0.42
MIR4764	142278	chr22:32304882-3230498	intra_enh	32304882	32304986	chr22	-0.44
LARGE	68540	chr22:32577585-3257816	intra_enh	32577585	32578168	chr22	-0.94
LARGE	30430	chr22:32615708-3261626	intra_enh	32615708	32616265	chr22	-0.54
LINC01399	31536	chr22:33925321-3392570	intra_enh	33925321	33925707	chr22	-0.98
APOL5	37856	chr22:34481585-3448185	intra_enh	34481585	34481855	chr22	-0.95
RBFOX2	23290	chr22:34589731-3459000	intra_enh	34589731	34590000	chr22	-0.81
RBFOX2	28409	chr22:34594765-3459520	intra_enh	34594765	34595205	chr22	-0.94
RBFOX2	29332	chr22:34595579-3459623	intra_enh	34595579	34596236	chr22	-0.93
RBFOX2	30376	chr22:34596541-3459736	intra_enh	34596541	34597363	chr22	-0.93

RBFOX2	36352	chr22:34602029-34603827	intra_enh	34602029	34603827	chr22	-0.75
RBFOX2	60287	chr22:34626505-34627221	intra_enh	34626505	34627221	chr22	-0.72
RBFOX2	60978	chr22:34627467-34627642	intra_enh	34627467	34627642	chr22	-0.77
RBFOX2	61830	chr22:34628169-34628643	intra_enh	34628169	34628643	chr22	-0.89
RBFOX2	72318	chr22:34638817-34638970	intra_enh	34638817	34638970	chr22	-0.72
RBFOX2	20062	chr22:34734416-34734525	intra_enh	34734416	34734525	chr22	-0.85
RBFOX2	16210	chr22:34738208-34738435	intra_enh	34738208	34738435	chr22	-0.88
RBFOX2	9204	chr22:34745026-34745630	intra_enh	34745026	34745630	chr22	-0.85
RBFOX2	6569	chr22:34747689-34748237	intra_enh	34747689	34748237	chr22	-0.56
MYH9	28478	chr22:35085337-35085824	intra_enh	35085337	35085824	chr22	-0.27
MYH9	7093	chr22:35106774-35107156	intra_enh	35106774	35107156	chr22	-0.65
MYH9	6272	chr22:35107584-35107988	intra_enh	35107584	35107988	chr22	-0.59
LOC100506271	27352	chr22:36108124-36108233	intra_enh	36108124	36108233	chr22	-0.91
LOC100506271	28441	chr22:36109134-36109400	intra_enh	36109134	36109400	chr22	-0.86
ELFN2	17600	chr22:36135600-36136104	intra_enh	36135600	36136104	chr22	-0.74
MFNG	11866	chr22:36224179-36224400	intra_enh	36224179	36224400	chr22	-0.35
C22orf23	19344	chr22:36660204-36660307	intra_enh	36660204	36660307	chr22	-0.58
TMEM184B	13421	chr22:36984703-36985687	intra_enh	36984703	36985687	chr22	-0.96
CSNK1E	3158	chr22:37121236-37121396	intra_enh	37121236	37121396	chr22	-0.30
GTPBP1	3762	chr22:37435219-37435810	intra_enh	37435219	37435810	chr22	-0.61
CBX6	3378	chr22:37594744-37594908	intra_enh	37594744	37594908	chr22	-0.75
CBX6	3044	chr22:37595090-37595231	intra_enh	37595090	37595231	chr22	-0.59
TAB1	12786	chr22:38138331-38138649	intra_enh	38138331	38138649	chr22	-0.84
TNRC6B	5868	chr22:38776487-38776781	intra_enh	38776487	38776781	chr22	-0.36
TNRC6B	31662	chr22:38935350-38935721	intra_enh	38935350	38935721	chr22	-0.47
TNRC6B	35690	chr22:38939480-38939648	intra_enh	38939480	38939648	chr22	-0.84
SGSM3	5429	chr22:39101674-39102204	intra_enh	39101674	39102204	chr22	-0.41
SGSM3	6302	chr22:39102400-39103225	intra_enh	39102400	39103225	chr22	-0.50
SGSM3	15708	chr22:39112147-39112289	intra_enh	39112147	39112289	chr22	-0.70
SREBF2	25136	chr22:40584084-40584244	intra_enh	40584084	40584244	chr22	-0.39
SREBF2	26374	chr22:40585127-40585676	intra_enh	40585127	40585676	chr22	-0.63
SREBF2	27346	chr22:40586271-40586478	intra_enh	40586271	40586478	chr22	-0.67
SREBF2	27997	chr22:40586914-40587136	intra_enh	40586914	40587136	chr22	-0.57
WBP2NL	24001	chr22:40748599-40748751	intra_enh	40748599	40748751	chr22	-0.80
A4GALT	18142	chr22:41428628-41428728	intra_enh	41428628	41428728	chr22	-0.82
A4GALT	16171	chr22:41430528-41430770	intra_enh	41430528	41430770	chr22	-0.83
A4GALT	15756	chr22:41430876-41431252	intra_enh	41430876	41431252	chr22	-0.83
A4GALT	13176	chr22:41433518-41433769	intra_enh	41433518	41433769	chr22	-0.92
ARFGAP3	38064	chr22:41621235-41621596	intra_enh	41621235	41621596	chr22	-0.66
PRR5-ARHGAP	8391	chr22:43485038-43485224	intra_enh	43485038	43485224	chr22	-0.88
MIR4762	7755	chr22:44542715-44542927	intra_enh	44542715	44542927	chr22	-0.65
MIR4762	9060	chr22:44543960-44544291	intra_enh	44543960	44544291	chr22	-0.57
MIR4762	9653	chr22:44544528-44544910	intra_enh	44544528	44544910	chr22	-0.79
LOC284930	158317	chr22:46564261-46564545	intra_enh	46564261	46564545	chr22	-0.60
LOC284930	209188	chr22:46615207-46615340	intra_enh	46615207	46615340	chr22	-0.54
LOC284930	209658	chr22:46615488-46616000	intra_enh	46615488	46616000	chr22	-0.46
FILIP1L	8778	chr3:101307099-10130744	intra_enh	101307099	101307441	chr3	-0.52
LNP1	4904	chr3:101597767-10159787	intra_enh	101597767	101597878	chr3	-0.59
LNP1	2383	chr3:101600251-10160043	intra_enh	101600251	101600435	chr3	-0.66
IMPG2	59445	chr3:102581482-10258162	intra_enh	102581482	102581628	chr3	-0.71
TRMT10C	2172	chr3:102765490-10276559	intra_enh	102765490	102765590	chr3	-0.83
PCNP	3168	chr3:102778793-10277900	intra_enh	102778793	102779003	chr3	-0.35
RPL24	3278	chr3:102884849-10288510	intra_enh	102884849	102885104	chr3	-0.72
NFKBIZ	9596	chr3:103019770-10302008	intra_enh	103019770	103020082	chr3	-0.75
NFKBIZ	3484	chr3:103032933-10303307	intra_enh	103032933	103033078	chr3	-0.77

NFKBIZ	9290	chr3:103038710-10303891	intra_enh	103038710	103038914	chr3	-0.65
NFKBIZ	9886	chr3:103039052-10303976	intra_enh	103039052	103039765	chr3	-0.74
ALCAM	5146	chr3:106573260-10657352	intra_enh	106573260	106573525	chr3	-0.82
ALCAM	9986	chr3:106577924-10657854	intra_enh	106577924	106578540	chr3	-0.91
ALCAM	19053	chr3:106587122-10658747	intra_enh	106587122	106587476	chr3	-0.76
CBLB	115575	chr3:106954468-10695553	intra_enh	106954468	106955538	chr3	-0.47
CBLB	21840	chr3:107048651-10704882	intra_enh	107048651	107048824	chr3	-0.43
LINC00882	122436	chr3:108319649-10831983	intra_enh	108319649	108319830	chr3	-0.57
LINC01215	8344	chr3:109335059-10933634	intra_enh	109335059	109336341	chr3	-0.34
MORC1	58803	chr3:110260797-11026096	intra_enh	110260797	110260965	chr3	-0.40
TMPRSS7	4044	chr3:113245077-11324532	intra_enh	113245077	113245320	chr3	-0.52
TMPRSS7	4432	chr3:113245427-11324574	intra_enh	113245427	113245744	chr3	-0.72
SLC9C1	47306	chr3:113448376-11344854	intra_enh	113448376	113448540	chr3	-0.82
BTLA	3195	chr3:113697484-11369832	intra_enh	113697484	113698322	chr3	-0.86
MIR4446	31674	chr3:114828036-11482813	intra_enh	114828036	114828137	chr3	-0.47
NAA50	9752	chr3:114937988-11493812	intra_enh	114937988	114938128	chr3	-0.37
NAA50	9296	chr3:114938250-11493877	intra_enh	114938250	114938778	chr3	-0.38
NAA50	8766	chr3:114938963-11493912	intra_enh	114938963	114939126	chr3	-0.48
ZDHHC23	33954	chr3:115183311-11518347	intra_enh	115183311	115183470	chr3	-0.85
LOC101929754	25186	chr3:115629823-11563006	intra_enh	115629823	115630062	chr3	-0.59
B4GALT4	18118	chr3:120460257-12046086	intra_enh	120460257	120460864	chr3	-0.77
ARHGAP31-AS	29536	chr3:120553708-12055396	intra_enh	120553708	120553960	chr3	-0.82
ARHGAP31-AS	30138	chr3:120554110-12055476	intra_enh	120554110	120554762	chr3	-0.93
ARHGAP31-AS	37136	chr3:120561354-12056151	intra_enh	120561354	120561515	chr3	-0.82
CD80	8934	chr3:120752137-12075233	intra_enh	120752137	120752338	chr3	-0.62
LRRC58	2292	chr3:121548341-12154882	intra_enh	121548341	121548827	chr3	-0.51
ILDR1	24200	chr3:123199413-12319982	intra_enh	123199413	123199824	chr3	-0.73
CD86	4008	chr3:123283111-12328367	intra_enh	123283111	123283672	chr3	-0.30
CSTA	66343	chr3:123460265-12346044	intra_enh	123460265	123460449	chr3	-0.28
CCDC58	3610	chr3:123581035-12358127	intra_enh	123581035	123581273	chr3	-0.84
FAM162A	2713	chr3:123588148-12358870	intra_enh	123588148	123588702	chr3	-0.34
FAM162A	3395	chr3:123589054-12358916	intra_enh	123589054	123589160	chr3	-0.26
SEMA5B	3120	chr3:124180694-12418088	intra_enh	124180694	124180889	chr3	-0.83
MYLK-AS2	34282	chr3:124925369-12492555	intra_enh	124925369	124925555	chr3	-0.33
CCDC14	3927	chr3:125158843-12515919	intra_enh	125158843	125159195	chr3	-0.89
CCDC14	2852	chr3:125160011-12516017	intra_enh	125160011	125160177	chr3	-0.79
MIR6083	94233	chr3:125670030-12567017	intra_enh	125670030	125670172	chr3	-0.46
RAF1	38497	chr3:12641996-12642410	intra_enh	12641996	12642410	chr3	-0.68
RAF1	15736	chr3:12664894-12665033	intra_enh	12664894	12665033	chr3	-0.58
RAF1	2270	chr3:12678338-12678522	intra_enh	12678338	12678522	chr3	-0.33
TMEM40	10318	chr3:12765438-12765543	intra_enh	12765438	12765543	chr3	-0.66
EEFSEC	24934	chr3:129379884-12937998	intra_enh	129379884	129379988	chr3	-0.71
ACAD9	2912	chr3:130083857-13008401	intra_enh	130083857	130084011	chr3	-0.70
IQSEC1	35606	chr3:13019125-13020482	intra_enh	13019125	13020482	chr3	-0.93
TMCC1	56078	chr3:131025919-13102611	intra_enh	131025919	131026110	chr3	-0.59
TMCC1	4846	chr3:131090198-13109032	intra_enh	131090198	131090329	chr3	-0.37
ATP2C1	6420	chr3:132102486-13210259	intra_enh	132102486	132102597	chr3	-0.76
ATP2C1	22278	chr3:132118150-13211865	intra_enh	132118150	132118650	chr3	-0.27
NUDT16P1	8524	chr3:132554804-13255490	intra_enh	132554804	132554905	chr3	-0.71
ACPP	8518	chr3:133527167-13352766	intra_enh	133527167	133527669	chr3	-0.88
ACPP	25698	chr3:133544527-13354466	intra_enh	133544527	133544668	chr3	-0.60
ACKR4	25792	chr3:133827379-13382754	intra_enh	133827379	133827544	chr3	-0.91
TMEM108-AS1	19800	chr3:134478373-13447853	intra_enh	134478373	134478539	chr3	-0.64
MSL2	14160	chr3:137381740-13738194	intra_enh	137381740	137381940	chr3	-0.72
NCK1	3750	chr3:138067195-13806778	intra_enh	138067195	138067780	chr3	-0.44

NCK1	28740	chr3:138103044-13810348	intra_enh	138103044	138103487	chr3	-0.81
NCK1	27480	chr3:138104443-13810461	intra_enh	138104443	138104610	chr3	-0.87
ZBTB38	12924	chr3:142538423-14253891	intra_enh	142538423	142538914	chr3	-0.68
ZBTB38	36687	chr3:142562369-14256249	intra_enh	142562369	142562493	chr3	-0.33
ATP1B3	3624	chr3:143081447-14308211	intra_enh	143081447	143082116	chr3	-0.67
ATP1B3	25206	chr3:143102753-14310397	intra_enh	143102753	143103976	chr3	-0.86
SLC6A6	4831	chr3:14423817-14424001	intra_enh	14423817	14424001	chr3	-0.80
SLC9A9	179098	chr3:144870610-14487132	intra_enh	144870610	144871321	chr3	-0.94
SLC9A9	174234	chr3:144875653-14487600	intra_enh	144875653	144876008	chr3	-0.48
C3orf20	10412	chr3:14701729-14702311	intra_enh	14701729	14702311	chr3	-0.69
HLTF	9190	chr3:150296062-15029638	intra_enh	150296062	150296383	chr3	-0.93
CP	18262	chr3:150404177-15040434	intra_enh	150404177	150404344	chr3	-0.62
CP	17843	chr3:150404502-15040485	intra_enh	150404502	150404856	chr3	-0.64
MRPS25	9690	chr3:15071898-15072361	intra_enh	15071898	15072361	chr3	-0.93
WWTR1	55478	chr3:150802907-15080314	intra_enh	150802907	150803140	chr3	-0.51
COL6A4P1	25602	chr3:15196485-15197252	intra_enh	15196485	15197252	chr3	-0.63
GPR171	56811	chr3:152346764-15234697	intra_enh	152346764	152346970	chr3	-0.50
P2RY14	12120	chr3:152466688-15246691	intra_enh	152466688	152466911	chr3	-0.32
SUCNR1	2340	chr3:153076352-15307656	intra_enh	153076352	153076568	chr3	-0.83
SH3BP5	37272	chr3:15311745-15311990	intra_enh	15311745	15311990	chr3	-0.34
TMEM14E	18096	chr3:153523257-15352349	intra_enh	153523257	153523490	chr3	-0.65
TMEM14E	102674	chr3:153643659-15364462	intra_enh	153643659	153644629	chr3	-0.30
DHX36	4880	chr3:155519932-15552026	intra_enh	155519932	155520268	chr3	-0.44
MME	47280	chr3:156327954-15632815	intra_enh	156327954	156328150	chr3	-0.61
MME	50416	chr3:156331074-15633130	intra_enh	156331074	156331302	chr3	-0.85
PLCH1	118112	chr3:156758359-15675901	intra_enh	156758359	156759016	chr3	-0.59
SLC33A1	8769	chr3:157046098-15704624	intra_enh	157046098	157046248	chr3	-0.74
SLC33A1	8230	chr3:157046518-15704690	intra_enh	157046518	157046907	chr3	-0.54
SLC33A1	4976	chr3:157049820-15705011	intra_enh	157049820	157050111	chr3	-0.68
KCNAB1	51384	chr3:157542805-15754290	intra_enh	157542805	157542900	chr3	-0.42
SSR3	2426	chr3:157753134-15775335	intra_enh	157753134	157753350	chr3	-0.72
PA2G4P4	15858	chr3:157996582-15799671	intra_enh	157996582	157996710	chr3	-0.83
ANKRD28	7838	chr3:15822319-15822748	intra_enh	15822319	15822748	chr3	-0.71
LOC100996447	218412	chr3:159553031-15955324	intra_enh	159553031	159553245	chr3	-0.53
RARRES1	4537	chr3:159928179-15992868	intra_enh	159928179	159928687	chr3	-0.40
LINC01100	8552	chr3:161212506-16121264	intra_enh	161212506	161212647	chr3	-0.53
LINC01100	8206	chr3:161212807-16121303	intra_enh	161212807	161213036	chr3	-0.45
SMC4	3651	chr3:161596073-16159619	intra_enh	161596073	161596193	chr3	-0.87
KPNA4	4876	chr3:161761117-16176127	intra_enh	161761117	161761272	chr3	-0.79
B3GALNT1	122126	chr3:162183086-16218341	intra_enh	162183086	162183419	chr3	-0.90
OXNAD1	100674	chr3:16382211-16382476	intra_enh	16382211	16382476	chr3	-0.91
RFTN1	89229	chr3:16440860-16441134	intra_enh	16440860	16441134	chr3	-0.63
RFTN1	88700	chr3:16441345-16441706	intra_enh	16441345	16441706	chr3	-0.62
RFTN1	76367	chr3:16453788-16453930	intra_enh	16453788	16453930	chr3	-0.80
RFTN1	74908	chr3:16455162-16455475	intra_enh	16455162	16455475	chr3	-0.44
RFTN1	74437	chr3:16455672-16455906	intra_enh	16455672	16455906	chr3	-0.64
SERPINI1	5651	chr3:168941736-16894197	intra_enh	168941736	168941974	chr3	-0.49
SERPINI1	26923	chr3:168963057-16896319	intra_enh	168963057	168963197	chr3	-0.44
PLCL2	7862	chr3:16909207-16909424	intra_enh	16909207	16909424	chr3	-0.60
PLCL2	8841	chr3:16909962-16910628	intra_enh	16909962	16910628	chr3	-0.66
PLCL2	14208	chr3:16915551-16915773	intra_enh	16915551	16915773	chr3	-0.27
PLCL2	14524	chr3:16915875-16916080	intra_enh	16915875	16916080	chr3	-0.34
PLCL2	22198	chr3:16923233-16924070	intra_enh	16923233	16924070	chr3	-0.84
GOLIM4	16346	chr3:169279586-16927994	intra_enh	169279586	169279946	chr3	-0.93
MIR3714	97238	chr3:17046806-17047049	intra_enh	17046806	17047049	chr3	-0.64

LRRIQ4	14506	chr3:171036725-17103709	intra_enh	171036725	171037092	chr3	-0.28
LRRIQ4	21234	chr3:171043420-17104385	intra_enh	171043420	171043852	chr3	-0.32
LRRC31	6310	chr3:171063801-17106441	intra_enh	171063801	171064414	chr3	-0.67
SAMD7	23078	chr3:171135128-17113537	intra_enh	171135128	171135376	chr3	-0.59
GPR160	11646	chr3:171250001-17125014	intra_enh	171250001	171250146	chr3	-0.34
GPR160	16656	chr3:171254933-17125523	intra_enh	171254933	171255235	chr3	-0.91
PHC3	55693	chr3:171326213-17132686	intra_enh	171326213	171326865	chr3	-0.96
PHC3	44214	chr3:171337870-17133816	intra_enh	171337870	171338166	chr3	-0.90
PHC3	37135	chr3:171344991-17134520	intra_enh	171344991	171345203	chr3	-0.86
PHC3	29168	chr3:171352981-17135314	intra_enh	171352981	171353148	chr3	-0.73
PHC3	28618	chr3:171353497-17135373	intra_enh	171353497	171353732	chr3	-0.39
PHC3	24102	chr3:171358030-17135823	intra_enh	171358030	171358231	chr3	-0.85
PHC3	7140	chr3:171374970-17137521	intra_enh	171374970	171375215	chr3	-0.78
PRKCI	36318	chr3:171459104-17145935	intra_enh	171459104	171459357	chr3	-0.43
PRKCI	55572	chr3:171478289-17147868	intra_enh	171478289	171478680	chr3	-0.66
SKIL	60764	chr3:171497191-17149761	intra_enh	171497191	171497614	chr3	-0.91
SKIL	12484	chr3:171572031-17157314	intra_enh	171572031	171573145	chr3	-0.64
MIR3714	246770	chr3:17196368-17196553	intra_enh	17196368	17196553	chr3	-0.31
MIR3714	249103	chr3:17198566-17199020	intra_enh	17198566	17199020	chr3	-0.40
MIR3714	257761	chr3:17206913-17207989	intra_enh	17206913	17207989	chr3	-0.52
MIR569	162950	chr3:172469951-17247043	intra_enh	172469951	172470434	chr3	-0.94
MIR3714	300180	chr3:17249785-17249954	intra_enh	17249785	17249954	chr3	-0.88
FNDC3B	47616	chr3:173288264-17328904	intra_enh	173288264	173289040	chr3	-0.97
FNDC3B	67790	chr3:173308645-17330900	intra_enh	173308645	173309008	chr3	-0.88
NCEH1	18273	chr3:173893199-17389365	intra_enh	173893199	173893659	chr3	-0.85
ECT2	3238	chr3:173954176-17395463	intra_enh	173954176	173954635	chr3	-0.76
TBC1D5	300826	chr3:17415560-17415820	intra_enh	17415560	17415820	chr3	-0.70
TBC1D5	300408	chr3:17415969-17416248	intra_enh	17415969	17416248	chr3	-0.67
TBL1XR1	110802	chr3:178286842-17828703	intra_enh	178286842	178287037	chr3	-0.91
TBL1XR1	109390	chr3:178288274-17828843	intra_enh	178288274	178288430	chr3	-0.87
LOC102724550	4022	chr3:179021196-17902153	intra_enh	179021196	179021539	chr3	-0.66
GNB4	14742	chr3:180637164-18063748	intra_enh	180637164	180637485	chr3	-0.52
FXR1	6276	chr3:182119163-18211924	intra_enh	182119163	182119241	chr3	-0.55
SOX2	3542	chr3:182908476-18290924	intra_enh	182908476	182909248	chr3	-0.92
LINC01206	3496	chr3:183155982-18315669	intra_enh	183155982	183156699	chr3	-0.84
DCUN1D1	12856	chr3:184167762-18416856	intra_enh	184167762	184168565	chr3	-0.65
B3GNT5	7250	chr3:184460815-18446113	intra_enh	184460815	184461134	chr3	-0.47
SATB1	5388	chr3:18447075-18447370	intra_enh	18447075	18447370	chr3	-0.71
MCF2L2	46438	chr3:184582131-18458249	intra_enh	184582131	184582496	chr3	-0.95
KLHL6-AS1	41560	chr3:184707474-18470783	intra_enh	184707474	184707837	chr3	-0.85
SATB1-AS1	44828	chr3:18506281-18506838	intra_enh	18506281	18506838	chr3	-0.94
VPS8	130938	chr3:186143467-18614365	intra_enh	186143467	186143656	chr3	-0.77
SENP2	2540	chr3:186789121-18678940	intra_enh	186789121	186789406	chr3	-0.45
IGF2BP2-AS1	52826	chr3:186860840-18686097	intra_enh	186860840	186860973	chr3	-0.26
ETV5	46672	chr3:187356176-18735636	intra_enh	187356176	187356360	chr3	-0.80
DGKG	120436	chr3:187442124-18744243	intra_enh	187442124	187442439	chr3	-0.66
DGKG	102304	chr3:187460307-18746052	intra_enh	187460307	187460522	chr3	-0.35
ST6GAL1	17270	chr3:188205002-18820517	intra_enh	188205002	188205174	chr3	-0.86
ST6GAL1	11697	chr3:188210540-18821078	intra_enh	188210540	188210782	chr3	-0.52
LOC101929106	16432	chr3:188424344-18842474	intra_enh	188424344	188424743	chr3	-0.61
LPP-AS2	11684	chr3:189365919-18936659	intra_enh	189365919	189366590	chr3	-0.94
FLJ42393	7730	chr3:189371217-18937137	intra_enh	189371217	189371370	chr3	-0.67
LPP	113842	chr3:189539621-18953983	intra_enh	189539621	189539834	chr3	-0.75
LPP	114422	chr3:189540136-18954048	intra_enh	189540136	189540481	chr3	-0.64
LPP-AS1	125826	chr3:189642865-18964378	intra_enh	189642865	189643780	chr3	-0.75

LPP-AS1	15780	chr3:189784594-18978526	intra_enh	189784594	189785262	chr3	-0.42
LPP-AS1	187784	chr3:189956376-18995748	intra_enh	189956376	189957488	chr3	-0.35
TPRG1-AS2	36518	chr3:190477458-19047773	intra_enh	190477458	190477734	chr3	-0.51
TP63	5395	chr3:190837242-19083736	intra_enh	190837242	190837364	chr3	-0.59
TP63	7601	chr3:190837541-19084147	intra_enh	190837541	190841477	chr3	-0.36
TP63	9870	chr3:190841627-19084192	intra_enh	190841627	190841929	chr3	-0.67
TP63	10639	chr3:190842137-19084295	intra_enh	190842137	190842957	chr3	-0.38
TP63	42916	chr3:190874258-19087539	intra_enh	190874258	190875391	chr3	-0.36
TP63	76870	chr3:190908371-19090918	intra_enh	190908371	190909184	chr3	-0.68
TP63	74474	chr3:190915209-19091612	intra_enh	190915209	190916127	chr3	-0.45
MIR944	9472	chr3:191020836-19102102	intra_enh	191020836	191021027	chr3	-0.72
MIR944	7116	chr3:191037422-19103761	intra_enh	191037422	191037617	chr3	-0.78
MIR944	15082	chr3:191045430-19104554	intra_enh	191045430	191045541	chr3	-0.86
CCDC50	27918	chr3:192501383-19250191	intra_enh	192501383	192501914	chr3	-0.95
FGF12-AS1	24882	chr3:193414055-19341440	intra_enh	193414055	193414406	chr3	-0.83
FGF12	77009	chr3:193532286-19353276	intra_enh	193532286	193532760	chr3	-0.80
FGF12	74388	chr3:193683857-19368398	intra_enh	193683857	193683984	chr3	-0.32
MB21D2	53177	chr3:194065424-19406551	intra_enh	194065424	194065510	chr3	-0.78
LOC100507391	21882	chr3:195932137-19593250	intra_enh	195932137	195932504	chr3	-0.34
LOC100507391	23574	chr3:195933936-19593408	intra_enh	195933936	195934087	chr3	-0.51
XXYLT1-AS1	6831	chr3:196303294-19630357	intra_enh	196303294	196303576	chr3	-0.75
XXYLT1-AS2	2996	chr3:196346735-19634704	intra_enh	196346735	196347049	chr3	-0.91
XXYLT1-AS2	10187	chr3:196359316-19636083	intra_enh	196359316	196360834	chr3	-0.78
XXYLT1-AS2	14662	chr3:196364181-19636491	intra_enh	196364181	196364919	chr3	-0.98
XXYLT1-AS2	25721	chr3:196375540-19637567	intra_enh	196375540	196375678	chr3	-0.92
XXYLT1-AS2	38312	chr3:196387567-19638883	intra_enh	196387567	196388834	chr3	-0.81
PPP1R2	10905	chr3:196740526-19674069	intra_enh	196740526	196740692	chr3	-0.90
PPP1R2	10462	chr3:196740939-19674116	intra_enh	196740939	196741165	chr3	-0.92
MUC4	16383	chr3:197006778-19700694	intra_enh	197006778	197006940	chr3	-0.79
MUC4	9098	chr3:197013926-19701436	intra_enh	197013926	197014361	chr3	-0.81
SENP5	2200	chr3:198081235-19808140	intra_enh	198081235	198081408	chr3	-0.47
KAT2B	6010	chr3:20062406-20062665	intra_enh	20062406	20062665	chr3	-0.80
UBE2E2	91740	chr3:23311309-23311744	intra_enh	23311309	23311744	chr3	-0.96
UBE2E2	142020	chr3:23361479-23362132	intra_enh	23361479	23362132	chr3	-0.97
UBE2E2	232092	chr3:23451632-23452123	intra_enh	23451632	23452123	chr3	-0.93
UBE2E2	234588	chr3:23454083-23454665	intra_enh	23454083	23454665	chr3	-0.98
UBE2E2	239800	chr3:23459516-23459655	intra_enh	23459516	23459655	chr3	-0.89
UBE2E1	19396	chr3:23846057-23846608	intra_enh	23846057	23846608	chr3	-0.81
NR1D2	7424	chr3:23969946-23970130	intra_enh	23969946	23970130	chr3	-0.84
TOP2B	16316	chr3:25664462-25664643	intra_enh	25664462	25664643	chr3	-0.51
TOP2B	7124	chr3:25673397-25674092	intra_enh	25673397	25674092	chr3	-0.71
SLC4A7	4472	chr3:27496170-27496719	intra_enh	27496170	27496719	chr3	-0.71
RBMS3	157917	chr3:29455635-29455811	intra_enh	29455635	29455811	chr3	-0.30
TGFBR2	14194	chr3:30636774-30637606	intra_enh	30636774	30637606	chr3	-0.81
TGFBR2	15592	chr3:30638143-30639032	intra_enh	30638143	30639032	chr3	-0.94
CHL1	29407	chr3:306651-307263	intra_enh	306651	307263	chr3	-0.65
STT3B	7453	chr3:31556164-31556734	intra_enh	31556164	31556734	chr3	-0.80
ZNF860	124308	chr3:31873847-31874074	intra_enh	31873847	31874074	chr3	-0.72
ZNF860	123860	chr3:31874313-31874503	intra_enh	31874313	31874503	chr3	-0.69
ZNF860	50394	chr3:31947592-31948156	intra_enh	31947592	31948156	chr3	-0.64
ZNF860	45069	chr3:31953062-31953336	intra_enh	31953062	31953336	chr3	-0.60
ZNF860	42765	chr3:31955440-31955566	intra_enh	31955440	31955566	chr3	-0.37
ZNF860	37596	chr3:31960620-31960725	intra_enh	31960620	31960725	chr3	-0.91
ZNF860	37178	chr3:31960899-31961282	intra_enh	31960899	31961282	chr3	-0.80
ZNF860	18844	chr3:31979094-31979754	intra_enh	31979094	31979754	chr3	-0.39

OSBPL10	3940	chr3:32002095-32002477	intra_enh	32002095	32002477	chr3	-0.84
CMTM8	58350	chr3:32313426-32313622	intra_enh	32313426	32313622	chr3	-0.44
CMTM7	46492	chr3:32454529-32454786	intra_enh	32454529	32454786	chr3	-0.92
CMTM7	49258	chr3:32457323-32457524	intra_enh	32457323	32457524	chr3	-0.68
CMTM6	4532	chr3:32514741-32515010	intra_enh	32514741	32515010	chr3	-0.50
CNOT10	5006	chr3:32716958-32717127	intra_enh	32716958	32717127	chr3	-0.65
TMPPE	34965	chr3:33078120-33078546	intra_enh	33078120	33078546	chr3	-0.74
TMPPE	33164	chr3:33079831-33080437	intra_enh	33079831	33080437	chr3	-0.83
TMPPE	31790	chr3:33081420-33081596	intra_enh	33081420	33081596	chr3	-0.85
CLASP2	2582	chr3:33732043-33732213	intra_enh	33732043	33732213	chr3	-0.74
ARPP21	12200	chr3:35670824-35671280	intra_enh	35670824	35671280	chr3	-0.47
ARPP21	17342	chr3:35676011-35676378	intra_enh	35676011	35676378	chr3	-0.60
TRANK1	49002	chr3:36912483-36912616	intra_enh	36912483	36912616	chr3	-0.77
ITGA9-AS1	124992	chr3:37753195-37753372	intra_enh	37753195	37753372	chr3	-0.62
MIR6822	10183	chr3:39144462-39144572	intra_enh	39144462	39144572	chr3	-0.55
CTNNB1	4664	chr3:41220490-41220725	intra_enh	41220490	41220725	chr3	-0.58
CTNNB1	5156	chr3:41220980-41221220	intra_enh	41220980	41221220	chr3	-0.40
CTNNB1	323330	chr3:41539134-41539414	intra_enh	41539134	41539414	chr3	-0.89
TRAK1	23017	chr3:42130485-42131045	intra_enh	42130485	42131045	chr3	-0.63
TRAK1	22146	chr3:42143415-42143754	intra_enh	42143415	42143754	chr3	-0.63
TRAK1	21512	chr3:42144135-42144302	intra_enh	42144135	42144302	chr3	-0.46
SEC22C	2472	chr3:42619924-42620173	intra_enh	42619924	42620173	chr3	-0.92
CYP8B1	28746	chr3:42863744-42864040	intra_enh	42863744	42864040	chr3	-0.87
ABHD5	13594	chr3:43720847-43721098	intra_enh	43720847	43721098	chr3	-0.92
LIMD1	17852	chr3:45628908-45629449	intra_enh	45628908	45629449	chr3	-0.88
LIMD1	18526	chr3:45629637-45630067	intra_enh	45629637	45630067	chr3	-0.88
LIMD1	19170	chr3:45630295-45630696	intra_enh	45630295	45630696	chr3	-0.80
CCR9	3240	chr3:45905954-45906521	intra_enh	45905954	45906521	chr3	-0.77
LRRC2-AS1	13414	chr3:46560353-46560599	intra_enh	46560353	46560599	chr3	-0.95
NRADDP	26558	chr3:47054396-47054787	intra_enh	47054396	47054787	chr3	-0.89
KLHL18	57128	chr3:47242077-47242330	intra_enh	47242077	47242330	chr3	-0.92
KIF9	10714	chr3:47309805-47310306	intra_enh	47309805	47310306	chr3	-0.74
KIF9	23390	chr3:47322519-47322945	intra_enh	47322519	47322945	chr3	-0.90
ZNF589	2946	chr3:48260297-48260792	intra_enh	48260297	48260792	chr3	-0.46
RHOA	25586	chr3:49398736-49399151	intra_enh	49398736	49399151	chr3	-0.63
MST1R	2946	chr3:49913131-49913596	intra_enh	49913131	49913596	chr3	-0.32
RBM6	6909	chr3:49959311-49959467	intra_enh	49959311	49959467	chr3	-0.60
ARL8B	14346	chr3:5153080-5153467	intra_enh	5153080	5153467	chr3	-0.75
ARL8B	14919	chr3:5153568-5154126	intra_enh	5153568	5154126	chr3	-0.62
ARL8B	16358	chr3:5154909-5155663	intra_enh	5154909	5155663	chr3	-0.87
ARL8B	17496	chr3:5156321-5156528	intra_enh	5156321	5156528	chr3	-0.89
TEX264	10121	chr3:51690409-51691197	intra_enh	51690409	51691197	chr3	-0.80
EDEM1	27183	chr3:5177120-5177230	intra_enh	5177120	5177230	chr3	-0.72
EDEM1	25998	chr3:5178119-5178601	intra_enh	5178119	5178601	chr3	-0.81
EDEM1	22815	chr3:5181186-5181900	intra_enh	5181186	5181900	chr3	-0.89
EDEM1	22000	chr3:5182045-5182671	intra_enh	5182045	5182671	chr3	-0.96
EDEM1	20798	chr3:5183332-5183789	intra_enh	5183332	5183789	chr3	-0.96
EDEM1	18132	chr3:5185787-5186664	intra_enh	5185787	5186664	chr3	-0.84
WDR82	3199	chr3:52284434-52284568	intra_enh	52284434	52284568	chr3	-0.32
CHDH	40940	chr3:53814439-53814602	intra_enh	53814439	53814602	chr3	-0.70
CHDH	2522	chr3:53852515-53853362	intra_enh	53852515	53853362	chr3	-0.79
WNT5A	34696	chr3:55531083-55531730	intra_enh	55531083	55531730	chr3	-0.87
ERC2-IT1	87339	chr3:55755784-55755970	intra_enh	55755784	55755970	chr3	-0.67
ERC2	161726	chr3:56315417-56315996	intra_enh	56315417	56315996	chr3	-0.98
ERC2	146275	chr3:56330954-56331360	intra_enh	56330954	56331360	chr3	-0.84

ARHGEF3	28760	chr3:56896710-56896849	intra_enh	56896710	56896849	chr3	-0.81
ARHGEF3-AS1	30524	chr3:56979470-56979790	intra_enh	56979470	56979790	chr3	-0.67
SPATA12	53008	chr3:57016445-57016556	intra_enh	57016445	57016556	chr3	-0.64
SPATA12	52668	chr3:57016662-57017018	intra_enh	57016662	57017018	chr3	-0.65
APPL1	7426	chr3:57244023-57244438	intra_enh	57244023	57244438	chr3	-0.51
FLNB	66126	chr3:58034929-58035654	intra_enh	58034929	58035654	chr3	-0.80
DNASE1L3	14106	chr3:58157460-58157868	intra_enh	58157460	58157868	chr3	-0.92
PDHB	44859	chr3:58349587-58349907	intra_enh	58349587	58349907	chr3	-0.88
PDHB	31714	chr3:58362788-58362995	intra_enh	58362788	58362995	chr3	-0.26
C3orf67	961043	chr3:59971741-59971857	intra_enh	59971741	59971857	chr3	-0.31
C3orf67	1026634	chr3:60036400-60038379	intra_enh	60036400	60038379	chr3	-0.89
FHIT	1001012	chr3:60211050-60211274	intra_enh	60211050	60211274	chr3	-0.89
PTPRG	69780	chr3:61591950-61592174	intra_enh	61591950	61592174	chr3	-0.80
PTPRG	70304	chr3:61592524-61592649	intra_enh	61592524	61592649	chr3	-0.87
PTPRG-AS1	130094	chr3:62149451-62149684	intra_enh	62149451	62149684	chr3	-0.56
CADPS	207714	chr3:62628309-62628471	intra_enh	62628309	62628471	chr3	-0.82
CADPS	203884	chr3:62632140-62632299	intra_enh	62632140	62632299	chr3	-0.73
CADPS	201422	chr3:62634542-62634822	intra_enh	62634542	62634822	chr3	-0.79
CADPS	148068	chr3:62687434-62688637	intra_enh	62687434	62688637	chr3	-0.92
CADPS	69869	chr3:62765686-62766784	intra_enh	62765686	62766784	chr3	-0.58
CADPS	4020	chr3:62831901-62832266	intra_enh	62831901	62832266	chr3	-0.94
ATXN7	7015	chr3:63832205-63832369	intra_enh	63832205	63832369	chr3	-0.91
ATXN7	34468	chr3:63893609-63894371	intra_enh	63893609	63894371	chr3	-0.57
ATXN7	33901	chr3:63894474-63894640	intra_enh	63894474	63894640	chr3	-0.78
MAGI1-AS1	161458	chr3:65693010-65693134	intra_enh	65693010	65693134	chr3	-0.73
SLC25A26	55510	chr3:66431727-66431925	intra_enh	66431727	66431925	chr3	-0.74
LRIG1	25352	chr3:66607887-66608482	intra_enh	66607887	66608482	chr3	-0.96
KBTBD8	6972	chr3:67137987-67138788	intra_enh	67137987	67138788	chr3	-0.84
GRM7-AS3	107460	chr3:6714523-6714828	intra_enh	6714523	6714828	chr3	-0.92
SUCLG2	3658	chr3:67783935-67784206	intra_enh	67783935	67784206	chr3	-0.43
ARL6IP5	2638	chr3:69219319-69219512	intra_enh	69219319	69219512	chr3	-0.66
FOXP1	53646	chr3:71142813-71143423	intra_enh	71142813	71143423	chr3	-0.78
FOXP1	4709	chr3:71201416-71201530	intra_enh	71201416	71201530	chr3	-0.82
FOXP1	4954	chr3:71201646-71201791	intra_enh	71201646	71201791	chr3	-0.64
FOXP1	51858	chr3:71488263-71488656	intra_enh	71488263	71488656	chr3	-0.60
FOXP1	98378	chr3:71534789-71535171	intra_enh	71534789	71535171	chr3	-0.61
FOXP1	10251	chr3:71685328-71685970	intra_enh	71685328	71685970	chr3	-0.90
RYBP	21044	chr3:72557251-72557589	intra_enh	72557251	72557589	chr3	-0.89
SHQ1	34060	chr3:72946129-72946327	intra_enh	72946129	72946327	chr3	-0.69
LOC101927296	36388	chr3:73616490-73617058	intra_enh	73616490	73617058	chr3	-0.86
LMCD1-AS1	8704	chr3:8509419-8509862	intra_enh	8509419	8509862	chr3	-0.87
LMCD1	5460	chr3:8523138-8524765	intra_enh	8523138	8524765	chr3	-0.93
ARPC4	10944	chr3:9798058-9798409	intra_enh	9798058	9798409	chr3	-0.36
ARPC4	10181	chr3:9798823-9799171	intra_enh	9798823	9799171	chr3	-0.88
MIR3684	32620	chr4:100170052-10017030	intra_enh	100170052	100170309	chr4	-0.61
LAMTOR3	38756	chr4:100995510-10099643	intra_enh	100995510	100996430	chr4	-0.73
LAMTOR3	34806	chr4:100999599-10100024	intra_enh	100999599	101000241	chr4	-0.93
MIR8066	87096	chr4:102293895-10229401	intra_enh	102293895	102294017	chr4	-0.75
SLC39A8	25279	chr4:103439124-10343930	intra_enh	103439124	103439302	chr4	-0.34
SLC39A8	3130	chr4:103482155-10348233	intra_enh	103482155	103482330	chr4	-0.40
HADH	39621	chr4:109169871-10917000	intra_enh	109169871	109170007	chr4	-0.28
SEC24B-AS1	5188	chr4:110579214-11058000	intra_enh	110579214	110580007	chr4	-0.80
EGF	57340	chr4:111110685-11111097	intra_enh	111110685	111110970	chr4	-0.85
ELOVL6	13747	chr4:111325346-11132560	intra_enh	111325346	111325600	chr4	-0.41
ENPEP	51202	chr4:111667707-11166804	intra_enh	111667707	111668049	chr4	-0.95

AP1AR	22008	chr4:113394284-11339441	intra_enh	113394284	113394415	chr4	-0.27
NEUROG2	44148	chr4:113700710-11370114	intra_enh	113700710	113701142	chr4	-0.89
CAMK2D	214390	chr4:114688046-11468823	intra_enh	114688046	114688238	chr4	-0.66
CAMK2D	193998	chr4:114708121-11470894	intra_enh	114708121	114708947	chr4	-0.67
CAMK2D	143552	chr4:114758907-11475905	intra_enh	114758907	114759053	chr4	-0.64
CAMK2D	143288	chr4:114759189-11475929	intra_enh	114759189	114759298	chr4	-0.30
CAMK2D	119688	chr4:114782766-11478292	intra_enh	114782766	114782923	chr4	-0.55
CAMK2D	84374	chr4:114817999-11481831	intra_enh	114817999	114818316	chr4	-0.33
UGT8	8698	chr4:115754090-11575445	intra_enh	115754090	115754455	chr4	-0.37
SYNPO2	79515	chr4:120108898-12010901	intra_enh	120108898	120109016	chr4	-0.65
MYOZ2	93848	chr4:120182406-12018267	intra_enh	120182406	120182671	chr4	-0.80
PRDM5	168870	chr4:121894456-12189474	intra_enh	121894456	121894748	chr4	-0.93
PRDM5	149381	chr4:121913534-12191464	intra_enh	121913534	121914648	chr4	-0.98
BBS7	29921	chr4:123040936-12304111	intra_enh	123040936	123041110	chr4	-0.59
SPRY1	152284	chr4:124384989-12438524	intra_enh	124384989	124385240	chr4	-0.76
LINC01091	81082	chr4:124995862-12499603	intra_enh	124995862	124996037	chr4	-0.45
LINC01091	82853	chr4:124997551-12499789	intra_enh	124997551	124997891	chr4	-0.40
PGRMC2	3917	chr4:129425370-12942566	intra_enh	129425370	129425664	chr4	-0.79
LOC100507487	26602	chr4:129595104-12959533	intra_enh	129595104	129595339	chr4	-0.85
LOC100507487	85973	chr4:129654469-12965471	intra_enh	129654469	129654717	chr4	-0.44
JADE1	8728	chr4:129961044-12996130	intra_enh	129961044	129961308	chr4	-0.90
JADE1	14992	chr4:129967353-12996752	intra_enh	129967353	129967528	chr4	-0.46
SCLT1	135105	chr4:130099022-13009919	intra_enh	130099022	130099192	chr4	-0.52
LINC01256	51088	chr4:133782698-13378286	intra_enh	133782698	133782863	chr4	-0.26
SLC7A11	3996	chr4:139378780-13937913	intra_enh	139378780	139379136	chr4	-0.80
NDUFC1	2767	chr4:140445871-14044597	intra_enh	140445871	140445975	chr4	-0.71
NDUFC1	3484	chr4:140446571-14044670	intra_enh	140446571	140446708	chr4	-0.58
NDUFC1	8850	chr4:140451666-14045234	intra_enh	140451666	140452345	chr4	-0.54
NDUFC1	9706	chr4:140452679-14045304	intra_enh	140452679	140453045	chr4	-0.48
NDUFC1	28706	chr4:140471819-14047190	intra_enh	140471819	140471904	chr4	-0.69
MAML3	177912	chr4:141116649-14111689	intra_enh	141116649	141116895	chr4	-0.85
MAML3	174980	chr4:141119607-14111980	intra_enh	141119607	141119800	chr4	-0.46
TBC1D9	128496	chr4:142025317-14202552	intra_enh	142025317	142025520	chr4	-0.87
GAB1	3112	chr4:144480084-14448100	intra_enh	144480084	144481005	chr4	-0.98
MIR3139	51212	chr4:144534816-14453573	intra_enh	144534816	144535733	chr4	-0.99
ANAPC10	4376	chr4:146243252-14624378	intra_enh	146243252	146243789	chr4	-0.42
ANAPC10	4983	chr4:146243979-14624427	intra_enh	146243979	146244275	chr4	-0.53
SMAD1-AS2	4948	chr4:146648249-14664881	intra_enh	146648249	146648811	chr4	-0.90
SMAD1-AS1	21730	chr4:146679432-14667961	intra_enh	146679432	146679619	chr4	-0.45
LOC101929095	16920	chr4:15021399-15022032	intra_enh	15021399	15022032	chr4	-0.48
LOC101929095	14938	chr4:15023494-15023902	intra_enh	15023494	15023902	chr4	-0.53
FBXL5	5426	chr4:15260614-15260803	intra_enh	15260614	15260803	chr4	-0.56
FBXL5	5101	chr4:15260916-15261150	intra_enh	15260916	15261150	chr4	-0.77
BST1	27596	chr4:15341136-15341396	intra_enh	15341136	15341396	chr4	-0.94
MIR3140	27164	chr4:153602649-15360305	intra_enh	153602649	153603059	chr4	-0.36
MIR3140	24708	chr4:153604843-15360577	intra_enh	153604843	153605778	chr4	-0.77
TMEM154	39540	chr4:153781163-15378129	intra_enh	153781163	153781293	chr4	-0.76
TMEM154	7637	chr4:153812944-15381331	intra_enh	153812944	153813318	chr4	-0.95
ARFIP1	6154	chr4:153926201-15392718	intra_enh	153926201	153927183	chr4	-0.77
CD38	7176	chr4:15395914-15396494	intra_enh	15395914	15396494	chr4	-0.87
CD38	27194	chr4:15415996-15416447	intra_enh	15415996	15416447	chr4	-0.62
TRIM2	3718	chr4:154297372-15429750	intra_enh	154297372	154297500	chr4	-0.90
KIAA0922	30088	chr4:154636965-15463710	intra_enh	154636965	154637102	chr4	-0.44
FAM198B	34430	chr4:159278609-15927886	intra_enh	159278609	159278867	chr4	-0.85
FAM198B	15773	chr4:159297223-15929756	intra_enh	159297223	159297567	chr4	-0.87

FAM198B	15360	chr4:159297678-15929793	intra_enh	159297678	159297937	chr4	-0.93
C4orf45	105111	chr4:160070543-16007080	intra_enh	160070543	160070803	chr4	-0.76
2-Mar	131392	chr4:164885536-16488570	intra_enh	164885536	164885700	chr4	-0.87
2-Mar	141412	chr4:164895399-16489587	intra_enh	164895399	164895878	chr4	-0.27
TLL1	172526	chr4:167186185-16718658	intra_enh	167186185	167186582	chr4	-0.83
PALLD	16396	chr4:170006014-17000623	intra_enh	170006014	170006238	chr4	-0.74
CBR4	3066	chr4:170164757-17016519	intra_enh	170164757	170165198	chr4	-0.49
LAP3	17339	chr4:17205269-17205457	intra_enh	17205269	17205457	chr4	-0.82
LOC101928551	41200	chr4:176030576-17603072	intra_enh	176030576	176030728	chr4	-0.76
ADAM29	7354	chr4:176083206-17608366	intra_enh	176083206	176083665	chr4	-0.73
WDR17	12942	chr4:177210792-17721128	intra_enh	177210792	177211280	chr4	-0.88
STOX2	15593	chr4:185078808-18507938	intra_enh	185078808	185079382	chr4	-0.85
LOC102723766	39135	chr4:185579266-18557991	intra_enh	185579266	185579912	chr4	-0.66
SNX25	55856	chr4:186423939-18642432	intra_enh	186423939	186424326	chr4	-0.89
LRP2BP	67529	chr4:186469511-18646972	intra_enh	186469511	186469723	chr4	-0.53
ANKRD37	4194	chr4:186558982-18655907	intra_enh	186558982	186559071	chr4	-0.66
SORBS2	59354	chr4:186755663-18675586	intra_enh	186755663	186755864	chr4	-0.64
SORBS2	47764	chr4:186767273-18676743	intra_enh	186767273	186767435	chr4	-0.81
CYP4V2	10288	chr4:187359852-18736005	intra_enh	187359852	187360055	chr4	-0.47
SLIT2-IT1	26850	chr4:20029516-20029999	intra_enh	20029516	20029999	chr4	-0.35
MXD4	29339	chr4:2262832-2262922	intra_enh	2262832	2262922	chr4	-0.42
MXD4	34536	chr4:2268014-2268133	intra_enh	2268014	2268133	chr4	-0.44
RNF4	11790	chr4:2452335-2453198	intra_enh	2452335	2453198	chr4	-0.49
PI4K2B	2869	chr4:24847274-24847964	intra_enh	24847274	24847964	chr4	-0.80
SEL1L3	7968	chr4:25465426-25466141	intra_enh	25465426	25466141	chr4	-0.29
SMIM20	12142	chr4:25536806-25537298	intra_enh	25536806	25537298	chr4	-0.41
RBPJ	52016	chr4:25983387-25983696	intra_enh	25983387	25983696	chr4	-0.26
STIM2	26742	chr4:26498040-26498263	intra_enh	26498040	26498263	chr4	-0.58
STIM2	142826	chr4:26613956-26614516	intra_enh	26613956	26614516	chr4	-0.46
TNIP2	7942	chr4:2719551-2719664	intra_enh	2719551	2719664	chr4	-0.52
ADD1	8860	chr4:2824459-2824610	intra_enh	2824459	2824610	chr4	-0.33
NOP14	3020	chr4:2931872-2932153	intra_enh	2931872	2932153	chr4	-0.89
HTT-AS	2759	chr4:3048693-3048905	intra_enh	3048693	3048905	chr4	-0.78
RGS12	14703	chr4:3326691-3326943	intra_enh	3326691	3326943	chr4	-0.93
RELL1	40514	chr4:37323566-37324195	intra_enh	37323566	37324195	chr4	-0.45
PTTG2	7511	chr4:37645704-37646218	intra_enh	37645704	37646218	chr4	-0.68
PTTG2	23938	chr4:37662324-37662451	intra_enh	37662324	37662451	chr4	-0.74
PTTG2	25482	chr4:37663413-37664452	intra_enh	37663413	37664452	chr4	-0.43
TMEM156	6412	chr4:38703897-38704150	intra_enh	38703897	38704150	chr4	-0.65
WDR19	14398	chr4:38845911-38846129	intra_enh	38845911	38846129	chr4	-0.79
RHOH	39846	chr4:39829080-39829275	intra_enh	39829080	39829275	chr4	-0.55
MIR4802	39568	chr4:40159006-40159646	intra_enh	40159006	40159646	chr4	-0.89
MIR4802	3940	chr4:40202777-40202891	intra_enh	40202777	40202891	chr4	-0.64
RBM47	19206	chr4:40231763-40232144	intra_enh	40231763	40232144	chr4	-0.79
RBM47	44116	chr4:40256621-40257108	intra_enh	40256621	40257108	chr4	-0.70
RBM47	55776	chr4:40270707-40271021	intra_enh	40270707	40271021	chr4	-0.81
PHOX2B	56106	chr4:41389586-41389689	intra_enh	41389586	41389689	chr4	-0.47
PHOX2B	55758	chr4:41389908-41390063	intra_enh	41389908	41390063	chr4	-0.42
BEND4	25376	chr4:41824015-41824538	intra_enh	41824015	41824538	chr4	-0.64
ATP8A1	8088	chr4:42345551-42346032	intra_enh	42345551	42346032	chr4	-0.91
ZBTB49	21264	chr4:4363848-4364328	intra_enh	4363848	4364328	chr4	-0.93
ZBTB49	27008	chr4:4369637-4370026	intra_enh	4369637	4370026	chr4	-0.78
ABCA11P	4143	chr4:462095-462187	intra_enh	462095	462187	chr4	-0.77
ATP10D	14381	chr4:47196019-47197075	intra_enh	47196019	47197075	chr4	-0.81
NFXL1	9018	chr4:47620287-47620632	intra_enh	47620287	47620632	chr4	-0.84

FRYL	144789	chr4:48332162-48332408	intra_enh	48332162	48332408	chr4	-0.74
SCFD2	4894	chr4:53922017-53922196	intra_enh	53922017	53922196	chr4	-0.27
FIP1L1	3686	chr4:53942121-53942404	intra_enh	53942121	53942404	chr4	-0.76
RPL21P44	29637	chr4:54577235-54578451	intra_enh	54577235	54578451	chr4	-0.95
CHIC2	33243	chr4:54592053-54592605	intra_enh	54592053	54592605	chr4	-0.92
CHIC2	31409	chr4:54594064-54594262	intra_enh	54594064	54594262	chr4	-0.85
SRD5A3	12678	chr4:55919607-55920036	intra_enh	55919607	55920036	chr4	-0.75
PPAT	6123	chr4:56990344-56990530	intra_enh	56990344	56990530	chr4	-0.50
PPAT	4192	chr4:56992156-56992580	intra_enh	56992156	56992580	chr4	-0.64
PPAT	3630	chr4:56992723-56993137	intra_enh	56992723	56993137	chr4	-0.53
REST	5552	chr4:57475288-57475485	intra_enh	57475288	57475485	chr4	-0.37
MAN2B2	23433	chr4:6651198-6651268	intra_enh	6651198	6651268	chr4	-0.26
STAP1	4518	chr4:68111395-68111721	intra_enh	68111395	68111721	chr4	-0.71
STAP1	5070	chr4:68112001-68112219	intra_enh	68112001	68112219	chr4	-0.33
YTHDC1	4212	chr4:68894177-68894239	intra_enh	68894177	68894239	chr4	-0.46
AMBN	9610	chr4:71502032-71502312	intra_enh	71502032	71502312	chr4	-0.49
MOB1B	40731	chr4:72027181-72028121	intra_enh	72027181	72028121	chr4	-0.30
DCK	13928	chr4:72064042-72064359	intra_enh	72064042	72064359	chr4	-0.63
DCK	13502	chr4:72064466-72064785	intra_enh	72064466	72064785	chr4	-0.72
DCK	15742	chr4:72093015-72094725	intra_enh	72093015	72094725	chr4	-0.52
COX18	16694	chr4:74170719-74171349	intra_enh	74170719	74171349	chr4	-0.94
ANKRD17	41879	chr4:74265679-74265955	intra_enh	74265679	74265955	chr4	-0.42
ANKRD17	3430	chr4:74339565-74340308	intra_enh	74339565	74340308	chr4	-0.53
RASSF6	15988	chr4:74689027-74689300	intra_enh	74689027	74689300	chr4	-0.63
RASSF6	7328	chr4:74697616-74698031	intra_enh	74697616	74698031	chr4	-0.91
MRPL1	49493	chr4:79052241-79052401	intra_enh	79052241	79052401	chr4	-0.65
LINC01094	7790	chr4:79793866-79794054	intra_enh	79793866	79794054	chr4	-0.89
LINC01094	16363	chr4:79802308-79802758	intra_enh	79802308	79802758	chr4	-0.94
BMP2K	5884	chr4:79922104-79922773	intra_enh	79922104	79922773	chr4	-0.82
BMP2K	21312	chr4:79937742-79937989	intra_enh	79937742	79937989	chr4	-0.95
ANTXR2	36164	chr4:81177237-81177440	intra_enh	81177237	81177440	chr4	-0.39
C4orf22	147290	chr4:81623086-81623285	intra_enh	81623086	81623285	chr4	-0.76
C4orf22	171851	chr4:81647681-81647813	intra_enh	81647681	81647813	chr4	-0.66
C4orf22	197404	chr4:81672925-81673676	intra_enh	81672925	81673676	chr4	-0.61
ABLIM2	27598	chr4:8183745-8183979	intra_enh	8183745	8183979	chr4	-0.54
BMP3	243238	chr4:81927669-81928138	intra_enh	81927669	81928138	chr4	-0.82
BMP3	155034	chr4:82015932-82016284	intra_enh	82015932	82016284	chr4	-0.43
BMP3	103972	chr4:82067120-82067221	intra_enh	82067120	82067221	chr4	-0.44
HTRA3	31684	chr4:8290642-8290770	intra_enh	8290642	8290770	chr4	-0.26
HNRNPD	13388	chr4:83500733-83500838	intra_enh	83500733	83500838	chr4	-0.72
HNRNPD	13104	chr4:83500947-83501194	intra_enh	83500947	83501194	chr4	-0.66
HNRNPD	11540	chr4:83502575-83502692	intra_enh	83502575	83502692	chr4	-0.63
HNRNPD	9106	chr4:83504982-83505154	intra_enh	83504982	83505154	chr4	-0.47
HNRNPD	8530	chr4:83505522-83505767	intra_enh	83505522	83505767	chr4	-0.41
HNRNPD	6734	chr4:83507369-83507510	intra_enh	83507369	83507510	chr4	-0.53
PLAC8	35519	chr4:84214435-84214599	intra_enh	84214435	84214599	chr4	-0.81
ACOX3	42312	chr4:8450956-8451125	intra_enh	8450956	8451125	chr4	-0.68
ARHGAP24	46102	chr4:86661309-86661506	intra_enh	86661309	86661506	chr4	-0.75
MIR4451	61339	chr4:86800976-86801634	intra_enh	86800976	86801634	chr4	-0.89
MIR4451	50185	chr4:86812261-86812657	intra_enh	86812261	86812657	chr4	-0.53
MIR4451	41066	chr4:86821504-86821652	intra_enh	86821504	86821652	chr4	-0.67
MIR4451	27031	chr4:86889624-86889726	intra_enh	86889624	86889726	chr4	-0.37
MIR4451	27618	chr4:86890232-86890292	intra_enh	86890232	86890292	chr4	-0.31
ARHGAP24	3586	chr4:86964289-86964676	intra_enh	86964289	86964676	chr4	-0.52
LOC100506746	3800	chr4:88071106-88071346	intra_enh	88071106	88071346	chr4	-0.88

AFF1	10116	chr4:88085116-88085467	intra_enh	88085116	88085467	chr4	-0.93
AFF1	12582	chr4:88087257-88088260	intra_enh	88087257	88088260	chr4	-0.90
AFF1	32162	chr4:88107218-88107458	intra_enh	88107218	88107458	chr4	-0.78
AFF1	28141	chr4:88118775-88119295	intra_enh	88118775	88119295	chr4	-0.97
AFF1	12394	chr4:88134546-88135018	intra_enh	88134546	88135018	chr4	-0.97
HERC3	21216	chr4:89753589-89754036	intra_enh	89753589	89754036	chr4	-0.54
GRID2	725520	chr4:94169976-94170208	intra_enh	94169976	94170208	chr4	-0.68
ATOH1	79510	chr4:94889494-94889687	intra_enh	94889494	94889687	chr4	-0.29
SLC2A9	15044	chr4:9617025-9617310	intra_enh	9617025	9617310	chr4	-0.52
BMPR1B	6025	chr4:96225460-96225818	intra_enh	96225460	96225818	chr4	-0.77
BMPR1B	97658	chr4:96329246-96329399	intra_enh	96329246	96329399	chr4	-0.84
LOC102467213	166788	chr5:106207704-10620794	intra_enh	106207704	106207949	chr5	-0.88
ANKRD33B	15303	chr5:10632287-10633187	intra_enh	10632287	10633187	chr5	-0.97
EFNA5	288137	chr5:106746196-10674652	intra_enh	106746196	106746522	chr5	-0.89
EFNA5	221189	chr5:106812765-10681384	intra_enh	106812765	106813849	chr5	-0.40
EFNA5	122141	chr5:106912133-10691257	intra_enh	106912133	106912577	chr5	-0.90
EFNA5	95836	chr5:106938453-10693886	intra_enh	106938453	106938867	chr5	-0.72
EFNA5	65365	chr5:106968870-10696939	intra_enh	106968870	106969392	chr5	-0.62
EFNA5	63056	chr5:106971175-10697170	intra_enh	106971175	106971704	chr5	-0.80
EFNA5	2295	chr5:107031958-10703244	intra_enh	107031958	107032444	chr5	-0.80
EFNA5	332366	chr5:107366755-10736697	intra_enh	107366755	107366970	chr5	-0.56
DAP	59468	chr5:10754797-10755042	intra_enh	10754797	10755042	chr5	-0.67
DAP	25464	chr5:10788742-10789107	intra_enh	10788742	10789107	chr5	-0.43
FER	111174	chr5:108222416-10822277	intra_enh	108222416	108222771	chr5	-0.54
MAN2A1	6199	chr5:109058630-10905969	intra_enh	109058630	109059696	chr5	-0.64
NREP	25186	chr5:111146895-111147106	intra_enh	111146895	111147106	chr5	-0.43
NREP-AS1	58588	chr5:111217295-11121773	intra_enh	111217295	111217734	chr5	-0.80
LOC101927023	48584	chr5:111640385-11164053	intra_enh	111640385	111640539	chr5	-0.87
MCC	48392	chr5:112610066-11261017	intra_enh	112610066	112610175	chr5	-0.54
MCC	35670	chr5:112694066-11269429	intra_enh	112694066	112694297	chr5	-0.46
YTHDC2	9292	chr5:112885807-11288735	intra_enh	112885807	112887352	chr5	-0.73
FEM1C	6396	chr5:114902037-11490215	intra_enh	114902037	114902150	chr5	-0.83
LOC100505811	46042	chr5:117599435-11760081	intra_enh	117599435	117600812	chr5	-0.98
DMXL1	4857	chr5:118439468-11844021	intra_enh	118439468	118440210	chr5	-0.28
TNFAIP8	12234	chr5:118730932-11873236	intra_enh	118730932	118732360	chr5	-0.62
SRFBP1	19396	chr5:121344754-12134514	intra_enh	121344754	121345145	chr5	-0.77
SRFBP1	20202	chr5:121345392-12134612	intra_enh	121345392	121346121	chr5	-0.90
SNCAIP	4455	chr5:121680089-12168025	intra_enh	121680089	121680257	chr5	-0.72
SNCAIP	4896	chr5:121680529-12168069	intra_enh	121680529	121680699	chr5	-0.94
CEP120	63898	chr5:122722951-12272362	intra_enh	122722951	122723625	chr5	-0.97
CSNK1G3	8844	chr5:122884366-12288470	intra_enh	122884366	122884703	chr5	-0.85
LINC01170	356876	chr5:123444999-12344547	intra_enh	123444999	123445474	chr5	-0.88
LINC01170	356168	chr5:123445664-12344622	intra_enh	123445664	123446223	chr5	-0.86
LINC01170	18822	chr5:123782945-12378363	intra_enh	123782945	123783635	chr5	-0.78
LOC101927421	154796	chr5:124555153-12455528	intra_enh	124555153	124555284	chr5	-0.36
LMNB1	4860	chr5:126145478-12614572	intra_enh	126145478	126145727	chr5	-0.63
LMNB1	9463	chr5:126150071-12615033	intra_enh	126150071	126150339	chr5	-0.53
LMNB1	17338	chr5:126157890-12615827	intra_enh	126157890	126158271	chr5	-0.42
LMNB1	24640	chr5:126165085-12616567	intra_enh	126165085	126165678	chr5	-0.53
4-Mar	32412	chr5:126361572-12636240	intra_enh	126361572	126362403	chr5	-0.85
MEGF10	23132	chr5:126677387-12667758	intra_enh	126677387	126677584	chr5	-0.56
CDC42SE2	93742	chr5:130721287-13072139	intra_enh	130721287	130721398	chr5	-0.63
CDC42SE2	111147	chr5:130738132-13073936	intra_enh	130738132	130739362	chr5	-0.89
CDC42SE2	114100	chr5:130741582-13074181	intra_enh	130741582	130741819	chr5	-0.44
CDC42SE2	118736	chr5:130746221-13074645	intra_enh	130746221	130746452	chr5	-0.82

CDC42SE2	119141	chr5:130746638-13074684	intra_enh	130746638	130746844	chr5	-0.73
RAPGEF6	12782	chr5:131011556-13101166	intra_enh	131011556	131011665	chr5	-0.59
FNIP1	3280	chr5:131157321-13115743	intra_enh	131157321	131157432	chr5	-0.62
MIR3936	7286	chr5:131721673-13172213	intra_enh	131721673	131722136	chr5	-0.75
C5orf56	4272	chr5:131778235-13177903	intra_enh	131778235	131779034	chr5	-0.79
MIR1289-2	183196	chr5:132607968-13260823	intra_enh	132607968	132608237	chr5	-0.76
C5orf15	10891	chr5:133321243-13332158	intra_enh	133321243	133321587	chr5	-0.69
VDAC1	10752	chr5:133357741-13335786	intra_enh	133357741	133357867	chr5	-0.47
DDX46	9112	chr5:134113074-13411334	intra_enh	134113074	134113345	chr5	-0.95
SPOCK1	475274	chr5:136387422-13638786	intra_enh	136387422	136387867	chr5	-0.36
MATR3	8982	chr5:138666236-13866640	intra_enh	138666236	138666400	chr5	-0.31
MATR3	11608	chr5:138668304-13866958	intra_enh	138668304	138669585	chr5	-0.33
MATR3	12568	chr5:138669771-13867003	intra_enh	138669771	138670037	chr5	-0.64
UBE2D2	10456	chr5:138931277-13893150	intra_enh	138931277	138931504	chr5	-0.62
CLPTM1L	4360	chr5:1393516-1393767	intra_enh	1393516	1393767	chr5	-0.82
PFDN1	20247	chr5:139642305-13964294	intra_enh	139642305	139642949	chr5	-0.79
PFDN1	6394	chr5:139656047-13965691	intra_enh	139656047	139656914	chr5	-0.91
SLC4A9	2985	chr5:139722893-13972301	intra_enh	139722893	139723017	chr5	-0.61
ANKHD1-EIF4E	3285	chr5:139764653-13976508	intra_enh	139764653	139765081	chr5	-0.26
PCDHGC4	2752	chr5:140841866-14084247	intra_enh	140841866	140842478	chr5	-0.96
PCDHGC5	33686	chr5:140882462-14088289	intra_enh	140882462	140882890	chr5	-0.92
LOC100505658	8067	chr5:140909613-14091037	intra_enh	140909613	140910373	chr5	-0.67
DIAPH1	14451	chr5:140964140-14096457	intra_enh	140964140	140964570	chr5	-0.96
DIAPH1	2824	chr5:140975886-14097607	intra_enh	140975886	140976079	chr5	-0.61
SPRY4	8243	chr5:141675855-14167599	intra_enh	141675855	141675991	chr5	-0.84
NR3C1	42763	chr5:142720369-14272100	intra_enh	142720369	142721001	chr5	-0.52
NR3C1	42104	chr5:142721102-14272158	intra_enh	142721102	142721585	chr5	-0.29
TRIO	114482	chr5:14311179-14311440	intra_enh	14311179	14311440	chr5	-0.90
KCTD16	17148	chr5:143547266-14354828	intra_enh	143547266	143548286	chr5	-0.38
KCTD16	21536	chr5:143552081-14355224	intra_enh	143552081	143552247	chr5	-0.68
LARS	8921	chr5:145533271-14553386	intra_enh	145533271	145533863	chr5	-0.88
RBM27	2720	chr5:145566015-14556613	intra_enh	145566015	145566133	chr5	-0.71
RBM27	4868	chr5:145568174-14556827	intra_enh	145568174	145568270	chr5	-0.43
FAM105A	13616	chr5:14648338-14648673	intra_enh	14648338	14648673	chr5	-0.60
FBXO38	19462	chr5:147763060-14776324	intra_enh	147763060	147763245	chr5	-0.88
MIR4637	24010	chr5:14854839-14855384	intra_enh	14854839	14855384	chr5	-0.96
PPARGC1B	19870	chr5:149111568-14911208	intra_enh	149111568	149112080	chr5	-0.84
PPARGC1B	5324	chr5:149136933-14913710	intra_enh	149136933	149137102	chr5	-0.33
PPARGC1B	7084	chr5:149138719-14913883	intra_enh	149138719	149138836	chr5	-0.83
PPARGC1B	9458	chr5:149140974-14914133	intra_enh	149140974	149141331	chr5	-0.77
LOC102546298	8792	chr5:149836757-14983715	intra_enh	149836757	149837156	chr5	-0.77
LOC102546298	8351	chr5:149837273-14983752	intra_enh	149837273	149837521	chr5	-0.87
SYNPO	8648	chr5:149985994-14998609	intra_enh	149985994	149986099	chr5	-0.30
CCDC69	26306	chr5:150557360-15055772	intra_enh	150557360	150557724	chr5	-0.64
CCDC69	7758	chr5:150576012-15057616	intra_enh	150576012	150576169	chr5	-0.36
SAP30L	2655	chr5:153808162-15380856	intra_enh	153808162	153808564	chr5	-0.45
MIR6075	22018	chr5:1541863-1542045	intra_enh	1541863	1542045	chr5	-0.47
CNOT8	4192	chr5:154222304-15422261	intra_enh	154222304	154222619	chr5	-0.63
MIR6075	21548	chr5:1542256-1542592	intra_enh	1542256	1542592	chr5	-0.46
TIMD4	28364	chr5:156294415-15629454	intra_enh	156294415	156294544	chr5	-0.53
ITK	24008	chr5:156564372-15656461	intra_enh	156564372	156564612	chr5	-0.50
ADAM19	27086	chr5:156908126-15690852	intra_enh	156908126	156908521	chr5	-0.89
CLINT1	37742	chr5:157180446-15718159	intra_enh	157180446	157181595	chr5	-0.60
CLINT1	34823	chr5:157183787-15718409	intra_enh	157183787	157184091	chr5	-0.83
CLINT1	33915	chr5:157184743-15718495	intra_enh	157184743	157184951	chr5	-0.85

CLINT1	33159	chr5:157185143-15718606	intra_enh	157185143	157186063	chr5	-0.86
CLINT1	32348	chr5:157186245-15718658	intra_enh	157186245	157186583	chr5	-0.75
CLINT1	28060	chr5:157190584-15719082	intra_enh	157190584	157190821	chr5	-0.88
CLINT1	26528	chr5:157191896-15719257	intra_enh	157191896	157192572	chr5	-0.79
CLINT1	6372	chr5:157212205-15721257	intra_enh	157212205	157212575	chr5	-0.54
CLINT1	4404	chr5:157214271-15721444	intra_enh	157214271	157214445	chr5	-0.55
LOC101927697	18958	chr5:157750335-15775046	intra_enh	157750335	157750469	chr5	-0.86
LOC101927697	340477	chr5:158109563-15811011	intra_enh	158109563	158110111	chr5	-0.64
EBF1	284571	chr5:158174739-15817485	intra_enh	158174739	158174851	chr5	-0.63
EBF1	253676	chr5:158205444-15820593	intra_enh	158205444	158205936	chr5	-0.44
EBF1	251835	chr5:158207288-15820777	intra_enh	158207288	158207774	chr5	-0.49
PWWP2A	21199	chr5:159457553-15945810	intra_enh	159457553	159458109	chr5	-0.86
PWWP2A	13362	chr5:159465578-15946575	intra_enh	159465578	159465757	chr5	-0.65
CCNG1	2468	chr5:162799531-16279971	intra_enh	162799531	162799713	chr5	-0.57
MAT2B	3718	chr5:162868367-16286928	intra_enh	162868367	162869289	chr5	-0.27
FAM134B	47014	chr5:16609020-16609224	intra_enh	16609020	16609224	chr5	-0.47
WWC1	37116	chr5:167688626-16768888	intra_enh	167688626	167688889	chr5	-0.88
FBXW11	40364	chr5:171325917-17132631	intra_enh	171325917	171326318	chr5	-0.89
FBXW11	38166	chr5:171328128-17132850	intra_enh	171328128	171328505	chr5	-0.36
FBXW11	17234	chr5:171349156-17134934	intra_enh	171349156	171349341	chr5	-0.94
STK10	48164	chr5:171499721-17149985	intra_enh	171499721	171499854	chr5	-0.67
STK10	46496	chr5:171501312-17150160	intra_enh	171501312	171501600	chr5	-0.35
STK10	10616	chr5:171537275-17153739	intra_enh	171537275	171537396	chr5	-0.72
EFCAB9	41476	chr5:171595118-17159539	intra_enh	171595118	171595394	chr5	-0.84
BNIP1	28901	chr5:172475065-17247523	intra_enh	172475065	172475233	chr5	-0.60
BASP1	38080	chr5:17308550-17308946	intra_enh	17308550	17308946	chr5	-0.26
CPEB4	12550	chr5:173260421-17326055	intra_enh	173260421	173260550	chr5	-0.38
CPEB4	25699	chr5:173273386-17327388	intra_enh	173273386	173273884	chr5	-0.90
CPEB4	36440	chr5:173284317-17328443	intra_enh	173284317	173284435	chr5	-0.58
CPEB4	36928	chr5:173284694-17328503	intra_enh	173284694	173285034	chr5	-0.55
UIMC1	19624	chr5:176346377-17634647	intra_enh	176346377	176346476	chr5	-0.74
UIMC1	18004	chr5:176347842-17634825	intra_enh	176347842	176348251	chr5	-0.90
UIMC1	17229	chr5:176348653-17634898	intra_enh	176348653	176348989	chr5	-0.89
UIMC1	8472	chr5:176357346-17635781	intra_enh	176357346	176357810	chr5	-0.27
NSD1	41728	chr5:176534804-17653552	intra_enh	176534804	176535527	chr5	-0.63
SLC34A1	6430	chr5:176750381-17675055	intra_enh	176750381	176750551	chr5	-0.81
COL23A1	117317	chr5:177832737-17783295	intra_enh	177832737	177832953	chr5	-0.87
TRIM41	3304	chr5:180586068-18058627	intra_enh	180586068	180586275	chr5	-0.82
TRIM52	4966	chr5:180615683-18061583	intra_enh	180615683	180615836	chr5	-0.34
DROSHA	52274	chr5:31515589-31515942	intra_enh	31515589	31515942	chr5	-0.91
MIR4279	83585	chr5:32055325-32055889	intra_enh	32055325	32055889	chr5	-0.61
PRLR	36048	chr5:35230244-35230557	intra_enh	35230244	35230557	chr5	-0.62
NADK2	15482	chr5:36293480-36293760	intra_enh	36293480	36293760	chr5	-0.81
NIPBL	5618	chr5:36917896-36918571	intra_enh	36917896	36918571	chr5	-0.44
C5orf42	137375	chr5:37147779-37148047	intra_enh	37147779	37148047	chr5	-0.81
C5orf42	128344	chr5:37156834-37157055	intra_enh	37156834	37157055	chr5	-0.86
C5orf42	128026	chr5:37157170-37157354	intra_enh	37157170	37157354	chr5	-0.73
NUP155	5002	chr5:37401922-37402046	intra_enh	37401922	37402046	chr5	-0.60
WDR70	27228	chr5:37442165-37442627	intra_enh	37442165	37442627	chr5	-0.95
GHR	55732	chr5:42657060-42657848	intra_enh	42657060	42657848	chr5	-0.58
HMGCS1	7154	chr5:43342123-43342313	intra_enh	43342123	43342313	chr5	-0.39
C5orf55	27270	chr5:468907-469069	intra_enh	468907	469069	chr5	-0.69
EMB	25620	chr5:49747153-49747591	intra_enh	49747153	49747591	chr5	-0.86
EMB	10810	chr5:49762002-49762363	intra_enh	49762002	49762363	chr5	-0.74
MAP3K1	22882	chr5:56169475-56169601	intra_enh	56169475	56169601	chr5	-0.38

MAP3K1	30382	chr5:56176842-56177235	intra_enh	56176842	56177235	chr5	-0.89
MAP3K1	37288	chr5:56183841-56184047	intra_enh	56183841	56184047	chr5	-0.87
PDE4D	87636	chr5:58520005-58520126	intra_enh	58520005	58520126	chr5	-0.76
PDE4D	58972	chr5:58976920-58977187	intra_enh	58976920	58977187	chr5	-0.94
PDE4D	75904	chr5:58993768-58994203	intra_enh	58993768	58994203	chr5	-0.92
DEPDC1B	101580	chr5:59929877-59930464	intra_enh	59929877	59930464	chr5	-0.62
CWC27	4742	chr5:64105024-64105459	intra_enh	64105024	64105459	chr5	-0.91
SGTB	2213	chr5:65051332-65051638	intra_enh	65051332	65051638	chr5	-0.51
ERBB2IP	5979	chr5:65264012-65264218	intra_enh	65264012	65264218	chr5	-0.48
ERBB2IP	7924	chr5:65265845-65266276	intra_enh	65265845	65266276	chr5	-0.29
ERBB2IP	8954	chr5:65266821-65267358	intra_enh	65266821	65267358	chr5	-0.31
MAST4	21083	chr5:65948738-65949288	intra_enh	65948738	65949288	chr5	-0.88
MAST4	105100	chr5:66032627-66033433	intra_enh	66032627	66033433	chr5	-0.96
MAST4	28820	chr5:66261160-66262105	intra_enh	66261160	66262105	chr5	-0.96
SRD5A1	32030	chr5:6718412-6718644	intra_enh	6718412	6718644	chr5	-0.40
LOC102467655	3805	chr5:67524942-67525584	intra_enh	67524942	67525584	chr5	-0.95
MRPS27	34916	chr5:71616681-71617167	intra_enh	71616681	71617167	chr5	-0.65
MRPS27	20717	chr5:71630628-71631618	intra_enh	71630628	71631618	chr5	-0.71
MRPS27	17078	chr5:71634705-71634818	intra_enh	71634705	71634818	chr5	-0.45
LINC01333	4497	chr5:73658443-73658683	intra_enh	73658443	73658683	chr5	-0.43
LINC01331	59380	chr5:73809007-73809349	intra_enh	73809007	73809349	chr5	-0.95
COL4A3BP	50642	chr5:74792451-74792686	intra_enh	74792451	74792686	chr5	-0.45
IQGAP2	146957	chr5:75587813-75587941	intra_enh	75587813	75587941	chr5	-0.46
IQGAP2	110080	chr5:75624497-75625012	intra_enh	75624497	75625012	chr5	-0.98
IQGAP2	65013	chr5:75669777-75669865	intra_enh	75669777	75669865	chr5	-0.82
IQGAP2	61004	chr5:75673737-75673922	intra_enh	75673737	75673922	chr5	-0.56
IQGAP2	70629	chr5:75805274-75805652	intra_enh	75805274	75805652	chr5	-0.94
IQGAP2	26654	chr5:75913580-75914460	intra_enh	75913580	75914460	chr5	-0.88
S100Z	18094	chr5:76199590-76199759	intra_enh	76199590	76199759	chr5	-0.39
PDE8B	83432	chr5:76625762-76626021	intra_enh	76625762	76626021	chr5	-0.45
LOC101929154	150410	chr5:77439800-77440673	intra_enh	77439800	77440673	chr5	-0.72
LOC101929154	151189	chr5:77440869-77441161	intra_enh	77440869	77441161	chr5	-0.76
AP3B1	2346	chr5:77623842-77624139	intra_enh	77623842	77624139	chr5	-0.69
ARSB	91686	chr5:78225636-78226035	intra_enh	78225636	78226035	chr5	-0.53
ARSB	4264	chr5:78313166-78313350	intra_enh	78313166	78313350	chr5	-0.76
CTD-2201I18.1	52898	chr5:79467986-79468297	intra_enh	79467986	79468297	chr5	-0.60
SERINC5	70725	chr5:79516758-79517108	intra_enh	79516758	79517108	chr5	-0.57
SERINC5	70074	chr5:79517533-79517636	intra_enh	79517533	79517636	chr5	-0.74
SERINC5	5956	chr5:79581552-79581852	intra_enh	79581552	79581852	chr5	-0.64
ACOT12	113148	chr5:80838835-80838948	intra_enh	80838835	80838948	chr5	-0.77
LINC00461	51925	chr5:88068148-88068454	intra_enh	88068148	88068454	chr5	-0.67
MEF2C	8632	chr5:88146815-88146920	intra_enh	88146815	88146920	chr5	-0.80
MEF2C	7890	chr5:88147256-88147964	intra_enh	88147256	88147964	chr5	-0.70
LINC01339	24792	chr5:89596789-89596915	intra_enh	89596789	89596915	chr5	-0.35
ANKRD32	228728	chr5:94208660-94209087	intra_enh	94208660	94209087	chr5	-0.96
MCTP1	231572	chr5:94211665-94211843	intra_enh	94211665	94211843	chr5	-0.33
CAST	8392	chr5:96096545-96096666	intra_enh	96096545	96096666	chr5	-0.75
ERAP2	6007	chr5:96243333-96243477	intra_enh	96243333	96243477	chr5	-0.74
LNPEP	5166	chr5:96314579-96314909	intra_enh	96314579	96314909	chr5	-0.88
LNPEP	4420	chr5:96315353-96315627	intra_enh	96315353	96315627	chr5	-0.90
LNPEP	9653	chr5:96329291-96329835	intra_enh	96329291	96329835	chr5	-0.67
LNPEP	10744	chr5:96330152-96331157	intra_enh	96330152	96331157	chr5	-0.78
ASCC3	84548	chr6:101351255-10135159	intra_enh	101351255	101351590	chr6	-0.40
PRDM1	3902	chr6:106644304-10664527	intra_enh	106644304	106645271	chr6	-0.91
RTN4IP1	19755	chr6:107164253-10716436	intra_enh	107164253	107164369	chr6	-0.47

RTN4IP1	12091	chr6:107171807-1071721	intra_enh	107171807	107172143	chr6	-0.62
QRSL1	3982	chr6:107188023-1071882	intra_enh	107188023	107188204	chr6	-0.86
QRSL1	6549	chr6:107190470-1071908	intra_enh	107190470	107190892	chr6	-0.78
PDSS2	129028	chr6:107757945-1077589	intra_enh	107757945	107758942	chr6	-0.34
LACE1	14369	chr6:108736951-1087373	intra_enh	108736951	108737367	chr6	-0.97
FOXO3	3887	chr6:108992135-1089931	intra_enh	108992135	108993159	chr6	-0.47
FOXO3	27177	chr6:109015778-1090160	intra_enh	109015778	109016096	chr6	-0.26
FOXO3	58672	chr6:109046945-1090479	intra_enh	109046945	109047920	chr6	-0.80
ARMC2-AS1	21474	chr6:109330277-1093307	intra_enh	109330277	109330776	chr6	-0.94
ARMC2-AS1	19165	chr6:109332487-1093331	intra_enh	109332487	109333183	chr6	-0.98
SESN1	21146	chr6:109501150-1095013	intra_enh	109501150	109501362	chr6	-0.86
SESN1	17796	chr6:109504544-1095046	intra_enh	109504544	109504668	chr6	-0.88
CEP57L1	11903	chr6:109545109-1095454	intra_enh	109545109	109545481	chr6	-0.57
CEP57L1	8694	chr6:109548349-1095486	intra_enh	109548349	109548659	chr6	-0.80
SYCP2L	2556	chr6:10997526-10997681	intra_enh	10997526	10997681	chr6	-0.90
WASF1	31719	chr6:110576084-11057627	intra_enh	110576084	110576278	chr6	-0.91
AMD1	15304	chr6:111227130-11122729	intra_enh	111227130	111227294	chr6	-0.51
AMD1	9578	chr6:111312176-11131233	intra_enh	111312176	111312337	chr6	-0.41
TRAF3IP2-AS1	71058	chr6:111840087-11184052	intra_enh	111840087	111840529	chr6	-0.89
TRAF3IP2-AS1	21316	chr6:111889985-11189011	intra_enh	111889985	111890114	chr6	-0.81
REV3L	3502	chr6:111915005-11191522	intra_enh	111915005	111915223	chr6	-0.87
REV3L	4168	chr6:111915534-11191602	intra_enh	111915534	111916025	chr6	-0.91
FYN	31490	chr6:112269790-11226992	intra_enh	112269790	112269927	chr6	-0.87
LOC101927686	7088	chr6:114070549-11407121	intra_enh	114070549	114071216	chr6	-0.89
LOC101927686	2859	chr6:114075057-11407516	intra_enh	114075057	114075165	chr6	-0.60
LOC101927686	2573	chr6:114075287-11407550	intra_enh	114075287	114075507	chr6	-0.86
NEDD9	50926	chr6:11439268-11440017	intra_enh	11439268	11440017	chr6	-0.58
TPI1P3	21483	chr6:116444903-11644530	intra_enh	116444903	116445303	chr6	-0.58
TPI1P3	21092	chr6:116445407-11644558	intra_enh	116445407	116445582	chr6	-0.71
ZUFSP	3493	chr6:117093095-11709325	intra_enh	117093095	117093251	chr6	-0.52
CEP85L	5181	chr6:119084728-11908506	intra_enh	119084728	119085062	chr6	-0.92
LOC285762	23606	chr6:119830461-11983065	intra_enh	119830461	119830659	chr6	-0.70
NCOA7	9102	chr6:126162623-1261627	intra_enh	126162623	126162781	chr6	-0.46
NCOA7-AS1	11717	chr6:126169908-1261700	intra_enh	126169908	126170054	chr6	-0.63
LAMA2	352862	chr6:129598229-1295994	intra_enh	129598229	129599452	chr6	-0.84
SAMD3	97563	chr6:130481039-1304812	intra_enh	130481039	130481283	chr6	-0.60
AKAP7	47550	chr6:131545989-1315461	intra_enh	131545989	131546148	chr6	-0.58
MOXD1	22852	chr6:132741375-1327416	intra_enh	132741375	132741653	chr6	-0.85
MOXD1	22484	chr6:132741802-1327419	intra_enh	132741802	132741962	chr6	-0.81
MOXD1	18700	chr6:132745525-1327458	intra_enh	132745525	132745806	chr6	-0.89
STX7	4216	chr6:132871758-1328718	intra_enh	132871758	132871871	chr6	-0.73
LOC285766	16274	chr6:134078-134342	intra_enh	134078	134342	chr6	-0.78
SGK1	58334	chr6:134598954-1345991	intra_enh	134598954	134599121	chr6	-0.80
GFOD1	23435	chr6:13539696-13539870	intra_enh	13539696	13539870	chr6	-0.43
MYB	10029	chr6:135553987-1355543	intra_enh	135553987	135554359	chr6	-0.80
MYB	10404	chr6:135554490-1355546	intra_enh	135554490	135554605	chr6	-0.77
MIR548H4	75318	chr6:135649600-1356501	intra_enh	135649600	135650108	chr6	-0.39
BCLAF1	7616	chr6:136644982-1366451	intra_enh	136644982	136645149	chr6	-0.52
IL22RA2	17662	chr6:137518561-1375190	intra_enh	137518561	137519071	chr6	-0.95
ECT2L	23052	chr6:139181673-13918231	intra_enh	139181673	139182310	chr6	-0.31
HECA	40193	chr6:139537973-1395382	intra_enh	139537973	139538293	chr6	-0.80
HECA	40597	chr6:139538456-13953861	intra_enh	139538456	139538618	chr6	-0.76
TXLNB	3848	chr6:139650950-1396511	intra_enh	139650950	139651158	chr6	-0.86
LOC100132735	70963	chr6:140204571-1402051	intra_enh	140204571	140205159	chr6	-0.29
HIVEP2	96955	chr6:143210882-14321127	intra_enh	143210882	143211272	chr6	-0.91

HIVEP2	96148	chr6:143211465-14321230	intra_enh	143211465	143212304	chr6	-0.84
HIVEP2	95197	chr6:143212750-14321292	intra_enh	143212750	143212920	chr6	-0.80
HIVEP2	94065	chr6:143213096-14321483	intra_enh	143213096	143214838	chr6	-0.79
HIVEP2	57824	chr6:143249952-14325046	intra_enh	143249952	143250463	chr6	-0.63
UTRN	19809	chr6:144674173-14467457	intra_enh	144674173	144674573	chr6	-0.85
UTRN	60908	chr6:144715365-14471557	intra_enh	144715365	144715579	chr6	-0.70
UTRN	168735	chr6:144823222-14482337	intra_enh	144823222	144823376	chr6	-0.83
FBXO30	5125	chr6:146172094-14617288	intra_enh	146172094	146172884	chr6	-0.35
LOC100128176	7240	chr6:149334681-14933482	intra_enh	149334681	149334827	chr6	-0.62
TAB2	46266	chr6:149634439-14963453	intra_enh	149634439	149634537	chr6	-0.51
TAB2	2700	chr6:149683765-14968389	intra_enh	149683765	149683892	chr6	-0.84
TAB2	5228	chr6:149686273-14968643	intra_enh	149686273	149686439	chr6	-0.89
ZC3H12D	13178	chr6:149834560-14983476	intra_enh	149834560	149834768	chr6	-0.35
LATS1	8378	chr6:150070683-15007106	intra_enh	150070683	150071069	chr6	-0.51
PCMT1	11783	chr6:150124235-15012437	intra_enh	150124235	150124375	chr6	-0.61
PCMT1	12189	chr6:150124508-15012491	intra_enh	150124508	150124914	chr6	-0.80
PPP1R14C	40252	chr6:150545912-15054635	intra_enh	150545912	150546353	chr6	-0.64
PLEKHG1	47508	chr6:151009794-15101060	intra_enh	151009794	151010602	chr6	-0.56
MTHFD1L	99630	chr6:151128403-15112934	intra_enh	151128403	151129348	chr6	-0.65
MTHFD1L	21909	chr6:151250948-15125119	intra_enh	151250948	151251190	chr6	-0.51
ESR1	15186	chr6:152185606-15218577	intra_enh	152185606	152185777	chr6	-0.79
FBXO5	4488	chr6:153341277-15334154	intra_enh	153341277	153341540	chr6	-0.82
JARID2	48000	chr6:15404956-15405171	intra_enh	15404956	15405171	chr6	-0.89
JARID2	92142	chr6:15448993-15449419	intra_enh	15448993	15449419	chr6	-0.82
IPCEF1	27976	chr6:154664744-15466512	intra_enh	154664744	154665121	chr6	-0.62
IPCEF1	27620	chr6:154665229-15466534	intra_enh	154665229	154665347	chr6	-0.75
TIAM2	58622	chr6:155520998-15552133	intra_enh	155520998	155521334	chr6	-0.97
MIR4466	7052	chr6:157149566-15714965	intra_enh	157149566	157149655	chr6	-0.60
MIR4466	197834	chr6:157340286-15734049	intra_enh	157340286	157340497	chr6	-0.75
MIR4466	255226	chr6:157397702-15739786	intra_enh	157397702	157397867	chr6	-0.88
DTNBP1	9226	chr6:15762007-15762077	intra_enh	15762007	15762077	chr6	-0.39
TULP4	16723	chr6:158669896-15867090	intra_enh	158669896	158670906	chr6	-0.40
MIR3918	25390	chr6:159131034-15913129	intra_enh	159131034	159131293	chr6	-0.57
LOC101929122	42250	chr6:159553042-15955351	intra_enh	159553042	159553513	chr6	-0.91
IGF2R	9717	chr6:160319753-16031992	intra_enh	160319753	160319921	chr6	-0.72
GMPR	249695	chr6:16596108-16596858	intra_enh	16596108	16596858	chr6	-0.98
LOC101929297	14485	chr6:166584614-16658524	intra_enh	166584614	166585248	chr6	-0.89
C6orf120	4374	chr6:169848462-16984864	intra_enh	169848462	169848646	chr6	-0.38
FOXC1	186502	chr6:1742056-1742304	intra_enh	1742056	1742304	chr6	-0.68
FOXC1	203808	chr6:1759235-1759738	intra_enh	1759235	1759738	chr6	-0.28
FOXC1	211595	chr6:1767095-1767451	intra_enh	1767095	1767451	chr6	-0.51
DEK	48930	chr6:18323783-18323912	intra_enh	18323783	18323912	chr6	-0.58
DEK	48685	chr6:18324013-18324173	intra_enh	18324013	18324173	chr6	-0.68
RNF144B	24880	chr6:18520357-18520518	intra_enh	18520357	18520518	chr6	-0.74
CASC14	231300	chr6:22023912-22024292	intra_enh	22023912	22024292	chr6	-0.51
KIAA0319	8356	chr6:24682984-24683171	intra_enh	24682984	24683171	chr6	-0.71
KIAA0319	8058	chr6:24683291-24683460	intra_enh	24683291	24683460	chr6	-0.80
C6orf62	2668	chr6:24824630-24824798	intra_enh	24824630	24824798	chr6	-0.46
FAM65B	13990	chr6:24971489-24971674	intra_enh	24971489	24971674	chr6	-0.85
FAM65B	7326	chr6:24992687-24993110	intra_enh	24992687	24993110	chr6	-0.71
FAM65B	13112	chr6:24998612-24998755	intra_enh	24998612	24998755	chr6	-0.73
FAM65B	16177	chr6:25001542-25001956	intra_enh	25001542	25001956	chr6	-0.87
FAM65B	16754	chr6:25002154-25002498	intra_enh	25002154	25002498	chr6	-0.92
FAM65B	9212	chr6:25010051-25010280	intra_enh	25010051	25010280	chr6	-0.39
FAM65B	10434	chr6:25029664-25029961	intra_enh	25029664	25029961	chr6	-0.77

FAM65B	11193	chr6:25030384-25030758	intra_enh	25030384	25030758	chr6	-0.73
FAM65B	9547	chr6:25034465-25034961	intra_enh	25034465	25034961	chr6	-0.84
FAM65B	15942	chr6:25060087-25060317	intra_enh	25060087	25060317	chr6	-0.54
FAM65B	50268	chr6:25100041-25100174	intra_enh	25100041	25100174	chr6	-0.55
CMAHP	30314	chr6:25215371-25216062	intra_enh	25215371	25216062	chr6	-0.98
LRRC16A	23536	chr6:25411009-25411332	intra_enh	25411009	25411332	chr6	-0.85
LRRC16A	33290	chr6:25420489-25421358	intra_enh	25420489	25421358	chr6	-0.41
LRRC16A	114925	chr6:25502314-25502804	intra_enh	25502314	25502804	chr6	-0.77
LRRC16A	137716	chr6:25525089-25525612	intra_enh	25525089	25525612	chr6	-0.91
HIST1H2BD	3292	chr6:26269553-26269683	intra_enh	26269553	26269683	chr6	-0.84
HIST1H2BD	4167	chr6:26270406-26270580	intra_enh	26270406	26270580	chr6	-0.87
HMGN4	3490	chr6:26649867-26650214	intra_enh	26649867	26650214	chr6	-0.93
MYLK4	17402	chr6:2678520-2678985	intra_enh	2678520	2678985	chr6	-0.64
ZSCAN16-AS1	3446	chr6:28209553-28209702	intra_enh	28209553	28209702	chr6	-0.82
ZSCAN12	3962	chr6:28471465-28471658	intra_enh	28471465	28471658	chr6	-0.72
ZSCAN12	3355	chr6:28472042-28472296	intra_enh	28472042	28472296	chr6	-0.37
BPHL	6092	chr6:3069737-3070295	intra_enh	3069737	3070295	chr6	-0.59
PSMG4	79162	chr6:3283204-3283439	intra_enh	3283204	3283439	chr6	-0.51
NUDT3	54981	chr6:34413352-34413558	intra_enh	34413352	34413558	chr6	-0.81
NUDT3	46101	chr6:34422298-34422372	intra_enh	34422298	34422372	chr6	-0.53
C6orf106	37692	chr6:34734516-34735313	intra_enh	34734516	34735313	chr6	-0.42
C6orf106	30006	chr6:34742522-34742677	intra_enh	34742522	34742677	chr6	-0.80
C6orf106	16946	chr6:34755408-34755912	intra_enh	34755408	34755912	chr6	-0.60
C6orf106	16450	chr6:34756085-34756228	intra_enh	34756085	34756228	chr6	-0.38
C6orf106	13170	chr6:34759371-34759502	intra_enh	34759371	34759502	chr6	-0.75
C6orf106	4345	chr6:34768193-34768329	intra_enh	34768193	34768329	chr6	-0.58
DEF6	3096	chr6:35376565-35376772	intra_enh	35376565	35376772	chr6	-0.73
FKBP5	6541	chr6:35758057-35758201	intra_enh	35758057	35758201	chr6	-0.45
MDGA1	9909	chr6:37763660-37764010	intra_enh	37763660	37764010	chr6	-0.93
BTBD9	43852	chr6:38627898-38628042	intra_enh	38627898	38628042	chr6	-0.56
KCNK5	31416	chr6:39273495-39274132	intra_enh	39273495	39274132	chr6	-0.89
KCNK5	10222	chr6:39294861-39295154	intra_enh	39294861	39295154	chr6	-0.97
LOC100507506	2331	chr6:4083334-4083936	intra_enh	4083334	4083936	chr6	-0.94
NFYA	3620	chr6:41151975-41152633	intra_enh	41151975	41152633	chr6	-0.52
NFYA	5308	chr6:41153899-41154086	intra_enh	41153899	41154086	chr6	-0.62
NFYA	5771	chr6:41154320-41154590	intra_enh	41154320	41154590	chr6	-0.74
CCND3	40266	chr6:42084084-42084605	intra_enh	42084084	42084605	chr6	-0.82
CCND3	29264	chr6:42095250-42095442	intra_enh	42095250	42095442	chr6	-0.94
CCND3	28472	chr6:42095994-42096283	intra_enh	42095994	42096283	chr6	-0.54
CCND3	4318	chr6:42120173-42120412	intra_enh	42120173	42120412	chr6	-0.66
MRPS10	3055	chr6:42290492-42290622	intra_enh	42290492	42290622	chr6	-0.84
UBR2	5554	chr6:42644949-42645631	intra_enh	42644949	42645631	chr6	-0.83
CNPY3	5367	chr6:42999377-42999561	intra_enh	42999377	42999561	chr6	-0.91
IRF4	98898	chr6:435386-435887	intra_enh	435386	435887	chr6	-0.54
ENPP4	8341	chr6:46213873-46214125	intra_enh	46213873	46214125	chr6	-0.85
CDYL	5102	chr6:4726417-4727144	intra_enh	4726417	4727144	chr6	-0.94
TNFRSF21	70082	chr6:47315482-47315638	intra_enh	47315482	47315638	chr6	-0.77
TNFRSF21	66941	chr6:47318440-47318962	intra_enh	47318440	47318962	chr6	-0.76
TNFRSF21	57354	chr6:47328139-47328438	intra_enh	47328139	47328438	chr6	-0.81
CDYL	25377	chr6:4746771-4747339	intra_enh	4746771	4747339	chr6	-0.87
CENPQ	2411	chr6:49541360-49541570	intra_enh	49541360	49541570	chr6	-0.45
DST	120584	chr6:56494884-56495256	intra_enh	56494884	56495256	chr6	-0.97
DST	102209	chr6:56512987-56513903	intra_enh	56512987	56513903	chr6	-0.96
F13A1	71825	chr6:6193936-6194262	intra_enh	6193936	6194262	chr6	-0.91
F13A1	65468	chr6:6331304-6331479	intra_enh	6331304	6331479	chr6	-0.80

PHF3	4465	chr6:64408725-64408893	intra_enh	64408725	64408893	chr6	-0.71
PHF3	17750	chr6:64431898-64432379	intra_enh	64431898	64432379	chr6	-0.77
PHF3	18508	chr6:64432534-64433259	intra_enh	64432534	64433259	chr6	-0.85
PHF3	26044	chr6:64440181-64440682	intra_enh	64440181	64440682	chr6	-0.90
B3GAT2	99728	chr6:71623706-71623857	intra_enh	71623706	71623857	chr6	-0.71
B3GAT2	99318	chr6:71624064-71624321	intra_enh	71624064	71624321	chr6	-0.79
SSR1	74546	chr6:7183927-7184072	intra_enh	7183927	7184072	chr6	-0.36
SSR1	74062	chr6:7184373-7184595	intra_enh	7184373	7184595	chr6	-0.51
KCNQ5-IT1	102498	chr6:73499344-73499535	intra_enh	73499344	73499535	chr6	-0.46
KCNQ5-IT1	139330	chr6:73535885-73536658	intra_enh	73535885	73536658	chr6	-0.36
KHDC1	4778	chr6:74071776-74071988	intra_enh	74071776	74071988	chr6	-0.83
TXNDC5	10707	chr6:7844529-7844677	intra_enh	7844529	7844677	chr6	-0.91
PIP5K1P1	22308	chr6:7908936-7909111	intra_enh	7908936	7909111	chr6	-0.95
PHIP	7732	chr6:79836840-79837155	intra_enh	79836840	79837155	chr6	-0.54
HMGN3-AS1	2324	chr6:79997659-79997909	intra_enh	79997659	79997909	chr6	-0.86
CYB5R4	2452	chr6:84628434-84628645	intra_enh	84628434	84628645	chr6	-0.56
CYB5R4	3102	chr6:84628752-84629628	intra_enh	84628752	84629628	chr6	-0.87
CYB5R4	3748	chr6:84629758-84629915	intra_enh	84629758	84629915	chr6	-0.81
ORC3	55212	chr6:88411593-88411836	intra_enh	88411593	88411836	chr6	-0.89
AKIRIN2	10046	chr6:88458541-88458776	intra_enh	88458541	88458776	chr6	-0.34
AKIRIN2	7684	chr6:88460716-88461323	intra_enh	88460716	88461323	chr6	-0.43
AKIRIN2	6824	chr6:88461474-88462287	intra_enh	88461474	88462287	chr6	-0.55
LOC101928911	41306	chr6:88592413-88592790	intra_enh	88592413	88592790	chr6	-0.68
LOC101928911	94234	chr6:88645125-88645935	intra_enh	88645125	88645935	chr6	-0.90
LOC101928911	123704	chr6:88674946-88675054	intra_enh	88674946	88675054	chr6	-0.74
CNR1	6816	chr6:88925605-88925734	intra_enh	88925605	88925734	chr6	-0.73
LOC101928936	102423	chr6:89407779-89408683	intra_enh	89407779	89408683	chr6	-0.55
CASP8AP2	5316	chr6:90601583-90601725	intra_enh	90601583	90601725	chr6	-0.30
BACH2	43348	chr6:91019931-91020070	intra_enh	91019931	91020070	chr6	-0.40
MAP3K7	49192	chr6:91304164-91304937	intra_enh	91304164	91304937	chr6	-0.58
FHL5	47469	chr6:97164527-97164699	intra_enh	97164527	97164699	chr6	-0.93
LOC101927365	7346	chr6:99972087-99972153	intra_enh	99972087	99972153	chr6	-0.50
LOC101927365	3426	chr6:99975850-99976230	intra_enh	99975850	99976230	chr6	-0.43
LINC01007	65134	chr7:100933782-10093396	intra_enh	100933782	100933961	chr7	-0.82
CUX1	49171	chr7:101296617-10129692	intra_enh	101296617	101296925	chr7	-0.84
CUX1	54446	chr7:101301951-10130214	intra_enh	101301951	101302142	chr7	-0.72
CUX1	70894	chr7:101318376-10131861	intra_enh	101318376	101318613	chr7	-0.84
CUX1	71773	chr7:101319290-10131945	intra_enh	101319290	101319456	chr7	-0.67
CUX1	124288	chr7:101371803-10137197	intra_enh	101371803	101371973	chr7	-0.34
CUX1	137060	chr7:101384441-10138488	intra_enh	101384441	101384880	chr7	-0.58
CUX1	164568	chr7:101411910-10141242	intra_enh	101411910	101412427	chr7	-0.33
KMT2E	13854	chr7:104455649-10445580	intra_enh	104455649	104455804	chr7	-0.44
ATXN7L1	67105	chr7:105236934-10523739	intra_enh	105236934	105237392	chr7	-0.55
CDHR3	30008	chr7:105420838-10542096	intra_enh	105420838	105420963	chr7	-0.37
PRKAR2B	8898	chr7:106480939-10648168	intra_enh	106480939	106481680	chr7	-0.98
DOCK4-AS1	179140	chr7:111414821-11141505	intra_enh	111414821	111415052	chr7	-0.78
C7orf60	73068	chr7:112294015-11229418	intra_enh	112294015	112294186	chr7	-0.73
LINC01510	40730	chr7:116001128-11600163	intra_enh	116001128	116001633	chr7	-0.63
CPED1	147040	chr7:120563657-12056378	intra_enh	120563657	120563783	chr7	-0.49
MIR592	398758	chr7:126086661-12608677	intra_enh	126086661	126086771	chr7	-0.54
MIR592	358945	chr7:126126472-12612658	intra_enh	126126472	126126586	chr7	-0.77
MIR592	358280	chr7:126127081-12612730	intra_enh	126127081	126127308	chr7	-0.86
SND1	86646	chr7:127165964-12716620	intra_enh	127165964	127166200	chr7	-0.73
SND1-IT1	126873	chr7:127297751-12729809	intra_enh	127297751	127298095	chr7	-0.73
IRF5	22916	chr7:128390650-12839109	intra_enh	128390650	128391099	chr7	-0.56

TNPO3	48158	chr7:128434025-12843458	intra_enh	128434025	128434586	chr7	-0.94
TNPO3	4237	chr7:128478147-12847830	intra_enh	128478147	128478307	chr7	-0.38
UBE2H	19536	chr7:129360370-12936059	intra_enh	129360370	129360598	chr7	-0.32
KLHDC10	43580	chr7:129540732-12954159	intra_enh	129540732	129541596	chr7	-0.55
LOC100506860	45632	chr7:130294335-13029445	intra_enh	130294335	130294453	chr7	-0.31
LOC101928782	313700	chr7:131559164-13155927	intra_enh	131559164	131559272	chr7	-0.81
PLXNA4	8056	chr7:131919847-13191999	intra_enh	131919847	131919994	chr7	-0.89
CHCHD3	212900	chr7:132204323-13220461	intra_enh	132204323	132204612	chr7	-0.86
LRGUK	149157	chr7:133313251-13331372	intra_enh	133313251	133313723	chr7	-0.81
LRGUK	76449	chr7:133385871-13338651	intra_enh	133385871	133386519	chr7	-0.95
LRGUK	81335	chr7:133543641-13354431	intra_enh	133543641	133544317	chr7	-0.86
LUZP6	33554	chr7:135278896-13527948	intra_enh	135278896	135279483	chr7	-0.96
LUZP6	15889	chr7:135296260-13529745	intra_enh	135296260	135297450	chr7	-0.88
LUZP6	14402	chr7:135298309-13529837	intra_enh	135298309	135298374	chr7	-0.73
LOC100130880	17780	chr7:137270745-13727096	intra_enh	137270745	137270960	chr7	-0.79
ZC3HAV1	10294	chr7:138434560-13843486	intra_enh	138434560	138434863	chr7	-0.83
MKRN1	3442	chr7:139822315-13982247	intra_enh	139822315	139822476	chr7	-0.40
CLCN1	9352	chr7:142732557-14273282	intra_enh	142732557	142732827	chr7	-0.95
TPK1	23050	chr7:144140780-14414128	intra_enh	144140780	144141281	chr7	-0.42
TPK1	8959	chr7:144154989-14415525	intra_enh	144154989	144155253	chr7	-0.94
TPK1	8361	chr7:144155524-14415591	intra_enh	144155524	144155914	chr7	-0.95
TPK1	3144	chr7:144160864-14416100	intra_enh	144160864	144161008	chr7	-0.85
C7orf33	313742	chr7:147604713-14760498	intra_enh	147604713	147604980	chr7	-0.54
C7orf33	285097	chr7:147633438-14763354	intra_enh	147633438	147633544	chr7	-0.74
EZH2	27200	chr7:148184277-14818439	intra_enh	148184277	148184392	chr7	-0.44
PRKAG2	45532	chr7:151097302-15109741	intra_enh	151097302	151097415	chr7	-0.38
KMT2C	16021	chr7:151747830-15174817	intra_enh	151747830	151748176	chr7	-0.64
LMBR1	27350	chr7:156351188-15635144	intra_enh	156351188	156351440	chr7	-0.78
MIR5707	42964	chr7:158119980-15812008	intra_enh	158119980	158120084	chr7	-0.84
HDAC9	115892	chr7:18208752-18209224	intra_enh	18208752	18209224	chr7	-0.84
HDAC9	116978	chr7:18209937-18210212	intra_enh	18209937	18210212	chr7	-0.77
HDAC9	139480	chr7:18362064-18362759	intra_enh	18362064	18362759	chr7	-0.26
HDAC9	105446	chr7:18396388-18396505	intra_enh	18396388	18396505	chr7	-0.26
HDAC9	35926	chr7:18465851-18466081	intra_enh	18465851	18466081	chr7	-0.69
HDAC9	5986	chr7:18509301-18509576	intra_enh	18509301	18509576	chr7	-0.78
HDAC9	5420	chr7:18509691-18510318	intra_enh	18509691	18510318	chr7	-0.66
HDAC9	7143	chr7:18522470-18522664	intra_enh	18522470	18522664	chr7	-0.84
HDAC9	15040	chr7:18530348-18530580	intra_enh	18530348	18530580	chr7	-0.34
HDAC9	15436	chr7:18530815-18530905	intra_enh	18530815	18530905	chr7	-0.32
HDAC9	62574	chr7:18577876-18578119	intra_enh	18577876	18578119	chr7	-0.50
LINC01162	75669	chr7:20917159-20917327	intra_enh	20917159	20917327	chr7	-0.66
RAPGEF5	23737	chr7:22339063-22339579	intra_enh	22339063	22339579	chr7	-0.82
RAPGEF5	10126	chr7:22352559-22353306	intra_enh	22352559	22353306	chr7	-0.91
RAPGEF5	65338	chr7:22428156-22428636	intra_enh	22428156	22428636	chr7	-0.80
RAPGEF5	69689	chr7:22432520-22432974	intra_enh	22432520	22432974	chr7	-0.93
STEAP1B	30794	chr7:22475555-22475710	intra_enh	22475555	22475710	chr7	-0.83
STEAP1B	11071	chr7:22495280-22495430	intra_enh	22495280	22495430	chr7	-0.61
LOC401312	3222	chr7:22668213-22668699	intra_enh	22668213	22668699	chr7	-0.96
GPNMB	15528	chr7:23268269-23268467	intra_enh	23268269	23268467	chr7	-0.29
MALSU1	58861	chr7:23364048-23364602	intra_enh	23364048	23364602	chr7	-0.35
MALSU1	67489	chr7:23372891-23373015	intra_enh	23372891	23373015	chr7	-0.54
CHST12	4004	chr7:2413683-2413765	intra_enh	2413683	2413765	chr7	-0.86
NPY	6052	chr7:24296250-24296514	intra_enh	24296250	24296514	chr7	-0.48
MPP6	37686	chr7:24617077-24617510	intra_enh	24617077	24617510	chr7	-0.89
MPP6	80062	chr7:24659597-24659744	intra_enh	24659597	24659744	chr7	-0.37

OSBPL3	54962	chr7:24843719-24843888	intra_enh	24843719	24843888	chr7	-0.70
OSBPL3	9884	chr7:24908588-24908713	intra_enh	24908588	24908713	chr7	-0.35
NFE2L3	14836	chr7:26173131-26173280	intra_enh	26173131	26173280	chr7	-0.37
NFE2L3	15086	chr7:26173405-26173506	intra_enh	26173405	26173506	chr7	-0.48
SNX10	13594	chr7:26311454-26311809	intra_enh	26311454	26311809	chr7	-0.46
SNX10	23203	chr7:26321119-26321363	intra_enh	26321119	26321363	chr7	-0.78
TTYH3	9556	chr7:2647575-2647793	intra_enh	2647575	2647793	chr7	-0.51
TTYH3	9916	chr7:2647897-2648190	intra_enh	2647897	2648190	chr7	-0.27
TAX1BP1	177912	chr7:27923990-27924309	intra_enh	27923990	27924309	chr7	-0.68
TAX1BP1	178760	chr7:27924701-27925294	intra_enh	27924701	27925294	chr7	-0.84
TAX1BP1	179422	chr7:27925602-27925719	intra_enh	27925602	27925719	chr7	-0.85
JAZF1-AS1	187473	chr7:27998948-27999306	intra_enh	27998948	27999306	chr7	-0.92
JAZF1-AS1	5882	chr7:28180575-28180861	intra_enh	28180575	28180861	chr7	-0.53
JAZF1-AS1	2332	chr7:28184169-28184368	intra_enh	28184169	28184368	chr7	-0.68
JAZF1	19856	chr7:28206638-28206998	intra_enh	28206638	28206998	chr7	-0.89
CREB5	30953	chr7:28336321-28336513	intra_enh	28336321	28336513	chr7	-0.30
LOC102724484	74182	chr7:29289240-29289347	intra_enh	29289240	29289347	chr7	-0.84
CARD11	71386	chr7:2978557-2978884	intra_enh	2978557	2978884	chr7	-0.38
SCRN1	31534	chr7:29964102-29964730	intra_enh	29964102	29964730	chr7	-0.62
FKBP14	5873	chr7:30026797-30027341	intra_enh	30026797	30027341	chr7	-0.67
PLEKHA8	34118	chr7:30068554-30068682	intra_enh	30068554	30068682	chr7	-0.54
DKFZP586I142	25083	chr7:30350741-30351473	intra_enh	30350741	30351473	chr7	-0.39
DKFZP586I142	22839	chr7:30353211-30353491	intra_enh	30353211	30353491	chr7	-0.36
NOD1	15234	chr7:30469617-30469751	intra_enh	30469617	30469751	chr7	-0.67
GGCT	2860	chr7:30508021-30508224	intra_enh	30508021	30508224	chr7	-0.84
FAM188B	26972	chr7:30804409-30804647	intra_enh	30804409	30804647	chr7	-0.65
FAM188B	29722	chr7:30807163-30807393	intra_enh	30807163	30807393	chr7	-0.90
LOC100129603	6717	chr7:3157787-3158243	intra_enh	3157787	3158243	chr7	-0.87
LOC100129603	5300	chr7:3159347-3159517	intra_enh	3159347	3159517	chr7	-0.85
NT5C3A	8288	chr7:33055385-33055796	intra_enh	33055385	33055796	chr7	-0.87
8-Sep	4611	chr7:35811675-35811787	intra_enh	35811675	35811787	chr7	-0.47
8-Sep	5016	chr7:35812003-35812270	intra_enh	35812003	35812270	chr7	-0.77
SDK1	387911	chr7:3747734-3748128	intra_enh	3747734	3748128	chr7	-0.63
SDK1	387337	chr7:3748314-3748696	intra_enh	3748314	3748696	chr7	-0.48
SDK1	368536	chr7:3767226-3767385	intra_enh	3767226	3767385	chr7	-0.45
TRG-AS1	28288	chr7:38375902-38376079	intra_enh	38375902	38376079	chr7	-0.57
CDK13	18416	chr7:39974655-39975140	intra_enh	39974655	39975140	chr7	-0.49
CDK13	19999	chr7:39976370-39976592	intra_enh	39976370	39976592	chr7	-0.61
CDK13	23610	chr7:39979884-39980300	intra_enh	39979884	39980300	chr7	-0.65
CDK13	26138	chr7:39982494-39982746	intra_enh	39982494	39982746	chr7	-0.81
CDK13	29396	chr7:39985633-39986123	intra_enh	39985633	39986123	chr7	-0.80
SUGCT	99304	chr7:40240161-40240642	intra_enh	40240161	40240642	chr7	-0.87
LINC01450	277320	chr7:40708670-40708814	intra_enh	40708670	40708814	chr7	-0.75
PSMA2	2446	chr7:42935472-42936296	intra_enh	42935472	42936296	chr7	-0.34
MIR3943	110425	chr7:43267380-43267506	intra_enh	43267380	43267506	chr7	-0.68
MIR3943	110738	chr7:43267692-43267821	intra_enh	43267692	43267821	chr7	-0.85
OGDH	24782	chr7:44636958-44637894	intra_enh	44636958	44637894	chr7	-0.25
C7orf72	49338	chr7:50155484-50155644	intra_enh	50155484	50155644	chr7	-0.47
C7orf72	56454	chr7:50162590-50162771	intra_enh	50162590	50162771	chr7	-0.84
IKZF1	58172	chr7:50387292-50387427	intra_enh	50387292	50387427	chr7	-0.68
ZNF713	15657	chr7:55963198-55963764	intra_enh	55963198	55963764	chr7	-0.60
CYTH3	13536	chr7:6265049-6265416	intra_enh	6265049	6265416	chr7	-0.31
ZNF736	6530	chr7:63417885-63418544	intra_enh	63417885	63418544	chr7	-0.84
ZNF92	5748	chr7:64481788-64481999	intra_enh	64481788	64481999	chr7	-0.54
ZNF92	13744	chr7:64489798-64489982	intra_enh	64489798	64489982	chr7	-0.95

AUTS2	6478	chr7:68708225-68708411	intra_enh	68708225	68708411	chr7	-0.53
AUTS2	14706	chr7:68716488-68716603	intra_enh	68716488	68716603	chr7	-0.62
AUTS2	15094	chr7:68716866-68717001	intra_enh	68716866	68717001	chr7	-0.72
AUTS2	21334	chr7:68723097-68723251	intra_enh	68723097	68723251	chr7	-0.28
AUTS2	48340	chr7:68749982-68750379	intra_enh	68749982	68750379	chr7	-0.89
AUTS2	128826	chr7:68830597-68830735	intra_enh	68830597	68830735	chr7	-0.79
AUTS2	149818	chr7:68851397-68851920	intra_enh	68851397	68851920	chr7	-0.78
AUTS2	157246	chr7:68858723-68859449	intra_enh	68858723	68859449	chr7	-0.57
AUTS2	159112	chr7:68860703-68861200	intra_enh	68860703	68861200	chr7	-0.65
AUTS2	164161	chr7:68865792-68866210	intra_enh	68865792	68866210	chr7	-0.85
AUTS2	181683	chr7:68883389-68883657	intra_enh	68883389	68883657	chr7	-0.75
AUTS2	202802	chr7:68904588-68904695	intra_enh	68904588	68904695	chr7	-0.64
AUTS2	203056	chr7:68904817-68904976	intra_enh	68904817	68904976	chr7	-0.31
AUTS2	207814	chr7:68909587-68909721	intra_enh	68909587	68909721	chr7	-0.79
AUTS2	260048	chr7:68961756-68962020	intra_enh	68961756	68962020	chr7	-0.31
AUTS2	352602	chr7:69054358-69054526	intra_enh	69054358	69054526	chr7	-0.51
WBSCR17	434276	chr7:69801097-69801266	intra_enh	69801097	69801266	chr7	-0.63
LIMK1	15570	chr7:73120410-73120534	intra_enh	73120410	73120534	chr7	-0.66
MIR590	7430	chr7:73235931-73236133	intra_enh	73235931	73236133	chr7	-0.27
MIR590	5455	chr7:73237911-73238103	intra_enh	73237911	73238103	chr7	-0.73
PMS2P3	91709	chr7:75086799-75087399	intra_enh	75086799	75087399	chr7	-0.96
HIP1	13423	chr7:75192623-75192983	intra_enh	75192623	75192983	chr7	-0.95
HIP1	7182	chr7:75198905-75199183	intra_enh	75198905	75199183	chr7	-0.91
YWHAG	3073	chr7:75823133-75823277	intra_enh	75823133	75823277	chr7	-0.33
PHTF2	19096	chr7:77326261-77326695	intra_enh	77326261	77326695	chr7	-0.63
PHTF2	63546	chr7:77370837-77371020	intra_enh	77370837	77371020	chr7	-0.45
RPL13AP17	92425	chr7:77721794-77722344	intra_enh	77721794	77722344	chr7	-0.76
PCLO	323229	chr7:82306676-82307134	intra_enh	82306676	82307134	chr7	-0.91
PCLO	237606	chr7:82392048-82393008	intra_enh	82392048	82393008	chr7	-0.78
PCLO	198405	chr7:82431301-82432157	intra_enh	82431301	82432157	chr7	-0.90
PCLO	109317	chr7:82520748-82520886	intra_enh	82520748	82520886	chr7	-0.82
KIAA1324L	5858	chr7:86438723-86439449	intra_enh	86438723	86439449	chr7	-0.94
KIAA1324L	13217	chr7:86446291-86446599	intra_enh	86446291	86446599	chr7	-0.40
CDK14	19084	chr7:90157478-90157647	intra_enh	90157478	90157647	chr7	-0.90
CDK14	3035	chr7:90173552-90173670	intra_enh	90173552	90173670	chr7	-0.43
CDK14	28916	chr7:90205880-90206080	intra_enh	90205880	90206080	chr7	-0.62
CDK14	29406	chr7:90206373-90206568	intra_enh	90206373	90206568	chr7	-0.57
CDK14	30034	chr7:90206767-90207428	intra_enh	90206767	90207428	chr7	-0.69
CDK14	44958	chr7:90221882-90222161	intra_enh	90221882	90222161	chr7	-0.82
FAM133B	3472	chr7:92053731-92053964	intra_enh	92053731	92053964	chr7	-0.46
FAM133B	30938	chr7:92088495-92088670	intra_enh	92088495	92088670	chr7	-0.45
CDK6	115676	chr7:92185420-92185564	intra_enh	92185420	92185564	chr7	-0.69
CDK6	101984	chr7:92199016-92199351	intra_enh	92199016	92199351	chr7	-0.92
CDK6	54774	chr7:92246315-92246473	intra_enh	92246315	92246473	chr7	-0.82
PPP1R9A	13574	chr7:94390544-94390893	intra_enh	94390544	94390893	chr7	-0.93
BHLHA15	12961	chr7:97666284-97666794	intra_enh	97666284	97666794	chr7	-0.98
BRI3	32762	chr7:97781558-97781793	intra_enh	97781558	97781793	chr7	-0.92
COX19	2598	chr7:979108-979220	intra_enh	979108	979220	chr7	-0.79
SMURF1	31900	chr7:98547522-98548038	intra_enh	98547522	98548038	chr7	-0.74
STAG3	12348	chr7:99625579-99625718	intra_enh	99625579	99625718	chr7	-0.59
STAG3	12706	chr7:99625845-99626167	intra_enh	99625845	99626167	chr7	-0.65
STAG3	13446	chr7:99626576-99626916	intra_enh	99626576	99626916	chr7	-0.70
PILRA	20053	chr7:99828961-99829149	intra_enh	99828961	99829149	chr7	-0.63
AGFG2	2730	chr7:99977384-99977613	intra_enh	99977384	99977613	chr7	-0.94
AGFG2	8776	chr7:99983274-99983815	intra_enh	99983274	99983815	chr7	-0.95

FBXO43	3011	chr8:101224098-10122443	intra_enh	101224098	101224432	chr8	-0.65
FBXO43	2424	chr8:101224639-10122506	intra_enh	101224639	101225065	chr8	-0.63
GRHL2	8911	chr8:102582555-10258295	intra_enh	102582555	102582951	chr8	-0.96
LOC104054148	60858	chr8:103126636-10312674	intra_enh	103126636	103126748	chr8	-0.52
UBR5	8384	chr8:103485330-10348609	intra_enh	103485330	103486090	chr8	-0.61
UBR5	6622	chr8:103487397-10348754	intra_enh	103487397	103487547	chr8	-0.30
AZIN1	5023	chr8:103940156-10394100	intra_enh	103940156	103941006	chr8	-0.53
ATP6V1C1	64500	chr8:104037772-10403807	intra_enh	104037772	104038073	chr8	-0.77
PRSS55	26472	chr8:10446743-10447128	intra_enh	10446743	10447128	chr8	-0.90
DCAF13	5866	chr8:104489966-10449053	intra_enh	104489966	104490535	chr8	-0.53
DCAF13	4882	chr8:104491191-10449127	intra_enh	104491191	104491276	chr8	-0.39
RP1L1	24583	chr8:10525289-10525601	intra_enh	10525289	10525601	chr8	-0.78
MIR1322	20039	chr8:10700266-10700384	intra_enh	10700266	10700384	chr8	-0.78
OXR1	59619	chr8:107679533-10767964	intra_enh	107679533	107679649	chr8	-0.91
EIF3E	4204	chr8:109325872-10932599	intra_enh	109325872	109325991	chr8	-0.68
EIF3E	3806	chr8:109326210-10932645	intra_enh	109326210	109326451	chr8	-0.64
MIR598	36717	chr8:10966807-10967071	intra_enh	10966807	10967071	chr8	-0.96
EBAG9	81222	chr8:110539778-11053998	intra_enh	110539778	110539986	chr8	-0.52
EBAG9	3869	chr8:110625788-11062601	intra_enh	110625788	110626010	chr8	-0.71
FAM167A-AS1	43100	chr8:11306317-11306522	intra_enh	11306317	11306522	chr8	-0.57
FAM167A	19196	chr8:11342353-11342626	intra_enh	11342353	11342626	chr8	-0.91
TRPS1	221450	chr8:116527712-11652821	intra_enh	116527712	116528215	chr8	-0.80
RAD21-AS1	6064	chr8:117949718-11794983	intra_enh	117949718	117949837	chr8	-0.69
SAMD12-AS1	54727	chr8:119647159-11964822	intra_enh	119647159	119648227	chr8	-0.41
DEPTOR	30164	chr8:120984927-12098554	intra_enh	120984927	120985549	chr8	-0.94
LOC101927543	58656	chr8:121783650-12178438	intra_enh	121783650	121784382	chr8	-0.83
LOC101927543	54230	chr8:121788392-12178849	intra_enh	121788392	121788491	chr8	-0.60
LOC101927543	18208	chr8:121823844-12182508	intra_enh	121823844	121825085	chr8	-0.97
SNTB1	7968	chr8:121884877-12188616	intra_enh	121884877	121886167	chr8	-0.91
RNF139-AS1	2794	chr8:125552802-12555316	intra_enh	125552802	125553161	chr8	-0.64
NDUFB9	55756	chr8:125676084-12567647	intra_enh	125676084	125676473	chr8	-0.32
NDUFB9	61756	chr8:125682083-12568247	intra_enh	125682083	125682474	chr8	-0.25
SQLE	5648	chr8:126085400-12608569	intra_enh	126085400	126085697	chr8	-0.37
TRIB1	167568	chr8:126344016-12634433	intra_enh	126344016	126344337	chr8	-0.55
LINC00824	9296	chr8:129636703-12963692	intra_enh	129636703	129636921	chr8	-0.31
ASAP1-IT1	94965	chr8:131282610-13128338	intra_enh	131282610	131283384	chr8	-0.75
ASAP1-IT1	36804	chr8:131340962-13134135	intra_enh	131340962	131341353	chr8	-0.92
ASAP1-IT1	10758	chr8:131367018-13136738	intra_enh	131367018	131367389	chr8	-0.92
ASAP1-IT1	57860	chr8:131435777-13143586	intra_enh	131435777	131435866	chr8	-0.84
DLC1	131674	chr8:13284968-13285285	intra_enh	13284968	13285285	chr8	-0.66
DLC1	131307	chr8:13285393-13285593	intra_enh	13285393	13285593	chr8	-0.71
EFR3A	12658	chr8:132997945-13299844	intra_enh	132997945	132998444	chr8	-0.66
MIR7848	87574	chr8:134040238-13404062	intra_enh	134040238	134040629	chr8	-0.66
ZFAT-AS1	3117	chr8:135676103-13567665	intra_enh	135676103	135676651	chr8	-0.61
ZFAT	4862	chr8:135772996-13577324	intra_enh	135772996	135773247	chr8	-0.32
ZFAT	4266	chr8:135773632-13577380	intra_enh	135773632	135773804	chr8	-0.45
AGO2	37818	chr8:141676890-14167712	intra_enh	141676890	141677129	chr8	-0.50
RNU6-31P	135521	chr8:141869844-14186992	intra_enh	141869844	141869922	chr8	-0.32
PTK2	109660	chr8:141970858-14197101	intra_enh	141970858	141971011	chr8	-0.50
PTK2	74804	chr8:142005703-14200587	intra_enh	142005703	142005878	chr8	-0.67
TSNARE1	15436	chr8:143466960-14346720	intra_enh	143466960	143467200	chr8	-0.67
MIR7112	53099	chr8:145336456-14533660	intra_enh	145336456	145336602	chr8	-0.44
PSD3	38394	chr8:18748997-18749163	intra_enh	18748997	18749163	chr8	-0.51
PSD3	102083	chr8:18813300-18813486	intra_enh	18813300	18813486	chr8	-0.81
CSGALNACT1	6208	chr8:19498021-19498235	intra_enh	19498021	19498235	chr8	-0.97

CSGALNACT1	20736	chr8:19563478-19563799	intra_enh	19563478	19563799	chr8	-0.97
XPO7	40712	chr8:21873777-21873895	intra_enh	21873777	21873895	chr8	-0.67
PPP3CC	10404	chr8:22343958-22344087	intra_enh	22343958	22344087	chr8	-0.48
SORBS3	2149	chr8:22467214-22467472	intra_enh	22467214	22467472	chr8	-0.26
PEBP4	11510	chr8:22829537-22830174	intra_enh	22829537	22830174	chr8	-0.80
BNIP3L	6604	chr8:26302719-26303366	intra_enh	26302719	26303366	chr8	-0.79
PTK2B	41733	chr8:27280333-27281125	intra_enh	27280333	27281125	chr8	-0.67
CHRNA2	13371	chr8:27379256-27379462	intra_enh	27379256	27379462	chr8	-0.37
NUGGC	11078	chr8:27986142-27986318	intra_enh	27986142	27986318	chr8	-0.81
PNOC	4350	chr8:28247622-28247841	intra_enh	28247622	28247841	chr8	-0.89
ZNF395	14872	chr8:28284969-28285080	intra_enh	28284969	28285080	chr8	-0.41
ZNF395	5732	chr8:28294036-28294291	intra_enh	28294036	28294291	chr8	-0.69
FBXO16	22088	chr8:28381541-28381790	intra_enh	28381541	28381790	chr8	-0.95
INTS9	6887	chr8:28796392-28796538	intra_enh	28796392	28796538	chr8	-0.68
INTS9	4954	chr8:28798197-28798599	intra_enh	28798197	28798599	chr8	-0.77
HMBOX1	15136	chr8:28818873-28819684	intra_enh	28818873	28819684	chr8	-0.59
HMBOX1	98954	chr8:28902845-28903346	intra_enh	28902845	28903346	chr8	-0.96
HMBOX1	110002	chr8:28913761-28914527	intra_enh	28913761	28914527	chr8	-0.98
SARAF	2784	chr8:30057065-30057898	intra_enh	30057065	30057898	chr8	-0.53
GTF2E2	7030	chr8:30628096-30628403	intra_enh	30628096	30628403	chr8	-0.56
GTF2E2	4042	chr8:30631138-30631337	intra_enh	30631138	30631337	chr8	-0.40
LOC101929550	151134	chr8:35536134-35536359	intra_enh	35536134	35536359	chr8	-0.87
WHSC1L1	22650	chr8:38335881-38336716	intra_enh	38335881	38336716	chr8	-0.78
WHSC1L1	16378	chr8:38342446-38342694	intra_enh	38342446	38342694	chr8	-0.89
FGFR1	36210	chr8:38408036-38408585	intra_enh	38408036	38408585	chr8	-0.45
FGFR1	25266	chr8:38418918-38419590	intra_enh	38418918	38419590	chr8	-0.78
TACC1	18875	chr8:38744945-38745061	intra_enh	38744945	38745061	chr8	-0.61
TACC1	18550	chr8:38745217-38745439	intra_enh	38745217	38745439	chr8	-0.42
TACC1	16124	chr8:38779845-38780160	intra_enh	38779845	38780160	chr8	-0.72
TACC1	16625	chr8:38780280-38780726	intra_enh	38780280	38780726	chr8	-0.91
IDO2	17103	chr8:39928406-39929060	intra_enh	39928406	39929060	chr8	-0.78
GOLGA7	17156	chr8:41484238-41484729	intra_enh	41484238	41484729	chr8	-0.87
GINS4	18893	chr8:41524563-41524983	intra_enh	41524563	41524983	chr8	-0.62
LOC102723729	5350	chr8:41560248-41560539	intra_enh	41560248	41560539	chr8	-0.40
LOC102723729	28390	chr8:41583343-41583524	intra_enh	41583343	41583524	chr8	-0.55
KAT6A	8252	chr8:42020325-42020494	intra_enh	42020325	42020494	chr8	-0.31
KAT6A	7157	chr8:42021089-42021921	intra_enh	42021089	42021921	chr8	-0.29
PLAT	4132	chr8:42180126-42180313	intra_enh	42180126	42180313	chr8	-0.77
IKBKB	13386	chr8:42261235-42261489	intra_enh	42261235	42261489	chr8	-0.65
FNTA	3182	chr8:43033673-43033888	intra_enh	43033673	43033888	chr8	-0.43
HGSNAT	23486	chr8:43138174-43138293	intra_enh	43138174	43138293	chr8	-0.48
SNTG1	704840	chr8:51691422-51692039	intra_enh	51691422	51692039	chr8	-0.94
SNTG1	706406	chr8:51693191-51693402	intra_enh	51693191	51693402	chr8	-0.27
SNTG1	728514	chr8:51715099-51715710	intra_enh	51715099	51715710	chr8	-0.83
PXDNL	413520	chr8:52470870-52471205	intra_enh	52470870	52471205	chr8	-0.62
TOX	166938	chr8:60027299-60027468	intra_enh	60027299	60027468	chr8	-0.67
CLVS1	180858	chr8:62543885-62543987	intra_enh	62543885	62543987	chr8	-0.36
LINC00251	5240	chr8:66249668-66250113	intra_enh	66249668	66250113	chr8	-0.45
MTFR1	2349	chr8:66721633-66721945	intra_enh	66721633	66721945	chr8	-0.50
PDE7A	45568	chr8:66818096-66818536	intra_enh	66818096	66818536	chr8	-0.91
PDE7A	11584	chr8:66904604-66905277	intra_enh	66904604	66905277	chr8	-0.42
C8orf46	10930	chr8:67578891-67579056	intra_enh	67578891	67579056	chr8	-0.83
C8orf44-SGK3	7112	chr8:67749391-67749514	intra_enh	67749391	67749514	chr8	-0.54
SGK3	3736	chr8:67790609-67791274	intra_enh	67790609	67791274	chr8	-0.92
PTTG3P	15643	chr8:67827094-67827208	intra_enh	67827094	67827208	chr8	-0.78

SNORD87	4638	chr8:67992503-67992896	intra_enh	67992503	67992896	chr8	-0.65
ARFGEF1	162353	chr8:68580543-68581095	intra_enh	68580543	68581095	chr8	-0.46
CPA6	143756	chr8:68677179-68677656	intra_enh	68677179	68677656	chr8	-0.91
CPA6	57772	chr8:68763201-68763602	intra_enh	68763201	68763602	chr8	-0.85
CPA6	21974	chr8:68798649-68799751	intra_enh	68798649	68799751	chr8	-0.98
SLCO5A1	111853	chr8:70795917-70796293	intra_enh	70795917	70796293	chr8	-0.76
LOC286190	8830	chr8:71691927-71692461	intra_enh	71691927	71692461	chr8	-0.69
UBE2W	42824	chr8:74910829-74910922	intra_enh	74910829	74910922	chr8	-0.64
UBE2W	18944	chr8:74934542-74934971	intra_enh	74934542	74934971	chr8	-0.60
TPD52	11288	chr8:81166775-81167045	intra_enh	81166775	81167045	chr8	-0.36
TPD52	15580	chr8:81171123-81171281	intra_enh	81171123	81171281	chr8	-0.80
TPD52	9798	chr8:81235909-81236475	intra_enh	81235909	81236475	chr8	-0.71
PAG1	110076	chr8:82076610-82076954	intra_enh	82076610	82076954	chr8	-0.67
PAG1	109532	chr8:82077262-82077390	intra_enh	82077262	82077390	chr8	-0.64
PAG1	37002	chr8:82149713-82149999	intra_enh	82149713	82149999	chr8	-0.67
SNX16	5281	chr8:82911667-82911923	intra_enh	82911667	82911923	chr8	-0.62
CA13	18353	chr8:86363239-86363399	intra_enh	86363239	86363399	chr8	-0.51
CPNE3	2964	chr8:87598634-87598833	intra_enh	87598634	87598833	chr8	-0.43
CPNE3	8943	chr8:87604416-87605010	intra_enh	87604416	87605010	chr8	-0.33
LOC101929709	31933	chr8:90807068-90807214	intra_enh	90807068	90807214	chr8	-0.82
C8orf88	65501	chr8:92000830-92001492	intra_enh	92000830	92001492	chr8	-0.88
C8orf88	48526	chr8:92017920-92018352	intra_enh	92017920	92018352	chr8	-0.96
TMEM55A	8756	chr8:92113399-92113848	intra_enh	92113399	92113848	chr8	-0.95
OTUD6B-AS1	2945	chr8:92148545-92148753	intra_enh	92148545	92148753	chr8	-0.88
TNKS	52823	chr8:9503582-9503772	intra_enh	9503582	9503772	chr8	-0.55
TP53INP1	3470	chr8:96026870-96027774	intra_enh	96026870	96027774	chr8	-0.75
C8orf37-AS1	20136	chr8:96329978-96330226	intra_enh	96329978	96330226	chr8	-0.83
C8orf37-AS1	19808	chr8:96330347-96330514	intra_enh	96330347	96330514	chr8	-0.87
MTDH	6936	chr8:98732449-98732588	intra_enh	98732449	98732588	chr8	-0.30
TGFBR1	32005	chr9:100939052-10093942	intra_enh	100939052	100939422	chr9	-0.36
NAMA	215788	chr9:101393050-10139324	intra_enh	101393050	101393245	chr9	-0.82
LOC101928438	190992	chr9:101430869-10143113	intra_enh	101430869	101431131	chr9	-0.94
ERP44	32260	chr9:101868596-10186918	intra_enh	101868596	101869189	chr9	-0.50
ERP44	9062	chr9:101892032-10189214	intra_enh	101892032	101892148	chr9	-0.41
LOC286367	4346	chr9:106571602-10657261	intra_enh	106571602	106572611	chr9	-0.76
ABCA1	64562	chr9:106665597-10666597	intra_enh	106665597	106665974	chr9	-0.65
ABCA1	58724	chr9:106671435-10667181	intra_enh	106671435	106671814	chr9	-0.52
ABCA1	16572	chr9:106713262-10671429	intra_enh	106713262	106714290	chr9	-0.94
ABCA1	15698	chr9:106714539-10671476	intra_enh	106714539	106714760	chr9	-0.92
ABCA1	15058	chr9:106714866-10671571	intra_enh	106714866	106715715	chr9	-0.87
SLC44A1	11837	chr9:107058420-10705868	intra_enh	107058420	107058682	chr9	-0.92
SLC44A1	13500	chr9:107059706-10706072	intra_enh	107059706	107060722	chr9	-0.90
SLC44A1	74336	chr9:107120622-10712147	intra_enh	107120622	107121477	chr9	-0.80
SLC44A1	86190	chr9:107132301-10713350	intra_enh	107132301	107133508	chr9	-0.95
TMEM245	17366	chr9:110904627-11090473	intra_enh	110904627	110904734	chr9	-0.61
TMEM245	9739	chr9:110912234-11091238	intra_enh	110912234	110912380	chr9	-0.44
TMEM245	8937	chr9:110912554-11091366	intra_enh	110912554	110913664	chr9	-0.64
TMEM245	6475	chr9:110915323-11091581	intra_enh	110915323	110915819	chr9	-0.71
PALM2	123957	chr9:111705913-11170679	intra_enh	111705913	111706793	chr9	-0.37
AKAP2	78534	chr9:111772097-11177223	intra_enh	111772097	111772230	chr9	-0.70
AKAP2	18581	chr9:111869170-11186938	intra_enh	111869170	111869388	chr9	-0.33
AKAP2	14606	chr9:111912884-11191310	intra_enh	111912884	111913105	chr9	-0.57
AKAP2	16298	chr9:111943675-11194412	intra_enh	111943675	111944122	chr9	-0.38
TXNDC8	28857	chr9:112110921-11211133	intra_enh	112110921	112111337	chr9	-0.92
MIR4668	12142	chr9:113721950-11372216	intra_enh	113721950	113722166	chr9	-0.69

SNX30	21422	chr9:114574298-11457445	intra_enh	114574298	114574454	chr9	-0.54
SNX30	23732	chr9:114576488-11457688	intra_enh	114576488	114576883	chr9	-0.91
RGS3	11060	chr9:115314274-11531489	intra_enh	115314274	115314899	chr9	-0.34
RGS3	4588	chr9:115378331-11537844	intra_enh	115378331	115378446	chr9	-0.71
AKNA	11169	chr9:116207616-11620773	intra_enh	116207616	116207734	chr9	-0.71
DFNB31	5924	chr9:116299225-11629955	intra_enh	116299225	116299559	chr9	-0.70
TRIM32	73573	chr9:118562587-11856335	intra_enh	118562587	118563359	chr9	-0.97
TLR4	2410	chr9:119508631-11950873	intra_enh	119508631	119508733	chr9	-0.39
MEGF9	2552	chr9:122513912-12251415	intra_enh	122513912	122514155	chr9	-0.36
PHF19	4362	chr9:122683637-12268394	intra_enh	122683637	122683943	chr9	-0.97
RAB14	46257	chr9:122957867-12295799	intra_enh	122957867	122957991	chr9	-0.69
RAB14	16690	chr9:122987431-12298756	intra_enh	122987431	122987561	chr9	-0.75
RAB14	5658	chr9:122998331-12299872	intra_enh	122998331	122998724	chr9	-0.32
MIR548D1	81399	chr9:123717281-12371744	intra_enh	123717281	123717449	chr9	-0.74
MIR548D1	4328	chr9:123794052-12379482	intra_enh	123794052	123794820	chr9	-0.42
MRRF	15284	chr9:124088149-12408834	intra_enh	124088149	124088343	chr9	-0.92
MRRF	16776	chr9:124089130-12409034	intra_enh	124089130	124090345	chr9	-0.85
PTGS1	15666	chr9:124193027-12419314	intra_enh	124193027	124193144	chr9	-0.82
RC3H2	7100	chr9:124700172-12470039	intra_enh	124700172	124700397	chr9	-0.62
MIR600HG	17644	chr9:124935132-12493531	intra_enh	124935132	124935312	chr9	-0.64
MIR600HG	19058	chr9:124936358-12493691	intra_enh	124936358	124936914	chr9	-0.85
MIR600HG	21794	chr9:124939277-12493946	intra_enh	124939277	124939466	chr9	-0.82
MIR600HG	62947	chr9:124980317-12498073	intra_enh	124980317	124980733	chr9	-0.70
NR6A1	35627	chr9:126537166-12653840	intra_enh	126537166	126538400	chr9	-0.86
GOLGA1	23750	chr9:126766807-12676711	intra_enh	126766807	126767110	chr9	-0.93
SCAI	17465	chr9:126928119-12692827	intra_enh	126928119	126928271	chr9	-0.33
MAPKAP1	72828	chr9:127436407-12743660	intra_enh	127436407	127436604	chr9	-0.52
MAPKAP1	72478	chr9:127436724-12743698	intra_enh	127436724	127436989	chr9	-0.46
ANGPTL2	40984	chr9:128965567-12896613	intra_enh	128965567	128966132	chr9	-0.96
ST6GALNAC6	2432	chr9:129704036-12970432	intra_enh	129704036	129704323	chr9	-0.78
SWI5	9288	chr9:130087401-13008766	intra_enh	130087401	130087662	chr9	-0.96
SPTAN1	3980	chr9:130358485-13035878	intra_enh	130358485	130358786	chr9	-0.47
FNBP1	45668	chr9:131799535-13179971	intra_enh	131799535	131799716	chr9	-0.52
FNBP1	24796	chr9:131820396-13182060	intra_enh	131820396	131820600	chr9	-0.71
FNBP1	21818	chr9:131823221-13182373	intra_enh	131823221	131823730	chr9	-0.68
FNBP1	16548	chr9:131828645-13182884	intra_enh	131828645	131828846	chr9	-0.78
FNBP1	14887	chr9:131830270-13183054	intra_enh	131830270	131830544	chr9	-0.64
FNBP1	14295	chr9:131830779-13183121	intra_enh	131830779	131831219	chr9	-0.61
FNBP1	13623	chr9:131831565-13183177	intra_enh	131831565	131831777	chr9	-0.70
FNBP1	8456	chr9:131836713-13183696	intra_enh	131836713	131836962	chr9	-0.63
FNBP1	6692	chr9:131838351-13183885	intra_enh	131838351	131838853	chr9	-0.74
C9orf9	10244	chr9:134754250-13475445	intra_enh	134754250	134754459	chr9	-0.36
NRARP	18589	chr9:139334861-13933536	intra_enh	139334861	139335365	chr9	-0.61
NFIB	4358	chr9:14299599-14299777	intra_enh	14299599	14299777	chr9	-0.81
ZDHHC21	4110	chr9:14678969-14679772	intra_enh	14678969	14679772	chr9	-0.40
SNAPC3	3760	chr9:15416216-15416864	intra_enh	15416216	15416864	chr9	-0.41
DENND4C	3208	chr9:19223846-19224094	intra_enh	19223846	19224094	chr9	-0.49
PTPLAD2	103976	chr9:20917613-20917706	intra_enh	20917613	20917706	chr9	-0.73
MTAP	11556	chr9:21804096-21804285	intra_enh	21804096	21804285	chr9	-0.50
LOC101929563	81682	chr9:23580513-23580920	intra_enh	23580513	23580920	chr9	-0.39
EQTN	70208	chr9:27357037-27357655	intra_enh	27357037	27357655	chr9	-0.80
EQTN	72584	chr9:27359679-27359764	intra_enh	27359679	27359764	chr9	-0.73
RFX3	95965	chr9:3289536-3289726	intra_enh	3289536	3289726	chr9	-0.87
RFX3	95346	chr9:3290106-3290394	intra_enh	3290106	3290394	chr9	-0.59
B4GALT1-AS1	41834	chr9:33115049-33115171	intra_enh	33115049	33115171	chr9	-0.48

B4GALT1-AS1	13444	chr9:33143036-33143964	intra_enh	33143036	33143964	chr9	-0.84
B4GALT1-AS1	12558	chr9:33144089-33144682	intra_enh	33144089	33144682	chr9	-0.84
UBE2R2	35376	chr9:33842471-33842641	intra_enh	33842471	33842641	chr9	-0.41
RFX3	9746	chr9:3469523-3469960	intra_enh	3469523	3469960	chr9	-0.93
TMEM8B	15378	chr9:35834759-35834986	intra_enh	35834759	35834986	chr9	-0.87
MELK	66688	chr9:36629352-36629739	intra_enh	36629352	36629739	chr9	-0.64
ZCCHC7	69396	chr9:37179739-37180242	intra_enh	37179739	37180242	chr9	-0.58
ZCCHC7	81173	chr9:37191632-37191902	intra_enh	37191632	37191902	chr9	-0.88
ZCCHC7	86711	chr9:37197135-37197475	intra_enh	37197135	37197475	chr9	-0.45
ZCCHC7	87284	chr9:37197617-37198138	intra_enh	37197617	37198138	chr9	-0.41
ZCCHC7	92074	chr9:37202438-37202898	intra_enh	37202438	37202898	chr9	-0.77
GRHPR	124500	chr9:37287484-37288927	intra_enh	37287484	37288927	chr9	-0.37
GRHPR	89464	chr9:37322777-37323708	intra_enh	37322777	37323708	chr9	-0.63
RCL1	20024	chr9:4802511-4803200	intra_enh	4802511	4803200	chr9	-0.64
RCL1	17544	chr9:4812107-4812340	intra_enh	4812107	4812340	chr9	-0.77
RLN1	2754	chr9:5326914-5327326	intra_enh	5326914	5327326	chr9	-0.74
RLN1	2302	chr9:5327442-5327701	intra_enh	5327442	5327701	chr9	-0.91
ERMP1	68694	chr9:5754240-5754536	intra_enh	5754240	5754536	chr9	-0.88
KANK1	60784	chr9:635909-636132	intra_enh	635909	636132	chr9	-0.65
KANK1	59707	chr9:637008-637186	intra_enh	637008	637186	chr9	-0.51
PIP5K1B	3059	chr9:70513083-70513331	intra_enh	70513083	70513331	chr9	-0.90
LOC101927069	26383	chr9:70753960-70754430	intra_enh	70753960	70754430	chr9	-0.94
LOC101927069	20476	chr9:70759804-70760399	intra_enh	70759804	70760399	chr9	-0.72
TJP2	11517	chr9:70998143-70998315	intra_enh	70998143	70998315	chr9	-0.83
SMC5	2182	chr9:72065787-72065970	intra_enh	72065787	72065970	chr9	-0.40
KLF9	8006	chr9:72211318-72211458	intra_enh	72211318	72211458	chr9	-0.79
ABHD17B	19924	chr9:73695236-73696852	intra_enh	73695236	73696852	chr9	-0.90
GCNT1	2900	chr9:78260884-78261088	intra_enh	78260884	78261088	chr9	-0.79
GCNT1	2572	chr9:78261200-78261428	intra_enh	78261200	78261428	chr9	-0.78
GCNT1	5694	chr9:78269370-78269791	intra_enh	78269370	78269791	chr9	-0.73
GCNT1	7650	chr9:78271357-78271716	intra_enh	78271357	78271716	chr9	-0.72
GCNT1	8499	chr9:78272216-78272554	intra_enh	78272216	78272554	chr9	-0.66
GCNT1	120656	chr9:78425742-78426305	intra_enh	78425742	78426305	chr9	-0.38
GCNT1	126113	chr9:78431079-78431883	intra_enh	78431079	78431883	chr9	-0.48
LINC01507	34106	chr9:81663235-81663505	intra_enh	81663235	81663505	chr9	-0.29
LINC01507	43088	chr9:81672129-81672576	intra_enh	81672129	81672576	chr9	-0.86
LINC01507	46692	chr9:81675872-81676040	intra_enh	81675872	81676040	chr9	-0.83
LINC01507	47169	chr9:81676242-81676624	intra_enh	81676242	81676624	chr9	-0.74
LINC01507	53925	chr9:81682892-81683486	intra_enh	81682892	81683486	chr9	-0.60
LINC01507	56164	chr9:81684950-81685906	intra_enh	81684950	81685906	chr9	-0.67
TLE1	23638	chr9:83469723-83469833	intra_enh	83469723	83469833	chr9	-0.73
UBQLN1	19050	chr9:85493605-85494271	intra_enh	85493605	85494271	chr9	-0.86
UBQLN1	11512	chr9:85501408-85501543	intra_enh	85501408	85501543	chr9	-0.74
ZCCHC6	6978	chr9:88152199-88152290	intra_enh	88152199	88152290	chr9	-0.57
ZCCHC6	6253	chr9:88152738-88153200	intra_enh	88152738	88153200	chr9	-0.48
DAPK1	19361	chr9:89322434-89322824	intra_enh	89322434	89322824	chr9	-0.92
DAPK1	21984	chr9:89324974-89325530	intra_enh	89324974	89325530	chr9	-0.93
DAPK1	57410	chr9:89360510-89360846	intra_enh	89360510	89360846	chr9	-0.98
ROR2	112577	chr9:93639611-93639767	intra_enh	93639611	93639767	chr9	-0.93
ROR2	112088	chr9:93640096-93640261	intra_enh	93640096	93640261	chr9	-0.68
NOL8	2828	chr9:94130433-94130618	intra_enh	94130433	94130618	chr9	-0.80
FAM120AOS	52045	chr9:95307608-95307874	intra_enh	95307608	95307874	chr9	-0.70
PTPRD-AS1	753850	chr9:9601756-9601976	intra_enh	9601756	9601976	chr9	-0.35
PTPRD-AS1	754212	chr9:9602096-9602360	intra_enh	9602096	9602360	chr9	-0.27
PTPRD-AS1	754788	chr9:9602549-9603060	intra_enh	9602549	9603060	chr9	-0.49

MIR2278	4172	chr9:96607772-96608012	intra_enh	96607772	96608012	chr9	-0.26
MIR2278	72206	chr9:96683993-96684548	intra_enh	96683993	96684548	chr9	-0.49
PTPRD	822546	chr9:9779979-9780376	intra_enh	9779979	9780376	chr9	-0.37
PTPRD	820282	chr9:9782162-9782723	intra_enh	9782162	9782723	chr9	-0.35
ZNF367	2990	chr9:98217435-98217566	intra_enh	98217435	98217566	chr9	-0.72
TSTD2	2317	chr9:99437931-99438271	intra_enh	99437931	99438271	chr9	-0.28
ANP32B	6566	chr9:99790961-99792788	intra_enh	99790961	99792788	chr9	-0.36
ANP32B	9336	chr9:99794587-99794700	intra_enh	99794587	99794700	chr9	-0.43
ANP32B	9918	chr9:99794929-99795524	intra_enh	99794929	99795524	chr9	-0.39
ANP32B	27368	chr9:99812562-99812790	intra_enh	99812562	99812790	chr9	-0.73
ANP32B	27716	chr9:99812918-99813130	intra_enh	99812918	99813130	chr9	-0.81
TRIM14	15999	chr9:99905397-99905517	intra_enh	99905397	99905517	chr9	-0.60
TRIM14	10046	chr9:99931340-99931665	intra_enh	99931340	99931665	chr9	-0.67
CLCN4	59462	chrX:10025306-10025739	intra_enh	10025306	10025739	chrX	-0.60
BTK	10369	chrX:100517060-10051793	intra_enh	100517060	100517938	chrX	-0.97
LOC286437	11815	chrX:103267693-10326788	intra_enh	103267693	103267885	chrX	-0.55
ACSL4	5084	chrX:108858132-10885825	intra_enh	108858132	108858256	chrX	-0.72
ACSL4	4684	chrX:108858475-10885871	intra_enh	108858475	108858712	chrX	-0.74
AMMECR1	3358	chrX:109450757-10945203	intra_enh	109450757	109452030	chrX	-0.95
AMMECR1	22982	chrX:109470781-10947125	intra_enh	109470781	109471254	chrX	-0.89
RGAG1	4318	chrX:109544447-10954479	intra_enh	109544447	109544798	chrX	-0.52
HCCS	33329	chrX:11072533-11072777	intra_enh	11072533	11072777	chrX	-0.66
AMELX	43159	chrX:11264309-11264913	intra_enh	11264309	11264913	chrX	-0.91
ARHGAP6	64880	chrX:11290751-11291142	intra_enh	11290751	11291142	chrX	-0.67
ARHGAP6	45914	chrX:11309739-11310085	intra_enh	11309739	11310085	chrX	-0.34
PGRMC1	2302	chrX:118256497-11825657	intra_enh	118256497	118256576	chrX	-0.35
NKRF	3098	chrX:118620709-11862084	intra_enh	118620709	118620844	chrX	-0.29
NKRF	14306	chrX:118638096-11863826	intra_enh	118638096	118638265	chrX	-0.85
MIR766	18096	chrX:118682847-11868302	intra_enh	118682847	118683025	chrX	-0.44
ZBTB33	11925	chrX:119280328-11928079	intra_enh	119280328	119280794	chrX	-0.92
THOC2	19006	chrX:122675406-12267575	intra_enh	122675406	122675753	chrX	-0.53
THOC2	18430	chrX:122676078-12267623	intra_enh	122676078	122676233	chrX	-0.42
XIAP	18359	chrX:122839516-12284059	intra_enh	122839516	122840594	chrX	-0.51
SH2D1A	158405	chrX:123465791-12346664	intra_enh	123465791	123466643	chrX	-0.93
TLR7	3902	chrX:12798976-12799073	intra_enh	12798976	12799073	chrX	-0.49
XPNPEP2	19234	chrX:128719703-12872001	intra_enh	128719703	128720018	chrX	-0.58
SASH3	7408	chrX:128748919-12874904	intra_enh	128748919	128749041	chrX	-0.62
RAB33A	11940	chrX:129145314-12914546	intra_enh	129145314	129145469	chrX	-0.55
ZNF280C	3164	chrX:129227253-12922762	intra_enh	129227253	129227627	chrX	-0.77
ZNF280C	2384	chrX:129227945-12922849	intra_enh	129227945	129228495	chrX	-0.53
ENOX2	69138	chrX:129795660-12979600	intra_enh	129795660	129796009	chrX	-0.86
GPC3	202309	chrX:132744934-13274512	intra_enh	132744934	132745128	chrX	-0.67
ZNF75D	4064	chrX:134301560-13430166	intra_enh	134301560	134301669	chrX	-0.44
DDX26B-AS1	35722	chrX:134517937-13451804	intra_enh	134517937	134518040	chrX	-0.59
FHL1	8866	chrX:135066995-13506754	intra_enh	135066995	135067542	chrX	-0.95
ARHGEF6	18043	chrX:135672974-13567328	intra_enh	135672974	135673280	chrX	-0.89
RAB9A	8558	chrX:13625507-13625929	intra_enh	13625507	13625929	chrX	-0.59
RAB9A	9310	chrX:13626371-13626568	intra_enh	13626371	13626568	chrX	-0.53
FMR1NB	43314	chrX:146913632-14691407	intra_enh	146913632	146914075	chrX	-0.39
AFF2	6243	chrX:147395990-14739615	intra_enh	147395990	147396156	chrX	-0.67
AFF2	25274	chrX:147414925-14741528	intra_enh	147414925	147415284	chrX	-0.92
AFF2	30232	chrX:147419897-14742022	intra_enh	147419897	147420227	chrX	-0.86
AFF2	79390	chrX:147469017-14746942	intra_enh	147469017	147469422	chrX	-0.90
AFF2	44517	chrX:147563730-14756384	intra_enh	147563730	147563848	chrX	-0.28
AFF2	52512	chrX:147660729-14766090	intra_enh	147660729	147660908	chrX	-0.41

MAMLD1	33486	chrX:149397713-14939801	intra_enh	149397713	149398011	chrX	-0.56
MAMLD1	33874	chrX:149398167-14939833	intra_enh	149398167	149398334	chrX	-0.52
ABCD1	10466	chrX:152653904-15265406	intra_enh	152653904	152654061	chrX	-0.64
PIR-FIGF	25926	chrX:15392915-15393940	intra_enh	15392915	15393940	chrX	-0.92
BRCC3	2264	chrX:153955091-15395521	intra_enh	153955091	153955214	chrX	-0.42
CTPS2	7222	chrX:16632960-16633119	intra_enh	16632960	16633119	chrX	-0.53
CTPS2	6749	chrX:16633337-16633689	intra_enh	16633337	16633689	chrX	-0.56
TXLNG	2795	chrX:16717173-16717365	intra_enh	16717173	16717365	chrX	-0.68
REPS2	60742	chrX:16935402-16935549	intra_enh	16935402	16935549	chrX	-0.65
SH3KBP1	8223	chrX:19607155-19607371	intra_enh	19607155	19607371	chrX	-0.83
SH3KBP1	8502	chrX:19607507-19607577	intra_enh	19607507	19607577	chrX	-0.60
SH3KBP1	44266	chrX:19683480-19683664	intra_enh	19683480	19683664	chrX	-0.90
SH3KBP1	23740	chrX:19704026-19704169	intra_enh	19704026	19704169	chrX	-0.67
SH3KBP1	7462	chrX:19719966-19720786	intra_enh	19719966	19720786	chrX	-0.81
SH3KBP1	6882	chrX:19720906-19721005	intra_enh	19720906	19721005	chrX	-0.64
SH3KBP1	37686	chrX:19777689-19778270	intra_enh	19777689	19778270	chrX	-0.32
KLHL15	6532	chrX:23948429-23948954	intra_enh	23948429	23948954	chrX	-0.72
KLHL15	5774	chrX:23949311-23949590	intra_enh	23949311	23949590	chrX	-0.65
ZFX	2870	chrX:24074531-24075093	intra_enh	24074531	24075093	chrX	-0.74
CXorf21	9425	chrX:30496390-30496668	intra_enh	30496390	30496668	chrX	-0.29
DMD	42742	chrX:31152020-31152387	intra_enh	31152020	31152387	chrX	-0.95
LOC101927476	4929	chrX:40011706-40012376	intra_enh	40011706	40012376	chrX	-0.91
GPR34	91865	chrX:41340886-41341720	intra_enh	41340886	41341720	chrX	-0.65
GPR34	84094	chrX:41348892-41349255	intra_enh	41348892	41349255	chrX	-0.93
GPR34	16072	chrX:41449094-41449387	intra_enh	41449094	41449387	chrX	-0.86
GPR82	16776	chrX:41451462-41451685	intra_enh	41451462	41451685	chrX	-0.69
KDM6A	16878	chrX:44634175-44634308	intra_enh	44634175	44634308	chrX	-0.73
KDM6A	24272	chrX:44641569-44641704	intra_enh	44641569	44641704	chrX	-0.82
KDM6A	35398	chrX:44652366-44653159	intra_enh	44652366	44653159	chrX	-0.72
SLC9A7	38372	chrX:46465105-46465256	intra_enh	46465105	46465256	chrX	-0.68
SLC9A7	15560	chrX:46487530-46488455	intra_enh	46487530	46488455	chrX	-0.88
SLC9A7	14898	chrX:46488560-46488749	intra_enh	46488560	46488749	chrX	-0.86
RP2	2812	chrX:46583995-46584210	intra_enh	46583995	46584210	chrX	-0.42
JADE3	42397	chrX:46698938-46699476	intra_enh	46698938	46699476	chrX	-0.89
JADE3	48514	chrX:46704850-46705798	intra_enh	46704850	46705798	chrX	-0.41
JADE3	56668	chrX:46713235-46713722	intra_enh	46713235	46713722	chrX	-0.77
OTUD5	4398	chrX:48695382-48695499	intra_enh	48695382	48695499	chrX	-0.44
IQSEC2	7847	chrX:53359208-53359594	intra_enh	53359208	53359594	chrX	-0.68
MIR4767	92044	chrX:6983735-6983976	intra_enh	6983735	6983976	chrX	-0.91
MIR4767	63422	chrX:7012334-7012623	intra_enh	7012334	7012623	chrX	-0.27
MIR4767	56954	chrX:7018642-7019251	intra_enh	7018642	7019251	chrX	-0.26
MIR4767	55822	chrX:7019955-7020200	intra_enh	7019955	7020200	chrX	-0.59
MIR4767	32630	chrX:7043175-7043365	intra_enh	7043175	7043365	chrX	-0.77
MIR4767	27135	chrX:7048708-7048822	intra_enh	7048708	7048822	chrX	-0.73
MIR4767	23918	chrX:7051733-7052230	intra_enh	7051733	7052230	chrX	-0.54
OGT	5746	chrX:70674962-70675801	intra_enh	70674962	70675801	chrX	-0.70
STS	11704	chrX:7158994-7159353	intra_enh	7158994	7159353	chrX	-0.60
MIR384	12136	chrX:76068161-76068470	intra_enh	76068161	76068470	chrX	-0.69
CYSLTR1	5830	chrX:77463929-77464099	intra_enh	77463929	77464099	chrX	-0.74
P2RY10	12466	chrX:78099599-78100301	intra_enh	78099599	78100301	chrX	-0.48
BRWD3	9711	chrX:79941978-79942380	intra_enh	79941978	79942380	chrX	-0.86
RPA4	47460	chrX:95977913-95978291	intra_enh	95977913	95978291	chrX	-0.49
RPA4	285172	chrX:96310548-96310921	intra_enh	96310548	96310921	chrX	-0.68
DIAPH2-AS1	237840	chrX:96468244-96468457	intra_enh	96468244	96468457	chrX	-0.42
DIAPH2-AS1	66281	chrX:96639661-96640157	intra_enh	96639661	96640157	chrX	-0.91

WWC3	46572	chrX:9990099-9990633	intra_enh	9990099	9990633	chrX	-0.90
UTY	99128	chrY:14002430-14003201	intra_enh	14002430	14003201	chrY	-0.97
UTY	63238	chrY:14038297-14039114	intra_enh	14038297	14039114	chrY	-0.92
KDM5D	32074	chrY:20333549-20334730	intra_enh	20333549	20334730	chrY	-0.97
KDM5D	26855	chrY:20339068-20339650	intra_enh	20339068	20339650	chrY	-0.94
EIF1AY	2577	chrY:21149483-21149639	intra_enh	21149483	21149639	chrY	-0.32
LINC00278	15475	chrY:2946339-2946683	intra_enh	2946339	2946683	chrY	-0.50
LINC00278	22804	chrY:2953463-2954218	intra_enh	2953463	2954218	chrY	-0.90
TBL1Y	150744	chrY:6989400-6989540	intra_enh	6989400	6989540	chrY	-0.41
TBL1Y	174884	chrY:7013502-7013719	intra_enh	7013502	7013719	chrY	-0.50
PRKY	4506	chrY:7206365-7206671	intra_enh	7206365	7206671	chrY	-0.42
PRKY	9152	chrY:7211062-7211265	intra_enh	7211062	7211265	chrY	-0.64
FRRS1	8414	chr1:100012220-10001248	inter_enh	100012220	100012483	chr1	-0.68
FRRS1	21170	chr1:100024860-10002535	inter_enh	100024860	100025355	chr1	-0.54
LOC101928370	14570	chr1:101459998-10146020	inter_enh	101459998	101460205	chr1	-0.42
S1PR1	9732	chr1:101484387-10148486	inter_enh	101484387	101484861	chr1	-0.57
S1PR1	13772	chr1:101488269-10148905	inter_enh	101488269	101489059	chr1	-0.75
MIR548H3	25802	chr1:105104030-10510459	inter_enh	105104030	105104591	chr1	-0.46
LINC01342	7378	chr1:1069496-1069776	inter_enh	1069496	1069776	chr1	-0.59
PRMT6	46088	chr1:107354546-10735485	inter_enh	107354546	107354855	chr1	-0.96
PRMT6	45582	chr1:107354990-10735542	inter_enh	107354990	107355423	chr1	-0.96
FNDC7	9128	chr1:109047863-10904803	inter_enh	109047863	109048037	chr1	-0.44
RBM15	14390	chr1:110697733-11069797	inter_enh	110697733	110697979	chr1	-0.48
LOC101929181	45971	chr1:11546137-11546269	inter_enh	11546137	11546269	chr1	-0.46
LOC101929181	45664	chr1:11546476-11546544	inter_enh	11546476	11546544	chr1	-0.36
MAN1A2	7748	chr1:117703733-11770398	inter_enh	117703733	117703984	chr1	-0.31
MAN1A2	7329	chr1:117704170-11770438	inter_enh	117704170	117704384	chr1	-0.61
KIAA2013	25641	chr1:11883294-11883568	inter_enh	11883294	11883568	chr1	-0.83
EMBP1	2596	chr1:120959627-12096004	inter_enh	120959627	120960046	chr1	-0.45
MIR7846	5168	chr1:12144229-12144608	inter_enh	12144229	12144608	chr1	-0.92
PRDM2	34552	chr1:13864688-13864848	inter_enh	13864688	13864848	chr1	-0.32
PRDM2	12512	chr1:13886693-13886923	inter_enh	13886693	13886923	chr1	-0.35
ENSA	7218	chr1:148860936-14886109	inter_enh	148860936	148861095	chr1	-0.50
CTSK	20433	chr1:149027014-14902720	inter_enh	149027014	149027204	chr1	-0.26
SETDB1	3838	chr1:149161547-14916165	inter_enh	149161547	149161652	chr1	-0.43
SETDB1	3506	chr1:149161862-14916200	inter_enh	149161862	149162002	chr1	-0.51
ZNF687	4876	chr1:149516237-14951684	inter_enh	149516237	149516840	chr1	-0.89
THEM4	10202	chr1:150158985-15015939	inter_enh	150158985	150159390	chr1	-0.79
THEM4	10730	chr1:150159637-15015979	inter_enh	150159637	150159794	chr1	-0.36
THEM4	11960	chr1:150160852-15016103	inter_enh	150160852	150161039	chr1	-0.63
S100A16	13860	chr1:151838212-15183834	inter_enh	151838212	151838344	chr1	-0.71
SHE	23358	chr1:152717712-15271787	inter_enh	152717712	152717871	chr1	-0.44
ADAR	42051	chr1:152909076-15290918	inter_enh	152909076	152909186	chr1	-0.58
SSR2	4980	chr1:154262281-15426244	inter_enh	154262281	154262442	chr1	-0.80
SEMA4A	3956	chr1:154382355-15438245	inter_enh	154382355	154382450	chr1	-0.43
C1orf61	16811	chr1:154682542-15468269	inter_enh	154682542	154682696	chr1	-0.76
NES	12482	chr1:154901270-15490139	inter_enh	154901270	154901393	chr1	-0.80
NES	12002	chr1:154925650-15492598	inter_enh	154925650	154925982	chr1	-0.28
FCRL5	46506	chr1:155742354-15574250	inter_enh	155742354	155742501	chr1	-0.32
FCRL5	17197	chr1:155806079-15580618	inter_enh	155806079	155806183	chr1	-0.71
FCRL3	46850	chr1:155890258-15589058	inter_enh	155890258	155890587	chr1	-0.81
FCRL3	33732	chr1:155970927-15597108	inter_enh	155970927	155971082	chr1	-0.79
CD5L	2704	chr1:156080803-15608112	inter_enh	156080803	156081121	chr1	-0.63
CD1D	16807	chr1:156399320-15639978	inter_enh	156399320	156399786	chr1	-0.90
CD1D	2959	chr1:156413208-15641359	inter_enh	156413208	156413594	chr1	-0.62

CD1C	5563	chr1:156520591-15652065	inter_enh	156520591	156520655	chr1	-0.77
IFI16	3948	chr1:157242130-15724258	inter_enh	157242130	157242581	chr1	-0.80
VANGL2	30267	chr1:158667197-15866730	inter_enh	158667197	158667309	chr1	-0.42
VANGL2	32010	chr1:158668823-15866916	inter_enh	158668823	158669169	chr1	-0.64
VANGL2	46794	chr1:158683119-15868444	inter_enh	158683119	158684441	chr1	-0.78
SLAMF6	48613	chr1:158710688-15871143	inter_enh	158710688	158711438	chr1	-0.90
CD84	27516	chr1:158843271-15884362	inter_enh	158843271	158843622	chr1	-0.83
SLAMF7	11850	chr1:158963468-15896377	inter_enh	158963468	158963773	chr1	-0.35
SLAMF7	5006	chr1:158970327-15897060	inter_enh	158970327	158970600	chr1	-0.75
DUSP12	8548	chr1:159977511-15997780	inter_enh	159977511	159977800	chr1	-0.53
NUF2	39648	chr1:161597936-16159805	inter_enh	161597936	161598053	chr1	-0.70
MGST3	18518	chr1:163848119-16384830	inter_enh	163848119	163848309	chr1	-0.92
ARHGEF19	24507	chr1:16387110-16387260	inter_enh	16387110	16387260	chr1	-0.76
RSG1	12029	chr1:16447804-16448746	inter_enh	16447804	16448746	chr1	-0.67
CREG1	14692	chr1:165774886-16577509	inter_enh	165774886	165775091	chr1	-0.75
CREG1	14188	chr1:165775310-16577567	inter_enh	165775310	165775674	chr1	-0.27
CREG1	13094	chr1:165776490-16577668	inter_enh	165776490	165776683	chr1	-0.76
RCSD1	9787	chr1:165855736-16585688	inter_enh	165855736	165856882	chr1	-0.40
RCSD1	3590	chr1:165862404-16586260	inter_enh	165862404	165862607	chr1	-0.86
SLC19A2	22788	chr1:167744410-16774483	inter_enh	167744410	167744831	chr1	-0.78
FMO2	11830	chr1:169408906-16940937	inter_enh	169408906	169409373	chr1	-0.90
TNFSF18	32966	chr1:171253421-17125410	inter_enh	171253421	171254100	chr1	-0.95
TNFSF18	11924	chr1:171274636-17127496	inter_enh	171274636	171274967	chr1	-0.75
RC3H1	26322	chr1:172255008-17225530	inter_enh	172255008	172255304	chr1	-0.54
PADI2	22140	chr1:17340403-17340948	inter_enh	17340403	17340948	chr1	-0.94
KIAA0040	2654	chr1:173431149-17343186	inter_enh	173431149	173431864	chr1	-0.88
KIAA0040	44305	chr1:173473040-17347327	inter_enh	173473040	173473274	chr1	-0.94
LOC730102	18240	chr1:176291935-17629207	inter_enh	176291935	176292077	chr1	-0.62
C1orf220	32360	chr1:176810861-17681096	inter_enh	176810861	176810963	chr1	-0.76
MIR4424	17731	chr1:176895351-17689619	inter_enh	176895351	176896199	chr1	-0.79
FAM20B	21682	chr1:177239965-17724006	inter_enh	177239965	177240064	chr1	-0.67
CEP350	2596	chr1:178187761-17818810	inter_enh	178187761	178188107	chr1	-0.28
CALML6	7478	chr1:1828472-1828821	inter_enh	1828472	1828821	chr1	-0.45
LINC01036	20782	chr1:185307697-18530793	inter_enh	185307697	185307931	chr1	-0.36
RGS1	29411	chr1:190840731-19084104	inter_enh	190840731	190841047	chr1	-0.71
RGS13	25448	chr1:190846223-19084666	inter_enh	190846223	190846660	chr1	-0.62
RGS13	20787	chr1:190850936-19085127	inter_enh	190850936	190851270	chr1	-0.81
DENND1B	2677	chr1:196013741-19601410	inter_enh	196013741	196014105	chr1	-0.94
DENND1B	3407	chr1:196014452-19601485	inter_enh	196014452	196014854	chr1	-0.91
CAPZB	2125	chr1:19686777-19686917	inter_enh	19686777	19686917	chr1	-0.51
NR5A2	49796	chr1:198213417-19821369	inter_enh	198213417	198213696	chr1	-0.45
LINC00862	4693	chr1:198613861-19861461	inter_enh	198613861	198614613	chr1	-0.95
KIF21B	2370	chr1:199261744-19926190	inter_enh	199261744	199261900	chr1	-0.76
TNNI1	14304	chr1:199671673-19967193	inter_enh	199671673	199671930	chr1	-0.73
PHLDA3	17902	chr1:199686935-19968710	inter_enh	199686935	199687105	chr1	-0.74
CSRP1	3701	chr1:199746497-19974692	inter_enh	199746497	199746925	chr1	-0.89
CSRP1	5716	chr1:199748631-19974882	inter_enh	199748631	199748821	chr1	-0.49
OTUD3	23315	chr1:20057952-20058366	inter_enh	20057952	20058366	chr1	-0.53
BTG2	5720	chr1:201546973-20154703	inter_enh	201546973	201547038	chr1	-0.30
BTG2	6060	chr1:201547219-20154747	inter_enh	201547219	201547473	chr1	-0.69
FMOD	11426	chr1:201575572-20157593	inter_enh	201575572	201575937	chr1	-0.73
FMOD	10740	chr1:201597802-20159803	inter_enh	201597802	201598038	chr1	-0.61
FMOD	15984	chr1:201603092-20160323	inter_enh	201603092	201603237	chr1	-0.86
ATP2B4	13464	chr1:201848873-20184927	inter_enh	201848873	201849271	chr1	-0.87
LAX1	9400	chr1:201991430-20199158	inter_enh	201991430	201991582	chr1	-0.83

LOC101929441	12350	chr1:202364714-20236490	inter_enh	202364714	202364903	chr1	-0.51
PIK3C2B	8697	chr1:202734697-20273489	inter_enh	202734697	202734893	chr1	-0.63
MDM4	12806	chr1:202739148-20273949	inter_enh	202739148	202739497	chr1	-0.55
MDM4	3778	chr1:202748280-20274842	inter_enh	202748280	202748421	chr1	-0.73
MDM4	2150	chr1:202749872-20275008	inter_enh	202749872	202750084	chr1	-0.84
MDM4	49836	chr1:202801846-20280208	inter_enh	202801846	202802082	chr1	-0.56
DSTYK	3436	chr1:203450491-20345108	inter_enh	203450491	203451081	chr1	-0.72
NUAK2	21298	chr1:203536063-20353635	inter_enh	203536063	203536353	chr1	-0.54
C1orf186	5952	chr1:204461097-20446134	inter_enh	204461097	204461346	chr1	-0.95
C1orf186	12940	chr1:204468129-20446829	inter_enh	204468129	204468290	chr1	-0.79
MAPKAPK2	12796	chr1:204912106-20491227	inter_enh	204912106	204912274	chr1	-0.60
MAPKAPK2	11780	chr1:204912982-20491343	inter_enh	204912982	204913430	chr1	-0.60
IL10	14584	chr1:204997581-20499817	inter_enh	204997581	204998175	chr1	-0.57
CD55	11382	chr1:205549850-20555026	inter_enh	205549850	205550263	chr1	-0.51
CR2	39618	chr1:205654538-20565475	inter_enh	205654538	205654757	chr1	-0.51
CR2	39330	chr1:205654875-20565499	inter_enh	205654875	205654998	chr1	-0.34
SLC30A1	3430	chr1:209822089-20982221	inter_enh	209822089	209822215	chr1	-0.66
NEK2	2341	chr1:209917855-20991801	inter_enh	209917855	209918019	chr1	-0.81
NEK2	5108	chr1:209920651-20992075	inter_enh	209920651	209920758	chr1	-0.83
NEK2	5532	chr1:209920939-20992131	inter_enh	209920939	209921317	chr1	-0.55
MIR3122	41245	chr1:210358710-21035893	inter_enh	210358710	210358932	chr1	-0.76
NENF	18052	chr1:210690818-21069098	inter_enh	210690818	210690987	chr1	-0.89
BATF3	28430	chr1:210911320-21091171	inter_enh	210911320	210911719	chr1	-0.56
EIF4G3	7324	chr1:21383155-21383428	inter_enh	21383155	21383428	chr1	-0.74
DUSP10	34966	chr1:220017048-22001716	inter_enh	220017048	220017167	chr1	-0.64
FAM177B	35210	chr1:221012324-22101245	inter_enh	221012324	221012455	chr1	-0.62
FAM177B	35780	chr1:221012751-22101317	inter_enh	221012751	221013170	chr1	-0.74
LBR	46096	chr1:223729198-22372935	inter_enh	223729198	223729355	chr1	-0.74
SDE2	29885	chr1:224283275-22428387	inter_enh	224283275	224283875	chr1	-0.56
ACBD3	14647	chr1:224455636-22445575	inter_enh	224455636	224455750	chr1	-0.76
PSEN2	45720	chr1:225079089-22507925	inter_enh	225079089	225079259	chr1	-0.44
ZBTB40	32565	chr1:22618167-22618563	inter_enh	22618167	22618563	chr1	-0.95
ZBTB40	22298	chr1:22628558-22628705	inter_enh	22628558	22628705	chr1	-0.89
ZBTB40	19674	chr1:22630984-22631527	inter_enh	22630984	22631527	chr1	-0.83
EPHA8	23955	chr1:22738531-22738739	inter_enh	22738531	22738739	chr1	-0.67
TSNAX-DISC1	12686	chr1:229718256-22971841	inter_enh	229718256	229718411	chr1	-0.77
TARBP1	8322	chr1:232689540-23269004	inter_enh	232689540	232690049	chr1	-0.77
LINC01354	6260	chr1:232727584-23272819	inter_enh	232727584	232728193	chr1	-0.93
LINC01132	48425	chr1:232974535-23297513	inter_enh	232974535	232975135	chr1	-0.27
LYST	39938	chr1:234153506-23415363	inter_enh	234153506	234153634	chr1	-0.41
MDS2	19829	chr1:23806407-23806755	inter_enh	23806407	23806755	chr1	-0.92
MDS2	9906	chr1:23816429-23816580	inter_enh	23816429	23816580	chr1	-0.87
RPL11	24198	chr1:23866316-23866997	inter_enh	23866316	23866997	chr1	-0.99
COX20	33796	chr1:243031340-24303158	inter_enh	243031340	243031588	chr1	-0.50
MIR3916	9191	chr1:245441097-24544125	inter_enh	245441097	245441257	chr1	-0.32
RCAN3	15440	chr1:24685862-24686110	inter_enh	24685862	24686110	chr1	-0.89
CLIC4	7746	chr1:24936375-24936826	inter_enh	24936375	24936826	chr1	-0.73
MAN1C1	17028	chr1:25799281-25799750	inter_enh	25799281	25799750	chr1	-0.90
STMN1	7861	chr1:26113644-26113990	inter_enh	26113644	26113990	chr1	-0.54
PDIK1L	5887	chr1:26304273-26304437	inter_enh	26304273	26304437	chr1	-0.37
PDIK1L	14635	chr1:26324981-26325997	inter_enh	26324981	26325997	chr1	-0.85
PDIK1L	15647	chr1:26326319-26326683	inter_enh	26326319	26326683	chr1	-0.94
PIGV	12330	chr1:26999497-26999690	inter_enh	26999497	26999690	chr1	-0.84
WDTC1	36252	chr1:27397234-27397447	inter_enh	27397234	27397447	chr1	-0.47
IFI6	8715	chr1:27862550-27862644	inter_enh	27862550	27862644	chr1	-0.89

THEMIS2	9162	chr1:28062350-28062607	inter_enh	28062350	28062607	chr1	-0.66
THEMIS2	18008	chr1:28089493-28089803	inter_enh	28089493	28089803	chr1	-0.60
PTAFR	41854	chr1:28334112-28334263	inter_enh	28334112	28334263	chr1	-0.92
PTAFR	41139	chr1:28334684-28335122	inter_enh	28334684	28335122	chr1	-0.40
TINAGL1	4918	chr1:31809580-31809928	inter_enh	31809580	31809928	chr1	-0.87
SPOCD1	12480	chr1:32066481-32066959	inter_enh	32066481	32066959	chr1	-0.87
SPOCD1	13062	chr1:32067150-32067453	inter_enh	32067150	32067453	chr1	-0.83
PTP4A2	17950	chr1:32194447-32194606	inter_enh	32194447	32194606	chr1	-0.86
KHDRBS1	32664	chr1:32218949-32219484	inter_enh	32218949	32219484	chr1	-0.83
SFPQ	8974	chr1:35440218-35440389	inter_enh	35440218	35440389	chr1	-0.27
SFPQ	9366	chr1:35440531-35440861	inter_enh	35440531	35440861	chr1	-0.50
AGO4	10304	chr1:36035927-36036294	inter_enh	36035927	36036294	chr1	-0.91
HEYL	14218	chr1:39892097-39892212	inter_enh	39892097	39892212	chr1	-0.83
MYCL	9028	chr1:40131019-40131474	inter_enh	40131019	40131474	chr1	-0.84
MFSD2A	8838	chr1:40184445-40184619	inter_enh	40184445	40184619	chr1	-0.84
MFSD2A	18723	chr1:40212024-40212162	inter_enh	40212024	40212162	chr1	-0.40
RLF	17033	chr1:40382534-40382652	inter_enh	40382534	40382652	chr1	-0.52
RLF	7170	chr1:40392373-40392540	inter_enh	40392373	40392540	chr1	-0.72
COL9A2	27634	chr1:40583092-40583227	inter_enh	40583092	40583227	chr1	-0.45
SMAP2	9669	chr1:40602234-40602356	inter_enh	40602234	40602356	chr1	-0.47
RIMS3	3579	chr1:40907409-40907573	inter_enh	40907409	40907573	chr1	-0.29
ERI3	7454	chr1:44600852-44601133	inter_enh	44600852	44601133	chr1	-0.80
AKR1A1	5316	chr1:45783548-45783899	inter_enh	45783548	45783899	chr1	-0.79
TSPAN1	15285	chr1:46398003-46398095	inter_enh	46398003	46398095	chr1	-0.40
POMGNT1	3533	chr1:46462030-46462164	inter_enh	46462030	46462164	chr1	-0.26
OSBPL9	38102	chr1:51816965-51817094	inter_enh	51816965	51817094	chr1	-0.32
CPT2	23402	chr1:53410976-53411596	inter_enh	53410976	53411596	chr1	-0.80
SSBP3	3224	chr1:54647770-54647990	inter_enh	54647770	54647990	chr1	-0.30
MIR4422	34934	chr1:55498618-55499050	inter_enh	55498618	55499050	chr1	-0.90
MYSM1	26701	chr1:58964831-58965243	inter_enh	58964831	58965243	chr1	-0.93
LINC01358	6758	chr1:59251884-59252069	inter_enh	59251884	59252069	chr1	-0.46
FGGY	30459	chr1:59504649-59504857	inter_enh	59504649	59504857	chr1	-0.84
FGGY	30068	chr1:59505084-59505203	inter_enh	59505084	59505203	chr1	-0.48
TM2D1	8477	chr1:61972019-61972303	inter_enh	61972019	61972303	chr1	-0.86
USP1	5330	chr1:62668784-62669681	inter_enh	62668784	62669681	chr1	-0.75
PDE4B	43284	chr1:66635859-66636006	inter_enh	66635859	66636006	chr1	-0.74
INSL5	12778	chr1:67026276-67027229	inter_enh	67026276	67027229	chr1	-0.95
LOC100505887	7732	chr1:6717822-6717985	inter_enh	6717822	6717985	chr1	-0.92
C1orf141	14538	chr1:67387700-67387860	inter_enh	67387700	67387860	chr1	-0.57
CAMTA1	16752	chr1:6751164-6751273	inter_enh	6751164	6751273	chr1	-0.86
CAMTA1	7588	chr1:6760166-6760599	inter_enh	6760166	6760599	chr1	-0.74
GADD45A	8738	chr1:67913773-67915644	inter_enh	67913773	67915644	chr1	-0.50
FAM73A	9054	chr1:78008557-78009126	inter_enh	78008557	78009126	chr1	-0.83
ELTD1	46360	chr1:79291323-79291565	inter_enh	79291323	79291565	chr1	-0.56
LOC102724539	38844	chr1:8152403-8152544	inter_enh	8152403	8152544	chr1	-0.27
CLCA3P	16792	chr1:86855680-86855829	inter_enh	86855680	86855829	chr1	-0.80
CA6	27398	chr1:8901013-8901146	inter_enh	8901013	8901146	chr1	-0.27
GBP1	4805	chr1:89308329-89308545	inter_enh	89308329	89308545	chr1	-0.28
SLC2A7	39456	chr1:8969425-8969647	inter_enh	8969425	8969647	chr1	-0.48
BARHL2	4514	chr1:90959827-90959966	inter_enh	90959827	90959966	chr1	-0.54
ZNF644	35767	chr1:91295783-91296551	inter_enh	91295783	91296551	chr1	-0.77
CDC7	47655	chr1:91786593-91787221	inter_enh	91786593	91787221	chr1	-0.98
FAM69A	3732	chr1:93203303-93203496	inter_enh	93203303	93203496	chr1	-0.52
FAM69A	9797	chr1:93209268-93209662	inter_enh	93209268	93209662	chr1	-0.94
FAM69A	16312	chr1:93215680-93216280	inter_enh	93215680	93216280	chr1	-0.57

FAM69A	17246	chr1:93216788-93217041	inter_enh	93216788	93217041	chr1	-0.78
FAM69A	29454	chr1:93228820-93229424	inter_enh	93228820	93229424	chr1	-0.85
FAM69A	43925	chr1:93243529-93243657	inter_enh	93243529	93243657	chr1	-0.79
LOC100506022	8407	chr1:9403082-9403228	inter_enh	9403082	9403228	chr1	-0.33
DPYD	16086	chr1:98175143-98175438	inter_enh	98175143	98175438	chr1	-0.81
ABCC2	5342	chr10:101526938-101527	inter_enh	101526938	101527065	chr10	-0.84
DNMBP	15558	chr10:101775163-1017752	inter_enh	101775163	101775284	chr10	-0.71
KAZALD1	6940	chr10:102817874-102817	inter_enh	102817874	102817981	chr10	-0.66
LINC01514	14240	chr10:102911774-1029118	inter_enh	102911774	102911882	chr10	-0.34
LBX1	15294	chr10:102963335-102963	inter_enh	102963335	102963494	chr10	-0.39
CALHM1	8109	chr10:105216572-105216	inter_enh	105216572	105216922	chr10	-0.41
PDCD4-AS1	17886	chr10:112602396-1126031	inter_enh	112602396	112603136	chr10	-0.84
PDCD4-AS1	7550	chr10:112612929-1126132	inter_enh	112612929	112613275	chr10	-0.96
USP6NL	13521	chr10:11707096-11707534	inter_enh	11707096	11707534	chr10	-0.69
USP6NL	34988	chr10:11728687-11728876	inter_enh	11728687	11728876	chr10	-0.70
ECHDC3	43106	chr10:11781118-11781390	inter_enh	11781118	11781390	chr10	-0.36
INPP5F	25388	chr10:121449785-121450	inter_enh	121449785	121450535	chr10	-0.76
CAMK1D	4745	chr10:12426729-1242695	inter_enh	12426729	12426957	chr10	-0.93
PWWP2B	9235	chr10:134051391-134051	inter_enh	134051391	134051519	chr10	-0.76
PTPLA	30572	chr10:17668707-1766890	inter_enh	17668707	17668909	chr10	-0.59
SPAG6	11956	chr10:22662128-2266271	inter_enh	22662128	22662716	chr10	-0.76
LOC100499489	45532	chr10:22812276-2281251	inter_enh	22812276	22812516	chr10	-0.82
OTUD1	25318	chr10:23742800-2374296	inter_enh	23742800	23742968	chr10	-0.79
OTUD1	9780	chr10:23777690-2377827	inter_enh	23777690	23778275	chr10	-0.77
OTUD1	12477	chr10:23780573-2378078	inter_enh	23780573	23780785	chr10	-0.37
MAP3K8	34102	chr10:30796797-3079731	inter_enh	30796797	30797315	chr10	-0.57
SVILP1	28946	chr10:30992157-3099236	inter_enh	30992157	30992366	chr10	-0.84
SVILP1	21304	chr10:30999696-3100011	inter_enh	30999696	31000113	chr10	-0.59
ITGB1	21350	chr10:33308518-3330878	inter_enh	33308518	33308781	chr10	-0.85
ITGB1	27666	chr10:33314788-3331514	inter_enh	33314788	33315145	chr10	-0.73
LINC00838	46703	chr10:34148191-3414844	inter_enh	34148191	34148443	chr10	-0.96
KLF6	27724	chr10:3789671-3789828	inter_enh	3789671	3789828	chr10	-0.92
KLF6	20176	chr10:3796870-3797725	inter_enh	3796870	3797725	chr10	-0.30
KLF6	18750	chr10:3798520-3798928	inter_enh	3798520	3798928	chr10	-0.35
ZNF248	7732	chr10:38194597-3819490	inter_enh	38194597	38194902	chr10	-0.69
ZNF22	4289	chr10:44811844-4481213	inter_enh	44811844	44812134	chr10	-0.90
SYT15	4329	chr10:46394861-4639501	inter_enh	46394861	46395013	chr10	-0.28
C10orf128	5846	chr10:50071925-5007267	inter_enh	50071925	50072672	chr10	-0.75
ASAH2	12437	chr10:51690650-5169097	inter_enh	51690650	51690976	chr10	-0.81
LINC01468	13571	chr10:53913780-5391396	inter_enh	53913780	53913962	chr10	-0.79
ASB13	36711	chr10:5711757-5711949	inter_enh	5711757	5711949	chr10	-0.75
GDI2	2817	chr10:5898170-5898500	inter_enh	5898170	5898500	chr10	-0.27
FBXO18	36110	chr10:5935377-5935483	inter_enh	5935377	5935483	chr10	-0.78
LINC00844	5886	chr10:60422600-6042419	inter_enh	60422600	60424192	chr10	-0.98
PFKFB3	9672	chr10:6217002-6217349	inter_enh	6217002	6217349	chr10	-0.41
LOC399715	20766	chr10:6387601-6387892	inter_enh	6387601	6387892	chr10	-0.79
LOC399715	6236	chr10:6402125-6402426	inter_enh	6402125	6402426	chr10	-0.85
ADO	49019	chr10:64185248-6418575	inter_enh	64185248	64185754	chr10	-0.98
ATOH7	19040	chr10:69642773-6964290	inter_enh	69642773	69642900	chr10	-0.59
PRF1	18524	chr10:72013865-7201416	inter_enh	72013865	72014162	chr10	-0.46
PSAP	32314	chr10:73313227-7331357	inter_enh	73313227	73313576	chr10	-0.85
DDIT4	16588	chr10:73686900-7368728	inter_enh	73686900	73687289	chr10	-0.79
USP54	16127	chr10:75021111-75022023	inter_enh	75021111	75022023	chr10	-0.60
CAMK2G	5467	chr10:75309643-7531000	inter_enh	75309643	75310003	chr10	-0.47
ITIH2	16102	chr10:7769048-7769229	inter_enh	7769048	7769229	chr10	-0.66

GRID1	21018	chr10:88137177-8813732	inter_enh	88137177	88137320	chr10	-0.45
MIR4679-2	21272	chr10:90834332-9083450	inter_enh	90834332	90834507	chr10	-0.80
CH25H	43396	chr10:90913571-9091374	inter_enh	90913571	90913740	chr10	-0.76
PANK1	6864	chr10:91401875-9140247	inter_enh	91401875	91402473	chr10	-0.91
LINC00865	31357	chr10:91610359-91610811	inter_enh	91610359	91610811	chr10	-0.61
HHEX	22570	chr10:94462040-94462421	inter_enh	94462040	94462421	chr10	-0.97
HHEX	30692	chr10:94470129-9447057	inter_enh	94470129	94470576	chr10	-0.87
CYP26A1	37125	chr10:94860629-9486089	inter_enh	94860629	94860893	chr10	-0.96
LGI1	15070	chr10:95492326-95492641	inter_enh	95492326	95492641	chr10	-0.78
PIK3AP1	6882	chr10:98476846-9847745	inter_enh	98476846	98477458	chr10	-0.97
PIK3AP1	35777	chr10:98505861-9850623	inter_enh	98505861	98506233	chr10	-0.95
PIK3AP1	37969	chr10:98507765-9850871	inter_enh	98507765	98508713	chr10	-0.93
ARHGAP42	6189	chr11:100057295-1000575	inter_enh	100057295	100057559	chr11	-0.36
BIRC3	27750	chr11:101665552-1016657	inter_enh	101665552	101665727	chr11	-0.34
TMEM123	22482	chr11:101851192-1018517	inter_enh	101851192	101851743	chr11	-0.63
TMEM123	23691	chr11:101852111-1018532	inter_enh	101852111	101853243	chr11	-0.29
DDX10	2366	chr11:108038452-1080387	inter_enh	108038452	108038737	chr11	-0.96
RDX	30846	chr11:109703216-1097037	inter_enh	109703216	109703773	chr11	-0.32
POU2AF1	3314	chr11:110758218-1107591	inter_enh	110758218	110759147	chr11	-0.28
HTR3A	26870	chr11:113323938-1133243	inter_enh	113323938	113324334	chr11	-0.86
IL10RA	26712	chr11:117335508-1173356	inter_enh	117335508	117335696	chr11	-0.70
DDX6	28538	chr11:118195420-1181960	inter_enh	118195420	118196020	chr11	-0.64
CXCR5	25886	chr11:118233705-1182338	inter_enh	118233705	118233891	chr11	-0.74
CXCR5	15734	chr11:118243888-1182440	inter_enh	118243888	118244012	chr11	-0.76
BCL9L	8432	chr11:118295200-1182953	inter_enh	118295200	118295311	chr11	-0.78
LOC102724301	22429	chr11:119127850-1191280	inter_enh	119127850	119128012	chr11	-0.32
SC5D	26762	chr11:120695453-120695	inter_enh	120695453	120695644	chr11	-0.94
SC5D	29178	chr11:120697826-1206981	inter_enh	120697826	120698103	chr11	-0.82
SC5D	41805	chr11:120710357-120710	inter_enh	120710357	120710825	chr11	-0.88
SC5D	43570	chr11:120712221-1207124	inter_enh	120712221	120712490	chr11	-0.89
SC5D	47388	chr11:120715872-1207164	inter_enh	120715872	120716476	chr11	-0.85
SC5D	48936	chr11:120717637-120717	inter_enh	120717637	120717806	chr11	-0.91
SORL1	29447	chr11:120798531-120798	inter_enh	120798531	120798815	chr11	-0.57
SORL1	16634	chr11:120811300-1208116	inter_enh	120811300	120811671	chr11	-0.65
SORL1	5246	chr11:120822694-120823	inter_enh	120822694	120823054	chr11	-0.60
UBASH3B	26389	chr11:122005129-122005	inter_enh	122005129	122005305	chr11	-0.77
OR10G7	32264	chr11:123446967-123447	inter_enh	123446967	123447396	chr11	-0.91
OR8D2	10154	chr11:123704933-123705	inter_enh	123704933	123705983	chr11	-0.83
FEZ1	18216	chr11:124889526-1248897	inter_enh	124889526	124889737	chr11	-0.78
PRDM10	11672	chr11:129389243-129389	inter_enh	129389243	129389981	chr11	-0.95
PRDM10	21623	chr11:129399306-129399	inter_enh	129399306	129399820	chr11	-0.77
APLP2	26258	chr11:129418540-1294187	inter_enh	129418540	129418792	chr11	-0.93
ST14	3592	chr11:129531052-129531	inter_enh	129531052	129531544	chr11	-0.59
SPON1	33880	chr11:13906694-13907061	inter_enh	13906694	13907061	chr11	-0.93
NUCB2	46286	chr11:17208452-1720869	inter_enh	17208452	17208695	chr11	-0.68
SAA4	6671	chr11:18208226-18208352	inter_enh	18208226	18208352	chr11	-0.92
PTPN5	10252	chr11:18781046-1878114	inter_enh	18781046	18781145	chr11	-0.28
E2F8	18456	chr11:19238092-1923837	inter_enh	19238092	19238375	chr11	-0.75
IFITM5	4183	chr11:293616-293802	inter_enh	293616	293802	chr11	-0.91
FSHB	25622	chr11:30183386-3018364	inter_enh	30183386	30183645	chr11	-0.36
FSHB	24869	chr11:30233953-30234061	inter_enh	30233953	30234061	chr11	-0.27
IFITM3	8881	chr11:319723-319867	inter_enh	319723	319867	chr11	-0.74
IFITM3	19633	chr11:330393-330701	inter_enh	330393	330701	chr11	-0.78
LOC100507144	18922	chr11:35096885-35097584	inter_enh	35096885	35097584	chr11	-0.93
TRIM44	6971	chr11:35633544-3563437	inter_enh	35633544	35634370	chr11	-0.98

RAG1	26710	chr11:36519337-36519520	inter_enh	36519337	36519520	chr11	-0.75
SYT13	12663	chr11:45276972-45277274	inter_enh	45276972	45277274	chr11	-0.64
SLC35C1	12465	chr11:45795626-45795736	inter_enh	45795626	45795736	chr11	-0.61
NUP160	2729	chr11:47829282-47829444	inter_enh	47829282	47829444	chr11	-0.76
NUP160	3223	chr11:47829732-47829982	inter_enh	47829732	47829982	chr11	-0.62
NUP160	8643	chr11:47835196-47835358	inter_enh	47835196	47835358	chr11	-0.71
NUP160	16732	chr11:47843272-47843459	inter_enh	47843272	47843459	chr11	-0.35
PTPRJ	6054	chr11:47952411-47952850	inter_enh	47952411	47952850	chr11	-0.72
OR5B21	16755	chr11:58048623-58049195	inter_enh	58048623	58049195	chr11	-0.62
OR5B21	17612	chr11:58049321-58050210	inter_enh	58049321	58050210	chr11	-0.57
GLYATL2	6206	chr11:58374727-58374834	inter_enh	58374727	58374834	chr11	-0.29
FAM111B	3238	chr11:58627912-58628077	inter_enh	58627912	58628077	chr11	-0.40
FAM111B	2853	chr11:58628268-58628490	inter_enh	58628268	58628490	chr11	-0.35
MRPL16	3390	chr11:59338097-59338528	inter_enh	59338097	59338528	chr11	-0.78
MRPL16	6287	chr11:59341094-59341324	inter_enh	59341094	59341324	chr11	-0.87
MRPL16	12098	chr11:59346899-59347141	inter_enh	59346899	59347141	chr11	-0.59
CD5	40644	chr11:60585781-60585939	inter_enh	60585781	60585939	chr11	-0.35
CD5	31826	chr11:60594616-60594741	inter_enh	60594616	60594741	chr11	-0.47
VPS37C	6102	chr11:60691515-60691673	inter_enh	60691515	60691673	chr11	-0.53
FEN1	4965	chr11:61321463-61321835	inter_enh	61321463	61321835	chr11	-0.65
HRASLS2	9284	chr11:63096568-63096865	inter_enh	63096568	63096865	chr11	-0.79
SF1	3919	chr11:64306675-64306947	inter_enh	64306675	64306947	chr11	-0.30
SYVN1	11918	chr11:64670392-64670603	inter_enh	64670392	64670603	chr11	-0.60
SPDYC	10958	chr11:64683198-64683451	inter_enh	64683198	64683451	chr11	-0.96
MALAT1	19231	chr11:65002472-65002682	inter_enh	65002472	65002682	chr11	-0.70
MALAT1	3801	chr11:65017820-65018194	inter_enh	65017820	65018194	chr11	-0.90
MALAT1	3077	chr11:65018595-65018867	inter_enh	65018595	65018867	chr11	-0.85
SSSCA1-AS1	4554	chr11:65089739-65090073	inter_enh	65089739	65090073	chr11	-0.79
RBM14	6485	chr11:66133812-66134474	inter_enh	66133812	66134474	chr11	-0.93
RBM14	5613	chr11:66134811-66135219	inter_enh	66134811	66135219	chr11	-0.93
GSTP1	3826	chr11:67103586-67104042	inter_enh	67103586	67104042	chr11	-0.35
OR2AG2	3555	chr11:6750235-6750403	inter_enh	6750235	6750403	chr11	-0.71
FCHSD2	7132	chr11:72537842-72538006	inter_enh	72537842	72538006	chr11	-0.85
RELT	3749	chr11:72761004-72761602	inter_enh	72761004	72761602	chr11	-0.89
MRPL48	3402	chr11:73173090-73173235	inter_enh	73173090	73173235	chr11	-0.79
UCP2	4226	chr11:73375525-73376003	inter_enh	73375525	73376003	chr11	-0.37
UCP3	10449	chr11:73387343-73387619	inter_enh	73387343	73387619	chr11	-0.77
LOC100506258	8002	chr11:7451526-7451761	inter_enh	7451526	7451761	chr11	-0.81
WNT11	25654	chr11:75620721-75621031	inter_enh	75620721	75621031	chr11	-0.26
LOC100506127	27302	chr11:75797209-75797428	inter_enh	75797209	75797428	chr11	-0.75
INTS4	5170	chr11:77388112-77388961	inter_enh	77388112	77388961	chr11	-0.71
TENM4	42283	chr11:78871282-78871972	inter_enh	78871282	78871972	chr11	-0.96
TMEM135	7024	chr11:86419357-86419659	inter_enh	86419357	86419659	chr11	-0.26
SESN3	15654	chr11:94620810-94621206	inter_enh	94620810	94621206	chr11	-0.85
SESN3	16745	chr11:94621838-94622360	inter_enh	94621838	94622360	chr11	-0.85
WEE1	33802	chr11:9586526-9586695	inter_enh	9586526	9586695	chr11	-0.86
WEE1	36456	chr11:9589050-9589477	inter_enh	9589050	9589477	chr11	-0.61
WEE1	44524	chr11:9597131-9597533	inter_enh	9597131	9597533	chr11	-0.47
SWAP70	34804	chr11:9607310-9607477	inter_enh	9607310	9607477	chr11	-0.43
SWAP70	20958	chr11:9621091-9621388	inter_enh	9621091	9621388	chr11	-0.44
MYBPC1	24588	chr12:100488185-1004883	inter_enh	100488185	100488315	chr12	-0.69
GNPTAB	8178	chr12:100756781-1007571	inter_enh	100756781	100757127	chr12	-0.73
DRAM1	22268	chr12:100772825-1007731	inter_enh	100772825	100773108	chr12	-0.84
C12orf45	11238	chr12:103892852-1038931	inter_enh	103892852	103893124	chr12	-0.83
C12orf75	8470	chr12:104239953-1042401	inter_enh	104239953	104240192	chr12	-0.95

TCP11L2	4972	chr12:105215449-1052160	inter_enh	105215449	105216003	chr12	-0.75
MTERF2	12637	chr12:105892328-1058925	inter_enh	105892328	105892546	chr12	-0.63
ASCL4	9734	chr12:106701720-1067023	inter_enh	106701720	106702328	chr12	-0.97
ISCU	11995	chr12:107491240-1074914	inter_enh	107491240	107491486	chr12	-0.97
SELPLG	13942	chr12:107535964-1075361	inter_enh	107535964	107536119	chr12	-0.69
CORO1C	2918	chr12:107652337-1076524	inter_enh	107652337	107652412	chr12	-0.40
ACACB	16608	chr12:108044919-1080450	inter_enh	108044919	108045034	chr12	-0.95
ACACB	16126	chr12:108045395-1080455	inter_enh	108045395	108045521	chr12	-0.90
ANAPC7	13878	chr12:109339496-1093400	inter_enh	109339496	109340095	chr12	-0.82
PPTC7	7809	chr12:109512969-1095135	inter_enh	109512969	109513545	chr12	-0.71
FAM109A	13610	chr12:110277632-1102777	inter_enh	110277632	110277763	chr12	-0.49
MIR6761	13289	chr12:110735255-1107353	inter_enh	110735255	110735363	chr12	-0.52
ERP29	12956	chr12:110948433-1109485	inter_enh	110948433	110948548	chr12	-0.62
DTX1	9278	chr12:111970625-1119709	inter_enh	111970625	111970907	chr12	-0.81
MED13L	48236	chr12:115247409-1152478	inter_enh	115247409	115247812	chr12	-0.68
PEBP1	15172	chr12:117043026-1170431	inter_enh	117043026	117043134	chr12	-0.75
PRKAB1	14810	chr12:118604815-1186050	inter_enh	118604815	118605089	chr12	-0.27
CIT	24784	chr12:118824177-1188243	inter_enh	118824177	118824348	chr12	-0.56
MIR7107	18222	chr12:120348218-1203484	inter_enh	120348218	120348413	chr12	-0.90
MORN3	17058	chr12:120608893-1206091	inter_enh	120608893	120609110	chr12	-0.57
BCL7A	13612	chr12:120930568-1209306	inter_enh	120930568	120930691	chr12	-0.66
BCL7A	4594	chr12:120939568-1209397	inter_enh	120939568	120939728	chr12	-0.79
VPS37B	2590	chr12:121948960-1219495	inter_enh	121948960	121949552	chr12	-0.79
VPS37B	5646	chr12:121952106-1219525	inter_enh	121952106	121952518	chr12	-0.93
CDK2AP1	5990	chr12:122328671-1223289	inter_enh	122328671	122328940	chr12	-0.57
UBC	4698	chr12:123960769-1239609	inter_enh	123960769	123960915	chr12	-0.36
GPR19	40221	chr12:12700101-12700233	inter_enh	12700101	12700233	chr12	-0.33
EP400NL	2975	chr12:131131696-1311319	inter_enh	131131696	131131914	chr12	-0.60
H2AFJ	6431	chr12:14824850-14825084	inter_enh	14824850	14825084	chr12	-0.76
LINC01489	7970	chr12:15037927-15038198	inter_enh	15037927	15038198	chr12	-0.86
LINC00942	45173	chr12:1524996-1525182	inter_enh	1524996	1525182	chr12	-0.78
PTPRO	48386	chr12:15317961-15318180	inter_enh	15317961	15318180	chr12	-0.57
WNT5B	8353	chr12:1587870-1588388	inter_enh	1587870	1588388	chr12	-0.75
STRAP	18191	chr12:15908122-15908604	inter_enh	15908122	15908604	chr12	-0.57
RERGL	10847	chr12:18145086-18145396	inter_enh	18145086	18145396	chr12	-0.71
RERGL	49388	chr12:18183311-18184254	inter_enh	18183311	18184254	chr12	-0.57
AEBP2	4938	chr12:19478753-19479119	inter_enh	19478753	19479119	chr12	-0.90
C12orf77	5552	chr12:25035964-25036213	inter_enh	25035964	25036213	chr12	-0.79
C12orf77	5145	chr12:25036445-25036545	inter_enh	25036445	25036545	chr12	-0.59
C12orf77	4434	chr12:25037039-25037372	inter_enh	25037039	25037372	chr12	-0.89
C12orf77	18016	chr12:25059403-25059909	inter_enh	25059403	25059909	chr12	-0.48
KRAS	12964	chr12:25307763-25308430	inter_enh	25307763	25308430	chr12	-0.98
BHLHE41	30899	chr12:26199814-26200524	inter_enh	26199814	26200524	chr12	-0.43
ITPR2	20942	chr12:26898221-26898459	inter_enh	26898221	26898459	chr12	-0.46
STK38L	22378	chr12:27265887-27266045	inter_enh	27265887	27266045	chr12	-0.87
AMN1	13960	chr12:31787018-31787653	inter_enh	31787018	31787653	chr12	-0.82
H3F3C	43218	chr12:31879526-31879793	inter_enh	31879526	31879793	chr12	-0.39
BICD1	46284	chr12:32105108-32105223	inter_enh	32105108	32105223	chr12	-0.76
BICD1	44138	chr12:32107237-32107387	inter_enh	32107237	32107387	chr12	-0.68
FGD4	15767	chr12:32530432-32530646	inter_enh	32530432	32530646	chr12	-0.88
FGD4	8396	chr12:32537595-32538225	inter_enh	32537595	32538225	chr12	-0.60
FGD4	3876	chr12:32542230-32542630	inter_enh	32542230	32542630	chr12	-0.80
YARS2	5774	chr12:32805832-32806023	inter_enh	32805832	32806023	chr12	-0.75
YARS2	6057	chr12:32806130-32806292	inter_enh	32806130	32806292	chr12	-0.50
PARP11	12383	chr12:3865192-3865326	inter_enh	3865192	3865326	chr12	-0.60

SLC2A13	31590	chr12:38817348-3881768	inter_enh	38817348	38817688	chr12	-0.77
LRRK2	16020	chr12:38888617-3888949	inter_enh	38888617	38889499	chr12	-0.71
LINC00938	6016	chr12:44401895-4440201	inter_enh	44401895	44402018	chr12	-0.63
DYRK4	24982	chr12:4544296-4544736	inter_enh	4544296	4544736	chr12	-0.33
DYRK4	5730	chr12:4563562-4563975	inter_enh	4563562	4563975	chr12	-0.75
HDAC7	8504	chr12:46508269-4650879	inter_enh	46508269	46508799	chr12	-0.62
CCDC65	13408	chr12:47570702-4757079	inter_enh	47570702	47570799	chr12	-0.53
RHEBL1	6045	chr12:47743913-4774408	inter_enh	47743913	47744081	chr12	-0.43
SPATS2	8242	chr12:48038656-4803876	inter_enh	48038656	48038769	chr12	-0.52
KCNH3	2176	chr12:48216979-4821708	inter_enh	48216979	48217082	chr12	-0.83
OR7E47P	26210	chr12:50799415-5080024	inter_enh	50799415	50800240	chr12	-0.42
HOXC8	3114	chr12:52685992-5268609	inter_enh	52685992	52686091	chr12	-0.59
SMUG1	2947	chr12:52871894-5287209	inter_enh	52871894	52872092	chr12	-0.69
SMUG1	18822	chr12:52887788-5288794	inter_enh	52887788	52887948	chr12	-0.42
SMARCC2	3736	chr12:54873286-5487342	inter_enh	54873286	54873423	chr12	-0.44
CS	2641	chr12:54982937-5498322	inter_enh	54982937	54983229	chr12	-0.72
SPRYD4	4195	chr12:55144253-5514448	inter_enh	55144253	55144489	chr12	-0.25
RBMS2	8066	chr12:55193737-5519387	inter_enh	55193737	55193878	chr12	-0.53
GPR182	7022	chr12:55667497-5566769	inter_enh	55667497	55667698	chr12	-0.77
ARHGAP9	3763	chr12:56163508-5616381	inter_enh	56163508	56163818	chr12	-0.92
CTDSP2	41636	chr12:56568439-5656886	inter_enh	56568439	56568861	chr12	-0.92
CD27	16342	chr12:6407712-6408223	inter_enh	6407712	6408223	chr12	-0.80
CD27	13268	chr12:6410949-6411135	inter_enh	6410949	6411135	chr12	-0.40
CD27	11620	chr12:6412261-6413120	inter_enh	6412261	6413120	chr12	-0.41
MIR6502	17636	chr12:64948473-6494905	inter_enh	64948473	64949055	chr12	-0.81
GAPDH	3325	chr12:6517934-6518004	inter_enh	6517934	6518004	chr12	-0.39
GRIP1	13301	chr12:65372203-6537278	inter_enh	65372203	65372783	chr12	-0.98
GRIP1	47615	chr12:65406616-6540699	inter_enh	65406616	65406998	chr12	-0.93
LOC101927901	28566	chr12:66437893-6643828	inter_enh	66437893	66438283	chr12	-0.91
IFNG	3812	chr12:66843304-6684389	inter_enh	66843304	66843895	chr12	-0.60
IL22	12281	chr12:66920959-6692157	inter_enh	66920959	66921575	chr12	-0.64
COPS7A	3423	chr12:6699613-6700361	inter_enh	6699613	6700361	chr12	-0.98
LOC100507195	11550	chr12:67142984-6714318	inter_enh	67142984	67143180	chr12	-0.31
SLC35E3	27088	chr12:67453092-6745348	inter_enh	67453092	67453489	chr12	-0.33
LYZ	18362	chr12:68009681-6801039	inter_enh	68009681	68010395	chr12	-0.60
FRS2	2918	chr12:68147329-6814762	inter_enh	68147329	68147622	chr12	-0.75
BEST3	2692	chr12:68382076-6838223	inter_enh	68382076	68382237	chr12	-0.91
WNK1	32726	chr12:699522-699722	inter_enh	699522	699722	chr12	-0.41
ATXN7L3B	47036	chr12:73170493-7317106	inter_enh	73170493	73171066	chr12	-0.63
APOBEC1	23840	chr12:7685804-7686057	inter_enh	7685804	7686057	chr12	-0.87
APOBEC1	20028	chr12:7689672-7689812	inter_enh	7689672	7689812	chr12	-0.76
FOXJ2	13377	chr12:8063037-8063457	inter_enh	8063037	8063457	chr12	-0.77
AICDA	16760	chr12:8673247-8673692	inter_enh	8673247	8673692	chr12	-0.46
DUSP6	33042	chr12:88237402-8823805	inter_enh	88237402	88238050	chr12	-0.88
BTG1	11796	chr12:91075241-9107595	inter_enh	91075241	91075959	chr12	-0.26
CLLU1OS	4646	chr12:91350586-9135081	inter_enh	91350586	91350819	chr12	-0.57
CLLU1OS	6630	chr12:91352608-9135276	inter_enh	91352608	91352764	chr12	-0.64
CLLU1OS	34054	chr12:91379920-9138030	inter_enh	91379920	91380301	chr12	-0.45
PLXNC1	46138	chr12:93020415-9302056	inter_enh	93020415	93020566	chr12	-0.38
CEP83-AS1	28476	chr12:93406317-9340645	inter_enh	93406317	93406451	chr12	-0.86
CEP83-AS1	28820	chr12:93406631-9340682	inter_enh	93406631	93406824	chr12	-0.94
MIR492	28464	chr12:93723656-9372402	inter_enh	93723656	93724024	chr12	-0.92
MIR3685	28489	chr12:94256211-9425642	inter_enh	94256211	94256423	chr12	-0.91
MIR3685	40170	chr12:94267830-9426816	inter_enh	94267830	94268167	chr12	-0.93
METAP2	45364	chr12:94346352-9434682	inter_enh	94346352	94346824	chr12	-0.57

LTA4H	18768	chr12:94980030-94980367	inter_enh	94980030	94980367	chr12	-0.73
ELK3	4084	chr12:95108135-95108368	inter_enh	95108135	95108368	chr12	-0.60
CDK17	3862	chr12:95321673-95323046	inter_enh	95321673	95323046	chr12	-0.98
CDK17	45418	chr12:95363660-95364172	inter_enh	95363660	95364172	chr12	-0.91
CLECL1	2572	chr12:9779669-9779800	inter_enh	9779669	9779800	chr12	-0.49
KLRF1	33252	chr12:9837656-9838524	inter_enh	9837656	9838524	chr12	-0.79
SLC10A2	32850	chr13:102484143-1024845	inter_enh	102484143	102484553	chr13	-0.55
ING1	12950	chr13:110178565-1101789	inter_enh	110178565	110178902	chr13	-0.49
MCF2L-AS1	25926	chr13:112644941-1126451	inter_enh	112644941	112645115	chr13	-0.66
MTMR6	4794	chr13:24764366-24764629	inter_enh	24764366	24764629	chr13	-0.85
LINC00412	7224	chr13:26702107-26702234	inter_enh	26702107	26702234	chr13	-0.77
MTIF3	11008	chr13:26933629-26933867	inter_enh	26933629	26933867	chr13	-0.78
KATNAL1	6199	chr13:29785429-29786217	inter_enh	29785429	29786217	chr13	-0.85
HMGB1	12002	chr13:29949968-29950201	inter_enh	29949968	29950201	chr13	-0.77
USPL1	6900	chr13:30082385-30083470	inter_enh	30082385	30083470	chr13	-0.86
USPL1	3252	chr13:30086322-30086831	inter_enh	30086322	30086831	chr13	-0.86
ALOX5AP	31794	chr13:30239328-30239548	inter_enh	30239328	30239548	chr13	-0.46
STARD13	45935	chr13:33194798-33195016	inter_enh	33194798	33195016	chr13	-0.68
RFC3	17800	chr13:33272297-33272510	inter_enh	33272297	33272510	chr13	-0.52
RFC3	17392	chr13:33272658-33272965	inter_enh	33272658	33272965	chr13	-0.29
RFXAP	12931	chr13:36277968-36278846	inter_enh	36277968	36278846	chr13	-0.89
TRPC4	17346	chr13:37359160-37359413	inter_enh	37359160	37359413	chr13	-0.87
LINC00571	24260	chr13:37639408-37639851	inter_enh	37639408	37639851	chr13	-0.59
LINC00571	37674	chr13:37652761-37653328	inter_enh	37652761	37653328	chr13	-0.37
LINC00598	13494	chr13:39966569-39966706	inter_enh	39966569	39966706	chr13	-0.56
LINC00598	13760	chr13:39966853-39966954	inter_enh	39966853	39966954	chr13	-0.49
LINC00598	44674	chr13:39997660-39997977	inter_enh	39997660	39997977	chr13	-0.64
FOXO1	28006	chr13:40166655-40166824	inter_enh	40166655	40166824	chr13	-0.47
FOXO1	30270	chr13:40168920-40169087	inter_enh	40168920	40169087	chr13	-0.67
MIR320D1	21172	chr13:40178748-40178933	inter_enh	40178748	40178933	chr13	-0.85
ELF1	4176	chr13:40495251-40496118	inter_enh	40495251	40496118	chr13	-0.85
ELF1	5552	chr13:40496755-40497364	inter_enh	40496755	40497364	chr13	-0.77
WBP4	20488	chr13:40513041-40513375	inter_enh	40513041	40513375	chr13	-0.47
LINC00563	36576	chr13:45806454-45806658	inter_enh	45806454	45806658	chr13	-0.49
KIAA0226L	10458	chr13:45872440-45872833	inter_enh	45872440	45872833	chr13	-0.45
KIAA0226L	11400	chr13:45873118-45874037	inter_enh	45873118	45874037	chr13	-0.55
ESD	37210	chr13:46232070-46232246	inter_enh	46232070	46232246	chr13	-0.77
RCBTB1	19526	chr13:49077035-49077458	inter_enh	49077035	49077458	chr13	-0.47
MIR3613	19806	chr13:49448757-49448907	inter_enh	49448757	49448907	chr13	-0.70
GUCY1B2	3896	chr13:50542092-50542288	inter_enh	50542092	50542288	chr13	-0.37
MIR4703	9794	chr13:51034433-51034602	inter_enh	51034433	51034602	chr13	-0.40
SLITRK5	8166	chr13:87130203-87131870	inter_enh	87130203	87131870	chr13	-0.98
GPC5	23476	chr13:90825317-90825476	inter_enh	90825317	90825476	chr13	-0.83
GPC5	23156	chr13:90825583-90825848	inter_enh	90825583	90825848	chr13	-0.68
OXGR1	2644	chr13:96446743-96447758	inter_enh	96446743	96447758	chr13	-0.86
OXGR1	32666	chr13:96477193-96477350	inter_enh	96477193	96477350	chr13	-0.90
DOCK9-AS2	38296	chr13:98575171-98575373	inter_enh	98575171	98575373	chr13	-0.38
DYNC1H1	3078	chr14:101497449-1014976	inter_enh	101497449	101497628	chr14	-0.50
TRAF3	2650	chr14:102310764-1023110	inter_enh	102310764	102311072	chr14	-0.44
AMN	8280	chr14:102450402-1024505	inter_enh	102450402	102450526	chr14	-0.48
APOPT1	32596	chr14:103131345-1031319	inter_enh	103131345	103131946	chr14	-0.56
ASPG	7702	chr14:103613984-1036141	inter_enh	103613984	103614160	chr14	-0.84
MIR4710	3618	chr14:104218663-1042188	inter_enh	104218663	104218836	chr14	-0.61
CDCA4	6306	chr14:104564685-1045648	inter_enh	104564685	104564866	chr14	-0.81
TEP1	2747	chr14:19954014-19954320	inter_enh	19954014	19954320	chr14	-0.62

KLHL33	3118	chr14:19976672-1997684	inter_enh	19976672	19976849	chr14	-0.88
ZNF219	2148	chr14:20644732-2064497	inter_enh	20644732	20644971	chr14	-0.43
SALL2	6438	chr14:21081430-2108182	inter_enh	21081430	21081827	chr14	-0.89
DAD1	38820	chr14:22089108-2208922	inter_enh	22089108	22089220	chr14	-0.35
DAD1	26348	chr14:22101521-2210175	inter_enh	22101521	22101750	chr14	-0.59
ABHD4	16300	chr14:22153204-2215336	inter_enh	22153204	22153367	chr14	-0.85
REM2	10680	chr14:22432680-2243322	inter_enh	22432680	22433221	chr14	-0.94
DCAF11	5688	chr14:23647772-2364834	inter_enh	23647772	23648341	chr14	-0.61
RABGGTA	2527	chr14:23813026-2381337	inter_enh	23813026	23813376	chr14	-0.91
RNU6-2	15760	chr14:31725111-3172536	inter_enh	31725111	31725369	chr14	-0.95
RNU6-2	12016	chr14:31728804-3172916	inter_enh	31728804	31729164	chr14	-0.87
EAPP	8241	chr14:34086861-3408700	inter_enh	34086861	34087009	chr14	-0.31
CFL2	8185	chr14:34261887-3426204	inter_enh	34261887	34262043	chr14	-0.51
IGBP1P1	9152	chr14:34469637-3446981	inter_enh	34469637	34469815	chr14	-0.69
NFKBIA	36899	chr14:34906627-3490699	inter_enh	34906627	34906999	chr14	-0.69
NFKBIA	8513	chr14:34952129-3495232	inter_enh	34952129	34952321	chr14	-0.78
SSTR1	10718	chr14:37736155-3773631	inter_enh	37736155	37736318	chr14	-0.67
LRR1	4272	chr14:49130233-4913155	inter_enh	49130233	49131551	chr14	-0.94
RPL36AL	2310	chr14:49154610-4915507	inter_enh	49154610	49155078	chr14	-0.74
MGAT2	4310	chr14:49161481-4916161	inter_enh	49161481	49161614	chr14	-0.86
NEMF	4644	chr14:49393933-4939444	inter_enh	49393933	49394440	chr14	-0.89
NEMF	17010	chr14:49406331-4940677	inter_enh	49406331	49406773	chr14	-0.52
ARF6	12486	chr14:49416926-4941706	inter_enh	49416926	49417069	chr14	-0.65
ARF6	6538	chr14:49435895-4943615	inter_enh	49435895	49436150	chr14	-0.72
MIR6076	20634	chr14:49482153-4948231	inter_enh	49482153	49482312	chr14	-0.85
MIR6076	19496	chr14:49483275-4948346	inter_enh	49483275	49483464	chr14	-0.89
LOC100506499	7610	chr14:49583772-4958415	inter_enh	49583772	49584153	chr14	-0.27
LOC100506499	25208	chr14:49601480-4960164	inter_enh	49601480	49601641	chr14	-0.37
VCPKMT	11612	chr14:49641366-4964150	inter_enh	49641366	49641505	chr14	-0.86
ABHD12B	11281	chr14:50397274-5039741	inter_enh	50397274	50397416	chr14	-0.49
SAMD4A	3236	chr14:54100788-5410089	inter_enh	54100788	54100897	chr14	-0.30
DAAM1	13058	chr14:58711808-5871234	inter_enh	58711808	58712340	chr14	-0.87
TMEM30B	28337	chr14:60789579-6079031	inter_enh	60789579	60790315	chr14	-0.66
HIF1A	24281	chr14:61207163-6120801	inter_enh	61207163	61208015	chr14	-0.50
SGPP1	31584	chr14:63295902-6329628	inter_enh	63295902	63296287	chr14	-0.29
LOC100128233	2584	chr14:64761259-6476154	inter_enh	64761259	64761546	chr14	-0.71
LOC100128233	9292	chr14:64767895-6476832	inter_enh	64767895	64768324	chr14	-0.54
LOC100128233	21950	chr14:64780578-6478095	inter_enh	64780578	64780958	chr14	-0.73
MIR4708	46082	chr14:64825271-6482587	inter_enh	64825271	64825872	chr14	-0.89
MIR4708	34476	chr14:64837086-6483727	inter_enh	64837086	64837271	chr14	-0.89
MIR4708	20290	chr14:64851285-6485144	inter_enh	64851285	64851442	chr14	-0.75
MIR4708	14079	chr14:64857347-6485780	inter_enh	64857347	64857803	chr14	-0.83
MIR4708	2466	chr14:64869106-6486927	inter_enh	64869106	64869270	chr14	-0.82
MIR4708	11840	chr14:64883173-6488381	inter_enh	64883173	64883815	chr14	-0.88
MIR4708	25372	chr14:64896618-6489743	inter_enh	64896618	64897435	chr14	-0.94
ZFP36L1	13053	chr14:68317276-6831738	inter_enh	68317276	68317386	chr14	-0.51
ZFP36L1	24568	chr14:68357080-6835748	inter_enh	68357080	68357484	chr14	-0.48
LINC01269	15352	chr14:70250448-7025058	inter_enh	70250448	70250589	chr14	-0.65
TMED10	47323	chr14:74760183-7476066	inter_enh	74760183	74760667	chr14	-0.96
FOS	49318	chr14:74765794-7476603	inter_enh	74765794	74766035	chr14	-0.84
JDP2	8096	chr14:74956053-7495627	inter_enh	74956053	74956276	chr14	-0.44
BATF	33608	chr14:75024838-7502501	inter_enh	75024838	75025017	chr14	-0.56
IRF2BPL	28196	chr14:76536449-7653675	inter_enh	76536449	76536751	chr14	-0.40
IRF2BPL	3480	chr14:76568212-7656834	inter_enh	76568212	76568340	chr14	-0.59
LOC283575	4418	chr14:76572474-7657297	inter_enh	76572474	76572978	chr14	-0.90

LOC102724190	5244	chr14:76617370-7661769	inter_enh	76617370	76617693	chr14	-0.92
OTUB2	14399	chr14:93547881-9354827	inter_enh	93547881	93548273	chr14	-0.80
SCARNA13	13704	chr14:95055685-9505634	inter_enh	95055685	95056346	chr14	-0.38
SCARNA13	2679	chr14:95066978-9506710	inter_enh	95066978	95067104	chr14	-0.67
TCL6	41428	chr14:95145781-9514589	inter_enh	95145781	95145895	chr14	-0.46
TCL1B	6347	chr14:95216030-9521628	inter_enh	95216030	95216288	chr14	-0.63
TCL1B	12830	chr14:95235234-9523543	inter_enh	95235234	95235439	chr14	-0.43
TCL1B	13318	chr14:95235621-9523602	inter_enh	95235621	95236027	chr14	-0.31
TCL1A	9917	chr14:95240060-9524067	inter_enh	95240060	95240678	chr14	-0.42
TCL1A	8872	chr14:95241189-9524164	inter_enh	95241189	95241640	chr14	-0.28
LOC730202	8046	chr14:96030298-9603044	inter_enh	96030298	96030443	chr14	-0.79
HERC2P10	25342	chr15:28922804-2892293	inter_enh	28922804	28922939	chr15	-0.75
LOC283710	24838	chr15:29334942-2933541	inter_enh	29334942	29335418	chr15	-0.75
LOC283710	40009	chr15:29350273-2935042	inter_enh	29350273	29350429	chr15	-0.68
KLF13	23034	chr15:29383245-2938338	inter_enh	29383245	29383383	chr15	-0.45
SPRED1	14312	chr15:36317950-3631810	inter_enh	36317950	36318109	chr15	-0.93
SPRED1	10596	chr15:36321468-3632202	inter_enh	36321468	36322023	chr15	-0.91
C15orf53	13465	chr15:36762593-3676265	inter_enh	36762593	36762657	chr15	-0.53
BMF	5588	chr15:38193744-3819418	inter_enh	38193744	38194189	chr15	-0.92
SPINT1	13548	chr15:38937417-3893754	inter_enh	38937417	38937546	chr15	-0.81
UBR1	12345	chr15:41197823-41198023	inter_enh	41197823	41198023	chr15	-0.64
LOC100419583	4710	chr15:42803589-4280394	inter_enh	42803589	42803944	chr15	-0.69
LOC100419583	3497	chr15:42804871-4280508	inter_enh	42804871	42805087	chr15	-0.45
BLOC1S6	14592	chr15:43651911-43652321	inter_enh	43651911	43652321	chr15	-0.58
AP4E1	29518	chr15:48958444-4895884	inter_enh	48958444	48958840	chr15	-0.65
MAPK6	12498	chr15:50085996-5008641	inter_enh	50085996	50086412	chr15	-0.93
MAPK6	10881	chr15:50087654-5008798	inter_enh	50087654	50087988	chr15	-0.76
MAPK6	10096	chr15:50088374-5008883	inter_enh	50088374	50088839	chr15	-0.90
BCL2L10	10386	chr15:50181738-5018201	inter_enh	50181738	50182017	chr15	-0.89
FAM214A	49451	chr15:50807494-5080765	inter_enh	50807494	50807656	chr15	-0.71
RFX7	3136	chr15:54325783-5432604	inter_enh	54325783	54326042	chr15	-0.53
SLTM	24066	chr15:57037089-57037331	inter_enh	57037089	57037331	chr15	-0.37
MYO1E	5111	chr15:57457243-5745770	inter_enh	57457243	57457707	chr15	-0.79
MYO1E	25461	chr15:57477694-5747795	inter_enh	57477694	57477956	chr15	-0.69
MYO1E	31462	chr15:57483694-5748395	inter_enh	57483694	57483957	chr15	-0.77
FOXB1	27631	chr15:58055956-5805620	inter_enh	58055956	58056206	chr15	-0.39
C2CD4B	40888	chr15:60203693-6020407	inter_enh	60203693	60204079	chr15	-0.91
C2CD4B	36198	chr15:60208340-6020881	inter_enh	60208340	60208813	chr15	-0.97
USP3	23928	chr15:61559671-6155999	inter_enh	61559671	61559997	chr15	-0.32
USP3	20663	chr15:61563014-6156318	inter_enh	61563014	61563184	chr15	-0.46
USP3	17216	chr15:61566410-61566681	inter_enh	61566410	61566681	chr15	-0.51
HERC1	47078	chr15:61960213-6196034	inter_enh	61960213	61960343	chr15	-0.90
PARP16	11058	chr15:63377030-63377231	inter_enh	63377030	63377231	chr15	-0.41
PARP16	11374	chr15:63377365-6337752	inter_enh	63377365	63377526	chr15	-0.47
DENND4A	4388	chr15:63875909-6387623	inter_enh	63875909	63876238	chr15	-0.95
TIPIN	3174	chr15:64439009-6443955	inter_enh	64439009	64439555	chr15	-0.87
MAP2K5	2730	chr15:65619157-6561953	inter_enh	65619157	65619530	chr15	-0.79
RNU6-2	10724	chr15:65929950-6593037	inter_enh	65929950	65930374	chr15	-0.42
RNU6-2	12950	chr15:65932303-6593247	inter_enh	65932303	65932472	chr15	-0.75
RNU6-2	13556	chr15:65932839-6593314	inter_enh	65932839	65933149	chr15	-0.51
RNU6-2	42661	chr15:65962042-6596215	inter_enh	65962042	65962156	chr15	-0.36
CALML4	15856	chr15:66269447-6626984	inter_enh	66269447	66269845	chr15	-0.95
CORO2B	3940	chr15:66654341-6665449	inter_enh	66654341	66654499	chr15	-0.76
NOX5	5280	chr15:67004555-6700467	inter_enh	67004555	67004670	chr15	-0.77
NOX5	4898	chr15:67004862-6700512	inter_enh	67004862	67005125	chr15	-0.96

LINC00593	26903	chr15:67941265-67941793	inter_enh	67941265	67941793	chr15	-0.84
SENP8	23348	chr15:70220723-70221342	inter_enh	70220723	70221342	chr15	-0.31
ADPGK-AS1	42425	chr15:70819522-70820084	inter_enh	70819522	70820084	chr15	-0.88
STOML1	26346	chr15:72045285-72045507	inter_enh	72045285	72045507	chr15	-0.45
CYP11A1	16380	chr15:72463343-72463685	inter_enh	72463343	72463685	chr15	-0.88
MIR6881	13504	chr15:72477111-72477533	inter_enh	72477111	72477533	chr15	-0.94
CSK	2748	chr15:72858619-72858838	inter_enh	72858619	72858838	chr15	-0.74
RPP25	3862	chr15:73040602-73040777	inter_enh	73040602	73040777	chr15	-0.86
C15orf27	2840	chr15:74136037-74136986	inter_enh	74136037	74136986	chr15	-0.84
LOC91450	3688	chr15:76069825-76070043	inter_enh	76069825	76070043	chr15	-0.82
WDR61	8828	chr15:76387752-76387896	inter_enh	76387752	76387896	chr15	-0.91
CTSH	6574	chr15:77030829-77031270	inter_enh	77030829	77031270	chr15	-0.26
BCL2A1	37639	chr15:78088258-78088416	inter_enh	78088258	78088416	chr15	-0.50
TM6SF1	15154	chr15:81552091-81552253	inter_enh	81552091	81552253	chr15	-0.76
ZNF592	14391	chr15:83078365-83078493	inter_enh	83078365	83078493	chr15	-0.77
ZNF592	12333	chr15:83080409-83080565	inter_enh	83080409	83080565	chr15	-0.88
MRPL46	17200	chr15:86794372-86794504	inter_enh	86794372	86794504	chr15	-0.37
MIR9-3	9432	chr15:87702723-87702914	inter_enh	87702723	87702914	chr15	-0.46
LINC00925	23942	chr15:87746020-87746416	inter_enh	87746020	87746416	chr15	-0.34
SEMA4B	6090	chr15:88522964-88523164	inter_enh	88522964	88523164	chr15	-0.61
ASB9P1	34800	chr15:91174049-91174983	inter_enh	91174049	91174983	chr15	-0.50
LOC100507217	3952	chr15:91223061-91223187	inter_enh	91223061	91223187	chr15	-0.79
MCTP2	36495	chr15:92605755-92606119	inter_enh	92605755	92606119	chr15	-0.28
ALDH1A3	29046	chr15:99208289-99208456	inter_enh	99208289	99208456	chr15	-0.82
TM2D3	10794	chr15:99999191-99999457	inter_enh	99999191	99999457	chr15	-0.63
ATF7IP2	3582	chr16:10383541-10384118	inter_enh	10383541	10384118	chr16	-0.27
CIITA	7044	chr16:10871258-10871762	inter_enh	10871258	10871762	chr16	-0.59
CIITA	5551	chr16:10872679-10873327	inter_enh	10872679	10873327	chr16	-0.54
PRM1	11940	chr16:11294532-11294737	inter_enh	11294532	11294737	chr16	-0.83
PRM1	13124	chr16:11295715-11295920	inter_enh	11295715	11295920	chr16	-0.53
PRM1	13694	chr16:11296282-11296495	inter_enh	11296282	11296495	chr16	-0.71
PRM1	30172	chr16:11312779-11312954	inter_enh	11312779	11312954	chr16	-0.47
RMI2	15462	chr16:11331184-11331512	inter_enh	11331184	11331512	chr16	-0.86
RMI2	25234	chr16:11371711-11372376	inter_enh	11371711	11372376	chr16	-0.51
LOC101927131	30542	chr16:11497060-11497255	inter_enh	11497060	11497255	chr16	-0.52
LITAF	15146	chr16:11603855-11604084	inter_enh	11603855	11604084	chr16	-0.72
SNN	16582	chr16:11653103-11653309	inter_enh	11653103	11653309	chr16	-0.45
TNFRSF17	14510	chr16:11951829-11952079	inter_enh	11951829	11952079	chr16	-0.28
TNFRSF17	3558	chr16:11969831-11970213	inter_enh	11969831	11970213	chr16	-0.70
LOC101927311	17903	chr16:13999183-13999763	inter_enh	13999183	13999763	chr16	-0.67
ARL6IP1	2682	chr16:18722747-18723333	inter_enh	18722747	18723333	chr16	-0.55
TMC5	30312	chr16:19298866-19299621	inter_enh	19298866	19299621	chr16	-0.89
TMC5	27994	chr16:19301477-19301646	inter_enh	19301477	19301646	chr16	-0.93
EEF2K	10776	chr16:22114105-22114526	inter_enh	22114105	22114526	chr16	-0.37
GGA2	9975	chr16:23439213-23439369	inter_enh	23439213	23439369	chr16	-0.81
PRKCB	28818	chr16:23725696-23726269	inter_enh	23725696	23726269	chr16	-0.85
CACNG3	4385	chr16:24169703-24170275	inter_enh	24169703	24170275	chr16	-0.96
LOC554206	16862	chr16:24967225-24967624	inter_enh	24967225	24967624	chr16	-0.61
LOC554206	19964	chr16:24970474-24970577	inter_enh	24970474	24970577	chr16	-0.72
LOC554206	20536	chr16:24970963-24971232	inter_enh	24970963	24971232	chr16	-0.64
LCMT1-AS1	37462	chr16:24992563-24993270	inter_enh	24992563	24993270	chr16	-0.70
LCMT1-AS1	17784	chr16:25012425-25012762	inter_enh	25012425	25012762	chr16	-0.56
C16orf82	46630	chr16:27032112-27032583	inter_enh	27032112	27032583	chr16	-0.36
KDM8	30032	chr16:27092224-27092324	inter_enh	27092224	27092324	chr16	-0.82
KDM8	24249	chr16:27097698-27098416	inter_enh	27097698	27098416	chr16	-0.54

KDM8	23613	chr16:27098554-27098832	inter_enh	27098554	27098832	chr16	-0.48
IL4R	14584	chr16:27217911-27218382	inter_enh	27217911	27218382	chr16	-0.74
SBK1	14794	chr16:28196490-28196601	inter_enh	28196490	28196601	chr16	-0.32
SULT1A2	5802	chr16:28521609-28521778	inter_enh	28521609	28521778	chr16	-0.68
CORO1A	16868	chr16:30085265-30085459	inter_enh	30085265	30085459	chr16	-0.78
SEPHS2	9197	chr16:30373863-30374127	inter_enh	30373863	30374127	chr16	-0.47
ZNF688	4070	chr16:30487050-30487269	inter_enh	30487050	30487269	chr16	-0.64
ZNF689	18344	chr16:30547873-30548011	inter_enh	30547873	30548011	chr16	-0.74
ITGAM	15620	chr16:31163082-31163255	inter_enh	31163082	31163255	chr16	-0.89
SLX4	14823	chr16:3615918-3616900	inter_enh	3615918	3616900	chr16	-0.45
MYLK3	24320	chr16:45363847-45364236	inter_enh	45363847	45364236	chr16	-0.69
C16orf87	3646	chr16:45426161-45426282	inter_enh	45426161	45426282	chr16	-0.57
SIAH1	45782	chr16:47022325-47022700	inter_enh	47022325	47022700	chr16	-0.56
N4BP1	2974	chr16:47204425-47204767	inter_enh	47204425	47204767	chr16	-0.66
C16orf78	31669	chr16:47996807-47997147	inter_enh	47996807	47997147	chr16	-0.95
C16orf78	33972	chr16:47999174-47999386	inter_enh	47999174	47999386	chr16	-0.91
HERPUD1	13790	chr16:55509535-55509888	inter_enh	55509535	55509888	chr16	-0.91
HERPUD1	4444	chr16:55518857-55519260	inter_enh	55518857	55519260	chr16	-0.95
CPNE2	5364	chr16:55678224-55678955	inter_enh	55678224	55678955	chr16	-0.91
ARL2BP	3918	chr16:55832503-55832738	inter_enh	55832503	55832738	chr16	-0.74
GINS3	32156	chr16:57015850-57016057	inter_enh	57015850	57016057	chr16	-0.93
GINS3	34770	chr16:57018513-57018622	inter_enh	57018513	57018622	chr16	-0.74
GOT2	21877	chr16:57347372-57347906	inter_enh	57347372	57347906	chr16	-0.35
LOC100505942	11220	chr16:66108854-66109007	inter_enh	66108854	66109007	chr16	-0.85
CTCF	8042	chr16:66145477-66146059	inter_enh	66145477	66146059	chr16	-0.72
CTCF	6280	chr16:66147226-66147833	inter_enh	66147226	66147833	chr16	-0.75
CTCF	5144	chr16:66148580-66148753	inter_enh	66148580	66148753	chr16	-0.61
CTCF	2722	chr16:66150979-66151197	inter_enh	66150979	66151197	chr16	-0.77
DPEP3	4525	chr16:66576265-66576693	inter_enh	66576265	66576693	chr16	-0.55
SLC7A6	2918	chr16:66852933-66853066	inter_enh	66852933	66853066	chr16	-0.86
SMPD3	38576	chr16:67078034-67078938	inter_enh	67078034	67078938	chr16	-0.94
SMPD3	39312	chr16:67079104-67079339	inter_enh	67079104	67079339	chr16	-0.91
PHLPP2	2364	chr16:70318118-70318823	inter_enh	70318118	70318823	chr16	-0.82
AP1G1	7858	chr16:70408105-70408566	inter_enh	70408105	70408566	chr16	-0.83
ATXN1L	3457	chr16:70433744-70434130	inter_enh	70433744	70434130	chr16	-0.64
ZFP1	7455	chr16:73732362-73732568	inter_enh	73732362	73732568	chr16	-0.78
ADAT1	28451	chr16:74186109-74186433	inter_enh	74186109	74186433	chr16	-0.93
NUDT7	42396	chr16:76271413-76271572	inter_enh	76271413	76271572	chr16	-0.79
BCO1	7444	chr16:79822249-79822454	inter_enh	79822249	79822454	chr16	-0.80
CMIP	20136	chr16:80016031-80016246	inter_enh	80016031	80016246	chr16	-0.94
CMIP	11140	chr16:80025023-80025246	inter_enh	80025023	80025246	chr16	-0.27
LOC100129617	49632	chr16:80305973-80306206	inter_enh	80305973	80306206	chr16	-0.72
TLDC1	4133	chr16:83099794-83100052	inter_enh	83099794	83100052	chr16	-0.93
USP10	12214	chr16:83278747-83278933	inter_enh	83278747	83278933	chr16	-0.55
LINC00311	22848	chr16:83851133-83851298	inter_enh	83851133	83851298	chr16	-0.38
MIR5093	4782	chr16:83902035-83902393	inter_enh	83902035	83902393	chr16	-0.31
MIR5093	6492	chr16:83903845-83904004	inter_enh	83903845	83904004	chr16	-0.89
MIR5093	24520	chr16:83921903-83922002	inter_enh	83921903	83922002	chr16	-0.42
MIR5093	28720	chr16:83926002-83926302	inter_enh	83926002	83926302	chr16	-0.55
C16orf74	11072	chr16:84353087-84353436	inter_enh	84353087	84353436	chr16	-0.90
LOC102724467	23162	chr16:86393335-86393502	inter_enh	86393335	86393502	chr16	-0.66
CDT1	3496	chr16:87394053-87394327	inter_enh	87394053	87394327	chr16	-0.59
SPIRE2	5854	chr16:88416366-88416737	inter_enh	88416366	88416737	chr16	-0.60
DEF8	3690	chr16:88538739-88539157	inter_enh	88538739	88539157	chr16	-0.89
C16orf72	31120	chr16:9061786-9062047	inter_enh	9061786	9062047	chr16	-0.92

C16orf72	29368	chr16:9063575-9063762	inter_enh	9063575	9063762	chr16	-0.95
C16orf72	18511	chr16:9074327-9074723	inter_enh	9074327	9074723	chr16	-0.45
C16orf72	43127	chr16:9136076-9136250	inter_enh	9136076	9136250	chr16	-0.69
C16orf72	43464	chr16:9136382-9136619	inter_enh	9136382	9136619	chr16	-0.53
MIR7641-2	39022	chr16:9604704-9604839	inter_enh	9604704	9604839	chr16	-0.89
ABR	12754	chr17:1050022-1050219	inter_enh	1050022	1050219	chr17	-0.61
ABR	25908	chr17:1063094-1063453	inter_enh	1063094	1063453	chr17	-0.33
ABR	30945	chr17:1068249-1068373	inter_enh	1068249	1068373	chr17	-0.61
ABR	31371	chr17:1068488-1068986	inter_enh	1068488	1068986	chr17	-0.47
MGC12916	48181	chr17:14195617-14196305	inter_enh	14195617	14196305	chr17	-0.91
ADORA2B	47152	chr17:15741713-15741892	inter_enh	15741713	15741892	chr17	-0.51
RAI1	15223	chr17:17510164-17510410	inter_enh	17510164	17510410	chr17	-0.80
SLC47A1	19626	chr17:19358042-19358223	inter_enh	19358042	19358223	chr17	-0.82
ALDH3A1	19690	chr17:19611811-19612244	inter_enh	19611811	19612244	chr17	-0.99
AKAP10	15242	chr17:19836944-19837065	inter_enh	19836944	19837065	chr17	-0.35
USP22	10938	chr17:20897731-20898034	inter_enh	20897731	20898034	chr17	-0.69
LINC01563	25158	chr17:20944494-20944742	inter_enh	20944494	20944742	chr17	-0.89
DHRS7B	7263	chr17:20963460-20963678	inter_enh	20963460	20963678	chr17	-0.57
DHRS7B	6754	chr17:20963973-20964182	inter_enh	20963973	20964182	chr17	-0.92
MAP2K3	6001	chr17:21122491-21122627	inter_enh	21122491	21122627	chr17	-0.60
MAP2K3	39924	chr17:21171766-21171962	inter_enh	21171766	21171962	chr17	-0.36
KCNJ12	30100	chr17:21189889-21190491	inter_enh	21189889	21190491	chr17	-0.50
MIR4522	12030	chr17:22633026-22633214	inter_enh	22633026	22633214	chr17	-0.62
PAFAH1B1	21498	chr17:2421877-2422470	inter_enh	2421877	2422470	chr17	-0.44
MIR4732	9486	chr17:24222279-24222442	inter_enh	24222279	24222442	chr17	-0.70
BLMH	8996	chr17:25652196-25652415	inter_enh	25652196	25652415	chr17	-0.49
TEFM	2739	chr17:26259893-26260409	inter_enh	26259893	26260409	chr17	-0.96
UTP6	11098	chr17:27263876-27264005	inter_enh	27263876	27264005	chr17	-0.45
UTP6	12099	chr17:27264867-27265015	inter_enh	27264867	27265015	chr17	-0.42
CCL2	12348	chr17:29593983-29594137	inter_enh	29593983	29594137	chr17	-0.94
CCL1	19740	chr17:29733909-29734303	inter_enh	29733909	29734303	chr17	-0.94
CCL1	35986	chr17:29750044-29750660	inter_enh	29750044	29750660	chr17	-0.98
SNORD7	3927	chr17:30920740-30920982	inter_enh	30920740	30920982	chr17	-0.51
RASL10B	4236	chr17:31078502-31078607	inter_enh	31078502	31078607	chr17	-0.76
RASL10B	4001	chr17:31078712-31078866	inter_enh	31078712	31078866	chr17	-0.81
LASP1	6400	chr17:34273086-34273385	inter_enh	34273086	34273385	chr17	-0.68
LASP1	2676	chr17:34276887-34277032	inter_enh	34276887	34277032	chr17	-0.56
ARL5C	4198	chr17:34579976-34580301	inter_enh	34579976	34580301	chr17	-0.92
STAC2	9874	chr17:34645364-34645515	inter_enh	34645364	34645515	chr17	-0.67
PPP1R1B	3588	chr17:35032969-35033258	inter_enh	35032969	35033258	chr17	-0.40
MSL1	9482	chr17:35522663-35523000	inter_enh	35522663	35523000	chr17	-0.34
GSG2	10868	chr17:3563007-3563145	inter_enh	3563007	3563145	chr17	-0.91
CCR7	26644	chr17:35943375-35943680	inter_enh	35943375	35943680	chr17	-0.31
SMARCE1	23764	chr17:36033766-36033966	inter_enh	36033766	36033966	chr17	-0.26
KLHL10	11986	chr17:37259146-37259963	inter_enh	37259146	37259963	chr17	-0.71
KLHL10	12811	chr17:37260316-37260442	inter_enh	37260316	37260442	chr17	-0.87
NAGLU	5376	chr17:37935969-37936230	inter_enh	37935969	37936230	chr17	-0.56
ATP2A3	2223	chr17:3816649-3816813	inter_enh	3816649	3816813	chr17	-0.44
G6PC	18370	chr17:38324484-38324931	inter_enh	38324484	38324931	chr17	-0.74
G6PC	19348	chr17:38325507-38325865	inter_enh	38325507	38325865	chr17	-0.58
G6PC	28374	chr17:38334532-38334891	inter_enh	38334532	38334891	chr17	-0.37
MEOX1	16436	chr17:39111019-39111429	inter_enh	39111019	39111429	chr17	-0.77
C17orf105	11200	chr17:39224464-39224593	inter_enh	39224464	39224593	chr17	-0.91
SLC4A1	21303	chr17:39679628-39679822	inter_enh	39679628	39679822	chr17	-0.80
SLC25A39	10068	chr17:39767711-39767912	inter_enh	39767711	39767912	chr17	-0.79

UBE2G1	7155	chr17:4223634-4224112	inter_enh	4223634	4224112	chr17	-0.92
UBE2G1	9590	chr17:4226224-4226393	inter_enh	4226224	4226393	chr17	-0.49
UBE2G1	22349	chr17:4238815-4239319	inter_enh	4238815	4239319	chr17	-0.95
UBE2G1	25546	chr17:4242196-4242331	inter_enh	4242196	4242331	chr17	-0.56
RPRML	12674	chr17:42424060-4242451	inter_enh	42424060	42424516	chr17	-0.83
CDC27	3596	chr17:42625100-4262544	inter_enh	42625100	42625448	chr17	-0.60
ITGB3	13702	chr17:42672441-4267256	inter_enh	42672441	42672567	chr17	-0.71
CDK5RAP3	31708	chr17:43434871-4343518	inter_enh	43434871	43435186	chr17	-0.86
SPOP	10134	chr17:45120609-4512070	inter_enh	45120609	45120708	chr17	-0.29
DLX3	11984	chr17:45439518-4543962	inter_enh	45439518	45439627	chr17	-0.48
LOC440446	36304	chr17:46805273-4680548	inter_enh	46805273	46805482	chr17	-0.82
SCIMP	2636	chr17:5081388-5081644	inter_enh	5081388	5081644	chr17	-0.64
SCIMP	3030	chr17:5081817-5082004	inter_enh	5081817	5082004	chr17	-0.77
SCIMP	8206	chr17:5086993-5087178	inter_enh	5086993	5087178	chr17	-0.80
MMD	41751	chr17:50896031-5089615	inter_enh	50896031	50896151	chr17	-0.79
MMD	45001	chr17:50899076-5089960	inter_enh	50899076	50899606	chr17	-0.52
CCDC182	9846	chr17:53167493-5316819	inter_enh	53167493	53168194	chr17	-0.89
VEZF1	5940	chr17:53426367-5342674	inter_enh	53426367	53426740	chr17	-0.83
MIR21	4914	chr17:55277664-5527898	inter_enh	55277664	55278980	chr17	-0.66
MIR21	12320	chr17:55285613-5528584	inter_enh	55285613	55285843	chr17	-0.72
CYB561	15254	chr17:58892613-5889280	inter_enh	58892613	58892803	chr17	-0.34
PECAM1	13386	chr17:59830896-5983136	inter_enh	59830896	59831364	chr17	-0.76
PECAM1	14204	chr17:59831758-5983213	inter_enh	59831758	59832138	chr17	-0.71
PECAM1	18576	chr17:59836271-5983636	inter_enh	59836271	59836368	chr17	-0.88
PECAM1	19984	chr17:59837651-5983780	inter_enh	59837651	59837804	chr17	-0.80
AMZ2P1	13328	chr17:60388680-6038899	inter_enh	60388680	60388996	chr17	-0.71
AMZ2P1	9606	chr17:60411561-60411984	inter_enh	60411561	60411984	chr17	-0.31
AMZ2P1	11478	chr17:60413513-6041377	inter_enh	60413513	60413775	chr17	-0.73
AMZ2P1	11928	chr17:60414032-6041415	inter_enh	60414032	60414157	chr17	-0.77
RGS9	15291	chr17:60548520-6054873	inter_enh	60548520	60548730	chr17	-0.85
CEP112	2248	chr17:61620821-6162102	inter_enh	61620821	61621023	chr17	-0.69
BPTF	24924	chr17:63227253-6322737	inter_enh	63227253	63227379	chr17	-0.25
BPTF	7471	chr17:63244567-6324497	inter_enh	63244567	63244971	chr17	-0.74
LOC440461	15972	chr17:63722285-6372244	inter_enh	63722285	63722448	chr17	-0.52
LINC01483	18605	chr17:65082685-6508354	inter_enh	65082685	65083549	chr17	-0.38
LINC01483	10648	chr17:65090925-6509122	inter_enh	65090925	65091222	chr17	-0.43
LINC00673	4898	chr17:68105358-6810551	inter_enh	68105358	68105514	chr17	-0.39
SSTR2	32408	chr17:68640276-6864041	inter_enh	68640276	68640415	chr17	-0.69
SSTR2	8785	chr17:68663898-6866404	inter_enh	68663898	68664040	chr17	-0.35
ASGR2	18001	chr17:6976576-6977134	inter_enh	6976576	6977134	chr17	-0.52
SLC25A19	8126	chr17:70805085-7080542	inter_enh	70805085	70805420	chr17	-0.49
NEURL4	2954	chr17:7175893-7176740	inter_enh	7175893	7176740	chr17	-0.79
UBALD2	4226	chr17:71768404-7176890	inter_enh	71768404	71768904	chr17	-0.70
RHBDF2	4874	chr17:72013833-7201412	inter_enh	72013833	72014122	chr17	-0.74
LOC101928514	17512	chr17:72324138-7232432	inter_enh	72324138	72324325	chr17	-0.78
LOC101928514	17886	chr17:72324501-7232471	inter_enh	72324501	72324712	chr17	-0.85
SEC14L1	5028	chr17:72591172-7259140	inter_enh	72591172	72591408	chr17	-0.83
FLJ45079	37118	chr17:73354458-7335483	inter_enh	73354458	73354835	chr17	-0.89
LOC100996291	20386	chr17:73765729-7376583	inter_enh	73765729	73765836	chr17	-0.68
SOCS3	3620	chr17:73863953-7386431	inter_enh	73863953	73864318	chr17	-0.40
NPTX1	10250	chr17:76075143-7607535	inter_enh	76075143	76075356	chr17	-0.56
NPTX1	10797	chr17:76075514-7607608	inter_enh	76075514	76076080	chr17	-0.69
LOC100130370	19505	chr17:76954200-7695430	inter_enh	76954200	76954302	chr17	-0.41
ACTG1	17504	chr17:77076938-7707702	inter_enh	77076938	77077029	chr17	-0.70
NOTUM	6204	chr17:77518405-7751869	inter_enh	77518405	77518698	chr17	-0.70

TEX19	9261	chr17:77901035-7790126	inter_enh	77901035	77901263	chr17	-0.81
UTS2R	6782	chr17:77918604-7791880	inter_enh	77918604	77918809	chr17	-0.93
FOXK2	12909	chr17:78057824-7805812	inter_enh	78057824	78058122	chr17	-0.77
PIK3R5	20012	chr17:8829627-8829906	inter_enh	8829627	8829906	chr17	-0.96
NAPG	34755	chr18:10481023-10481211	inter_enh	10481023	10481211	chr18	-0.34
SLC35G4	49262	chr18:11550210-1155037	inter_enh	11550210	11550379	chr18	-0.93
LOC101927571	4198	chr18:18624854-1862513	inter_enh	18624854	18625138	chr18	-0.62
CABLES1	42977	chr18:18925328-1892576	inter_enh	18925328	18925766	chr18	-0.71
CABLES1	2504	chr18:18965913-1896612	inter_enh	18965913	18966128	chr18	-0.71
TAF4B	11830	chr18:22048930-2204909	inter_enh	22048930	22049099	chr18	-0.77
TAF4B	8882	chr18:22051726-2205219	inter_enh	22051726	22052199	chr18	-0.79
LINC01543	16237	chr18:22272934-2227345	inter_enh	22272934	22273452	chr18	-0.57
CBX3P2	17498	chr18:2627843-2627948	inter_enh	2627843	2627948	chr18	-0.36
CBX3P2	16792	chr18:2628524-2628679	inter_enh	2628524	2628679	chr18	-0.39
CBX3P2	14266	chr18:2630955-2631300	inter_enh	2630955	2631300	chr18	-0.87
MEP1B	31634	chr18:27992253-2799244	inter_enh	27992253	27992448	chr18	-0.50
LPIN2	25603	chr18:3027400-3027698	inter_enh	3027400	3027698	chr18	-0.81
LPIN2	48813	chr18:3050675-3050843	inter_enh	3050675	3050843	chr18	-0.91
ZNF396	9530	chr18:31220734-3122092	inter_enh	31220734	31220926	chr18	-0.34
GALNT1	30296	chr18:31458047-3145842	inter_enh	31458047	31458422	chr18	-0.94
MYL12B	35032	chr18:3287703-3287794	inter_enh	3287703	3287794	chr18	-0.40
SKA1	18117	chr18:46137206-4613733	inter_enh	46137206	46137336	chr18	-0.28
POLI	5414	chr18:50044098-5004476	inter_enh	50044098	50044765	chr18	-0.98
LINC-ROR	17132	chr18:52907431-5290752	inter_enh	52907431	52907528	chr18	-0.84
MALT1	20920	chr18:54468370-54468981	inter_enh	54468370	54468981	chr18	-0.96
PMAIP1	46459	chr18:55671419-5567200	inter_enh	55671419	55672003	chr18	-0.64
PMAIP1	23542	chr18:55694516-55694741	inter_enh	55694516	55694741	chr18	-0.79
CD226	2342	chr18:65777490-6577761	inter_enh	65777490	65777619	chr18	-0.60
FAM69C	49278	chr18:70225983-7022643	inter_enh	70225983	70226430	chr18	-0.70
CTDP1	35774	chr18:75504935-7550509	inter_enh	75504935	75505093	chr18	-0.47
CTDP1	35333	chr18:75505284-7550562	inter_enh	75505284	75505626	chr18	-0.46
NDUFV2	19562	chr18:9072670-9073457	inter_enh	9072670	9073457	chr18	-0.49
DNMT1	3914	chr19:10170474-1017086	inter_enh	10170474	10170866	chr19	-0.40
DNMT1	4575	chr19:10171216-1017144	inter_enh	10171216	10171446	chr19	-0.68
DNMT1	6032	chr19:10172738-1017283	inter_enh	10172738	10172838	chr19	-0.72
MIR4322	10434	chr19:10191545-1019176	inter_enh	10191545	10191764	chr19	-0.71
MIR4322	9940	chr19:10192088-10192207	inter_enh	10192088	10192207	chr19	-0.62
S1PR2	4196	chr19:10207080-1020720	inter_enh	10207080	10207208	chr19	-0.73
S1PR2	6662	chr19:10209498-10209721	inter_enh	10209498	10209721	chr19	-0.88
S1PR2	7876	chr19:10210754-1021089	inter_enh	10210754	10210894	chr19	-0.90
MRPL4	6570	chr19:10217005-10217131	inter_enh	10217005	10217131	chr19	-0.45
MRPL4	6267	chr19:10217249-1021749	inter_enh	10217249	10217493	chr19	-0.68
PDE4A	5746	chr19:10382564-1038283	inter_enh	10382564	10382839	chr19	-0.97
C19orf52	10948	chr19:10911089-10911651	inter_enh	10911089	10911651	chr19	-0.92
ELOF1	5558	chr19:11536472-1153674	inter_enh	11536472	11536749	chr19	-0.79
ACP5	2862	chr19:11553559-11553768	inter_enh	11553559	11553768	chr19	-0.45
ACP5	3209	chr19:11553925-11554097	inter_enh	11553925	11554097	chr19	-0.83
ACP5	5295	chr19:11556002-11556192	inter_enh	11556002	11556192	chr19	-0.74
ZNF833P	34562	chr19:11611119-11611381	inter_enh	11611119	11611381	chr19	-0.30
ZNF439	15593	chr19:11822175-11822323	inter_enh	11822175	11822323	chr19	-0.76
ZNF763	16790	chr19:11953363-11953953	inter_enh	11953363	11953953	chr19	-0.98
ZNF564	22778	chr19:12545833-1254643	inter_enh	12545833	12546434	chr19	-0.47
JUNB	7836	chr19:12755398-1275554	inter_enh	12755398	12755546	chr19	-0.30
IER2	22127	chr19:13144180-1314463	inter_enh	13144180	13144634	chr19	-0.89
C19orf53	9347	chr19:13755532-1375567	inter_enh	13755532	13755674	chr19	-0.79

ZSWIM4	6330	chr19:13760832-13761052	inter_enh	13760832	13761052	chr19	-0.60
RFX1	9414	chr19:13987272-13987824	inter_enh	13987272	13987824	chr19	-0.79
RLN3	8835	chr19:13990978-13991384	inter_enh	13990978	13991384	chr19	-0.68
CD97	27525	chr19:14325384-14325474	inter_enh	14325384	14325474	chr19	-0.71
CD97	14414	chr19:14338220-14338860	inter_enh	14338220	14338860	chr19	-0.68
NDUFB7	2509	chr19:14546293-14546505	inter_enh	14546293	14546505	chr19	-0.72
NDUFB7	5318	chr19:14549132-14549285	inter_enh	14549132	14549285	chr19	-0.88
CLEC17A	5078	chr19:14549650-14549983	inter_enh	14549650	14549983	chr19	-0.88
BRD4	20465	chr19:15272467-15272987	inter_enh	15272467	15272987	chr19	-0.68
BRD4	21832	chr19:15273981-15274206	inter_enh	15273981	15274206	chr19	-0.54
RASAL3	2560	chr19:15438809-15439075	inter_enh	15438809	15439075	chr19	-0.70
OR10H1	2324	chr19:15782197-15782323	inter_enh	15782197	15782323	chr19	-0.33
TCF3	8836	chr19:1612010-1612317	inter_enh	1612010	1612317	chr19	-0.46
TCF3	13607	chr19:1616734-1617136	inter_enh	1616734	1617136	chr19	-0.38
KLF2	21511	chr19:16275080-16275198	inter_enh	16275080	16275198	chr19	-0.94
KLF2	2874	chr19:16293687-16293864	inter_enh	16293687	16293864	chr19	-0.90
TCF3	38492	chr19:1641752-1641888	inter_enh	1641752	1641888	chr19	-0.69
ONECUT3	5564	chr19:1699026-1699166	inter_enh	1699026	1699166	chr19	-0.35
PLVAP	5376	chr19:17354227-17354801	inter_enh	17354227	17354801	chr19	-0.36
MVB12A	6904	chr19:17384369-17385132	inter_enh	17384369	17385132	chr19	-0.34
ARRDC2	36134	chr19:18016010-18016209	inter_enh	18016010	18016209	chr19	-0.78
IFI30	7208	chr19:18152739-18152852	inter_enh	18152739	18152852	chr19	-0.26
LSM4	5716	chr19:18300419-18301018	inter_enh	18300419	18301018	chr19	-0.30
LRRC25	4146	chr19:18373505-18373619	inter_enh	18373505	18373619	chr19	-0.39
LRRC25	10643	chr19:18379923-18380195	inter_enh	18379923	18380195	chr19	-0.49
ADAT3	9879	chr19:1846369-1846613	inter_enh	1846369	1846613	chr19	-0.42
GATAD2A	10686	chr19:19346815-19347092	inter_enh	19346815	19347092	chr19	-0.70
GATAD2A	4628	chr19:19352800-19353223	inter_enh	19352800	19353223	chr19	-0.96
MKNK2	15868	chr19:1986303-1986448	inter_enh	1986303	1986448	chr19	-0.72
MKNK2	3800	chr19:2005951-2006136	inter_enh	2005951	2006136	chr19	-0.56
OAZ1	4800	chr19:2215627-2215741	inter_enh	2215627	2215741	chr19	-0.29
OAZ1	2946	chr19:2217431-2217646	inter_enh	2217431	2217646	chr19	-0.61
OAZ1	2626	chr19:2217771-2217945	inter_enh	2217771	2217945	chr19	-0.36
GADD45B	10222	chr19:2437309-2437379	inter_enh	2437309	2437379	chr19	-0.71
GADD45B	14812	chr19:2441720-2442148	inter_enh	2441720	2442148	chr19	-0.64
GNG7	8458	chr19:2662090-2662318	inter_enh	2662090	2662318	chr19	-0.31
ZNF57	13160	chr19:2838658-2838811	inter_enh	2838658	2838811	chr19	-0.37
ZNF77	6082	chr19:2901923-2902182	inter_enh	2901923	2902182	chr19	-0.98
THEG	8686	chr19:335591-335808	inter_enh	335591	335808	chr19	-0.80
CCNE1	25231	chr19:35019878-35020064	inter_enh	35019878	35020064	chr19	-0.68
CCNE1	25714	chr19:35020314-35020595	inter_enh	35020314	35020595	chr19	-0.44
GRAMD1A	2731	chr19:40180216-40180490	inter_enh	40180216	40180490	chr19	-0.76
FAM187B	23436	chr19:40387926-40388138	inter_enh	40387926	40388138	chr19	-0.61
FAM187B	20694	chr19:40390692-40390855	inter_enh	40390692	40390855	chr19	-0.73
FAM187B	17810	chr19:40393451-40393864	inter_enh	40393451	40393864	chr19	-0.61
FAM187B	16678	chr19:40394444-40395137	inter_enh	40394444	40395137	chr19	-0.50
CD22	8517	chr19:40502899-40503883	inter_enh	40502899	40503883	chr19	-0.37
CD22	4866	chr19:40506829-40507254	inter_enh	40506829	40507254	chr19	-0.55
FFAR1	2762	chr19:40531424-40531620	inter_enh	40531424	40531620	chr19	-0.77
FFAR2	9166	chr19:40641429-40641815	inter_enh	40641429	40641815	chr19	-0.84
FFAR2	9583	chr19:40641941-40642137	inter_enh	40641941	40642137	chr19	-0.69
FFAR2	12984	chr19:40645031-40645850	inter_enh	40645031	40645850	chr19	-0.77
HAUS5	2502	chr19:40792752-40793213	inter_enh	40792752	40793213	chr19	-0.66
LRFN3	5081	chr19:41114626-41114932	inter_enh	41114626	41114932	chr19	-0.50
RPS16	4140	chr19:44622321-44622876	inter_enh	44622321	44622876	chr19	-0.89

EID2	2356	chr19:44724731-4472533	inter_enh	44724731	44725336	chr19	-0.94
MAP3K10	47520	chr19:45341735-4534220	inter_enh	45341735	45342206	chr19	-0.96
SERTAD3	7293	chr19:45632972-4563313	inter_enh	45632972	45633134	chr19	-0.82
ERICH4	6524	chr19:46647344-46647507	inter_enh	46647344	46647507	chr19	-0.87
LINC01480	4982	chr19:46728407-4672902	inter_enh	46728407	46729024	chr19	-0.88
CEACAM3	11365	chr19:46980859-46981131	inter_enh	46980859	46981131	chr19	-0.80
CEACAM3	11004	chr19:46981255-4698145	inter_enh	46981255	46981456	chr19	-0.83
FEM1A	9744	chr19:4732856-4733109	inter_enh	4732856	4733109	chr19	-0.88
MIR4323	21396	chr19:47350622-4735118	inter_enh	47350622	47351183	chr19	-0.74
FEM1A	15648	chr19:4758324-4758424	inter_enh	4758324	4758424	chr19	-0.51
PLIN3	8188	chr19:4826879-4827058	inter_enh	4826879	4827058	chr19	-0.49
SMG9	10842	chr19:48961717-4896193	inter_enh	48961717	48961930	chr19	-0.84
CEACAM16	23152	chr19:49917331-4991749	inter_enh	49917331	49917494	chr19	-0.81
CBLC	7784	chr19:49965115-4996524	inter_enh	49965115	49965246	chr19	-0.63
CBLC	7270	chr19:49965650-4996573	inter_enh	49965650	49965738	chr19	-0.39
QPCTL	15172	chr19:50902550-5090295	inter_enh	50902550	50902954	chr19	-0.81
NANOS2	12924	chr19:51122713-51122887	inter_enh	51122713	51122887	chr19	-0.44
CCDC8	18138	chr19:51626652-5162714	inter_enh	51626652	51627145	chr19	-0.97
CALM3	11421	chr19:51807487-5180805	inter_enh	51807487	51808055	chr19	-0.83
PTGIR	8211	chr19:51811761-5181220	inter_enh	51811761	51812205	chr19	-0.78
PTGIR	7674	chr19:51812443-5181259	inter_enh	51812443	51812598	chr19	-0.81
PTGIR	6174	chr19:51813807-5181423	inter_enh	51813807	51814232	chr19	-0.73
PTGIR	5168	chr19:51814793-5181525	inter_enh	51814793	51815258	chr19	-0.74
SNAR-E	5596	chr19:52020169-5202024	inter_enh	52020169	52020244	chr19	-0.76
AP2S1	5046	chr19:52051061-5205121	inter_enh	52051061	52051214	chr19	-0.37
BBC3	8845	chr19:52436504-5243691	inter_enh	52436504	52436914	chr19	-0.59
INAFM1	13548	chr19:52483438-52483617	inter_enh	52483438	52483617	chr19	-0.64
NAPA	3004	chr19:52712935-5271373	inter_enh	52712935	52713730	chr19	-0.89
NAPA	3898	chr19:52714034-52714417	inter_enh	52714034	52714417	chr19	-0.93
ZNF541	22067	chr19:52772769-52773217	inter_enh	52772769	52773217	chr19	-0.69
ZNF541	22693	chr19:52773392-5277384	inter_enh	52773392	52773846	chr19	-0.85
SLC6A16	2650	chr19:54522790-54523081	inter_enh	54522790	54523081	chr19	-0.77
SLC6A16	4278	chr19:54524446-54524681	inter_enh	54524446	54524681	chr19	-0.66
CD37	2686	chr19:54527662-5452794	inter_enh	54527662	54527942	chr19	-0.71
PTH2	2493	chr19:54615899-5461613	inter_enh	54615899	54616135	chr19	-0.96
SLC17A7	2490	chr19:54639045-5463917	inter_enh	54639045	54639174	chr19	-0.32
IZUMO2	15727	chr19:55373798-5537435	inter_enh	55373798	55374356	chr19	-0.90
NAPSB	2456	chr19:55542192-5554235	inter_enh	55542192	55542356	chr19	-0.29
C19orf84	5112	chr19:56590546-5659095	inter_enh	56590546	56590959	chr19	-0.60
SIGLEC8	16740	chr19:56636693-5663686	inter_enh	56636693	56636866	chr19	-0.33
LINC01530	13314	chr19:56802387-5680313	inter_enh	56802387	56803134	chr19	-0.91
HAS1	12778	chr19:56906194-5690636	inter_enh	56906194	56906366	chr19	-0.94
NLRP12	18057	chr19:59037391-5903766	inter_enh	59037391	59037663	chr19	-0.79
LILRA4	12720	chr19:59554773-5955513	inter_enh	59554773	59555134	chr19	-0.94
PPP1R12C	3228	chr19:60323569-60324447	inter_enh	60323569	60324447	chr19	-0.97
NLRP8	4050	chr19:61146838-61147079	inter_enh	61146838	61147079	chr19	-0.87
TNFSF9	11522	chr19:6470414-6470558	inter_enh	6470414	6470558	chr19	-0.66
TNFSF9	5074	chr19:6486992-6487173	inter_enh	6486992	6487173	chr19	-0.29
TNFSF9	5616	chr19:6487441-6487806	inter_enh	6487441	6487806	chr19	-0.28
CD70	7672	chr19:6549676-6549995	inter_enh	6549676	6549995	chr19	-0.33
TNFSF14	28700	chr19:6592706-6593095	inter_enh	6592706	6593095	chr19	-0.78
C3	7700	chr19:6679307-6679418	inter_enh	6679307	6679418	chr19	-0.67
FCER2	3803	chr19:7676636-7677034	inter_enh	7676636	7677034	chr19	-0.70
FBN3	13606	chr19:8131892-8132093	inter_enh	8131892	8132093	chr19	-0.54
CERS4	16773	chr19:8163397-8163489	inter_enh	8163397	8163489	chr19	-0.72

ACTL9	35118	chr19:8634976-8635147	inter_enh	8634976	8635147	chr19	-0.75
CHST10	36117	chr2:100364342-10036454	inter_enh	100364342	100364548	chr2	-0.61
MIR5696	19170	chr2:101311414-10131160	inter_enh	101311414	101311609	chr2	-0.45
LINC01159	16372	chr2:104871731-10487198	inter_enh	104871731	104871986	chr2	-0.91
NCK2	6253	chr2:105721252-10572214	inter_enh	105721252	105722142	chr2	-0.70
FLJ42351	7294	chr2:113110864-11311100	inter_enh	113110864	113111005	chr2	-0.62
SLC20A1	45056	chr2:113164875-11316504	inter_enh	113164875	113165044	chr2	-0.30
IL1RN	21743	chr2:113623255-11362344	inter_enh	113623255	113623447	chr2	-0.92
CBWD2	30720	chr2:113880936-11388109	inter_enh	113880936	113881095	chr2	-0.89
MIR4782	22122	chr2:114173137-11417345	inter_enh	114173137	114173450	chr2	-0.61
CCDC93	33026	chr2:118520973-11852149	inter_enh	118520973	118521498	chr2	-0.77
INSIG2	28536	chr2:118533864-11853409	inter_enh	118533864	118534099	chr2	-0.83
DBI	10080	chr2:119851673-11985192	inter_enh	119851673	119851927	chr2	-0.71
DBI	16248	chr2:119857742-11985819	inter_enh	119857742	119858195	chr2	-0.84
CYP27C1	46708	chr2:127632845-12763336	inter_enh	127632845	127633366	chr2	-0.89
IMP4	6370	chr2:130823270-13082338	inter_enh	130823270	130823385	chr2	-0.59
PTPN18	5330	chr2:130824657-13082477	inter_enh	130824657	130824779	chr2	-0.50
ANKRD30BL	18582	chr2:132750505-13275068	inter_enh	132750505	132750682	chr2	-0.38
MGAT5	48220	chr2:134680011-13468014	inter_enh	134680011	134680145	chr2	-0.79
MGAT5	47912	chr2:134680336-13468043	inter_enh	134680336	134680437	chr2	-0.56
MGAT5	41460	chr2:134686631-13468704	inter_enh	134686631	134687045	chr2	-0.90
DARS	33984	chr2:136493625-13649379	inter_enh	136493625	136493791	chr2	-0.90
ARHGAP15	18488	chr2:143584739-14358502	inter_enh	143584739	143585020	chr2	-0.58
ARHGAP15	8133	chr2:143594971-14359549	inter_enh	143594971	143595499	chr2	-0.81
GTDC1	7181	chr2:144813314-14481419	inter_enh	144813314	144814192	chr2	-0.50
TEX41	37352	chr2:145104500-14510480	inter_enh	145104500	145104800	chr2	-0.32
ERMN	36775	chr2:157928983-15792935	inter_enh	157928983	157929351	chr2	-0.69
TANK	47839	chr2:161653770-16165397	inter_enh	161653770	161653972	chr2	-0.60
TANK	33360	chr2:161668188-16166851	inter_enh	161668188	161668511	chr2	-0.88
TANK	31552	chr2:161669895-16167042	inter_enh	161669895	161670420	chr2	-0.96
TANK	20294	chr2:161681197-16168163	inter_enh	161681197	161681635	chr2	-0.67
GALNT3	21450	chr2:166380229-16638077	inter_enh	166380229	166380772	chr2	-0.68
FAM49A	22264	chr2:16732816-16732944	inter_enh	16732816	16732944	chr2	-0.37
FAM49A	47413	chr2:16757821-16758237	inter_enh	16757821	16758237	chr2	-0.29
TLK1	35006	chr2:171830820-17183133	inter_enh	171830820	171831333	chr2	-0.64
CYBRD1	8085	chr2:172078855-17207897	inter_enh	172078855	172078979	chr2	-0.72
SLC25A12	8812	chr2:172467773-17246797	inter_enh	172467773	172467976	chr2	-0.61
ZAK	16108	chr2:173632428-17363297	inter_enh	173632428	173632976	chr2	-0.70
ZAK	15660	chr2:173633077-17363322	inter_enh	173633077	173633224	chr2	-0.32
CDCA7	5436	chr2:173922309-17392243	inter_enh	173922309	173922432	chr2	-0.52
SP3	25831	chr2:174564037-17456497	inter_enh	174564037	174564977	chr2	-0.25
ATP5G3	21900	chr2:175776552-17577671	inter_enh	175776552	175776719	chr2	-0.49
MSGN1	5656	chr2:17866682-17867163	inter_enh	17866682	17867163	chr2	-0.86
MSGN1	6080	chr2:17867268-17867425	inter_enh	17867268	17867425	chr2	-0.41
MIR4437	8053	chr2:181886366-18188698	inter_enh	181886366	181886988	chr2	-0.51
MIR4437	46630	chr2:181925185-18192532	inter_enh	181925185	181925323	chr2	-0.43
ITGA4	47688	chr2:181981832-18198251	inter_enh	181981832	181982516	chr2	-0.76
FRZB	21181	chr2:183460519-18346133	inter_enh	183460519	183461331	chr2	-0.88
NT5C1B	10578	chr2:18644693-18645118	inter_enh	18644693	18645118	chr2	-0.95
ASNSD1	3292	chr2:190230795-19023135	inter_enh	190230795	190231357	chr2	-0.51
NAB1	11536	chr2:191210400-19121071	inter_enh	191210400	191210711	chr2	-0.32
NABP1	48842	chr2:192201924-19220247	inter_enh	192201924	192202476	chr2	-0.37
STK17B	15199	chr2:196759689-19675987	inter_enh	196759689	196759873	chr2	-0.38
LOC101927619	6714	chr2:198954710-19895485	inter_enh	198954710	198954851	chr2	-0.86
FZD7	29100	chr2:202578060-20257884	inter_enh	202578060	202578849	chr2	-0.90

NOP58	5852	chr2:202832812-20283300	inter_enh	202832812	202833000	chr2	-0.94
CD28	49664	chr2:204229561-20422999	inter_enh	204229561	204229996	chr2	-0.95
CTLA4	6417	chr2:204434281-20443439	inter_enh	204434281	204434393	chr2	-0.87
CREB1	4341	chr2:208098386-20809865	inter_enh	208098386	208098652	chr2	-0.69
METTL21A	38806	chr2:208236669-20823737	inter_enh	208236669	208237379	chr2	-0.88
IKZF2	5810	chr2:213730251-21373052	inter_enh	213730251	213730526	chr2	-0.42
IKZF2	14134	chr2:213738196-21373922	inter_enh	213738196	213739228	chr2	-0.64
IKZF2	15014	chr2:213739417-21373976	inter_enh	213739417	213739766	chr2	-0.62
LOC100130451	47150	chr2:213809827-21381022	inter_enh	213809827	213810222	chr2	-0.45
CXCR1	19646	chr2:218759510-21875970	inter_enh	218759510	218759706	chr2	-0.60
WNT10A	18114	chr2:219471491-21947173	inter_enh	219471491	219471733	chr2	-0.54
WDFY1	5722	chr2:224523798-22452423	inter_enh	224523798	224524237	chr2	-0.87
ARMC9	18548	chr2:231752831-23175307	inter_enh	231752831	231753077	chr2	-0.79
ARMC9	16609	chr2:231754813-23175497	inter_enh	231754813	231754973	chr2	-0.47
ATG16L1	27774	chr2:233797064-23379729	inter_enh	233797064	233797296	chr2	-0.60
SPP2	48298	chr2:234672052-23467271	inter_enh	234672052	234672712	chr2	-0.69
ACKR3	4476	chr2:237138312-23713897	inter_enh	237138312	237138971	chr2	-0.86
COPS8	28006	chr2:237630684-23763094	inter_enh	237630684	237630948	chr2	-0.93
TCF23	25306	chr2:27250629-27250880	inter_enh	27250629	27250880	chr2	-0.79
TCF23	25710	chr2:27251023-27251294	inter_enh	27251023	27251294	chr2	-0.48
ATRAID	26132	chr2:27262115-27262425	inter_enh	27262115	27262425	chr2	-0.79
YPEL5	48528	chr2:30174572-30174876	inter_enh	30174572	30174876	chr2	-0.80
YPEL5	31244	chr2:30191829-30192186	inter_enh	30191829	30192186	chr2	-0.67
EHD3	7445	chr2:31302836-31303038	inter_enh	31302836	31303038	chr2	-0.82
QPCT	10197	chr2:37414766-37415352	inter_enh	37414766	37415352	chr2	-0.83
LINC00211	6801	chr2:37903484-37903630	inter_enh	37903484	37903630	chr2	-0.79
LINC00211	16758	chr2:37973207-37973328	inter_enh	37973207	37973328	chr2	-0.33
ATL2	39402	chr2:38497177-38497499	inter_enh	38497177	38497499	chr2	-0.92
ATL2	41044	chr2:38498876-38499084	inter_enh	38498876	38499084	chr2	-0.69
LOC101929596	8367	chr2:38604653-38604853	inter_enh	38604653	38604853	chr2	-0.74
LOC101929596	11862	chr2:38607936-38608561	inter_enh	38607936	38608561	chr2	-0.82
HNRNPLL	2570	chr2:38685850-38686655	inter_enh	38685850	38686655	chr2	-0.89
GALM	21923	chr2:38724503-38724759	inter_enh	38724503	38724759	chr2	-0.94
SRSF7	3010	chr2:38834840-38835461	inter_enh	38834840	38835461	chr2	-0.37
SOS1	8586	chr2:39209546-39209842	inter_enh	39209546	39209842	chr2	-0.85
EML4	45164	chr2:42204681-42204976	inter_enh	42204681	42204976	chr2	-0.87
EML4	27360	chr2:42222444-42222820	inter_enh	42222444	42222820	chr2	-0.91
PLEKHH2	2360	chr2:43715350-43715814	inter_enh	43715350	43715814	chr2	-0.88
SOCS5	16186	chr2:46763307-46763524	inter_enh	46763307	46763524	chr2	-0.93
HCG2040054	40314	chr2:47567469-47568258	inter_enh	47567469	47568258	chr2	-0.58
MSH6	47564	chr2:47815472-47816848	inter_enh	47815472	47816848	chr2	-0.79
MSH6	17279	chr2:47846375-47846515	inter_enh	47846375	47846515	chr2	-0.75
C2orf73	19664	chr2:54391686-54392134	inter_enh	54391686	54392134	chr2	-0.95
RTN4	5628	chr2:55136816-55136916	inter_enh	55136816	55136916	chr2	-0.76
MIR4432	24232	chr2:60492230-60492402	inter_enh	60492230	60492402	chr2	-0.83
BCL11A	48887	chr2:60682895-60683155	inter_enh	60682895	60683155	chr2	-0.89
UGP2	21288	chr2:63899771-63900852	inter_enh	63899771	63900852	chr2	-0.70
UGP2	20368	chr2:63901014-63901451	inter_enh	63901014	63901451	chr2	-0.85
UGP2	19481	chr2:63901607-63902631	inter_enh	63901607	63902631	chr2	-0.91
VPS54	6968	chr2:64106553-64106818	inter_enh	64106553	64106818	chr2	-0.75
VPS54	30630	chr2:64130233-64130464	inter_enh	64130233	64130464	chr2	-0.79
SERTAD2	11398	chr2:64745799-64746098	inter_enh	64745799	64746098	chr2	-0.88
SERTAD2	27904	chr2:64762377-64762532	inter_enh	64762377	64762532	chr2	-0.72
LOC101927438	25304	chr2:64918914-64919018	inter_enh	64918914	64919018	chr2	-0.43
CEP68	26829	chr2:65110093-65110245	inter_enh	65110093	65110245	chr2	-0.68

RAB1A	32858	chr2:65243525-65244071	inter_enh	65243525	65244071	chr2	-0.77
PPP3R1	23891	chr2:68356746-68357348	inter_enh	68356746	68357348	chr2	-0.93
PLEK	6871	chr2:68438873-68439033	inter_enh	68438873	68439033	chr2	-0.75
FBXO48	46809	chr2:68500928-68501242	inter_enh	68500928	68501242	chr2	-0.84
FBXO48	25180	chr2:68522637-68522790	inter_enh	68522637	68522790	chr2	-0.79
NRIR	30454	chr2:6867441-6867742	inter_enh	6867441	6867742	chr2	-0.78
NRIR	12266	chr2:6885638-6885923	inter_enh	6885638	6885923	chr2	-0.69
GKN2	27629	chr2:69005904-69006050	inter_enh	69005904	69006050	chr2	-0.61
LOC100133985	17905	chr2:70187973-70188121	inter_enh	70187973	70188121	chr2	-0.73
LOC100133985	10740	chr2:70216487-70216897	inter_enh	70216487	70216897	chr2	-0.39
SPR	24830	chr2:72943110-72943266	inter_enh	72943110	72943266	chr2	-0.34
STAMBP	6453	chr2:73902934-73903260	inter_enh	73902934	73903260	chr2	-0.77
C2orf81	4036	chr2:74494240-74494393	inter_enh	74494240	74494393	chr2	-0.90
LINC00298	27638	chr2:8061942-8062127	inter_enh	8061942	8062127	chr2	-0.69
TMSB10	14165	chr2:85000116-85000758	inter_enh	85000116	85000758	chr2	-0.27
KCMF1	32368	chr2:85019221-85019522	inter_enh	85019221	85019522	chr2	-0.58
KCMF1	2782	chr2:85048870-85049047	inter_enh	85048870	85049047	chr2	-0.83
GNLY	10711	chr2:85785553-85785717	inter_enh	85785553	85785717	chr2	-0.57
LOC90784	29644	chr2:86074763-86074954	inter_enh	86074763	86074954	chr2	-0.39
LOC90784	24424	chr2:86079829-86080328	inter_enh	86079829	86080328	chr2	-0.47
LOC101929567	30133	chr2:8610984-8611498	inter_enh	8610984	8611498	chr2	-0.40
REEP1	20956	chr2:86439594-86439753	inter_enh	86439594	86439753	chr2	-0.75
KDM3A	47043	chr2:86474411-86475063	inter_enh	86474411	86475063	chr2	-0.82
ASAP2	31508	chr2:9232707-9232966	inter_enh	9232707	9232966	chr2	-0.74
ADRA2B	3956	chr2:96149566-96149769	inter_enh	96149566	96149769	chr2	-0.92
ITPRIPL1	6182	chr2:96348513-96348700	inter_enh	96348513	96348700	chr2	-0.90
ITPRIPL1	5490	chr2:96349130-96349466	inter_enh	96349130	96349466	chr2	-0.79
FAHD2B	46320	chr2:97077924-97078057	inter_enh	97077924	97078057	chr2	-0.70
FAHD2B	46060	chr2:97078170-97078330	inter_enh	97078170	97078330	chr2	-0.64
LOC100289473	22574	chr20:1730891-1731041	inter_enh	1730891	1731041	chr20	-0.59
SIRPA	43431	chr20:1779224-1779538	inter_enh	1779224	1779538	chr20	-0.91
MGME1	34787	chr20:17932375-17932719	inter_enh	17932375	17932719	chr20	-0.61
SIRPA	22922	chr20:1799803-1799977	inter_enh	1799803	1799977	chr20	-0.52
PDYN	39924	chr20:1881393-1881664	inter_enh	1881393	1881664	chr20	-0.73
LOC284788	45218	chr20:22303997-22304131	inter_enh	22303997	22304131	chr20	-0.29
MIR3193	14852	chr20:29673398-29673602	inter_enh	29673398	29673602	chr20	-0.91
DUSP15	11228	chr20:29910160-29910308	inter_enh	29910160	29910308	chr20	-0.73
KIF3B	7018	chr20:30322023-30322168	inter_enh	30322023	30322168	chr20	-0.80
C20orf203	24246	chr20:30679140-30679255	inter_enh	30679140	30679255	chr20	-0.49
COMMD7	2514	chr20:30797863-30798117	inter_enh	30797863	30798117	chr20	-0.36
SNTA1	16885	chr20:31512004-31512486	inter_enh	31512004	31512486	chr20	-0.62
EIF2S2	12168	chr20:32175827-32176001	inter_enh	32175827	32176001	chr20	-0.88
EIF2S2	12550	chr20:32176198-32176395	inter_enh	32176198	32176395	chr20	-0.91
ASIP	17608	chr20:32294105-32294338	inter_enh	32294105	32294338	chr20	-0.39
ITCH	22966	chr20:32391651-32391818	inter_enh	32391651	32391818	chr20	-0.63
RBCK1	7198	chr20:329337-329683	inter_enh	329337	329683	chr20	-0.86
MANBAL	14351	chr20:35336932-35337294	inter_enh	35336932	35337294	chr20	-0.83
SRC	8278	chr20:35398138-35398307	inter_enh	35398138	35398307	chr20	-0.78
SRC	7781	chr20:35398640-35398798	inter_enh	35398640	35398798	chr20	-0.62
BLCAP	6837	chr20:35596512-35596658	inter_enh	35596512	35596658	chr20	-0.52
SLC32A1	7346	chr20:36793808-36793920	inter_enh	36793808	36793920	chr20	-0.37
TOP1	48063	chr20:39042722-39042900	inter_enh	39042722	39042900	chr20	-0.87
TOP1	34752	chr20:39055945-39056298	inter_enh	39055945	39056298	chr20	-0.83
TOP1	34096	chr20:39056607-39056948	inter_enh	39056607	39056948	chr20	-0.59
TOP1	31862	chr20:39058802-39059223	inter_enh	39058802	39059223	chr20	-0.59

ZHX3	6260	chr20:39368135-39368694	inter_enh	39368135	39368694	chr20	-0.67
CHD6	31454	chr20:39711827-39712177	inter_enh	39711827	39712177	chr20	-0.93
SMOX	39826	chr20:4037521-4037674	inter_enh	4037521	4037674	chr20	-0.35
GTSF1L	6968	chr20:41795940-41796109	inter_enh	41795940	41796109	chr20	-0.75
YWHAB	17670	chr20:42929906-42930059	inter_enh	42929906	42930059	chr20	-0.58
MATN4	11030	chr20:43381503-43381725	inter_enh	43381503	43381725	chr20	-0.83
MATN4	12545	chr20:43383020-43383238	inter_enh	43383020	43383238	chr20	-0.70
WFDC3	20736	chr20:43833141-43833295	inter_enh	43833141	43833295	chr20	-0.59
WFDC3	20430	chr20:43833463-43833586	inter_enh	43833463	43833586	chr20	-0.56
TP53RK	4910	chr20:44756449-44756739	inter_enh	44756449	44756739	chr20	-0.70
NCOA3	47688	chr20:45516215-45516421	inter_enh	45516215	45516421	chr20	-0.79
NCOA3	34570	chr20:45529168-45529705	inter_enh	45529168	45529705	chr20	-0.39
NCOA3	22312	chr20:45541592-45541797	inter_enh	45541592	45541797	chr20	-0.72
NCOA3	18516	chr20:45545354-45545625	inter_enh	45545354	45545625	chr20	-0.72
NCOA3	17206	chr20:45546486-45547115	inter_enh	45546486	45547115	chr20	-0.48
NCOA3	15724	chr20:45548192-45548372	inter_enh	45548192	45548372	chr20	-0.69
NCOA3	13518	chr20:45550419-45550556	inter_enh	45550419	45550556	chr20	-0.55
PREX1	4550	chr20:46882073-46882683	inter_enh	46882073	46882683	chr20	-0.94
SNORD12	17212	chr20:47347761-47347915	inter_enh	47347761	47347915	chr20	-0.86
B4GALT5	11300	chr20:47775086-47775171	inter_enh	47775086	47775171	chr20	-0.78
B4GALT5	23592	chr20:47787247-47787594	inter_enh	47787247	47787594	chr20	-0.92
SLC9A8	36448	chr20:47826072-47826345	inter_enh	47826072	47826345	chr20	-0.49
SLC9A8	25702	chr20:47836846-47837063	inter_enh	47836846	47837063	chr20	-0.60
SLC9A8	11906	chr20:47850585-47850915	inter_enh	47850585	47850915	chr20	-0.62
SLC9A8	11508	chr20:47851027-47851270	inter_enh	47851027	47851270	chr20	-0.50
SLC9A8	10707	chr20:47851686-47852212	inter_enh	47851686	47852212	chr20	-0.51
SNAI1	3976	chr20:48028880-48029005	inter_enh	48028880	48029005	chr20	-0.53
PTPN1	45578	chr20:48514589-48514783	inter_enh	48514589	48514783	chr20	-0.50
PTPN1	21716	chr20:48538332-48538763	inter_enh	48538332	48538763	chr20	-0.39
KCNG1	30770	chr20:49042045-49042579	inter_enh	49042045	49042579	chr20	-0.76
NFATC2	32312	chr20:49644716-49645463	inter_enh	49644716	49645463	chr20	-0.53
TMEM230	22632	chr20:5018918-5019285	inter_enh	5018918	5019285	chr20	-0.67
LOC101927770	19997	chr20:51582569-51582865	inter_enh	51582569	51582865	chr20	-0.55
ZNF217	4298	chr20:51637145-51637540	inter_enh	51637145	51637540	chr20	-0.31
ZNF217	38560	chr20:51671381-51671828	inter_enh	51671381	51671828	chr20	-0.30
ZNF217	44719	chr20:51677692-51677834	inter_enh	51677692	51677834	chr20	-0.39
SUMO1P1	48638	chr20:51876864-51877171	inter_enh	51876864	51877171	chr20	-0.94
SUMO1P1	40749	chr20:51884814-51885000	inter_enh	51884814	51885000	chr20	-0.64
SUMO1P1	37664	chr20:51887906-51888077	inter_enh	51887906	51888077	chr20	-0.77
SUMO1P1	31362	chr20:51956785-51957251	inter_enh	51956785	51957251	chr20	-0.42
SUMO1P1	33554	chr20:51959049-51959370	inter_enh	51959049	51959370	chr20	-0.71
GPCPD1	35614	chr20:5575189-5575383	inter_enh	5575189	5575383	chr20	-0.65
GPCPD1	39547	chr20:5579061-5579377	inter_enh	5579061	5579377	chr20	-0.44
C20orf196	35518	chr20:5643430-5643617	inter_enh	5643430	5643617	chr20	-0.38
TUBB1	2365	chr20:57025002-57025672	inter_enh	57025002	57025672	chr20	-0.36
RSPO4	3414	chr20:934223-934420	inter_enh	934223	934420	chr20	-0.38
LOC388813	41312	chr21:14978491-14978732	inter_enh	14978491	14978732	chr21	-0.54
LOC388813	42593	chr21:14979679-14980107	inter_enh	14979679	14980107	chr21	-0.59
BACH1	4832	chr21:29587962-29588346	inter_enh	29587962	29588346	chr21	-0.92
EVA1C	8808	chr21:32697757-32697855	inter_enh	32697757	32697855	chr21	-0.85
LINC01548	29548	chr21:33493882-33494037	inter_enh	33493882	33494037	chr21	-0.70
IFNAR2	29778	chr21:33494200-33494379	inter_enh	33494200	33494379	chr21	-0.73
IFNGR2	22882	chr21:33674116-33674259	inter_enh	33674116	33674259	chr21	-0.76
PIGP	8268	chr21:37358642-37358770	inter_enh	37358642	37358770	chr21	-0.81
LOC101928435	28938	chr21:39300264-39300751	inter_enh	39300264	39300751	chr21	-0.74

LOC101928435	39113	chr21:39310535-39310831	inter_enh	39310535	39310831	chr21	-0.94
LOC101928435	39550	chr21:39310981-39311259	inter_enh	39310981	39311259	chr21	-0.72
ZNF295-AS1	6908	chr21:42322216-42322493	inter_enh	42322216	42322493	chr21	-0.26
TFF3	5942	chr21:42602747-42602921	inter_enh	42602747	42602921	chr21	-0.39
TFF2	13229	chr21:42631009-42631089	inter_enh	42631009	42631089	chr21	-0.37
UBASH3A	46122	chr21:42743121-42743198	inter_enh	42743121	42743198	chr21	-0.60
PKNOX1	36994	chr21:43230611-43230778	inter_enh	43230611	43230778	chr21	-0.66
CBS	9822	chr21:43379270-43379457	inter_enh	43379270	43379457	chr21	-0.86
U2AF1	17864	chr21:43418289-43418955	inter_enh	43418289	43418955	chr21	-0.82
LINC00322	41236	chr21:43535078-43535146	inter_enh	43535078	43535146	chr21	-0.69
CSTB	3511	chr21:44024124-44024266	inter_enh	44024124	44024266	chr21	-0.32
CSTB	6518	chr21:44027042-44027363	inter_enh	44027042	44027363	chr21	-0.63
AGPAT3	22376	chr21:44087021-44087312	inter_enh	44087021	44087312	chr21	-0.52
ICOSLG	28602	chr21:44456484-44456944	inter_enh	44456484	44456944	chr21	-0.82
PEX26	8833	chr22:16931287-16932415	inter_enh	16931287	16932415	chr22	-0.97
LINC00895	48280	chr22:17982460-17982825	inter_enh	17982460	17982825	chr22	-0.33
TOP3B	46654	chr22:20713827-20713961	inter_enh	20713827	20713961	chr22	-0.46
VPREB1	38568	chr22:20890253-20891008	inter_enh	20890253	20891008	chr22	-0.55
VPREB1	37018	chr22:20892026-20892335	inter_enh	20892026	20892335	chr22	-0.75
VPREB1	34942	chr22:20894063-20894449	inter_enh	20894063	20894449	chr22	-0.69
VPREB1	4382	chr22:20933121-20934040	inter_enh	20933121	20934040	chr22	-0.66
BMS1P20	45082	chr22:21027452-21027635	inter_enh	21027452	21027635	chr22	-0.76
POM121L1P	27598	chr22:21289322-21289507	inter_enh	21289322	21289507	chr22	-0.33
GGTLC2	35262	chr22:21353795-21354289	inter_enh	21353795	21354289	chr22	-0.67
GGTLC2	47420	chr22:21366146-21366254	inter_enh	21366146	21366254	chr22	-0.69
MIR650	2660	chr22:21497802-21498054	inter_enh	21497802	21498054	chr22	-0.83
IGLL5	22637	chr22:21536786-21537856	inter_enh	21536786	21537856	chr22	-0.69
IGLL5	44579	chr22:21604344-21604730	inter_enh	21604344	21604730	chr22	-0.68
GNAZ	15742	chr22:21726748-21727104	inter_enh	21726748	21727104	chr22	-0.72
MIF-AS1	12422	chr22:22583449-22583630	inter_enh	22583449	22583630	chr22	-0.94
MIF-AS1	15605	chr22:22586383-22587063	inter_enh	22586383	22587063	chr22	-0.60
MIAT	11808	chr22:25371507-25371765	inter_enh	25371507	25371765	chr22	-0.28
CCDC117	12254	chr22:27486060-27486752	inter_enh	27486060	27486752	chr22	-0.41
XBP1	8892	chr22:27517566-27517769	inter_enh	27517566	27517769	chr22	-0.83
XBP1	7198	chr22:27519270-27519454	inter_enh	27519270	27519454	chr22	-0.71
XBP1	6308	chr22:27520083-27520421	inter_enh	27520083	27520421	chr22	-0.85
XBP1	11570	chr22:27537918-27538342	inter_enh	27537918	27538342	chr22	-0.96
XBP1	16476	chr22:27542759-27543312	inter_enh	27542759	27543312	chr22	-0.94
XBP1	22191	chr22:27548602-27548900	inter_enh	27548602	27548900	chr22	-0.87
XBP1	23690	chr22:27550128-27550372	inter_enh	27550128	27550372	chr22	-0.92
OSM	8938	chr22:29001587-29001950	inter_enh	29001587	29001950	chr22	-0.40
SMTN	16411	chr22:29790817-29790921	inter_enh	29790817	29790921	chr22	-0.86
PIK3IP1	14240	chr22:30032674-30032845	inter_enh	30032674	30032845	chr22	-0.38
PIK3IP1	15911	chr22:30034106-30034756	inter_enh	30034106	30034756	chr22	-0.67
AP1B1P1	16251	chr22:30864138-30864288	inter_enh	30864138	30864288	chr22	-0.26
HMOX1	3706	chr22:34103229-34103475	inter_enh	34103229	34103475	chr22	-0.59
CARD10	19966	chr22:36265037-36265206	inter_enh	36265037	36265206	chr22	-0.66
LGALS1	3067	chr22:36398439-36398543	inter_enh	36398439	36398543	chr22	-0.75
MICALL1	9670	chr22:36622107-36622753	inter_enh	36622107	36622753	chr22	-0.52
PICK1	3062	chr22:36779804-36780483	inter_enh	36779804	36780483	chr22	-0.98
APOBEC3B-AS1	4688	chr22:37728778-37728942	inter_enh	37728778	37728942	chr22	-0.87
APOBEC3G	10908	chr22:37791982-37792110	inter_enh	37791982	37792110	chr22	-0.87
APOBEC3G	8706	chr22:37794122-37794373	inter_enh	37794122	37794373	chr22	-0.97
APOBEC3H	13779	chr22:37836616-37837290	inter_enh	37836616	37837290	chr22	-0.84
APOBEC3H	17818	chr22:37840848-37841137	inter_enh	37840848	37841137	chr22	-0.95

APOBEC3H	18670	chr22:37841548-37842140	inter_enh	37841548	37842140	chr22	-0.92
APOBEC3H	25128	chr22:37848227-37848378	inter_enh	37848227	37848378	chr22	-0.83
LOC100506472	10576	chr22:38168564-38168808	inter_enh	38168564	38168808	chr22	-0.69
MKL1	9561	chr22:39372128-39372334	inter_enh	39372128	39372334	chr22	-0.56
TNFRSF13C	4550	chr22:40647879-40648557	inter_enh	40647879	40648557	chr22	-0.70
CENPM	4014	chr22:40662089-40662222	inter_enh	40662089	40662222	chr22	-0.66
OGFRP1	27180	chr22:41022811-41022953	inter_enh	41022811	41022953	chr22	-0.56
OGFRP1	27550	chr22:41023071-41023434	inter_enh	41023071	41023434	chr22	-0.89
OGFRP1	29778	chr22:41025275-41025686	inter_enh	41025275	41025686	chr22	-0.69
LINC01315	12604	chr22:41082479-41082630	inter_enh	41082479	41082630	chr22	-0.63
SERHL2	4283	chr22:41275297-41275757	inter_enh	41275297	41275757	chr22	-0.90
LINC01310	31867	chr22:47616519-47616915	inter_enh	47616519	47616915	chr22	-0.84
PIM3	14596	chr22:48725491-48725608	inter_enh	48725491	48725608	chr22	-0.68
PDCL3P4	10432	chr3:102903191-10290387	inter_enh	102903191	102903876	chr3	-0.99
ZPLD1	19240	chr3:103617143-10361747	inter_enh	103617143	103617474	chr3	-0.84
LOC101929607	5118	chr3:108626699-10862799	inter_enh	108626699	108627998	chr3	-0.56
SLC9C1	2868	chr3:113498482-11349878	inter_enh	113498482	113498782	chr3	-0.35
SLC9C1	3719	chr3:113498973-11349999	inter_enh	113498973	113499993	chr3	-0.51
CD200R1L	31857	chr3:114015499-11401576	inter_enh	114015499	114015763	chr3	-0.75
CD200R1L	29064	chr3:114076467-11407663	inter_enh	114076467	114076636	chr3	-0.49
LINC00901	35080	chr3:118087569-11808820	inter_enh	118087569	118088202	chr3	-0.50
GSK3B	3091	chr3:121298907-12129918	inter_enh	121298907	121299183	chr3	-0.83
POLQ	3114	chr3:122750415-12275090	inter_enh	122750415	122750900	chr3	-0.54
PARP15	30763	chr3:123847625-12384832	inter_enh	123847625	123848329	chr3	-0.61
CNBP	3644	chr3:130389045-13038924	inter_enh	130389045	130389242	chr3	-0.83
CNBP	4110	chr3:130389466-13038975	inter_enh	130389466	130389754	chr3	-0.77
IQSEC1	4744	chr3:13094211-13094512	inter_enh	13094211	13094512	chr3	-0.77
IQSEC1	5382	chr3:13094634-13095367	inter_enh	13094634	13095367	chr3	-0.92
IQSEC1	38104	chr3:13127064-13128380	inter_enh	13127064	13128380	chr3	-0.28
IQSEC1	40937	chr3:13130421-13130689	inter_enh	13130421	13130689	chr3	-0.38
PIK3R4	13246	chr3:131961531-13196173	inter_enh	131961531	131961734	chr3	-0.60
TOPBP1	2192	chr3:134865551-13486568	inter_enh	134865551	134865689	chr3	-0.54
AMOTL2	5016	chr3:135581725-13558220	inter_enh	135581725	135582208	chr3	-0.95
PISRT1	31146	chr3:140403876-14040394	inter_enh	140403876	140403941	chr3	-0.49
ZBTB38	3286	chr3:142522297-14252262	inter_enh	142522297	142522620	chr3	-0.80
LINC01267	22882	chr3:14346130-14346251	inter_enh	14346130	14346251	chr3	-0.81
HPS3	8955	chr3:150321022-15032118	inter_enh	150321022	150321188	chr3	-0.48
CP	21604	chr3:150443945-15044430	inter_enh	150443945	150444306	chr3	-0.93
RNF13	4412	chr3:151008634-15100887	inter_enh	151008634	151008871	chr3	-0.39
RNF13	3912	chr3:151009141-15100936	inter_enh	151009141	151009364	chr3	-0.35
TSC22D2	35294	chr3:151573781-15157458	inter_enh	151573781	151574583	chr3	-0.25
MBNL1	43961	chr3:153424387-15342472	inter_enh	153424387	153424727	chr3	-0.42
COLQ	35100	chr3:15573304-15573420	inter_enh	15573304	15573420	chr3	-0.75
COLQ	36202	chr3:15574399-15574530	inter_enh	15574399	15574530	chr3	-0.46
MME	30858	chr3:156249025-15624951	inter_enh	156249025	156249516	chr3	-0.95
PLCH1	33830	chr3:156938456-15693858	inter_enh	156938456	156938589	chr3	-0.53
TIPARP	30549	chr3:157844223-15784447	inter_enh	157844223	157844475	chr3	-0.68
CCNL1	5998	chr3:158367126-15836722	inter_enh	158367126	158367223	chr3	-0.66
OTOL1	13892	chr3:162711035-16271132	inter_enh	162711035	162711324	chr3	-0.92
LINC00690	14796	chr3:16567531-16567718	inter_enh	16567531	16567718	chr3	-0.32
PLCL2	16711	chr3:16884346-16885140	inter_enh	16884346	16885140	chr3	-0.88
LINC01330	31314	chr3:169065022-16906520	inter_enh	169065022	169065206	chr3	-0.53
LINC01330	13890	chr3:169082327-16908274	inter_enh	169082327	169082749	chr3	-0.44
MECOM	13358	chr3:170877433-17087780	inter_enh	170877433	170877800	chr3	-0.46
TERC	6122	chr3:170959341-17095949	inter_enh	170959341	170959498	chr3	-0.91

TERC	5719	chr3:170959641-17096000	inter_enh	170959641	170960005	chr3	-0.96
TERC	2164	chr3:170963299-17096345	inter_enh	170963299	170963458	chr3	-0.55
LOC100128164	23277	chr3:171143697-17114418	inter_enh	171143697	171144181	chr3	-0.83
SEC62	32210	chr3:171199258-17119970	inter_enh	171199258	171199707	chr3	-0.84
PHC3	7770	chr3:171389823-17139018	inter_enh	171389823	171390180	chr3	-0.42
SKIL	4586	chr3:171553380-17155377	inter_enh	171553380	171553779	chr3	-0.27
SLC7A14	47970	chr3:171834437-17183462	inter_enh	171834437	171834620	chr3	-0.29
TNIK	31378	chr3:172692091-17269244	inter_enh	172692091	172692449	chr3	-0.51
TBL1XR1	46326	chr3:178443908-17844422	inter_enh	178443908	178444229	chr3	-0.35
LINC00501	44712	chr3:178539424-17853984	inter_enh	178539424	178539845	chr3	-0.31
LINC00578	30932	chr3:178611150-17861178	inter_enh	178611150	178611789	chr3	-0.46
LOC102724550	38080	chr3:178979155-17897937	inter_enh	178979155	178979377	chr3	-0.93
KCNMB2	13708	chr3:179722932-17972320	inter_enh	179722932	179723207	chr3	-0.88
ZMAT3	12364	chr3:180284518-18028491	inter_enh	180284518	180284910	chr3	-0.83
ZNF639	7394	chr3:180516680-18051702	inter_enh	180516680	180517021	chr3	-0.40
GNB4	23042	chr3:180675028-18067518	inter_enh	180675028	180675187	chr3	-0.67
GNB4	25071	chr3:180676942-18067733	inter_enh	180676942	180677332	chr3	-0.53
GNB4	25510	chr3:180677516-18067763	inter_enh	180677516	180677637	chr3	-0.54
ACTL6A	11474	chr3:180751805-18075204	inter_enh	180751805	180752047	chr3	-0.81
ACTL6A	11038	chr3:180752281-18075244	inter_enh	180752281	180752443	chr3	-0.87
LINC01206	9102	chr3:183143682-18314380	inter_enh	183143682	183143801	chr3	-0.70
FLJ46066	4289	chr3:183691091-18369117	inter_enh	183691091	183691175	chr3	-0.79
FLJ46066	4814	chr3:183691341-18369197	inter_enh	183691341	183691974	chr3	-0.92
FLJ46066	15716	chr3:183702351-18370276	inter_enh	183702351	183702768	chr3	-0.95
MCF2L2	7866	chr3:184636477-18463676	inter_enh	184636477	184636760	chr3	-0.94
ETV5	33600	chr3:187342884-18734350	inter_enh	187342884	187343508	chr3	-0.98
BCL6	24772	chr3:188970880-18897108	inter_enh	188970880	188971081	chr3	-0.77
LPP	16642	chr3:189337561-18933786	inter_enh	189337561	189337864	chr3	-0.33
LOC647323	31555	chr3:195235300-19523609	inter_enh	195235300	195236094	chr3	-0.89
LOC647323	43828	chr3:195247672-19524826	inter_enh	195247672	195248269	chr3	-0.87
HES1	28042	chr3:195308392-19530877	inter_enh	195308392	195308771	chr3	-0.94
LOC100505920	7010	chr3:195399701-19539986	inter_enh	195399701	195399860	chr3	-0.69
ACAP2	3251	chr3:196648060-19664865	inter_enh	196648060	196648654	chr3	-0.64
LINC00885	26827	chr3:197326927-19732722	inter_enh	197326927	197327223	chr3	-0.75
NRROS	6205	chr3:197844755-19784493	inter_enh	197844755	197844939	chr3	-0.42
DLG1	6804	chr3:198517116-19851757	inter_enh	198517116	198517573	chr3	-0.89
OXSM	29085	chr3:25835496-25835806	inter_enh	25835496	25835806	chr3	-0.51
TGFBR2	7512	chr3:30614992-30615977	inter_enh	30614992	30615977	chr3	-0.64
GADL1	39871	chr3:30950939-30951119	inter_enh	30950939	30951119	chr3	-0.89
EPM2AIP1	23338	chr3:36986372-36986553	inter_enh	36986372	36986553	chr3	-0.39
XIRP1	15592	chr3:39224246-39225117	inter_enh	39224246	39225117	chr3	-0.82
XIRP1	40374	chr3:39249401-39249526	inter_enh	39249401	39249526	chr3	-0.66
CX3CR1	5210	chr3:39303326-39303555	inter_enh	39303326	39303555	chr3	-0.49
SNRK	40273	chr3:43262682-43262784	inter_enh	43262682	43262784	chr3	-0.50
RTP3	9304	chr3:46505113-46505254	inter_enh	46505113	46505254	chr3	-0.93
SMARCC1	7758	chr3:47806055-47806282	inter_enh	47806055	47806282	chr3	-0.55
EDEM1	4285	chr3:5199871-5200275	inter_enh	5199871	5200275	chr3	-0.92
APPL1	2560	chr3:57234164-57234324	inter_enh	57234164	57234324	chr3	-0.86
LINC01266	33980	chr3:574499-575113	inter_enh	574499	575113	chr3	-0.92
SYNPR	49235	chr3:63189656-63189778	inter_enh	63189656	63189778	chr3	-0.48
LINC01212	21435	chr3:70152926-70153112	inter_enh	70152926	70153112	chr3	-0.74
RYBP	49456	chr3:72627843-72627996	inter_enh	72627843	72627996	chr3	-0.79
SSUH2	13591	chr3:8681942-8682768	inter_enh	8681942	8682768	chr3	-0.64
CGGBP1	28464	chr3:88162225-88162518	inter_enh	88162225	88162518	chr3	-0.66
THUMPD3	9826	chr3:9369839-9369941	inter_enh	9369839	9369941	chr3	-0.41

THUMPD3	8100	chr3:9371336-9371897	inter_enh	9371336	9371897	chr3	-0.67
GPR15	14351	chr3:99747516-99748050	inter_enh	99747516	99748050	chr3	-0.96
CPOX	29845	chr3:99764937-99765665	inter_enh	99764937	99765665	chr3	-0.99
EIF4E	2154	chr4:100072884-10007304	inter_enh	100072884	100073045	chr4	-0.83
DAPP1	8510	chr4:100948419-10094856	inter_enh	100948419	100948565	chr4	-0.70
LOC101929353	24228	chr4:101305806-10130616	inter_enh	101305806	101306161	chr4	-0.48
TMED11P	14318	chr4:1121137-1121403	inter_enh	1121137	1121403	chr4	-0.73
C4orf32	45380	chr4:113240509-11324073	inter_enh	113240509	113240732	chr4	-0.79
TIFA	4302	chr4:113430675-11343094	inter_enh	113430675	113430945	chr4	-0.89
PDE5A	34711	chr4:120804058-12080422	inter_enh	120804058	120804224	chr4	-0.41
PDE5A	35535	chr4:120804724-12080520	inter_enh	120804724	120805206	chr4	-0.42
MAD2L1	3096	chr4:121210446-12121067	inter_enh	121210446	121210671	chr4	-0.93
MAD2L1	4324	chr4:121211660-12121191	inter_enh	121211660	121211913	chr4	-0.87
EXOSC9	5162	chr4:122936582-12293693	inter_enh	122936582	122936934	chr4	-0.85
SPRY1	43961	chr4:124583846-12458426	inter_enh	124583846	124584264	chr4	-0.35
MGARP	48084	chr4:140372743-14037297	inter_enh	140372743	140372972	chr4	-0.96
TNRC18P1	30480	chr4:141753069-14175333	inter_enh	141753069	141753338	chr4	-0.93
OTUD4	2769	chr4:146322751-14632335	inter_enh	146322751	146323351	chr4	-0.83
OTUD4	15746	chr4:146335934-14633612	inter_enh	146335934	146336121	chr4	-0.72
MMAA	9704	chr4:146750180-14675038	inter_enh	146750180	146750387	chr4	-0.62
LINC01095	48170	chr4:147214188-14721450	inter_enh	147214188	147214503	chr4	-0.74
CC2D2A	12260	chr4:15068224-15068428	inter_enh	15068224	15068428	chr4	-0.50
FAM160A1	46176	chr4:152503600-15250374	inter_enh	152503600	152503741	chr4	-0.65
MIR4453	16932	chr4:153693641-15369427	inter_enh	153693641	153694279	chr4	-0.95
MIR4453	18164	chr4:153694690-15369569	inter_enh	153694690	153695693	chr4	-0.90
MIR4453	23406	chr4:153700269-15370059	inter_enh	153700269	153700599	chr4	-0.78
MIR4453	25048	chr4:153701814-15370233	inter_enh	153701814	153702337	chr4	-0.64
MIR4453	41836	chr4:153718595-15371913	inter_enh	153718595	153719133	chr4	-0.68
CD38	6680	chr4:15382129-15382567	inter_enh	15382129	15382567	chr4	-0.95
TMEM154	16723	chr4:153837439-15383754	inter_enh	153837439	153837543	chr4	-0.36
KIAA0922	37652	chr4:154569229-15456935	inter_enh	154569229	154569359	chr4	-0.65
KIAA0922	36974	chr4:154569532-15457041	inter_enh	154569532	154570412	chr4	-0.32
KIAA0922	30406	chr4:154576342-15457673	inter_enh	154576342	154576739	chr4	-0.87
TLR2	40822	chr4:154783962-15478417	inter_enh	154783962	154784174	chr4	-0.54
FGFBP1	47178	chr4:15502127-15502440	inter_enh	15502127	15502440	chr4	-0.94
TMEM144	16713	chr4:159334037-15933423	inter_enh	159334037	159334237	chr4	-0.79
MIR3688-1	3472	chr4:160272768-16027316	inter_enh	160272768	160273168	chr4	-0.96
MIR3688-1	21963	chr4:160290851-16029206	inter_enh	160290851	160292067	chr4	-0.97
MIR3688-1	25224	chr4:160293970-16029547	inter_enh	160293970	160295471	chr4	-0.97
MIR3688-1	31310	chr4:160300151-16030146	inter_enh	160300151	160301460	chr4	-0.99
MIR3688-1	43530	chr4:160312640-16031341	inter_enh	160312640	160313413	chr4	-0.98
MIR3688-1	45351	chr4:160314515-16031517	inter_enh	160314515	160315179	chr4	-0.98
TMEM192	20414	chr4:166273613-16627416	inter_enh	166273613	166274163	chr4	-0.84
HMGB2	3153	chr4:174495255-17449539	inter_enh	174495255	174495391	chr4	-0.80
HMGB2	3433	chr4:174495523-17449568	inter_enh	174495523	174495683	chr4	-0.84
HMGB2	5970	chr4:174497948-17449833	inter_enh	174497948	174498332	chr4	-0.71
LCORL	35792	chr4:17668327-17668421	inter_enh	17668327	17668421	chr4	-0.50
IRF2	6979	chr4:185639642-18563975	inter_enh	185639642	185639756	chr4	-0.73
PDLIM3	48064	chr4:186741446-18674209	inter_enh	186741446	186742095	chr4	-0.95
ZNF595	23730	chr4:19364-19532	inter_enh	19364	19532	chr4	-0.46
SEL1L3	21060	chr4:25495319-25495432	inter_enh	25495319	25495432	chr4	-0.57
SMIM20	9380	chr4:25515411-25515650	inter_enh	25515411	25515650	chr4	-0.71
RBPJ	7030	chr4:25923302-25923494	inter_enh	25923302	25923494	chr4	-0.75
LOC100133461	11602	chr4:3637698-3637857	inter_enh	3637698	3637857	chr4	-0.91
TLR6	4048	chr4:38538797-38538967	inter_enh	38538797	38538967	chr4	-0.38

KLHL5	2325	chr4:38720256-38720782	inter_enh	38720256	38720782	chr4	-0.57
UBE2K	15794	chr4:39360094-39360433	inter_enh	39360094	39360433	chr4	-0.97
NSUN7	26894	chr4:40419570-40419983	inter_enh	40419570	40419983	chr4	-0.42
NSG1	38582	chr4:4400220-4400380	inter_enh	4400220	4400380	chr4	-0.60
GABRA4	16794	chr4:46707901-46708051	inter_enh	46707901	46708051	chr4	-0.70
FRYL	12254	chr4:48489144-48489511	inter_enh	48489144	48489511	chr4	-0.61
FRYL	14962	chr4:48491947-48492126	inter_enh	48491947	48492126	chr4	-0.90
STK32B	15416	chr4:5088913-5089106	inter_enh	5088913	5089106	chr4	-0.82
DANCR	11327	chr4:53261920-53262178	inter_enh	53261920	53262178	chr4	-0.85
DANCR	10948	chr4:53262328-53262529	inter_enh	53262328	53262529	chr4	-0.87
SPINK2	17642	chr4:57364585-57364923	inter_enh	57364585	57364923	chr4	-0.69
SPINK2	14830	chr4:57397553-57397690	inter_enh	57397553	57397690	chr4	-0.60
CENPC	6484	chr4:68100246-68100425	inter_enh	68100246	68100425	chr4	-0.48
IGJ	2498	chr4:71753617-71753802	inter_enh	71753617	71753802	chr4	-0.57
IGJ	5630	chr4:71756716-71756968	inter_enh	71756716	71756968	chr4	-0.37
UTP3	8073	chr4:71764813-71765157	inter_enh	71764813	71765157	chr4	-0.52
UTP3	7218	chr4:71765539-71766142	inter_enh	71765539	71766142	chr4	-0.64
UTP3	6591	chr4:71766359-71766575	inter_enh	71766359	71766575	chr4	-0.68
RASSF6	33510	chr4:74738480-74738964	inter_enh	74738480	74738964	chr4	-0.64
LINC01094	32146	chr4:79753942-79754105	inter_enh	79753942	79754105	chr4	-0.74
LINC01094	31859	chr4:79754281-79754341	inter_enh	79754281	79754341	chr4	-0.61
LINC01094	7287	chr4:79778480-79779286	inter_enh	79778480	79779286	chr4	-0.94
BMP2K	41606	chr4:79874726-79875169	inter_enh	79874726	79875169	chr4	-0.96
PRDM8	12778	chr4:81312524-81312813	inter_enh	81312524	81312813	chr4	-0.80
HTRA3	46254	chr4:8368565-8368723	inter_enh	8368565	8368723	chr4	-0.25
HTRA3	47718	chr4:8370023-8370193	inter_enh	8370023	8370193	chr4	-0.27
COQ2	29088	chr4:84395941-84396068	inter_enh	84395941	84396068	chr4	-0.68
HPSE	31308	chr4:84506574-84506703	inter_enh	84506574	84506703	chr4	-0.54
C4orf36	15998	chr4:88048337-88048859	inter_enh	88048337	88048859	chr4	-0.83
GPRIN3	23578	chr4:90471420-90472105	inter_enh	90471420	90472105	chr4	-0.63
SLCO6A1	24581	chr5:101887087-10188731	inter_enh	101887087	101887315	chr5	-0.76
EFNA5	3126	chr5:107037509-10703773	inter_enh	107037509	107037734	chr5	-0.80
LOC100289673	46452	chr5:109293178-10929328	inter_enh	109293178	109293285	chr5	-0.33
LOC100289673	46748	chr5:109293468-10929358	inter_enh	109293468	109293589	chr5	-0.81
WDR36	8712	chr5:110446947-11044716	inter_enh	110446947	110447165	chr5	-0.70
LOC102467214	23416	chr5:111968546-11196868	inter_enh	111968546	111968682	chr5	-0.93
DTWD2	28350	chr5:118380226-11838075	inter_enh	118380226	118380755	chr5	-0.81
DTWD2	33164	chr5:118384946-11838566	inter_enh	118384946	118385663	chr5	-0.83
DTWD2	33727	chr5:118385814-11838592	inter_enh	118385814	118385920	chr5	-0.87
DTWD2	40168	chr5:118392234-11839238	inter_enh	118392234	118392383	chr5	-0.32
SLC12A7	22456	chr5:1187523-1187733	inter_enh	1187523	1187733	chr5	-0.71
SNCAIP	11294	chr5:121664240-12166460	inter_enh	121664240	121664609	chr5	-0.95
SNCAIP	10773	chr5:121664767-12166512	inter_enh	121664767	121665123	chr5	-0.79
LOC101927421	36948	chr5:124363091-12436385	inter_enh	124363091	124363856	chr5	-0.32
LOC101927421	25474	chr5:124374888-12437500	inter_enh	124374888	124375009	chr5	-0.41
TEX43	44706	chr5:126039962-12604007	inter_enh	126039962	126040074	chr5	-0.28
C5orf63	15857	chr5:126452775-12645310	inter_enh	126452775	126453107	chr5	-0.94
CDC42SE2	33374	chr5:130593999-13059445	inter_enh	130593999	130594452	chr5	-0.65
CDC42SE2	10090	chr5:130617402-13061761	inter_enh	130617402	130617617	chr5	-0.83
CDC42SE2	5997	chr5:130621477-13062172	inter_enh	130621477	130621729	chr5	-0.25
RAPGEF6	5214	chr5:131003940-13100414	inter_enh	131003940	131004143	chr5	-0.54
CSF2	27214	chr5:131464507-13146468	inter_enh	131464507	131464685	chr5	-0.64
CSF2	27467	chr5:131464789-13146490	inter_enh	131464789	131464909	chr5	-0.65
P4HA2-AS1	4772	chr5:131543540-13154384	inter_enh	131543540	131543848	chr5	-0.84
IRF1	10768	chr5:131865059-13186520	inter_enh	131865059	131865205	chr5	-0.58

ZCCHC10	4072	chr5:132394130-13239436	inter_enh	132394130	132394362	chr5	-0.67
FSTL4	5928	chr5:132981948-13298215	inter_enh	132981948	132982153	chr5	-0.78
C5orf15	48723	chr5:133283481-13328368	inter_enh	133283481	133283685	chr5	-0.92
C5orf15	39648	chr5:133292429-13329288	inter_enh	133292429	133292887	chr5	-0.78
TCF7	23763	chr5:133454312-13345476	inter_enh	133454312	133454762	chr5	-0.71
SMAD5	21894	chr5:135474336-13547474	inter_enh	135474336	135474741	chr5	-0.79
FAM13B	2882	chr5:137399483-13739968	inter_enh	137399483	137399686	chr5	-0.79
SPATA24	3670	chr5:138770857-13877183	inter_enh	138770857	138771835	chr5	-0.64
CXXC5	38956	chr5:139047390-13904749	inter_enh	139047390	139047490	chr5	-0.31
HBEGF	5152	chr5:139711416-13971163	inter_enh	139711416	139711631	chr5	-0.73
SLC4A9	2574	chr5:139717287-13971750	inter_enh	139717287	139717505	chr5	-0.37
FAM105A	46844	chr5:14587870-14588222	inter_enh	14587870	14588222	chr5	-0.92
JAKMIP2	27074	chr5:147169480-14716987	inter_enh	147169480	147169877	chr5	-0.89
ADRB2	20340	chr5:148165823-14816619	inter_enh	148165823	148166194	chr5	-0.84
PPARGC1B	49577	chr5:149040253-14904060	inter_enh	149040253	149040605	chr5	-0.93
PPARGC1B	49141	chr5:149040793-14904093	inter_enh	149040793	149040937	chr5	-0.79
RPS14	13659	chr5:149795803-14979590	inter_enh	149795803	149795903	chr5	-0.77
RPS14	7750	chr5:149816861-14981766	inter_enh	149816861	149817664	chr5	-0.93
IRGM	7394	chr5:150213515-15021382	inter_enh	150213515	150213824	chr5	-0.72
ANXA6	6918	chr5:150524466-15052464	inter_enh	150524466	150524642	chr5	-0.50
ANXA6	7258	chr5:150524821-15052496	inter_enh	150524821	150524967	chr5	-0.33
MFAP3	33346	chr5:153431979-15343213	inter_enh	153431979	153432132	chr5	-0.30
PPP1R2P3	39464	chr5:156249370-15624980	inter_enh	156249370	156249809	chr5	-0.88
PPP1R2P3	42156	chr5:156251774-15625279	inter_enh	156251774	156252790	chr5	-0.98
ADAM19	32008	chr5:156967354-15696748	inter_enh	156967354	156967483	chr5	-0.84
THG1L	12769	chr5:157078076-15707818	inter_enh	157078076	157078186	chr5	-0.80
LOC101927697	11742	chr5:157780791-15778141	inter_enh	157780791	157781413	chr5	-0.58
LOC101927740	20187	chr5:158480076-15848043	inter_enh	158480076	158480434	chr5	-0.49
LOC285627	38559	chr5:158787205-15878740	inter_enh	158787205	158787401	chr5	-0.71
MIR146A	23410	chr5:159868213-15986847	inter_enh	159868213	159868479	chr5	-0.74
CCNG1	29066	chr5:162768007-16276816	inter_enh	162768007	162768169	chr5	-0.29
LINC01366	4104	chr5:169686433-16968730	inter_enh	169686433	169687307	chr5	-0.98
DUSP1	6506	chr5:172137030-17213760	inter_enh	172137030	172137602	chr5	-0.42
CREBRF	3938	chr5:172411779-17241226	inter_enh	172411779	172412265	chr5	-0.95
CREBRF	3104	chr5:172412452-17241326	inter_enh	172412452	172413260	chr5	-0.93
BOD1	2658	chr5:172978801-17297906	inter_enh	172978801	172979060	chr5	-0.37
LOC401177	13540	chr5:17426815-17426945	inter_enh	17426815	17426945	chr5	-0.50
LOC401177	25786	chr5:17466157-17466255	inter_enh	17466157	17466255	chr5	-0.43
SFXN1	13514	chr5:174824561-17482464	inter_enh	174824561	174824648	chr5	-0.69
NSD1	18863	chr5:176473737-17647390	inter_enh	176473737	176473905	chr5	-0.32
NHP2	6552	chr5:177520071-17752017	inter_enh	177520071	177520170	chr5	-0.84
CANX	2084	chr5:179056367-17905653	inter_enh	179056367	179056534	chr5	-0.43
SUB1	47910	chr5:32573291-32573608	inter_enh	32573291	32573608	chr5	-0.81
SUB1	45246	chr5:32575993-32576235	inter_enh	32575993	32576235	chr5	-0.30
SUB1	12480	chr5:32608768-32608991	inter_enh	32608768	32608991	chr5	-0.71
IL7R	2720	chr5:35889889-35890135	inter_enh	35889889	35890135	chr5	-0.27
NIPBL-AS1	6238	chr5:36906227-36906405	inter_enh	36906227	36906405	chr5	-0.66
NIPBL-AS1	5888	chr5:36906546-36906785	inter_enh	36906546	36906785	chr5	-0.79
C9	5682	chr5:39405913-39406275	inter_enh	39405913	39406275	chr5	-0.47
LINC00603	7028	chr5:40080996-40081244	inter_enh	40080996	40081244	chr5	-0.95
LINC00603	6602	chr5:40081462-40081631	inter_enh	40081462	40081631	chr5	-0.87
EMB	4384	chr5:49777186-49777567	inter_enh	49777186	49777567	chr5	-0.52
PPAP2A	3751	chr5:54870055-54870775	inter_enh	54870055	54870775	chr5	-0.41
PPAP2A	5258	chr5:54871699-54872145	inter_enh	54871699	54872145	chr5	-0.84
PPAP2A	5780	chr5:54872370-54872517	inter_enh	54872370	54872517	chr5	-0.70

GAPT	15094	chr5:57838020-57838339	inter_enh	57838020	57838339	chr5	-0.91
ERBB2IP	9640	chr5:65248418-65248574	inter_enh	65248418	65248574	chr5	-0.76
ERBB2IP	9204	chr5:65248824-65249041	inter_enh	65248824	65249041	chr5	-0.84
CD180	12406	chr5:66540696-66540863	inter_enh	66540696	66540863	chr5	-0.27
TMEM174	19486	chr5:72485228-72485357	inter_enh	72485228	72485357	chr5	-0.42
F2RL1	44428	chr5:76106082-76106237	inter_enh	76106082	76106237	chr5	-0.40
BHMT	21954	chr5:78464994-78465630	inter_enh	78464994	78465630	chr5	-0.66
HOMER1	42696	chr5:78888013-78888210	inter_enh	78888013	78888210	chr5	-0.77
ZFYVE16	8362	chr5:79730976-79731472	inter_enh	79730976	79731472	chr5	-0.63
HAPLN1	10514	chr5:83063081-83063250	inter_enh	83063081	83063250	chr5	-0.73
HAPLN1	10856	chr5:83063399-83063618	inter_enh	83063399	83063618	chr5	-0.88
HAPLN1	19834	chr5:83072206-83072767	inter_enh	83072206	83072767	chr5	-0.89
HAPLN1	24168	chr5:83076659-83076981	inter_enh	83076659	83076981	chr5	-0.80
MIR4280	13451	chr5:86432957-86433197	inter_enh	86432957	86433197	chr5	-0.60
RFESD	2460	chr5:95005672-95005880	inter_enh	95005672	95005880	chr5	-0.72
LINC01554	17413	chr5:95230959-95231247	inter_enh	95230959	95231247	chr5	-0.63
ERAP2	6696	chr5:96230615-96230790	inter_enh	96230615	96230790	chr5	-0.31
C6orf203	30526	chr6:107425477-1074256	inter_enh	107425477	107425608	chr6	-0.33
LINC00222	17779	chr6:109161493-1091620	inter_enh	109161493	109162045	chr6	-0.95
WISP3	25804	chr6:112456075-11245625	inter_enh	112456075	112456257	chr6	-0.70
NEDD9	4118	chr6:11494148-11495224	inter_enh	11494148	11495224	chr6	-0.88
MAN1A1	45384	chr6:119757892-11975813	inter_enh	119757892	119758135	chr6	-0.84
LOC285762	41774	chr6:119812262-11981252	inter_enh	119812262	119812523	chr6	-0.70
LOC285762	32388	chr6:119886124-11988698	inter_enh	119886124	119886985	chr6	-0.97
LOC285762	33145	chr6:119887191-11988743	inter_enh	119887191	119887431	chr6	-0.93
ARHGAP18	34149	chr6:130107003-1301074	inter_enh	130107003	130107423	chr6	-0.76
TAAR1	2222	chr6:133006441-1330067	inter_enh	133006441	133006786	chr6	-0.94
SNORA33	6092	chr6:133186071-13318621	inter_enh	133186071	133186212	chr6	-0.79
TBC1D7	11730	chr6:13448455-13448594	inter_enh	13448455	13448594	chr6	-0.79
MYB	39336	chr6:135504565-1355050	inter_enh	135504565	135505051	chr6	-0.97
MYB	36963	chr6:135506969-1355073	inter_enh	135506969	135507393	chr6	-0.73
MYB	36336	chr6:135507706-13550791	inter_enh	135507706	135507911	chr6	-0.41
MYB	35720	chr6:135508270-13550857	inter_enh	135508270	135508578	chr6	-0.59
MYB	4544	chr6:135539359-1355398	inter_enh	135539359	135539840	chr6	-0.63
LOC102723649	15440	chr6:138043865-1380439	inter_enh	138043865	138043962	chr6	-0.74
LOC100507406	29496	chr6:138131280-1381314	inter_enh	138131280	138131448	chr6	-0.71
HEBP2	10068	chr6:138756822-1387570	inter_enh	138756822	138757098	chr6	-0.87
HECA	9776	chr6:139487969-1394883	inter_enh	139487969	139488358	chr6	-0.91
CITED2	9788	chr6:139727199-13972731	inter_enh	139727199	139727312	chr6	-0.59
MIR4465	19996	chr6:141026536-1410267	inter_enh	141026536	141026755	chr6	-0.83
MIR4465	27392	chr6:141073857-14107421	inter_enh	141073857	141074211	chr6	-0.93
MIR4465	27990	chr6:141074380-1410748	inter_enh	141074380	141074884	chr6	-0.88
CD83	20582	chr6:14204831-14204934	inter_enh	14204831	14204934	chr6	-0.67
LINC01108	19166	chr6:14374122-14374874	inter_enh	14374122	14374874	chr6	-0.97
LINC01108	35554	chr6:14428990-14429446	inter_enh	14428990	14429446	chr6	-0.94
RAET1L	4409	chr6:150392525-15039301	inter_enh	150392525	150393017	chr6	-0.36
IYD	49217	chr6:150780783-1507810	inter_enh	150780783	150781091	chr6	-0.37
PLEKHG1	9244	chr6:150953299-1509535	inter_enh	150953299	150953594	chr6	-0.69
MYCT1	15044	chr6:153045543-15304581	inter_enh	153045543	153045814	chr6	-0.95
MYCT1	12906	chr6:153047478-1530481	inter_enh	153047478	153048153	chr6	-0.93
TFB1M	36945	chr6:155714123-1557143	inter_enh	155714123	155714387	chr6	-0.64
TFB1M	37279	chr6:155714498-1557146	inter_enh	155714498	155714680	chr6	-0.64
ARID1B	44124	chr6:157096464-1570967	inter_enh	157096464	157096795	chr6	-0.81
ARID1B	43707	chr6:157096962-1570971	inter_enh	157096962	157097132	chr6	-0.88
ARID1B	9697	chr6:157130914-1571312	inter_enh	157130914	157131200	chr6	-0.58

ARID1B	2786	chr6:157137912-15713802	inter_enh	157137912	157138025	chr6	-0.68
TULP4	19549	chr6:158633999-15863425	inter_enh	158633999	158634259	chr6	-0.38
RSPH3	8432	chr6:159349561-15934967	inter_enh	159349561	159349675	chr6	-0.28
RSPH3	20023	chr6:159360815-15936160	inter_enh	159360815	159361603	chr6	-0.88
FNDC1	43976	chr6:159466371-15946650	inter_enh	159466371	159466508	chr6	-0.58
FNDC1	18080	chr6:159492253-15949241	inter_enh	159492253	159492418	chr6	-0.43
SOD2	7755	chr6:160041985-16004221	inter_enh	160041985	160042213	chr6	-0.89
MIR4639	41908	chr6:16291559-16291784	inter_enh	16291559	16291784	chr6	-0.38
PRR18	32694	chr6:166609098-16660923	inter_enh	166609098	166609237	chr6	-0.81
LOC100289495	9483	chr6:166685302-16668588	inter_enh	166685302	166685880	chr6	-0.39
FGFR1OP	49396	chr6:167382029-16738235	inter_enh	167382029	167382352	chr6	-0.83
CCR6	37723	chr6:167407415-16740770	inter_enh	167407415	167407707	chr6	-0.92
CCR6	31802	chr6:167413112-16741385	inter_enh	167413112	167413851	chr6	-0.64
LINC00242	4664	chr6:169945298-16994572	inter_enh	169945298	169945723	chr6	-0.44
RNF144B	49656	chr6:18445603-18446202	inter_enh	18445603	18446202	chr6	-0.76
E2F3	24056	chr6:20485845-20486270	inter_enh	20485845	20486270	chr6	-0.78
DUSP22	31916	chr6:204872-205407	inter_enh	204872	205407	chr6	-0.95
SOX4	10090	chr6:21711563-21712517	inter_enh	21711563	21712517	chr6	-0.98
DUSP22	5274	chr6:231726-231837	inter_enh	231726	231837	chr6	-0.61
LOC101928663	4316	chr6:25373870-25373991	inter_enh	25373870	25373991	chr6	-0.49
HIST1H2BF	2172	chr6:26309802-26310069	inter_enh	26309802	26310069	chr6	-0.77
ABT1	10480	chr6:26715579-26715678	inter_enh	26715579	26715678	chr6	-0.89
HIST1H2BJ	3206	chr6:27205254-27205443	inter_enh	27205254	27205443	chr6	-0.78
MIR3143	14318	chr6:27237376-27238023	inter_enh	27237376	27238023	chr6	-0.38
LINC01012	22230	chr6:27747380-27747744	inter_enh	27747380	27747744	chr6	-0.68
HIST1H2BL	15921	chr6:27867031-27868503	inter_enh	27867031	27868503	chr6	-0.60
HIST1H4J	4374	chr6:27895437-27895575	inter_enh	27895437	27895575	chr6	-0.44
HIST1H2AL	3240	chr6:27937672-27938016	inter_enh	27937672	27938016	chr6	-0.96
SERPINB9P1	3009	chr6:2824583-2824923	inter_enh	2824583	2824923	chr6	-0.97
LOC101927730	2494	chr6:2826615-2826838	inter_enh	2826615	2826838	chr6	-0.49
SERPINB6	16806	chr6:2890440-2890757	inter_enh	2890440	2890757	chr6	-0.29
IRF4	13512	chr6:322933-323518	inter_enh	322933	323518	chr6	-0.36
ITPR3	11548	chr6:33685444-33685723	inter_enh	33685444	33685723	chr6	-0.90
HMGA1	9448	chr6:34303029-34303182	inter_enh	34303029	34303182	chr6	-0.62
C6orf1	24460	chr6:34349241-34349408	inter_enh	34349241	34349408	chr6	-0.84
PPARD	15140	chr6:35403055-35403288	inter_enh	35403055	35403288	chr6	-0.48
CLPSL2	5486	chr6:35846784-35846940	inter_enh	35846784	35846940	chr6	-0.40
PANDAR	25040	chr6:36725704-36725981	inter_enh	36725704	36725981	chr6	-0.85
TBCC	5298	chr6:42816489-42816638	inter_enh	42816489	42816638	chr6	-0.88
TBCC	33380	chr6:42854994-42855489	inter_enh	42854994	42855489	chr6	-0.83
TBCC	34218	chr6:42855914-42856246	inter_enh	42855914	42856246	chr6	-0.89
GLTSCR1L	31124	chr6:42865564-42865727	inter_enh	42865564	42865727	chr6	-0.31
ZNF318	5720	chr6:43450784-43450977	inter_enh	43450784	43450977	chr6	-0.83
ZNF318	16975	chr6:43461952-43462318	inter_enh	43461952	43462318	chr6	-0.54
ENPP5	5193	chr6:46251686-46252112	inter_enh	46251686	46252112	chr6	-0.79
GPR110	5206	chr6:47123134-47123363	inter_enh	47123134	47123363	chr6	-0.67
CD2AP	30796	chr6:47522484-47522887	inter_enh	47522484	47522887	chr6	-0.86
DEFB113	9040	chr6:50054182-50054495	inter_enh	50054182	50054495	chr6	-0.42
MCM3	37419	chr6:52294915-52295199	inter_enh	52294915	52295199	chr6	-0.49
PAQR8	9542	chr6:52325097-52325588	inter_enh	52325097	52325588	chr6	-0.51
PAQR8	2281	chr6:52332553-52332653	inter_enh	52332553	52332653	chr6	-0.54
KHDRBS2	12411	chr6:63066250-63066692	inter_enh	63066250	63066692	chr6	-0.75
KHDRBS2	13008	chr6:63066898-63067238	inter_enh	63066898	63067238	chr6	-0.61
PTP4A1	46554	chr6:64293237-64293402	inter_enh	64293237	64293402	chr6	-0.75
EXOC2	29194	chr6:667246-667426	inter_enh	667246	667426	chr6	-0.38

OGFRL1	38302	chr6:72016676-72017111	inter_enh	72016676	72017111	chr6	-0.85
OGFRL1	37712	chr6:72017301-72017666	inter_enh	72017301	72017666	chr6	-0.93
OGFRL1	37238	chr6:72017844-72018072	inter_enh	72017844	72018072	chr6	-0.92
MIR30C2	10772	chr6:72132441-72132928	inter_enh	72132441	72132928	chr6	-0.94
LCA5	7294	chr6:80311036-80311284	inter_enh	80311036	80311284	chr6	-0.95
LCA5	7668	chr6:80311399-80311670	inter_enh	80311399	80311670	chr6	-0.38
AKIRIN2	23292	chr6:88491699-88492294	inter_enh	88491699	88492294	chr6	-0.33
AKIRIN2	26386	chr6:88495005-88495174	inter_enh	88495005	88495174	chr6	-0.30
CNR1	9438	chr6:88902010-88902665	inter_enh	88902010	88902665	chr6	-0.57
GABRR1	8098	chr6:90005769-90005878	inter_enh	90005769	90005878	chr6	-0.86
GABRR1	8455	chr6:90006074-90006288	inter_enh	90006074	90006288	chr6	-0.80
MIR4464	6443	chr6:91085435-91085811	inter_enh	91085435	91085811	chr6	-0.70
MIR4464	7754	chr6:91086629-91087240	inter_enh	91086629	91087240	chr6	-0.40
MIR4464	39169	chr6:91118270-91118428	inter_enh	91118270	91118428	chr6	-0.49
KLHL32	2688	chr6:97476300-97476756	inter_enh	97476300	97476756	chr6	-0.31
LHFPL3-AS2	23580	chr7:104377719-10437809	inter_enh	104377719	104378097	chr7	-0.58
LHFPL3-AS2	24112	chr7:104378326-10437855	inter_enh	104378326	104378553	chr7	-0.82
LINC01004	9892	chr7:104408900-10440901	inter_enh	104408900	104409011	chr7	-0.33
LINC01004	9395	chr7:104428201-10442828	inter_enh	104428201	104428285	chr7	-0.44
SYPL1	35535	chr7:105503533-10550545	inter_enh	105503533	105505453	chr7	-0.56
SYPL1	29000	chr7:105510956-10551109	inter_enh	105510956	105511099	chr7	-0.55
SYPL1	36110	chr7:105576342-10557653	inter_enh	105576342	105576537	chr7	-0.61
LSM8	5522	chr7:117605572-11760602	inter_enh	117605572	117606023	chr7	-0.94
LSM8	4234	chr7:117606931-11760724	inter_enh	117606931	117607241	chr7	-0.82
KCP	8948	chr7:128346687-12834722	inter_enh	128346687	128347229	chr7	-0.84
MEST	12662	chr7:129900442-12990073	inter_enh	129900442	129900735	chr7	-0.74
LUZP6	3086	chr7:135315717-13531594	inter_enh	135315717	135315944	chr7	-0.85
LUZP6	4007	chr7:135316346-13531715	inter_enh	135316346	135317156	chr7	-0.94
LUZP6	5094	chr7:135317446-13531822	inter_enh	135317446	135318229	chr7	-0.95
MIR4468	38141	chr7:137497086-13749728	inter_enh	137497086	137497280	chr7	-0.26
TRY2P	29735	chr7:141648209-14164836	inter_enh	141648209	141648365	chr7	-0.74
PRSS1	9578	chr7:142127150-14212747	inter_enh	142127150	142127479	chr7	-0.92
PRSS1	9204	chr7:142127614-14212776	inter_enh	142127614	142127763	chr7	-0.85
TAS2R40	16025	chr7:142613168-14261336	inter_enh	142613168	142613366	chr7	-0.79
CNTNAP2	27646	chr7:145416622-14541685	inter_enh	145416622	145416853	chr7	-0.77
EZH2	29093	chr7:148241390-14824154	inter_enh	148241390	148241544	chr7	-0.70
INTS1	8448	chr7:1518904-1519079	inter_enh	1518904	1519079	chr7	-0.79
INTS1	8776	chr7:1519235-1519405	inter_enh	1519235	1519405	chr7	-0.38
NOM1	21388	chr7:156413728-15641384	inter_enh	156413728	156413847	chr7	-0.87
PSMG3-AS1	22108	chr7:1598259-1598425	inter_enh	1598259	1598425	chr7	-0.66
SNX13	6549	chr7:17952733-17953677	inter_enh	17952733	17953677	chr7	-0.71
CDCA7L	17765	chr7:21969627-21970039	inter_enh	21969627	21970039	chr7	-0.30
RAPGEF5	33786	chr7:22396667-22397022	inter_enh	22396667	22397022	chr7	-0.97
LOC401312	12371	chr7:22683964-22684134	inter_enh	22683964	22684134	chr7	-0.81
LOC401312	29562	chr7:22701165-22701315	inter_enh	22701165	22701315	chr7	-0.88
IL6	30424	chr7:22702746-22702986	inter_enh	22702746	22702986	chr7	-0.88
IL6	16860	chr7:22716296-22716564	inter_enh	22716296	22716564	chr7	-0.83
FAM126A	10488	chr7:23030610-23030958	inter_enh	23030610	23030958	chr7	-0.66
TRA2A	13150	chr7:23550911-23551762	inter_enh	23550911	23551762	chr7	-0.57
NPY	15305	chr7:24305393-24305877	inter_enh	24305393	24305877	chr7	-0.43
NPY	37962	chr7:24327993-24328591	inter_enh	24327993	24328591	chr7	-0.71
NPY	40941	chr7:24331030-24331512	inter_enh	24331030	24331512	chr7	-0.64
CYCS	7452	chr7:25123572-25124535	inter_enh	25123572	25124535	chr7	-0.30
CYCS	7357	chr7:25138801-25138925	inter_enh	25138801	25138925	chr7	-0.34
NPVF	17985	chr7:25216559-25216731	inter_enh	25216559	25216731	chr7	-0.86

NPVF	31555	chr7:25266050-25266320	inter_enh	25266050	25266320	chr7	-0.44
MIR148A	3654	chr7:25959736-25959836	inter_enh	25959736	25959836	chr7	-0.73
MIR148A	4104	chr7:25959992-25960481	inter_enh	25959992	25960481	chr7	-0.92
GNA12	34222	chr7:2884647-2884769	inter_enh	2884647	2884769	chr7	-0.87
MTURN	29565	chr7:30170587-30170695	inter_enh	30170587	30170695	chr7	-0.30
ZNRF2	36378	chr7:30253711-30254425	inter_enh	30253711	30254425	chr7	-0.44
ZNRF2	2894	chr7:30287362-30287742	inter_enh	30287362	30287742	chr7	-0.74
TRG-AS1	22293	chr7:38325150-38325668	inter_enh	38325150	38325668	chr7	-0.87
TRG-AS1	21605	chr7:38325942-38326252	inter_enh	38325942	38326252	chr7	-0.79
HECW1	39930	chr7:43078720-43078865	inter_enh	43078720	43078865	chr7	-0.84
HECW1	34407	chr7:43084151-43084479	inter_enh	43084151	43084479	chr7	-0.88
POLD2	4272	chr7:44133569-44134362	inter_enh	44133569	44134362	chr7	-0.97
PURB	6114	chr7:44897387-44897860	inter_enh	44897387	44897860	chr7	-0.96
TNS3	7720	chr7:47595823-47596153	inter_enh	47595823	47596153	chr7	-0.78
UPP1	20934	chr7:48116244-48116371	inter_enh	48116244	48116371	chr7	-0.44
FKBP9P1	46807	chr7:55676328-55676498	inter_enh	55676328	55676498	chr7	-0.71
FKBP9P1	46323	chr7:55676676-55677118	inter_enh	55676676	55677118	chr7	-0.75
FAM220A	25654	chr7:6329409-6329515	inter_enh	6329409	6329515	chr7	-0.48
ZNF736	8473	chr7:63403077-63403345	inter_enh	63403077	63403345	chr7	-0.37
ZNF736	7752	chr7:63403736-63404128	inter_enh	63403736	63404128	chr7	-0.61
LOC441242	38652	chr7:64911812-64911957	inter_enh	64911812	64911957	chr7	-0.48
LOC100507468	20164	chr7:68680176-68680333	inter_enh	68680176	68680333	chr7	-0.74
BAZ1B	4962	chr7:72579260-72579769	inter_enh	72579260	72579769	chr7	-0.86
EIF4H	22701	chr7:73203848-73204030	inter_enh	73203848	73204030	chr7	-0.52
RFC2	12336	chr7:73318918-73319201	inter_enh	73318918	73319201	chr7	-0.44
CLIP2	4415	chr7:73337223-73337427	inter_enh	73337223	73337427	chr7	-0.73
HSPB1	4164	chr7:75773888-75774059	inter_enh	75773888	75774059	chr7	-0.82
HSPB1	11649	chr7:75781409-75781509	inter_enh	75781409	75781509	chr7	-0.48
PTPN12	7730	chr7:76996929-76997027	inter_enh	76996929	76997027	chr7	-0.81
PTPN12	6308	chr7:76998326-76998473	inter_enh	76998326	76998473	chr7	-0.41
TMEM243	7130	chr7:86693777-86694420	inter_enh	86693777	86694420	chr7	-0.34
TMEM243	47808	chr7:86734685-86734868	inter_enh	86734685	86734868	chr7	-0.89
ABCB4	23547	chr7:86966440-86966566	inter_enh	86966440	86966566	chr7	-0.46
MTERF1	36822	chr7:91311027-91311270	inter_enh	91311027	91311270	chr7	-0.77
GNG11	4830	chr7:93383996-93384245	inter_enh	93383996	93384245	chr7	-0.63
ASB4	15237	chr7:94937523-94938299	inter_enh	94937523	94938299	chr7	-0.54
ASB4	8590	chr7:94944473-94944643	inter_enh	94944473	94944643	chr7	-0.72
PPP1R35	8644	chr7:99880579-99880768	inter_enh	99880579	99880768	chr7	-0.82
ANKRD46	4218	chr8:101645336-10164548	inter_enh	101645336	101645480	chr8	-0.33
UBR5	19746	chr8:103513763-10351391	inter_enh	103513763	103513917	chr8	-0.89
ODF1	19572	chr8:103613353-10361354	inter_enh	103613353	103613548	chr8	-0.79
ODF1	13122	chr8:103646059-10364622	inter_enh	103646059	103646228	chr8	-0.65
ODF1	16380	chr8:103649341-10364946	inter_enh	103649341	103649464	chr8	-0.53
ODF1	44540	chr8:103677502-10367762	inter_enh	103677502	103677621	chr8	-0.77
KLF10	36145	chr8:103699047-10369939	inter_enh	103699047	103699399	chr8	-0.89
KLF10	3852	chr8:103741073-10374124	inter_enh	103741073	103741242	chr8	-0.27
TMEM74	44636	chr8:109824114-10982450	inter_enh	109824114	109824505	chr8	-0.89
MTMR9	32828	chr8:11146369-11146791	inter_enh	11146369	11146791	chr8	-0.89
MTMR9	15042	chr8:11164317-11164416	inter_enh	11164317	11164416	chr8	-0.71
BLK	11928	chr8:11376897-11377103	inter_enh	11376897	11377103	chr8	-0.76
EIF3H	3430	chr8:117840346-11784100	inter_enh	117840346	117841001	chr8	-0.71
UTP23	4746	chr8:117843026-11784332	inter_enh	117843026	117843325	chr8	-0.43
RAD21	4294	chr8:117960357-11796080	inter_enh	117960357	117960802	chr8	-0.79
DEPTOR	6495	chr8:120948509-12094864	inter_enh	120948509	120948649	chr8	-0.83
TRMT12	10006	chr8:125522095-12552234	inter_enh	125522095	125522349	chr8	-0.68

TRIB1	7280	chr8:126504266-12650466	inter_enh	126504266	126504663	chr8	-0.70
MIR1204	5772	chr8:128883082-12888323	inter_enh	128883082	128883238	chr8	-0.82
MIR1204	6892	chr8:128884122-12888443	inter_enh	128884122	128884437	chr8	-0.96
MIR1208	41318	chr8:129272794-12927292	inter_enh	129272794	129272925	chr8	-0.60
CHRAC1	2990	chr8:141587462-14158771	inter_enh	141587462	141587713	chr8	-0.56
ARC	4996	chr8:143687777-14368790	inter_enh	143687777	143687903	chr8	-0.62
ARC	20515	chr8:143713292-14371341	inter_enh	143713292	143713410	chr8	-0.63
FGL1	44019	chr8:17753076-17753274	inter_enh	17753076	17753274	chr8	-0.45
CHMP7	2418	chr8:23154592-23154759	inter_enh	23154592	23154759	chr8	-0.48
DOCK5	14608	chr8:25083506-25083683	inter_enh	25083506	25083683	chr8	-0.54
PPP2R2A	33292	chr8:26171410-26171850	inter_enh	26171410	26171850	chr8	-0.48
PBK	2670	chr8:27754106-27754297	inter_enh	27754106	27754297	chr8	-0.86
PBK	3161	chr8:27754445-27754941	inter_enh	27754445	27754941	chr8	-0.83
ZNF395	17166	chr8:28316927-28317198	inter_enh	28316927	28317198	chr8	-0.40
ZNF395	18932	chr8:28318691-28318964	inter_enh	28318691	28318964	chr8	-0.50
ZNF395	33081	chr8:28332862-28333092	inter_enh	28332862	28333092	chr8	-0.52
LEPROTL1	2315	chr8:30069999-30070295	inter_enh	30069999	30070295	chr8	-0.68
C8orf86	19966	chr8:38485165-38485580	inter_enh	38485165	38485580	chr8	-0.98
PLEKHA2	17300	chr8:38860448-38860767	inter_enh	38860448	38860767	chr8	-0.61
ADAM2	10377	chr8:39825246-39825440	inter_enh	39825246	39825440	chr8	-0.94
ADAM2	14952	chr8:39829716-39830120	inter_enh	39829716	39830120	chr8	-0.97
C8orf4	44778	chr8:40085101-40085627	inter_enh	40085101	40085627	chr8	-0.79
NKX6-3	10779	chr8:41612914-41613600	inter_enh	41612914	41613600	chr8	-0.69
CHRNA6	21540	chr8:42764543-42764710	inter_enh	42764543	42764710	chr8	-0.51
POTEA	38622	chr8:43227868-43228367	inter_enh	43227868	43228367	chr8	-0.79
POTEA	37368	chr8:43229242-43229502	inter_enh	43229242	43229502	chr8	-0.91
SNAI2	4577	chr8:50000934-50001324	inter_enh	50000934	50001324	chr8	-0.25
SNAI2	16294	chr8:50012676-50013015	inter_enh	50012676	50013015	chr8	-0.92
PCMTD1	40172	chr8:53014111-53014832	inter_enh	53014111	53014832	chr8	-0.36
NPBWR1	46064	chr8:54060902-54061265	inter_enh	54060902	54061265	chr8	-0.31
NPBWR1	46492	chr8:54061381-54061642	inter_enh	54061381	54061642	chr8	-0.55
LYN	12718	chr8:56942061-56942380	inter_enh	56942061	56942380	chr8	-0.72
RPS20	19117	chr8:57168747-57168875	inter_enh	57168747	57168875	chr8	-0.42
MOS	5175	chr8:57183746-57184096	inter_enh	57183746	57184096	chr8	-0.90
TOX	28716	chr8:60222908-60223169	inter_enh	60222908	60223169	chr8	-0.51
LOC100130298	18764	chr8:62024016-62024181	inter_enh	62024016	62024181	chr8	-0.48
C8orf46	45419	chr8:67613046-67613880	inter_enh	67613046	67613880	chr8	-0.49
TERF1	22121	chr8:74061347-74061711	inter_enh	74061347	74061711	chr8	-0.92
SBSPON	19234	chr8:74187236-74187357	inter_enh	74187236	74187357	chr8	-0.64
SBSPON	23081	chr8:74190993-74191293	inter_enh	74190993	74191293	chr8	-0.49
UBE2W	14381	chr8:74968015-74968147	inter_enh	74968015	74968147	chr8	-0.37
UBE2W	16824	chr8:74970309-74970740	inter_enh	74970309	74970740	chr8	-0.48
TPD52	2894	chr8:81248933-81249754	inter_enh	81248933	81249754	chr8	-0.88
CLDN23	31177	chr8:8565724-8566070	inter_enh	8565724	8566070	chr8	-0.86
CLDN23	23846	chr8:8573135-8573322	inter_enh	8573135	8573322	chr8	-0.68
CLDN23	23478	chr8:8573499-8573694	inter_enh	8573499	8573694	chr8	-0.87
CLDN23	37428	chr8:8634358-8634647	inter_enh	8634358	8634647	chr8	-0.95
TNKS	3578	chr8:9447096-9447457	inter_enh	9447096	9447457	chr8	-0.84
TP53INP1	14532	chr8:96045240-96045409	inter_enh	96045240	96045409	chr8	-0.72
NDUFAF6	37302	chr8:96068885-96069286	inter_enh	96068885	96069286	chr8	-0.86
MIR3150B	20620	chr8:96174674-96175367	inter_enh	96174674	96175367	chr8	-0.43
PLEKHF2	2180	chr8:96212770-96213118	inter_enh	96212770	96213118	chr8	-0.56
PLEKHF2	29212	chr8:96243875-96244797	inter_enh	96243875	96244797	chr8	-0.62
LOC100500773	7780	chr8:97021516-97022429	inter_enh	97021516	97022429	chr8	-0.87
GABBR2	17574	chr9:100528460-10052928	inter_enh	100528460	100529287	chr9	-0.56

GABBR2	18188	chr9:100529389-10052958	inter_enh	100529389	100529587	chr9	-0.69
ALG2	39940	chr9:100984020-10098423	inter_enh	100984020	100984235	chr9	-0.34
ALG2	34576	chr9:100989115-10098986	inter_enh	100989115	100989869	chr9	-0.96
GRIN3A	30736	chr9:103571091-10357175	inter_enh	103571091	103571750	chr9	-0.96
ABCA1	33254	chr9:106763497-10676370	inter_enh	106763497	106763706	chr9	-0.73
FSD1L	44604	chr9:107205419-10720564	inter_enh	107205419	107205642	chr9	-0.67
RGS3	28872	chr9:115424847-11542540	inter_enh	115424847	115425405	chr9	-0.48
DFNB31	34536	chr9:116341801-11634238	inter_enh	116341801	116342387	chr9	-0.72
ATP6V1G1	13046	chr9:116376605-11637693	inter_enh	116376605	116376930	chr9	-0.95
C9orf91	7234	chr9:116406182-11640640	inter_enh	116406182	116406403	chr9	-0.79
LOC100505478	28572	chr9:116455533-11645570	inter_enh	116455533	116455702	chr9	-0.72
LOC100505478	28216	chr9:116455913-11645603	inter_enh	116455913	116456034	chr9	-0.85
LOC100505478	44119	chr9:116528075-11652854	inter_enh	116528075	116528543	chr9	-0.94
TNFSF15	17764	chr9:116576589-11657714	inter_enh	116576589	116577146	chr9	-0.52
TNFSF8	8572	chr9:116740984-11674155	inter_enh	116740984	116741553	chr9	-0.75
TLR4	11075	chr9:119494856-11949553	inter_enh	119494856	119495538	chr9	-0.62
C5	10094	chr9:122862359-12286258	inter_enh	122862359	122862580	chr9	-0.50
CRB2	18030	chr9:125140032-12514044	inter_enh	125140032	125140441	chr9	-0.71
CRB2	9567	chr9:125148653-12514874	inter_enh	125148653	125148745	chr9	-0.31
FAM102A	4362	chr9:129786920-12978707	inter_enh	129786920	129787073	chr9	-0.87
FAM102A	10772	chr9:129793308-12979350	inter_enh	129793308	129793505	chr9	-0.75
FAM102A	26364	chr9:129808934-12980906	inter_enh	129808934	129809062	chr9	-0.81
NAIF1	31824	chr9:129837526-12983766	inter_enh	129837526	129837667	chr9	-0.52
IER5L	42988	chr9:131023211-13102348	inter_enh	131023211	131023488	chr9	-0.72
NTMT1	24426	chr9:131386457-13138665	inter_enh	131386457	131386654	chr9	-0.44
PTGES	15474	chr9:131539609-13153977	inter_enh	131539609	131539776	chr9	-0.48
EXOSC2	3892	chr9:132554927-13255522	inter_enh	132554927	132555222	chr9	-0.51
RAPGEF1	9880	chr9:133612536-13361271	inter_enh	133612536	133612717	chr9	-0.63
RAPGEF1	11049	chr9:133613373-13361421	inter_enh	133613373	133614217	chr9	-0.90
WDR5	8420	chr9:135982531-13598269	inter_enh	135982531	135982690	chr9	-0.81
WDR5	7160	chr9:135983722-13598401	inter_enh	135983722	135984017	chr9	-0.57
UBAC1	29181	chr9:138022129-13802232	inter_enh	138022129	138022329	chr9	-0.52
RRAGA	2424	chr9:19041713-19041874	inter_enh	19041713	19041874	chr9	-0.91
IFNW1	22805	chr9:21109126-21109552	inter_enh	21109126	21109552	chr9	-0.63
C9orf72	14370	chr9:27578150-27578317	inter_enh	27578150	27578317	chr9	-0.38
ACO1	5520	chr9:32368747-32369412	inter_enh	32368747	32369412	chr9	-0.74
SPINK4	14240	chr9:33215828-33216081	inter_enh	33215828	33216081	chr9	-0.65
FAM166B	7221	chr9:35560971-35561263	inter_enh	35560971	35561263	chr9	-0.74
OR2S2	17446	chr9:35930271-35931141	inter_enh	35930271	35931141	chr9	-0.97
OR2S2	12190	chr9:35935749-35936174	inter_enh	35935749	35936174	chr9	-0.37
OR2S2	19136	chr9:35966692-35967884	inter_enh	35966692	35967884	chr9	-0.98
RECK	29458	chr9:35997114-35997787	inter_enh	35997114	35997787	chr9	-0.93
RECK	27761	chr9:35999090-35999204	inter_enh	35999090	35999204	chr9	-0.68
EBLN3	4272	chr9:37065508-37065733	inter_enh	37065508	37065733	chr9	-0.51
EBLN3	2960	chr9:37066542-37067321	inter_enh	37066542	37067321	chr9	-0.26
EBLN3	2222	chr9:37067520-37067819	inter_enh	37067520	37067819	chr9	-0.32
GRHPR	48582	chr9:37364040-37364208	inter_enh	37364040	37364208	chr9	-0.54
GRHPR	47364	chr9:37365144-37365539	inter_enh	37365144	37365539	chr9	-0.58
GRHPR	41912	chr9:37370714-37370873	inter_enh	37370714	37370873	chr9	-0.41
JAK2	48957	chr9:4925854-4926720	inter_enh	4925854	4926720	chr9	-0.83
JAK2	48218	chr9:4926837-4927216	inter_enh	4926837	4927216	chr9	-0.96
RIC1	46184	chr9:5572893-5572974	inter_enh	5572893	5572974	chr9	-0.74
RIC1	37922	chr9:5581136-5581257	inter_enh	5581136	5581257	chr9	-0.26
RANBP6	36274	chr9:6041827-6042000	inter_enh	6041827	6042000	chr9	-0.35
UHRF2	2402	chr9:6400667-6400830	inter_enh	6400667	6400830	chr9	-0.72

KDM4C	30647	chr9:6679891-6680539	inter_enh	6679891	6680539	chr9	-0.53
LINC01506	37831	chr9:70389093-70389245	inter_enh	70389093	70389245	chr9	-0.33
PIP5K1B	21804	chr9:70488150-70488539	inter_enh	70488150	70488539	chr9	-0.84
FXN	8000	chr9:70832146-70832450	inter_enh	70832146	70832450	chr9	-0.57
TMEM2	6294	chr9:73579722-73580106	inter_enh	73579722	73580106	chr9	-0.72
KANK1	44422	chr9:741151-741300	inter_enh	741151	741300	chr9	-0.61
C9orf41	25968	chr9:76858924-76859271	inter_enh	76858924	76859271	chr9	-0.93
RFK	22285	chr9:78176893-78177065	inter_enh	78176893	78177065	chr9	-0.95
RFK	21319	chr9:78177873-78178017	inter_enh	78177873	78178017	chr9	-0.65
RFK	21011	chr9:78178192-78178314	inter_enh	78178192	78178314	chr9	-0.55
RPSAP9	3656	chr9:78206933-78207046	inter_enh	78206933	78207046	chr9	-0.65
TLE4	3344	chr9:81373098-81373227	inter_enh	81373098	81373227	chr9	-0.60
TLE4	2958	chr9:81373345-81373752	inter_enh	81373345	81373752	chr9	-0.72
LINC01507	11562	chr9:81617244-81618160	inter_enh	81617244	81618160	chr9	-0.60
UBQLN1	6410	chr9:85519326-85519470	inter_enh	85519326	85519470	chr9	-0.63
DAPK1	17046	chr9:89284758-89285074	inter_enh	89284758	89285074	chr9	-0.92
SYK	25834	chr9:92577779-92578116	inter_enh	92577779	92578116	chr9	-0.80
NFIL3	8618	chr9:93235261-93235435	inter_enh	93235261	93235435	chr9	-0.82
PCAT7	45420	chr9:96311547-96311906	inter_enh	96311547	96311906	chr9	-0.96
PCAT7	44752	chr9:96312323-96312465	inter_enh	96312323	96312465	chr9	-0.80
PCAT7	44234	chr9:96312750-96313074	inter_enh	96312750	96313074	chr9	-0.72
PCAT7	43479	chr9:96313535-96313799	inter_enh	96313535	96313799	chr9	-0.80
PCAT7	42836	chr9:96314144-96314475	inter_enh	96314144	96314475	chr9	-0.92
PCAT7	27765	chr9:96329094-96329668	inter_enh	96329094	96329668	chr9	-0.95
DMRT3	30818	chr9:997650-997919	inter_enh	997650	997919	chr9	-0.35
ANP32B	3191	chr9:99781819-99782415	inter_enh	99781819	99782415	chr9	-0.96
NANS	18020	chr9:99840666-99840851	inter_enh	99840666	99840851	chr9	-0.64
NANS	17509	chr9:99841170-99841368	inter_enh	99841170	99841368	chr9	-0.66
XKRX	10582	chrX:100080864-10008140	inter_enh	100080864	100081407	chrX	-0.88
TMSB15B	3756	chrX:103107529-10310769	inter_enh	103107529	103107691	chrX	-0.64
ZCCHC18	14022	chrX:103229762-10322993	inter_enh	103229762	103229938	chrX	-0.73
GUCY2F	5525	chrX:108617255-10861767	inter_enh	108617255	108617679	chrX	-0.97
SOWAHD	4564	chrX:118771953-11877212	inter_enh	118771953	118772122	chrX	-0.31
SOWAHD	4157	chrX:118772358-11877253	inter_enh	118772358	118772532	chrX	-0.69
SOWAHD	3466	chrX:118772924-11877334	inter_enh	118772924	118773347	chrX	-0.32
RHOXF2	42227	chrX:119053408-11905361	inter_enh	119053408	119053610	chrX	-0.74
XIAP	29462	chrX:122791780-12279198	inter_enh	122791780	122791980	chrX	-0.33
TLR7	23036	chrX:12771532-12772640	inter_enh	12771532	12772640	chrX	-0.58
TLR8	14324	chrX:12820057-12820611	inter_enh	12820057	12820611	chrX	-0.96
TMSB4X	29630	chrX:12932714-12932837	inter_enh	12932714	12932837	chrX	-0.72
FAM9C	21654	chrX:12950998-12951370	inter_enh	12950998	12951370	chrX	-0.56
FAM9C	32733	chrX:13005508-13005634	inter_enh	13005508	13005634	chrX	-0.47
FAM9C	39988	chrX:13012682-13012971	inter_enh	13012682	13012971	chrX	-0.60
FAM9C	44474	chrX:13017257-13017367	inter_enh	13017257	13017367	chrX	-0.60
STK26	35674	chrX:130948881-13094962	inter_enh	130948881	130949620	chrX	-0.36
LINC01203	10045	chrX:13272884-13273766	inter_enh	13272884	13273766	chrX	-0.49
HPRT1	2562	chrX:133419057-13341949	inter_enh	133419057	133419498	chrX	-0.73
IRAK1	11246	chrX:152927148-15292743	inter_enh	152927148	152927433	chrX	-0.90
SH3KBP1	18739	chrX:19834248-19834562	inter_enh	19834248	19834562	chrX	-0.94
RPS6KA3	48424	chrX:20242974-20243219	inter_enh	20242974	20243219	chrX	-0.81
RPS6KA3	48780	chrX:20243335-20243570	inter_enh	20243335	20243570	chrX	-0.69
ACOT9	13152	chrX:23684392-23684568	inter_enh	23684392	23684568	chrX	-0.29
SAT1	19392	chrX:23730504-23730669	inter_enh	23730504	23730669	chrX	-0.49
SAT1	34453	chrX:23745595-23745699	inter_enh	23745595	23745699	chrX	-0.28
CXorf21	20028	chrX:30525898-30526067	inter_enh	30525898	30526067	chrX	-0.45

DYNLT3	23278	chrX:37568126-37568985	inter_enh	37568126	37568985	chrX	-0.77
MID1IP1-AS1	5876	chrX:38553753-38554160	inter_enh	38553753	38554160	chrX	-0.92
MID1IP1-AS1	7766	chrX:38555325-38556367	inter_enh	38555325	38556367	chrX	-0.80
BCOR	31242	chrX:39952672-39952865	inter_enh	39952672	39952865	chrX	-0.86
MED14	14242	chrX:40493781-40494200	inter_enh	40493781	40494200	chrX	-0.51
MED14	14648	chrX:40494313-40494480	inter_enh	40494313	40494480	chrX	-0.30
PPP1R2P9	5340	chrX:42517016-42517163	inter_enh	42517016	42517163	chrX	-0.70
CHST7	10952	chrX:46306987-46307237	inter_enh	46306987	46307237	chrX	-0.76
ARAF	5064	chrX:47300244-47300513	inter_enh	47300244	47300513	chrX	-0.51
RBM3	2628	chrX:48314928-48315184	inter_enh	48314928	48315184	chrX	-0.62
CLCN5	11920	chrX:49562005-49562082	inter_enh	49562005	49562082	chrX	-0.38
NUDT11	39898	chrX:51216147-51216457	inter_enh	51216147	51216457	chrX	-0.81
MAGED1	24123	chrX:51677317-51677801	inter_enh	51677317	51677801	chrX	-0.93
PAGE2B	17362	chrX:55100751-55100950	inter_enh	55100751	55100950	chrX	-0.51
LINC01420	2318	chrX:56770056-56770192	inter_enh	56770056	56770192	chrX	-0.65
SPIN2B	3904	chrX:57168518-57168719	inter_enh	57168518	57168719	chrX	-0.73
MTMR8	32362	chrX:63564332-63564508	inter_enh	63564332	63564508	chrX	-0.64
HDHD1	32858	chrX:7109018-7109162	inter_enh	7109018	7109162	chrX	-0.85
HDHD1	33371	chrX:7109539-7109667	inter_enh	7109539	7109667	chrX	-0.85
CYSLTR1	5922	chrX:77475556-77475976	inter_enh	77475556	77475976	chrX	-0.93
GPR174	31865	chrX:78280497-78282021	inter_enh	78280497	78282021	chrX	-0.71
BRWD3	2446	chrX:79954229-79954442	inter_enh	79954229	79954442	chrX	-0.75
WWC3	19650	chrX:9924048-9924240	inter_enh	9924048	9924240	chrX	-0.31
RPS4Y2	29626	chrY:21297501-21297926	inter_enh	21297501	21297926	chrY	-0.40
TTTY16	23552	chrY:7652560-7653120	inter_enh	7652560	7653120	chrY	-0.78

Supplementary Table 6 - Genes with 50% H3K4me2 loss and KMT2D binindg in OCI-LY1 vs OCI-LY7 used for GSEA

Genes With 50% Density Loss in H3K4me2 ChIPseq in OCI-LY1 vs OCI-LY7 used to generate GSEA plot from Figure 5b

symbol	symbol	symbol	symbol	symbol	symbol	symbol	symbol	symbol
A4GALT	CBFA2T2	ENC1	IKZF3	LOC554206	NRXN1	RNASE6	TENM4	ZNF644
AA06	CBFA2T3	ENDOD1	IL10	LOC647323	NSD1	RNASEH1-AS1	TEP1	ZNF664-FAM101A
AAGAB	CBFB	ENKUR	IL10RA	LOC727896	NSG1	RNASEH2B	TERC	ZNF669
AASDH	CBL	ENOPH1	IL12RB1	LOC728730	NSL1	RNASEH2B-AS	TERF1	ZNF680
ABCA1	CBLC	ENOSF1	IL15RA	LOC728739	NSMCE1	RNASET2	TERT	ZNF687
ABCA11P	CBS	ENOX2	IL16	LOC729683	NSUN4	RNF113A	TET1	ZNF688
ABCC1	CBWD2	ENPEP	IL17RA	LOC730101	NT5C1B	RNF122	TET3	ZNF689
ABCC2	CBX3P2	ENPP3	IL17RD	LOC730102	NT5C2	RNF125	TEX19	ZNF69
ABCC5-AS1	CBX6	ENPP4	IL1RAP	LOC730202	NT5C3A	RNF139-AS1	TEX264	ZNF701
ABCD1	CC2D2B	ENPP5	IL1RN	LOC91450	NTF3	RNF14	TEX41	ZNF709
ABCD2	CCBL1	ENSA	IL21R	LOC93622	NTMT1	RNF144B	TEX9	ZNF710
ABCE1	CCDC102A	ENTPD1	IL22	LONRF1	NTN1	RNF145	TFB1M	ZNF713
ABCG1	CCDC112	ENTPD5	IL22RA2	LPCAT3	NTN3	RNF157	TFCP2	ZNF724P
ABHD11-AS1	CCDC12	ENY2	IL23A	LPIN2	NTN4	RNF167	TFCP2L1	ZNF730
ABHD12B	CCDC126	EP400NL	IL24	LPP	NTNG1	RNF186	TFF1	ZNF736
ABHD17B	CCDC14	EPB41L1	IL4R	LPP-AS1	NUAK2	RNF187	TFIP11	ZNF750
ABHD4	CCDC141	EPB41L2	IL6	LPP-AS2	NUBPL	RNF19B	TGFBR2	ZNF763
ABHD5	CCDC144B	EPB41L4A	ILDR1	LPXN	NUCB1-AS1	RNF4	TGIF1	ZNF77
ABHD8	CCDC147-AS1	EPB41L4A-AS1	ILF3	LRCH1	NUCB2	RNF43	TGM6	ZNF775
ABI1	CCDC155	EPHA4	IMMT	LRFN3	NUCKS1	RNLS	THADA	ZNF782
ABI2	CCDC167	EPHA8	IMP4	LRG1	NUDT11	RNU4ATAC	THAP5	ZNF784
ABLIM1	CCDC174	EPHB3	IMPA2	LRGUK	NUDT16P1	RNU6-2	THAP9-AS1	ZNF79
ABLIM2	CCDC178	EPN2	IMPG2	LRIG1	NUDT17	ROCK1	THEG	ZNF804A
ABR	CCDC18	EPN2-AS1	INAFM1	LRMP	NUDT3	ROCK2	THEM4	ZNF821
ABT1	CCDC182	EPN2-IT1	INF2	LRP2BP	NUDT5	ROR1	THEMIS2	ZNF830
ACACB	CCDC183	EPRS	ING3	LRR1	NUDT7	ROR2	THG1L	ZNF831
ACAD10	CCDC28A	EPS15	INO80B-WBP1	LRRC10	NUF2	RP1L1	THNSL1	ZNF839
ACAD9	CCDC50	EPS8	INO80C	LRRC16A	NUGGC	RPA4	THOC1	ZNF843
ACADVL	CCDC58	EPS8L2	INPP4A	LRRC2-AS1	NUMB	RPAP3	THOC2	ZNF85
ACAP1	CCDC6	EQTN	INPP5A	LRRC23	NUP155	RPARP-AS1	THRA	ZNF860
ACAP2	CCDC65	ERAP2	INPP5B	LRRC31	NUP160	RPF2	THUMPD3	ZNF92
ACAT1	CCDC66	ERBB2IP	INPP5F	LRRC37A3	NUP205	RPGR	THY1	ZNRF1
ACBD3	CCDC69	ERC1	INSC	LRRC3C	NUP62CL	RPL11	TIAM1	ZNRF2
ACKR3	CCDC8	ERC2	INSIG2	LRRC4C	NUP93	RPL13AP17	TIAM2	ZPBP2
ACKR4	CCDC80	ERC2-IT1	INSL5	LRRC58	NUPL2	RPL19	TIFA	ZPLD1

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ACOX3
ACOXL
ACP5
ACPP
ACSL1
ACSL3
ACSL4
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ACTG1
ACTL6A
ACTL9
ACTR3
ACVR1B
ACY3
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ADAT3
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ADD3
ADD3-AS1
ADK
ADNP-AS1
ADO
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ADPGK-AS1
ADRA2B
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CCDC94
CCL1
CCL2
CCL25
CCL3
CCM2
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CCNG1
CCNL1
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CCNYL1
CCR6
CCR7
CCR9
CCSER2
CCT3
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CD1D
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CD38
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ERICH4
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EXOC6
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EXOSC3
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EYA3
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EZH2
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FALEC
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FAM102B
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INTS4
INTS9
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IPO11
IPO7
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IQCH-AS1
IQGAP2
IQGAP3
IQSEC1
IQSEC2
IQSEC3
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IRAK3
IRF1
IRF2
IRF2BPL
IRF4
IRF5
IRF7
IRGM
ISCA2
ISCU
ISYNA1
ITCH
ITGA4
ITGA9-AS1
ITGAM
ITGB1
ITGB2
ITGB3
ITGB6
ITIH2
ITK
ITPK1-AS1
ITPKB
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LRRC9
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LRRK2
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LSP1
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LTBP1
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LUZP6
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LYN
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LYRM9
LYZ
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MAD2L1
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MAF
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MAGI1-AS1
MAGOHB
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MAN1A2
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MAN2A1
MANBAL
MAP2K3
MAP2K5
MAP2K6
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NYX
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OAZ1
ODF1
OGFRL1
OGFRP1
OGT
OIP5-AS1
OPA3
OPN5
OPTC
OR10G7
OR1F2P
OR2AG2
OR2B6
OR2S2
OR5B21
OR6P1
OR7E47P
OR8D2
ORC1
ORC3
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OSBPL8
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OTUB2
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OTUD3
OTUD4
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Supplementary Table 6 (cont.). Genes with 50% H3K4me2 loss and KMT2D binindg in OCI-LY1 vs OCI-LY7 used for GSEA

Genes With 50% Density Loss in H3K4me2 ChIPseq in OCI-LY1 vsOCI-LY7 that have KMT2D binding used to perform GSEA analysis from Figure 5d and pathway analysis from figure 5e

symbol	symbol	symbol	symbol	symbol	symbol	symbol	symbol
A4GALT	CBL	ENC1	ID3	LOC730101	NUCB1-AS1	RGSL1	TLR8
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ABCA1	CBWD2	ENKUR	IFI6	LOC93622	NUDT7	RHOC	TM9SF4
ABCC1	CBX3P2	ENOSF1	IFITM1	LONRF1	NUGGC	RHOXF2	TMA16
ABCD2	CBX6	ENTPD1	IFNLR1	LPP	NUMB	RIC8B	TMA7
ABCG1	CCBL1	EPB41L2	IFT81	LRFN3	NUP62CL	RILPL1	TMBIM1
ABHD11-AS1	CCDC112	EPB41L4A-AS1	IGF1R	LRIG1	NUPL2	RMI2	TMED10
ABLIM2	CCDC144B	EPHB3	IGF2R	LRRC23	NYX	RNASEH2B	TMED9
ABR	CCDC155	EPN2-AS1	IGLL5	LRRC37A3	OAZ1	RNASEH2B-AS	TMEM114
ACAD10	CCDC183	ERCC1	IKBKB	LRRC8C	ODF1	RNASET2	TMEM123
ACADVL	CCDC50	ERI1	IKZF3	LSP1	OGFRP1	RNF122	TMEM143
ACBD3	CCDC6	ERN1	IL12RB1	LXN	OIP5-AS1	RNF125	TMEM165
ACN9	CCDC65	ETV6	IL17RA	MACF1	OR7E47P	RNF186	TMEM184B
ACOXL	CCDC69	EVL	IL1RAP	MAD2L1BP	OTUD5	RNF187	TMEM19
ACP5	CCDC8	EZH2	IL21R	MALAT1	OXR1	RNF4	TMEM214
ACTR3	CCDC85C	FAAH2	IL23A	MAN1A1	P2RX1	RNU6-2	TMEM229B
ACY3	CCDC90B	FABP5P3	IL24	MANBAL	P2RX5	RPARP-AS1	TMEM241
ADA	CCL1	FALEC	IL4R	MAP3K10	PACSIN1	RPGR	TMEM245
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ADAM9	CCM2	FAM102B	INPP5A	MAP3K13	PAG1	RPL23	TMEM40
ADAMTS13	CCND3	FAM109A	INSC	MAP4K1	PAIP2B	RPL26	TMEM41A
ADAP1	CCR6	FAM110A	INSR	MAP9	PAK4	RPL39	TMEM50B
ADARB1	CCT3	FAM126A	INTS1	MAPKAPK2	PAPLN	RPPH1	TMEM55A
ADAT3	CD19	FAM129C	INTS4	MATN4	PCAT7	RPS14	TNFRSF10B
ADO	CD1D	FAM13B	INTS9	MDM2	PCCB	RPS26	TNFRSF13B
ADRB2	CD22	FAM155B	IQGAP2	MDM4	PCDH12	RPS29	TNFRSF17
AFMID	CD28	FAM160B2	IQGAP3	MDS2	PCDH9	RPS6KA1	TNFRSF1A
AGO2	CD2AP	FAM167A	IQSEC1	MED12L	PCGF2	RTP3	TNFRSF21
AHDC1	CD38	FAM167A-AS1	IQSEC3	MEF2D	PCLO	RXFP4	TNNI1
AKNA	CD46	FAM170B	IRF1	MEIS1	PCNA	S100A16	TNNI3
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RELB
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SSR1
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