Supplemental Material to:

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A cell epigenotype specific model for the correction of brain cellular heterogeneity bias and its application to age, brain region, and major depression

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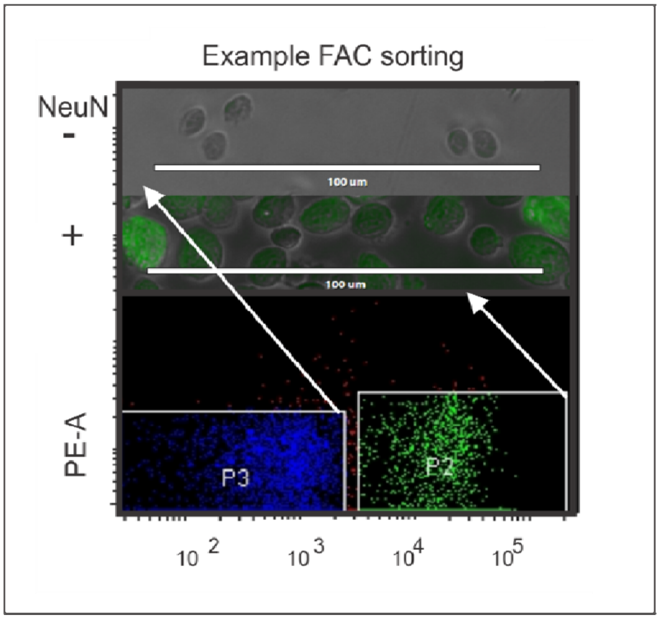
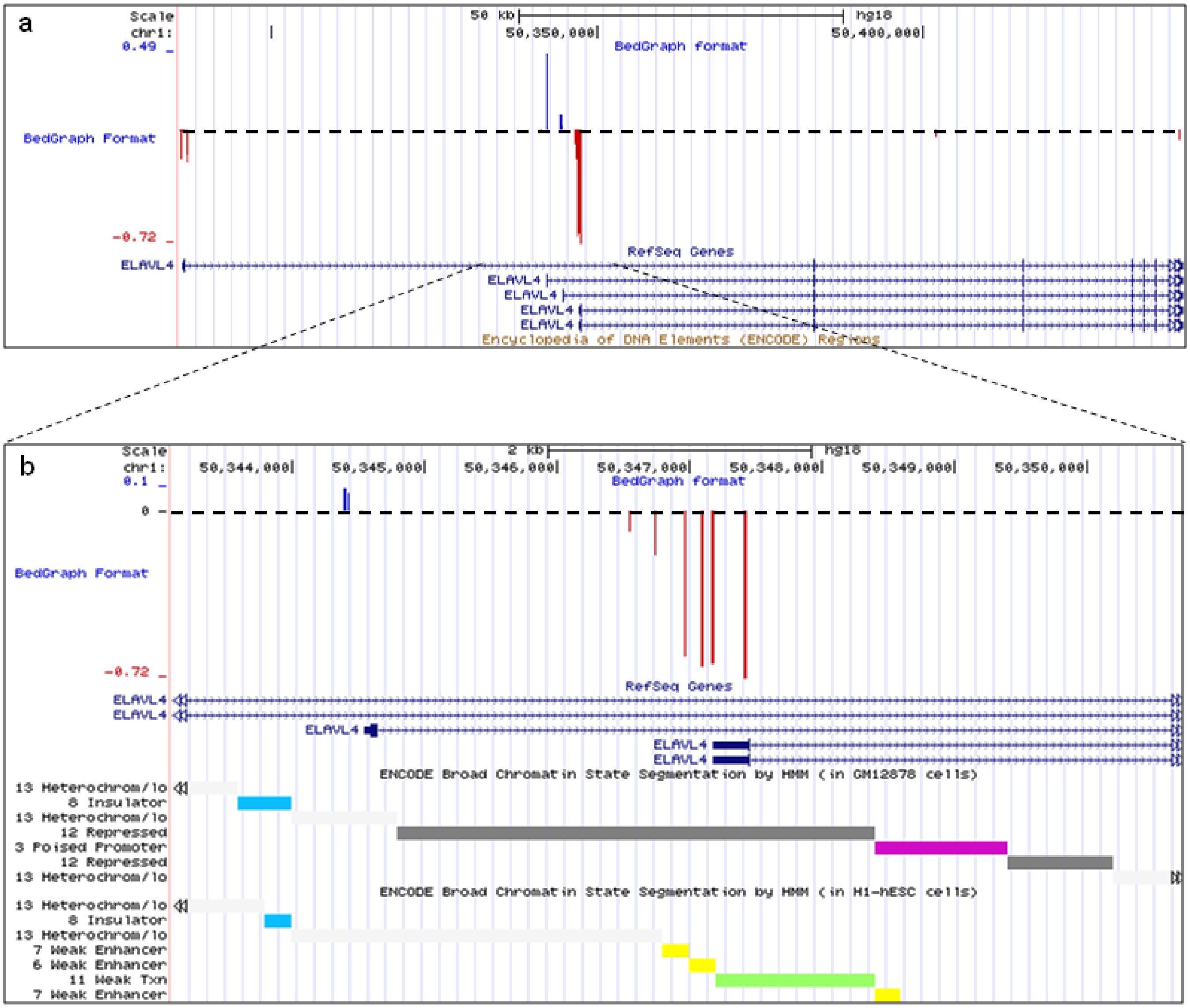
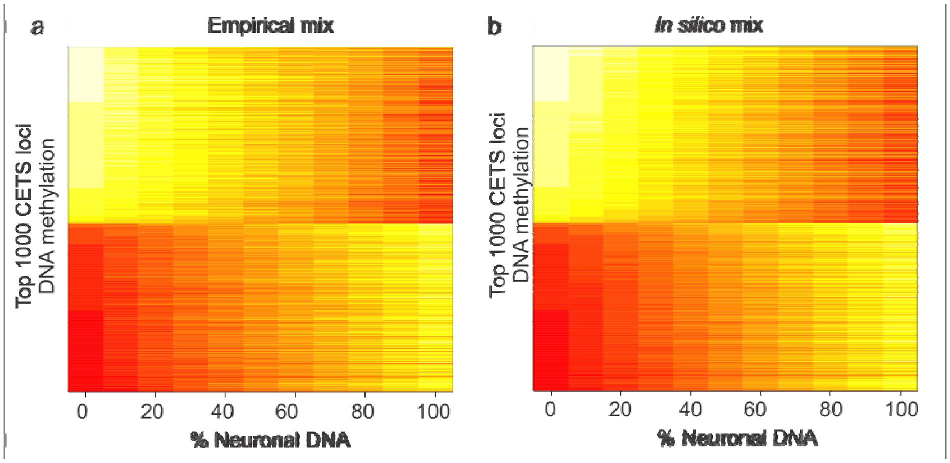


Supplementary Figure 1. FAC Sorting of neuronal and non-neuronal nuclei
Fluorescent microscopy image of FACS isolated neuronal and non-neuronal nuclei and an example plot of FACS sorting gates distinguishing NeuN positive neurons from NeuN negative non-neuronal cells.



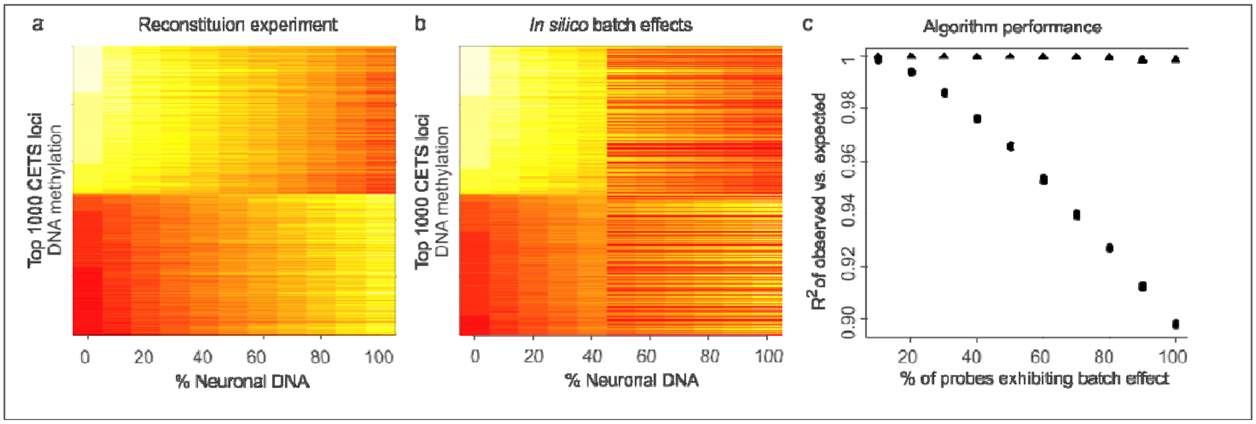
Supplementary Figure 2. UCSC genome browser tracks of cell-type specific DNA methylation differences

A.) An image derived from the UCSC genome browser (http://genome.ucsc.edu/) depicting cell-type specific epigenetic patterns via Bedgraph tracks over RefSeq gene tracks of the *ELAVL4* gene, a gene thought to be involved in neuron specific RNA processing. The mean percentage of neurons minus non-neurons (y-axis) is depicted as a function of the relative genomic coordinates per CpG on the hg18 human genome build (x-axis). Positive values are depicted in blue and negative values are depicted in red. B.) A blow up of the promoter region of an alternatively spliced variate of *ELAVL4*. ENCODE Chromatin State Segmentation by HMM tracks are depicted for the GM12878 lymphoblastoid cell line and the H1-hESC human embryonic stem cell line and demonstrate that cell-type specific epigenetic patterns fall within regulatory regions that appear to vary based on alternative splice variants of the gene. Yellow, green, blue, purple, and grey tracks depict weak enhancers, weak transcription start sites, insulator sequences, poised promoters, and heterochromatic regions, respectively.

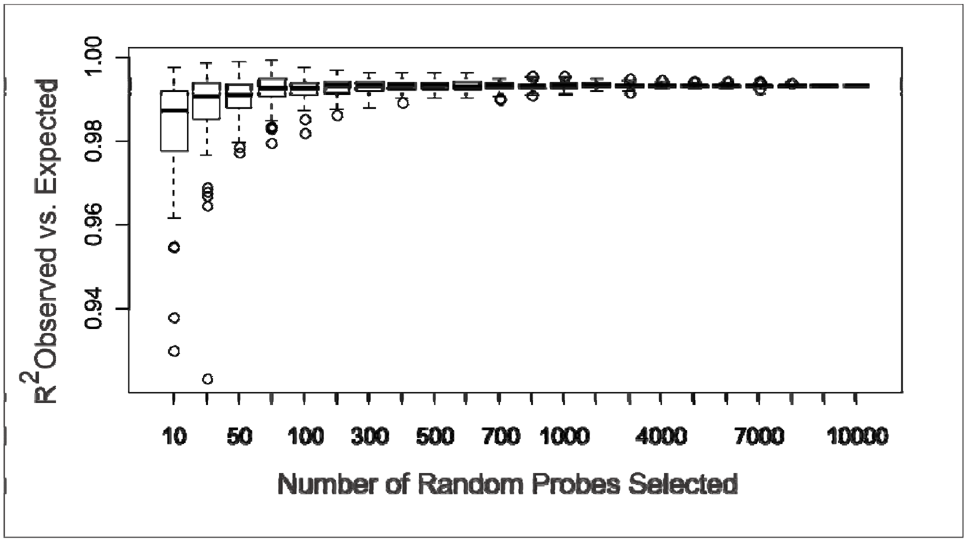


Supplementary Figure 3. Reconstitution experiment

A.) Heat maps of DNA methylation at the top 1000 CETS markers as measured by HM450 microarray probes vs. the proportion of mixed non-neuronal to neuronal DNA content in the empirically mixed reconstitution experiment. B.) An *in silico* profile using only DNA methylation profiles from 100% neurons and 100% non-neurons. Yellow and red denote beta values of methylated and un-methyated DNA, respectively.



Supplementary Figure 4. Induction and evaluation of robustness to batch effects
A.)Heat maps of DNA methylation at the top 1000 CETS markers as measured by HM450 microarray probes vs. the proportion of mixed non-neuronal to neuronal DNA content in the empirically mixed reconstitution experiment. B.) An example of an *in silico* batch effect where a randomly selected 40% of loci have an induced increase in DNA methylation percentage by 20%. C.) Performance of the CETS model prediction (triangles) and the quadratic programming algorithm (circles) at predicting the proper proportions of empirical mixes in the reconstitution experiment (x-axis) as a function of the percentage of probes randomly influenced by the batch effect.



Supplementary Figure 5. Performance of randomly selected CETS loci
Box plots of the R^2 value obtained predicting the neuronal composition of the reconstitution experiment (y-axis) at variable numbers of randomly selected probes within the top 10000 CETS marker loci (x-axis).

Supplementary Table 1: *Significantly Over-represented Gene Ontology Categories at top 1000 CETS loci*

Gene Ontology	Corrected P value	Expected Freq	Observed Freq	Description
GO:0007399	3.1E-14	0.19	0.07	nervous system development
GO:0048731	3.7E-11	0.29	0.05	system development
GO:0048856	2.9E-10	0.31	0.05	anatomical structure development
GO:0022008	4.8E-10	0.13	0.07	neurogenesis
GO:0048468	1.2E-09	0.15	0.06	cell development
GO:0007275	1.3E-09	0.31	0.05	multicellular organismal development
GO:0032502	1.8E-09	0.34	0.05	developmental process
GO:0048699	3.7E-09	0.12	0.07	generation of neurons
GO:0009653	4.3E-09	0.19	0.06	anatomical structure morphogenesis
GO:0048667	1.0E-08	0.08	0.09	cell morphogenesis involved in neuron differentiation
GO:0048812	1.6E-08	0.08	0.09	neuron projection morphogenesis
GO:0048666	4.4E-08	0.10	0.08	neuron development
GO:0031175	4.7E-08	0.09	0.08	neuron projection development
GO:0030182	1.0E-07	0.11	0.07	neuron differentiation
GO:0045202	1.6E-07	0.07	0.09	synapse
GO:0032990	2.3E-07	0.09	0.08	cell part morphogenesis
GO:0030030	2.7E-07	0.10	0.07	cell projection organization
GO:0048858	3.4E-07	0.09	0.08	cell projection morphogenesis
GO:0007154	5.2E-07	0.36	0.04	cell communication
GO:0007409	6.4E-07	0.07	0.08	axonogenesis
GO:0000904	7.0E-07	0.09	0.08	cell morphogenesis involved in differentiation
GO:0035637	7.8E-07	0.09	0.07	multicellular organismal signaling
GO:0032501	1.1E-06	0.39	0.04	multicellular organismal process
GO:0019226	1.6E-06	0.09	0.07	transmission of nerve impulse
GO:0030154	1.7E-06	0.22	0.05	cell differentiation
GO:0023052	2.2E-06	0.35	0.04	signaling
GO:0048869	6.3E-06	0.23	0.05	cellular developmental process
GO:0032989	1.2E-05	0.10	0.06	cellular component morphogenesis
GO:0007268	2.1E-05	0.08	0.07	synaptic transmission
GO:0000902	2.2E-05	0.10	0.06	cell morphogenesis
GO:0043005	2.2E-05	0.08	0.07	neuron projection
GO:0071842	3.8E-05	0.25	0.05	cellular component organization at cellular level

GO:0016043	5.4E-05	0.30	0.04	cellular component organization
GO:0023051	5.8E-05	0.17	0.05	regulation of signaling
GO:0042995	8.5E-05	0.12	0.06	cell projection
GO:0050794	1.5E-04	0.50	0.04	regulation of cellular process
GO:0048519	1.9E-04	0.24	0.04	negative regulation of biological process
GO:0046903	2.1E-04	0.09	0.06	secretion
GO:0065007	2.3E-04	0.55	0.04	biological regulation
GO:0010646	2.4E-04	0.13	0.05	regulation of cell communication
GO:0051552	2.6E-04	0.01	0.83	flavone metabolic process
GO:0050804	2.9E-04	0.04	0.11	regulation of synaptic transmission
GO:0071841	3.4E-04	0.25	0.04	cellular component organization or biogenesis at cellular level
GO:0048523	3.9E-04	0.22	0.05	negative regulation of cellular process
GO:0030425	4.5E-04	0.05	0.09	dendrite
GO:0071840	5.0E-04	0.30	0.04	cellular component organization or biogenesis
GO:0050877	5.3E-04	0.11	0.06	neurological system process
GO:0003008	8.8E-04	0.14	0.05	system process
GO:0051969	9.4E-04	0.04	0.10	regulation of transmission of nerve impulse
GO:0065008	1.6E-03	0.20	0.05	regulation of biological quality
GO:0044456	1.6E-03	0.05	0.08	synapse part
GO:0051179	1.8E-03	0.29	0.04	localization
GO:0030234	2.1E-03	0.09	0.06	enzyme regulator activity
GO:0050789	2.1E-03	0.52	0.04	regulation of biological process
GO:0051716	2.6E-03	0.35	0.04	cellular response to stimulus
GO:0060589	2.6E-03	0.05	0.07	nucleoside-triphosphatase regulator activity
GO:0031644	2.7E-03	0.04	0.10	regulation of neurological system process
GO:0006836	3.1E-03	0.03	0.12	neurotransmitter transport
GO:0003001	3.2E-03	0.05	0.08	generation of a signal involved in cell-cell signaling
GO:0023061	3.2E-03	0.05	0.08	signal release
GO:0008092	3.5E-03	0.07	0.07	cytoskeletal protein binding
GO:0052695	5.2E-03	0.01	0.40	cellular glucuronidation
GO:0007165	5.9E-03	0.30	0.04	signal transduction
GO:0050896	6.0E-03	0.44	0.04	response to stimulus
GO:0007267	7.2E-03	0.10	0.05	cell-cell signaling
GO:0009790	7.5E-03	0.09	0.06	embryo development

GO:0007010	7.7E-03	0.08	0.06	cytoskeleton organization
GO:0015020	8.2E-03	0.01	0.24	glucuronosyltransferase activity
GO:0007269	8.9E-03	0.02	0.14	neurotransmitter secretion
GO:0007411	1.0E-02	0.05	0.08	axon guidance
GO:0008289	1.1E-02	0.07	0.06	lipid binding
GO:0030695	1.1E-02	0.05	0.07	GTPase regulator activity
GO:0040011	1.2E-02	0.11	0.05	locomotion
GO:0044327	1.4E-02	0.02	0.12	dendritic spine head
GO:0014069	1.4E-02	0.02	0.12	postsynaptic density
GO:0044309	1.4E-02	0.03	0.10	neuron spine
GO:0043197	1.4E-02	0.03	0.10	dendritic spine
GO:0048513	1.8E-02	0.18	0.04	organ development
GO:0007417	1.8E-02	0.07	0.06	central nervous system development
GO:0032940	1.9E-02	0.07	0.06	secretion by cell
GO:0001505	2.1E-02	0.02	0.11	regulation of neurotransmitter levels
GO:0052696	2.2E-02	0.01	0.67	flavonoid glucuronidation
GO:0052697	2.2E-02	0.01	0.67	xenobiotic glucuronidation
GO:0009966	2.2E-02	0.14	0.05	regulation of signal transduction
GO:0005856	2.2E-02	0.14	0.05	cytoskeleton
GO:0030054	2.3E-02	0.07	0.06	cell junction
GO:0051234	2.5E-02	0.24	0.04	establishment of localization
GO:0044057	2.5E-02	0.05	0.07	regulation of system process
GO:0006063	3.6E-02	0.01	0.30	uronic acid metabolic process
GO:0019585	3.6E-02	0.01	0.30	glucuronate metabolic process
GO:0016758	3.7E-02	0.03	0.09	transferase activity, transferring hexosyl groups
GO:0016020	4.2E-02	0.49	0.04	membrane
GO:0035556	4.3E-02	0.14	0.05	intracellular signal transduction
GO:0009987	4.6E-02	0.74	0.03	cellular process
GO:0044297	4.6E-02	0.04	0.08	cell body

Supplementary Table 2: *DMRs Identified Between MDD and Controls in the SMRI Cohort using CETS Model Normalized Data*

Chr	DMR Start Position	DMR End Position	Strand	Con M value	MDD M value	P value	Q value	Gene
chr1	149205007	149207269	-	-0.17	0.22	3.9E-05	0.02	CERS2
chrX	46963843	46965626	+	-0.23	0.07	4.9E-05	0.02	CDK16
chr1	177258142	177260823	+	-0.16	0.19	8.1E-05	0.03	FAM20B
chr4	24639056	24640556	-	-0.13	0.16	5.7E-04	0.09	LGI2
chr11	64165119	64166240	-	-0.17	0.09	9.2E-04	0.09	NRXN2
chr11	2646100	2647390	+	-0.20	0.19	9.9E-04	0.09	KCNQ1
chr11	2646100	2647390	-	-0.20	0.19	9.9E-04	0.09	KCNQ1OT1
chr2	27457680	27458835	-	-0.19	0.34	1.0E-03	0.09	PPM1G
chr2	240722028	240723321	-	-0.12	0.17	1.0E-03	0.09	MYEOV2
chr2	240722028	240723321	-	-0.12	0.17	1.0E-03	0.09	OTOS
chr12	128901255	128903704	-	-0.16	0.14	1.2E-03	0.09	TMEM132D
chr18	72665010	72666135	+	-0.22	0.29	1.2E-03	0.09	ZNF236
chr8	65454106	65455384	+	0.08	-0.10	1.4E-03	0.09	MIR124-2
chr9	35596963	35598217	-	-0.10	0.30	1.4E-03	0.09	CD72
chr9	35596963	35598217	+	-0.10	0.30	1.4E-03	0.09	MIR4667
chr9	35596963	35598217	+	-0.10	0.30	1.4E-03	0.09	TESK1
chr15	41448049	41448880	+	-0.29	0.33	1.4E-03	0.09	TUBGCP4
chr15	41448049	41448880	-	-0.29	0.33	1.4E-03	0.09	ZSCAN29
chr6	19942656	19943598	+	-0.20	0.17	1.4E-03	0.09	ID4
chr10	71682451	71683820	-	-0.18	0.11	1.5E-03	0.09	NPFFR1
chr21	42514676	42515666	+	-0.17	0.05	1.5E-03	0.09	ABCG1
chr11	61205037	61206245	+	-0.18	0.15	1.8E-03	0.09	DAGLA
chr18	42748311	42749636	-	-0.21	0.08	1.8E-03	0.09	PIAS2
chr5	10810689	10813272	-	-0.12	0.25	2.0E-03	0.09	DAP
chr16	24930974	24932491	-	-0.18	0.18	2.0E-03	0.09	ARHGAP17
chr17	41333088	41334478	+	-0.15	0.06	2.0E-03	0.09	MAPT
chr2	46776712	46779284	+	-0.13	0.12	2.1E-03	0.09	SOCS5
chr2	66524037	66525057	+	0.19	-0.09	2.3E-03	0.09	MEIS1
chr13	31897083	31898689	-	-0.17	0.16	2.5E-03	0.09	N4BP2L1
chr6	1566549	1567892	-	0.17	-0.08	2.6E-03	0.09	GMDS
chr3	48447035	48447980	-	-0.20	0.22	2.6E-03	0.09	CCDC51
chr12	12738945	12739887	-	-0.21	0.31	2.6E-03	0.09	GPR19
chr9	102276236	102277338	+	-0.13	0.02	2.7E-03	0.09	C9orf30-TMEFF1
chr9	102276236	102277338	+	-0.13	0.02	2.7E-03	0.09	TMEFF1
chr2	45727957	45728971	+	-0.17	0.15	2.8E-03	0.09	PRKCE
chr1	152793949	152794964	-	-0.14	0.17	2.8E-03	0.09	UBE2Q1
chr19	18806136	18809906	+	-0.15	0.18	2.8E-03	0.09	UPF1
chr7	99527097	99528437	+	-0.12	0.22	2.9E-03	0.09	COPS6
chr7	99527097	99528437	-	-0.12	0.22	2.9E-03	0.09	MCM7
chr7	99527097	99528437	-	-0.12	0.22	2.9E-03	0.09	MIR106B
chr7	99527097	99528437	-	-0.12	0.22	2.9E-03	0.09	MIR25
chr7	99527097	99528437	-	-0.12	0.22	2.9E-03	0.09	MIR93

chr14	59625050	59626775	+	-0.25	0.25	3.1E-03	0.09	C14orf135
chr6	43349584	43350421	+	-0.25	0.19	3.1E-03	0.09	TTBK1
chr8	123864819	123865925	+	-0.21	0.05	3.1E-03	0.09	ZHX2
chr11	67734524	67735497	-	-0.15	0.14	3.6E-03	0.09	SUV420H1
chr12	619020	620405	-	-0.21	0.17	3.6E-03	0.09	NINJ2
chr18	10717206	10718300	-	-0.22	0.17	3.6E-03	0.09	PIEZO2
chr15	63453612	63454521	-	-0.21	0.23	3.7E-03	0.09	IGDCC3
chr18	19338642	19341009	+	-0.21	0.13	3.7E-03	0.09	C18orf8
chr16	30290036	30290945	+	-0.15	0.15	3.8E-03	0.09	MYLPF
chr11	82119685	82120597	-	-0.13	0.02	3.8E-03	0.09	FAM181B
chr14	73252127	73253442	-	-0.21	0.19	3.8E-03	0.09	C14orf43
chr3	148605310	148606048	+	0.22	-0.17	3.9E-03	0.09	ZIC1
chr3	148605310	148606048	-	0.22	-0.17	3.9E-03	0.09	ZIC4
chrX	49011887	49012808	+	-0.15	0.00	3.9E-03	0.09	PPP1R3F
chr19	59336763	59337884	+	-0.16	0.27	4.1E-03	0.09	CNOT3
chr8	1748166	1749177	+	-0.28	0.18	4.1E-03	0.09	MIR596
chr2	28643762	28645072	+	-0.15	0.25	4.1E-03	0.09	PLB1
chr9	135226940	135227953	-	-0.11	0.13	4.3E-03	0.09	SURF4
chr7	131913456	131914368	-	-0.18	0.29	4.5E-03	0.09	PLXNA4
chr7	142765236	142766108	-	-0.13	0.24	4.5E-03	0.09	FAM131B
chr1	45857508	45858521	-	-0.23	0.09	5.0E-03	0.10	CCDC17
chr1	90060313	90061188	+	-0.13	0.09	5.1E-03	0.10	LRRC8D
chr13	40664060	40665179	-	-0.14	0.23	5.2E-03	0.10	KBTBD7
chr1	145112378	145113308	+	-0.20	0.08	5.2E-03	0.10	PDIA3P
chr17	6864655	6865600	+	-0.12	0.14	5.3E-03	0.10	BCL6B
chr17	8472272	8473007	-	-0.11	0.04	5.3E-03	0.10	MYH10
chr19	10393453	10394257	+	-0.15	0.11	5.4E-03	0.10	PDE4A
chr19	44571225	44572032	+	-0.13	0.26	5.5E-03	0.10	MED29
chr19	44571225	44572032	-	-0.13	0.26	5.5E-03	0.10	PAF1
chr20	17538065	17538760	-	-0.26	0.14	5.5E-03	0.10	RRBP1
chr8	141605860	141606708	-	-0.19	0.07	5.8E-03	0.10	EIF2C2
chr21	42029452	42030526	-	-0.14	0.16	5.8E-03	0.10	RIPK4
chr8	117846305	117847314	+	-0.25	0.10	5.9E-03	0.10	UTP23
chr21	46688703	46689662	+	-0.22	0.15	5.9E-03	0.10	PCNT
chr17	61726624	61727730	+	-0.14	0.19	5.9E-03	0.10	PRKCA
chr4	108858413	108859265	-	-0.15	0.03	6.2E-03	0.10	PAPSS1
chr14	104335698	104337022	+	-0.21	0.16	6.7E-03	0.11	ZBTB42
chr1	241705671	241706511	+	-0.12	0.23	7.1E-03	0.11	SDCCAG8
chr17	7321840	7322572	+	-0.13	0.02	7.5E-03	0.11	SLC35G6
chr17	7321840	7322572	-	-0.13	0.02	7.5E-03	0.11	ZBTB4
chr19	63146186	63147161	-	-0.16	0.17	7.6E-03	0.11	ZNF256
chr1	191356259	191357046	+	-0.19	0.05	7.8E-03	0.11	CDC73
chr9	113434899	113436010	+	-0.19	0.13	7.9E-03	0.11	DNAJC25-GNG10
chr9	113434899	113436010	+	-0.19	0.13	7.9E-03	0.11	DNAJC25
chr2	130828273	130829181	+	-0.18	0.19	7.9E-03	0.11	PTPN18
chr9	118490209	118490911	-	-0.15	0.03	8.0E-03	0.11	ASTN2
chr9	118490209	118490911	+	-0.15	0.03	8.0E-03	0.11	TRIM32

chrX	48662051	48662717	-	-0.16	0.02	8.0E-03	0.11	OTUD5
chr1	35793439	35794207	-	-0.14	0.05	8.0E-03	0.11	KIAA0319L
chr1	35793439	35794207	+	-0.14	0.05	8.0E-03	0.11	NCDN
chr6	117974266	117975034	+	-0.07	0.25	8.1E-03	0.11	DCBLD1
chrX	122923708	122924379	+	-0.13	0.00	8.5E-03	0.12	STAG2
chr11	71490269	71491178	-	-0.09	0.17	8.6E-03	0.12	LAMTOR1
chr11	71490269	71491178	+	-0.09	0.17	8.6E-03	0.12	LRTOMT
chr1	165154952	165155747	-	-0.15	0.15	8.6E-03	0.12	ILDR2
chr1	167340362	167341097	+	-0.24	0.11	9.3E-03	0.12	ATP1B1
chr1	231008657	231009287	+	-0.20	0.08	9.4E-03	0.12	KIAA1383
chr1	154447763	154448357	+	-0.26	0.21	9.5E-03	0.12	PMF1-BGLAP
chr1	154447763	154448357	+	-0.26	0.21	9.5E-03	0.12	PMF1
chr1	154447763	154448357	+	-0.26	0.21	9.5E-03	0.12	SLC25A44
chrX	68300264	68300942	-	-0.20	0.08	9.7E-03	0.12	PJA1
chr19	46574695	46575406	+	-0.16	0.16	9.9E-03	0.12	TMEM91
chr6	109875204	109875903	-	-0.20	0.21	9.9E-03	0.12	MICAL1
chr11	1721356	1721917	-	-0.15	0.27	9.9E-03	0.12	IFITM10
chr11	1721356	1721917	-	-0.15	0.27	9.9E-03	0.12	MOB2
chr2	98592630	98593365	+	-0.15	0.27	1.0E-02	0.12	UNC50
chr5	96170866	96172056	-	-0.13	0.17	1.0E-02	0.12	ERAP1
chr8	31008436	31009105	-	-0.26	0.25	1.0E-02	0.12	PURG
chr8	31008436	31009105	+	-0.26	0.25	1.0E-02	0.12	WRN
chr11	1861935	1862643	+	-0.20	0.29	1.0E-02	0.12	LSP1
chr10	14687772	14688330	-	-0.25	0.14	1.0E-02	0.12	FAM107B
chr10	448015	448714	-	-0.19	0.16	1.1E-02	0.12	DIP2C
chr4	141394232	141395189	+	-0.16	0.04	1.1E-02	0.12	SCOC
chr15	98696403	98697183	-	-0.13	0.11	1.1E-02	0.12	ADAMTS17
chrX	46658048	46658687	+	-0.18	0.05	1.1E-02	0.12	PHF16
chr10	42289709	42290303	+	-0.22	0.24	1.1E-02	0.12	LOC84856
chr7	44127559	44128331	-	-0.19	0.21	1.1E-02	0.12	POLD2
chrX	48652807	48653506	-	-0.16	0.03	1.1E-02	0.12	PIM2
chrX	48652807	48653506	-	-0.16	0.03	1.1E-02	0.12	SLC35A2
chr12	68267498	68268230	+	-0.25	0.28	1.1E-02	0.12	CCT2
chr1	201539178	201540054	+	-0.06	0.21	1.1E-02	0.12	BTG2
chr1	201539178	201540054	-	-0.06	0.21	1.1E-02	0.12	LOC730227
chr1	247070836	247071446	-	-0.22	0.39	1.2E-02	0.12	SH3BP5L
chr11	304013	305240	+	0.11	-0.14	1.2E-02	0.12	IFITM1
chr10	75200551	75201325	+	-0.18	0.08	1.2E-02	0.12	FUT11
chr10	75200551	75201325	+	-0.18	0.08	1.2E-02	0.12	SEC24C
chr1	119963865	119964588	-	-0.16	0.21	1.2E-02	0.12	ZNF697
chr5	83052359	83053195	-	-0.16	0.08	1.2E-02	0.12	HAPLN1
chr9	35063775	35064737	-	-0.10	0.18	1.2E-02	0.12	FANCG
chr1	101477375	101478182	+	0.14	-0.12	1.2E-02	0.12	S1PR1
chr18	46337590	46338545	+	-0.17	0.10	1.2E-02	0.12	MAPK4
chr12	6545756	6546918	-	-0.14	0.12	1.2E-02	0.12	CHD4
chr12	6545756	6546918	-	-0.14	0.12	1.2E-02	0.12	NOP2
chr10	126671127	126671960	-	-0.17	0.16	1.3E-02	0.12	CTBP2
chr5	180552907	180553597	-	-0.27	0.13	1.3E-02	0.12	TRIM7

chrX	48319718	48320404	+	-0.25	0.18	1.3E-02	0.12	RBM3
chrX	48545640	48546273	+	-0.17	0.01	1.3E-02	0.12	HDAC6
chr4	483878	484652	+	-0.20	0.22	1.3E-02	0.12	PIGG
chr19	47273762	47274425	+	-0.18	0.09	1.3E-02	0.12	ZNF574
chr11	45126068	45126922	+	-0.19	0.19	1.3E-02	0.12	PRDM11
chr17	62392962	62393523	+	-0.13	0.06	1.4E-02	0.12	CACNG4
chr9	100596282	100597515	-	-0.14	0.20	1.4E-02	0.12	ANKS6
chr11	6460616	6461207	+	-0.39	0.29	1.4E-02	0.13	FXC1
chr3	51407226	51407994	+	-0.14	0.20	1.4E-02	0.13	RBM15B
chr3	51407226	51407994	-	-0.14	0.20	1.4E-02	0.13	VPRBP
chr17	7080439	7081174	-	-0.14	0.23	1.4E-02	0.13	GABARAP
chr17	7080439	7081174	-	-0.14	0.23	1.4E-02	0.13	PHF23
chrX	48822257	48823492	-	-0.09	0.14	1.4E-02	0.13	WDR45
chr4	2252556	2253666	-	-0.14	0.15	1.5E-02	0.13	ZFYVE28
chrX	153648386	153649052	+	-0.21	0.20	1.5E-02	0.13	DKC1
chrX	153648386	153649052	+	-0.21	0.20	1.5E-02	0.13	SNORA36A
chr4	48189773	48190508	-	-0.16	0.17	1.5E-02	0.13	FRYL
chr4	48189773	48190508	+	-0.16	0.17	1.5E-02	0.13	ZAR1
chr12	54786518	54787701	+	-0.14	0.25	1.5E-02	0.13	PA2G4
chr17	39387600	39388733	-	-0.15	0.11	1.5E-02	0.13	PYY
chrX	48786644	48787167	-	-0.14	0.02	1.5E-02	0.13	TFE3
chr2	96849334	96849964	+	-0.17	0.22	1.5E-02	0.13	CNNM3
chr13	31896076	31896864	-	-0.23	0.11	1.5E-02	0.13	N4BP2L1
chr20	16499455	16500052	-	-0.32	0.31	1.5E-02	0.13	KIF16B
chr20	33048988	33049549	+	-0.28	0.04	1.6E-02	0.13	MYH7B
chr9	111443375	111443903	+	-0.13	0.03	1.6E-02	0.13	PALM2
chr20	29772762	29773392	-	-0.16	0.07	1.6E-02	0.13	BCL2L1
chr1	6290253	6291438	-	-0.06	0.25	1.6E-02	0.13	ACOT7
chr11	30559392	30560166	-	-0.19	0.20	1.6E-02	0.13	MPPED2
chr17	78268497	78269865	+	-0.10	0.23	1.6E-02	0.13	FN3KRP
chr2	3683652	3684754	+	-0.12	0.16	1.6E-02	0.13	ALLC
chr5	11435762	11436356	-	-0.15	0.27	1.7E-02	0.13	CTNND2
chr18	74928557	74929212	+	-0.28	0.19	1.7E-02	0.13	ATP9B
chr6	112516541	112517126	+	-0.22	0.09	1.7E-02	0.13	C6orf225
chr3	192528827	192529382	+	-0.13	0.06	1.7E-02	0.13	CCDC50
chr3	192528827	192529382	-	-0.13	0.06	1.7E-02	0.13	UTS2D
chr4	54787801	54788500	+	0.07	-0.14	1.7E-02	0.13	PDGFRA
chr16	79666962	79667733	-	-0.12	0.07	1.7E-02	0.13	C16orf46
chr7	149702311	149704338	+	-0.13	0.18	1.7E-02	0.13	ZNF775
chrX	50572120	50572679	-	-0.20	0.08	1.7E-02	0.13	SHROOM4
chr7	36155998	36156641	+	-0.33	0.21	1.7E-02	0.13	EEPD1
chr18	58343569	58344251	+	-0.13	0.04	1.7E-02	0.13	ZCCHC2
chr2	73150164	73150884	-	-0.13	0.03	1.7E-02	0.13	RAB11FIP5
chr2	73150164	73150884	-	-0.13	0.03	1.7E-02	0.13	SFXN5
chr2	24866640	24867598	+	-0.18	0.18	1.8E-02	0.13	CENPO
chr2	24866640	24867598	-	-0.18	0.18	1.8E-02	0.13	PTRHD1
chr13	24340632	24341121	+	-0.20	0.22	1.8E-02	0.13	RNF17
chr19	48838529	48839365	-	-0.21	0.20	1.8E-02	0.13	PLAUR

chr14	94853971	94854568	-	-0.18	0.04	1.8E-02	0.13	CLMN
chr6	88008796	88009476	+	-0.22	0.23	1.8E-02	0.13	ZNF292
chr4	21558225	21558858	-	-0.13	0.03	1.8E-02	0.13	KCNIP4
chr10	72103618	72104348	+	-0.17	0.12	1.9E-02	0.13	ADAMTS14
chr6	109909114	109909849	-	-0.13	0.30	1.9E-02	0.13	ZBTB24
chr10	106103791	106104678	+	-0.10	0.25	1.9E-02	0.13	CCDC147
chr6	144370101	144370715	-	0.11	-0.16	1.9E-02	0.13	HYMAI
chr6	144370101	144370715	-	0.11	-0.16	1.9E-02	0.13	PLAGL1
chr8	42025071	42025710	-	-0.20	0.20	1.9E-02	0.13	KAT6A
chr18	5283123	5283748	-	-0.25	0.26	2.0E-02	0.13	ZFP161
chr5	16752065	16752933	-	-0.12	0.13	2.0E-02	0.13	MYO10
chr17	69708402	69709077	+	-0.18	0.15	2.0E-02	0.13	RPL38
chr17	45941315	45942125	+	-0.21	0.22	2.0E-02	0.13	MYCBPAP
chr9	964916	965699	+	0.09	-0.08	2.0E-02	0.13	DMRT3
chr2	3453436	3454102	+	-0.12	0.17	2.0E-02	0.13	TTC15
chr11	133286858	133287527	-	-0.11	0.11	2.0E-02	0.13	IGSF9B
chr4	1159532	1160054	-	-0.18	0.22	2.1E-02	0.13	SPON2
chr3	58254377	58255004	+	-0.19	0.11	2.1E-02	0.13	ABHD6
chr18	33397919	33398483	-	-0.14	0.03	2.1E-02	0.13	CELF4
chr9	123892239	123893541	-	-0.15	0.04	2.1E-02	0.13	TTLL11
chr11	2865116	2865609	-	-0.12	0.18	2.1E-02	0.13	SLC22A18AS
chr14	56806614	56807172	+	-0.29	0.36	2.1E-02	0.13	MUDENG
chr1	172393314	172393959	+	-0.19	0.19	2.1E-02	0.13	RABGAP1L
chr10	79351812	79352483	-	-0.20	0.16	2.2E-02	0.13	DLG5
chr22	30668396	30669235	-	-0.24	0.15	2.2E-02	0.13	C22orf24
chr22	30668396	30669235	+	-0.24	0.15	2.2E-02	0.13	YWHAH
chr12	122810256	122810917	+	-0.15	0.18	2.2E-02	0.13	ATP6V0A2
chr12	122810256	122810917	+	-0.15	0.18	2.2E-02	0.13	DNAH10
chr4	83700648	83701242	-	-0.17	0.11	2.2E-02	0.13	TMEM150C
chr5	112848374	112849448	-	-0.27	0.22	2.2E-02	0.13	MCC
chr16	75784275	75784839	+	-0.23	0.26	2.2E-02	0.13	MON1B
chr8	87587760	87588516	-	-0.16	0.18	2.2E-02	0.13	FAM82B
chr17	32381040	32383521	+	-0.22	0.26	2.2E-02	0.13	AATF
chr8	23369164	23369692	-	-0.19	0.13	2.3E-02	0.13	ENTPD4
chr2	96788621	96789179	+	-0.23	0.21	2.3E-02	0.13	CNNM4
chr1	53457074	53457923	-	-0.22	0.12	2.3E-02	0.13	C1orf123
chr4	8443294	8444156	-	-0.16	0.15	2.3E-02	0.13	ACOX3
chrX	11684329	11685138	+	-0.21	0.08	2.3E-02	0.13	MSL3
chrX	48907521	48908136	+	-0.13	0.22	2.4E-02	0.13	MAGIX
chr12	55758479	55759146	-	0.01	-0.22	2.4E-02	0.13	TMEM194A
chr11	2676311	2676665	+	-0.13	-0.02	2.4E-02	0.13	KCNQ1
chr11	2676311	2676665	-	-0.13	-0.02	2.4E-02	0.13	KCNQ1OT1
chr11	74822002	74822491	-	-0.16	0.15	2.4E-02	0.13	GDPD5
chr19	15440703	15441300	-	-0.21	0.34	2.4E-02	0.13	PGLYRP2
chr14	103094209	103094836	-	-0.20	0.16	2.4E-02	0.13	BAG5
chr16	65747456	65747969	+	-0.14	0.20	2.4E-02	0.13	FBXL8
chr16	65747456	65747969	-	-0.14	0.20	2.4E-02	0.13	TRADD
chr1	57663713	57664358	-	-0.23	0.26	2.4E-02	0.13	DAB1

chr12	27287335	27288136	+	-0.21	0.23	2.4E-02	0.13	STK38L
chr9	37642272	37643031	+	-0.04	0.26	2.4E-02	0.13	FRMPD1
chrX	47307607	47309064	+	-0.21	0.14	2.5E-02	0.13	ARAF
chr10	131823502	131823955	+	-0.28	0.18	2.5E-02	0.13	GLRX3
chr22	29696207	29696816	+	-0.15	0.04	2.5E-02	0.13	TUG1
chr11	46319608	46320334	+	-0.17	0.12	2.5E-02	0.13	DGKZ
chr1	201201028	201201796	-	-0.20	0.23	2.5E-02	0.13	CYB5R1
chr1	220859486	220860119	+	-0.16	0.22	2.5E-02	0.13	MIA3
chr17	4786819	4787482	-	-0.10	0.22	2.6E-02	0.13	PFN1
chr17	4786819	4787482	+	-0.10	0.22	2.6E-02	0.13	RNF167
chr1	59050928	59051796	+	-0.23	0.09	2.6E-02	0.13	LOC100131060
chr7	149167479	149167971	+	-0.20	0.19	2.6E-02	0.13	ZNF862
chr11	66811620	66812250	+	-0.09	0.16	2.7E-02	0.13	ANKRD13D
chr11	65236788	65237484	+	-0.09	0.13	2.7E-02	0.13	KAT5
chr19	5159373	5160045	-	-0.40	0.18	2.7E-02	0.13	PTPRS
chr11	61485922	61486519	+	-0.10	0.13	2.7E-02	0.13	BEST1
chr11	61485922	61486519	-	-0.10	0.13	2.7E-02	0.13	FTH1
chr7	134503991	134504516	-	-0.20	0.20	2.7E-02	0.13	C7orf49
chr13	101842779	101843855	-	-0.16	0.07	2.8E-02	0.13	FGF14-IT1
chr13	101842779	101843855	-	-0.16	0.07	2.8E-02	0.13	FGF14
chr13	101842779	101843855	+	-0.16	0.07	2.8E-02	0.13	LOC283481
chr7	7977782	7978500	+	-0.09	0.02	2.8E-02	0.13	GLCCI1
chr3	173911076	173911636	-	0.13	-0.15	2.8E-02	0.13	NCEH1
chr20	11818365	11818911	+	-0.11	0.03	2.8E-02	0.13	BTBD3
chr17	37517127	37517814	-	-0.10	0.12	2.8E-02	0.13	DHX58
chr17	37517127	37517814	-	-0.10	0.12	2.8E-02	0.13	KAT2A
chrX	151750686	151751139	+	-0.23	0.03	2.8E-02	0.13	NSDHL
chr19	4345046	4345666	-	-0.20	0.15	2.8E-02	0.13	SH3GL1
chr9	111297986	111299000	-	-0.21	0.21	2.8E-02	0.13	PTPN3
chr20	18217674	18218608	+	-0.16	0.14	2.8E-02	0.13	ZNF133
chr2	72966377	72967118	+	-0.15	0.24	2.8E-02	0.13	SPR
chr7	75797667	75798120	-	-0.25	0.15	2.8E-02	0.13	YWHAG
chrX	15603098	15603788	+	0.05	-0.24	2.9E-02	0.13	CA5BP1
chr3	124226674	124227328	-	-0.19	0.10	2.9E-02	0.13	SEMA5B
chr7	31341062	31341653	-	-0.11	0.17	2.9E-02	0.13	NEUROD6
chr6	41756041	41756668	-	-0.09	0.23	2.9E-02	0.13	TFEB
chr6	31742300	31742756	+	-0.17	0.04	2.9E-02	0.13	CSNK2B
chr6	31742300	31742756	+	-0.17	0.04	2.9E-02	0.13	LY6G5B
chr16	83241772	83242396	+	-0.12	0.25	2.9E-02	0.13	KLHL36
chr17	28644700	28645440	-	-0.15	0.07	2.9E-02	0.13	ACCN1
chr12	6471443	6472328	-	-0.07	0.24	2.9E-02	0.13	MRPL51
chr12	6471443	6472328	+	-0.07	0.24	2.9E-02	0.13	NCAPD2
chr11	2628364	2628957	+	-0.11	0.02	3.0E-02	0.13	KCNQ1
chr11	2628364	2628957	-	-0.11	0.02	3.0E-02	0.13	KCNQ1OT1
chr12	32148845	32149833	+	-0.16	0.21	3.0E-02	0.13	BICD1
chrX	30815860	30816520	-	-0.15	0.00	3.0E-02	0.13	TAB3
chr11	33745709	33746195	-	-0.16	0.21	3.0E-02	0.13	FBXO3
chr19	41126098	41127029	+	-0.27	0.19	3.0E-02	0.13	LRFN3

chr10	718075	718793	-	-0.15	0.19	3.0E-02	0.13	DIP2C
chr3	49036537	49037180	-	-0.13	0.12	3.0E-02	0.13	IMPDH2
chr3	187560715	187561207	-	-0.14	0.07	3.0E-02	0.13	DGKG
chr5	138560183	138561157	-	-0.15	0.21	3.0E-02	0.13	SIL1
chr19	51939847	51940406	+	-0.12	0.05	3.1E-02	0.13	FKRP
chr19	51939847	51940406	-	-0.12	0.05	3.1E-02	0.13	STRN4
chr10	30386596	30387049	-	-0.12	0.06	3.1E-02	0.13	KIAA1462
chr19	52708584	52709337	-	-0.16	0.13	3.1E-02	0.13	NAPA
chr13	35440501	35441050	-	-0.14	0.18	3.1E-02	0.13	DCLK1
chr17	40746938	40747424	-	-0.19	0.11	3.1E-02	0.13	MAP3K14
chr7	49781252	49781834	+	-0.15	0.26	3.1E-02	0.13	VWC2
chr11	109482228	109482717	+	-0.28	0.12	3.1E-02	0.13	ZC3H12C
chr19	3934249	3934705	-	-0.17	0.08	3.2E-02	0.13	EEF2
chr12	48509053	48509686	+	-0.16	0.28	3.2E-02	0.13	LOC100286844
chr3	180852398	180852858	+	-0.16	0.03	3.2E-02	0.13	USP13
chr17	25728563	25729177	+	-0.18	0.11	3.2E-02	0.13	CPD
chr18	27928280	27929061	+	-0.18	0.17	3.2E-02	0.13	RNF138
chr8	118031930	118032668	+	-0.15	0.22	3.3E-02	0.13	SLC30A8
chr1	117010061	117010550	-	-0.19	0.10	3.3E-02	0.13	IGSF3
chr15	57519355	57520073	+	-0.15	0.24	3.3E-02	0.13	FAM81A
chr5	114540890	114541509	-	-0.10	0.25	3.3E-02	0.13	TRIM36
chr17	2253255	2253875	-	-0.15	0.18	3.3E-02	0.13	LOC284009
chr8	29172908	29173522	-	-0.18	0.08	3.3E-02	0.13	KIF13B
chr12	122764552	122765113	+	-0.15	0.25	3.3E-02	0.13	ATP6V0A2
chr6	112514720	112515281	+	0.07	-0.16	3.4E-02	0.13	C6orf225
chr6	112514720	112515281	-	0.07	-0.16	3.4E-02	0.13	TUBE1
chr22	47267067	47267700	+	-0.12	0.12	3.4E-02	0.13	FAM19A5
chr19	63760156	63760853	+	-0.12	0.10	3.4E-02	0.13	LOC100131691
chr19	63760156	63760853	-	-0.12	0.10	3.4E-02	0.13	UBE2M
chr10	717061	717862	-	-0.10	0.26	3.4E-02	0.13	DIP2C
chr22	28026417	28027337	+	-0.16	0.19	3.4E-02	0.13	EWSR1
chr21	32169637	32170152	+	-0.16	0.06	3.4E-02	0.13	HUNK
chr10	627677	628238	-	-0.20	0.11	3.4E-02	0.13	DIP2C
chrX	48659914	48660439	-	-0.16	0.07	3.4E-02	0.13	OTUD5
chrX	48659914	48660439	-	-0.16	0.07	3.4E-02	0.13	PIM2
chr14	22602056	22602581	-	-0.16	0.23	3.4E-02	0.13	ACIN1
chr11	111404692	111405870	+	-0.22	0.12	3.4E-02	0.13	DLAT
chr4	47607910	47608450	-	-0.19	0.14	3.4E-02	0.13	NFXL1
chr17	2595144	2595741	-	-0.24	0.17	3.5E-02	0.13	MIR1253
chr12	13047385	13047970	+	-0.21	0.22	3.5E-02	0.13	HTR7P1
chr5	176489559	176490322	+	-0.15	0.12	3.5E-02	0.13	NSD1
chr9	22435479	22436177	+	-0.23	0.27	3.5E-02	0.13	DMRTA1
chr11	129442869	129443874	+	-0.22	0.14	3.5E-02	0.13	APLP2
chr10	18984451	18985048	+	-0.13	0.27	3.5E-02	0.13	ARL5B
chr16	31140226	31140871	+	-0.24	0.17	3.5E-02	0.13	TRIM72
chr11	17053254	17054110	-	-0.17	0.22	3.5E-02	0.13	RPS13
chr7	120283648	120284242	-	-0.12	0.11	3.6E-02	0.13	TSPAN12
chr14	28313409	28313938	+	0.07	-0.14	3.6E-02	0.13	C14orf23

chrX	100490943	100491468	-	-0.15	0.03	3.6E-02	0.13	BTK
chr18	45271846	45272338	-	-0.11	0.05	3.7E-02	0.13	RPL17-C18ORF32
chr18	45271846	45272338	-	-0.11	0.05	3.7E-02	0.13	RPL17
chr18	45271846	45272338	-	-0.11	0.05	3.7E-02	0.13	SNORD58B
chr8	19843358	19843919	+	-0.14	0.13	3.7E-02	0.13	LPL
chr20	61044569	61045097	+	-0.23	0.16	3.7E-02	0.13	C20orf11
chrX	70360230	70360797	+	-0.16	0.08	3.8E-02	0.13	GJB1
chr19	40730494	40731162	-	-0.17	0.13	3.8E-02	0.13	ATP4A
chr12	47648751	47649299	-	-0.17	0.09	3.8E-02	0.13	WNT10B
chr17	7084638	7085220	-	-0.11	0.01	3.8E-02	0.13	CTDNEP1
chr17	7084638	7085220	-	-0.11	0.01	3.8E-02	0.13	GABARAP
chr13	38163297	38163822	+	-0.12	0.26	3.8E-02	0.13	FREM2
chr8	81245286	81245745	-	-0.18	0.07	3.8E-02	0.13	TPD52
chr3	194442742	194443333	+	-0.14	0.05	3.8E-02	0.13	HRASLS
chr3	194442742	194443333	+	-0.14	0.05	3.8E-02	0.13	MGC2889
chr2	9482490	9483232	+	-0.35	0.16	3.8E-02	0.13	CPSF3
chrX	113726128	113726653	+	-0.14	0.04	3.8E-02	0.13	HTR2C
chr17	33873596	33874124	+	-0.17	0.05	3.8E-02	0.13	ARHGAP23
chr2	73315753	73316506	+	-0.13	0.14	3.8E-02	0.13	CCT7
chrX	9401174	9401806	+	-0.18	0.25	3.9E-02	0.13	TBL1X
chr7	6179112	6179634	-	0.13	-0.07	3.9E-02	0.13	CYTH3
chr17	33862654	33863074	+	-0.23	0.08	3.9E-02	0.13	ARHGAP23
chr12	107571939	107575062	-	-0.13	0.11	3.9E-02	0.13	CORO1C
chr2	241857067	241857595	-	-0.07	0.26	3.9E-02	0.13	HDLBP
chr1	154314843	154315422	-	-0.15	0.27	3.9E-02	0.13	MEX3A
chr1	32442122	32442679	+	-0.11	0.17	3.9E-02	0.13	CCDC28B
chr1	32442122	32442679	+	-0.11	0.17	3.9E-02	0.13	IQCC
chr8	10502949	10503579	-	-0.14	0.24	3.9E-02	0.13	RP1L1
chr11	6586698	6587224	+	-0.16	0.22	3.9E-02	0.13	ILK
chr11	6586698	6587224	-	-0.16	0.22	3.9E-02	0.13	TAF10
chr11	6586698	6587224	-	-0.16	0.22	3.9E-02	0.13	TPP1
chr11	66949660	66951976	+	-0.19	0.12	3.9E-02	0.13	RPS6KB2
chr2	97645203	97645688	-	-0.14	0.08	4.0E-02	0.13	ACTR1B
chr10	79064449	79064961	-	-0.11	0.02	4.0E-02	0.13	KCNMA1
chr19	50235063	50235555	+	-0.16	0.17	4.0E-02	0.13	CLASRP
chr2	238198882	238199431	+	-0.11	0.21	4.0E-02	0.13	LRRFIP1
chr21	44230555	44231116	+	-0.18	0.08	4.0E-02	0.13	AGPAT3
chr15	81410867	81411320	-	-0.10	0.10	4.0E-02	0.13	HOMER2
chr19	44030070	44030901	-	-0.19	0.09	4.1E-02	0.13	HNRNPL
chr3	161187883	161188548	+	-0.15	0.25	4.1E-02	0.13	IL12A
chr7	6582296	6582791	+	-0.18	0.25	4.1E-02	0.13	ZDHHC4
chr6	150501718	150502280	+	-0.15	0.21	4.1E-02	0.13	PPP1R14C
chr16	54780036	54780705	-	-0.15	0.08	4.1E-02	0.13	DKFZP434H168
chr16	54780036	54780705	+	-0.15	0.08	4.1E-02	0.13	GNAO1
chr16	54780036	54780705	-	-0.15	0.08	4.1E-02	0.13	LOC283856
chr1	31853842	31854363	+	-0.15	0.22	4.2E-02	0.13	HCRTR1
chr7	142690513	142691038	+	-0.18	0.20	4.2E-02	0.13	TMEM139

chr4	7099357	7099921	+	-0.07	0.14	4.2E-02	0.13	TADA2B
chr11	63767443	63767896	+	-0.15	0.28	4.2E-02	0.13	FKBP2
chr11	63767443	63767896	-	-0.15	0.28	4.2E-02	0.13	PPP1R14B
chr15	41573307	41573927	-	-0.13	0.07	4.2E-02	0.13	TP53BP1
chr16	65169614	65170214	+	-0.11	0.17	4.2E-02	0.13	CKLF-CMTM1
chr16	65169614	65170214	+	-0.11	0.17	4.2E-02	0.13	CMTM1
chr16	65169614	65170214	+	-0.11	0.17	4.2E-02	0.13	CMTM2
chr4	187530917	187531475	-	-0.15	0.13	4.2E-02	0.13	LOC285441
chr12	31999188	31999939	+	-0.18	0.22	4.2E-02	0.13	C12orf35
chr2	25325753	25326311	-	-0.04	0.24	4.2E-02	0.13	DNMT3A
chr14	23779701	23780226	-	-0.17	0.27	4.2E-02	0.13	TINF2
chr13	22939387	22939912	+	-0.19	0.11	4.3E-02	0.13	LINC00327
chr20	36321174	36321881	-	-0.15	0.00	4.3E-02	0.13	KIAA1755
chr11	22320376	22320800	+	0.10	-0.16	4.3E-02	0.13	SLC17A6
chr7	4866074	4866527	-	-0.26	0.21	4.4E-02	0.13	PAPOLB
chr7	4866074	4866527	-	-0.26	0.21	4.4E-02	0.13	RADIL
chrX	96026295	96026845	+	-0.13	0.16	4.4E-02	0.13	DIAPH2
chrX	96026295	96026845	+	-0.13	0.16	4.4E-02	0.13	RPA4
chr11	31781425	31781989	-	0.09	-0.10	4.4E-02	0.13	PAX6
chr17	33859199	33859763	+	-0.18	0.09	4.4E-02	0.13	ARHGAP23
chr18	9696406	9696970	+	-0.16	0.22	4.4E-02	0.13	RAB31
chr8	22074998	22075518	+	-0.11	0.22	4.4E-02	0.13	BMP1
chr8	22074998	22075518	+	-0.11	0.22	4.4E-02	0.13	SFTPC
chr9	135209461	135210152	-	-0.16	0.12	4.4E-02	0.13	SURF1
chr9	135209461	135210152	+	-0.16	0.12	4.4E-02	0.13	SURF2
chrX	118622830	118623396	-	-0.12	0.02	4.4E-02	0.13	NKRF
chr6	26647985	26648477	+	-0.14	0.27	4.4E-02	0.13	HMGN4
chr19	4916933	4917488	+	-0.15	0.11	4.4E-02	0.13	KDM4B
chr11	125583297	125583846	+	-0.08	0.18	4.4E-02	0.13	FAM118B
chr11	125583297	125583846	-	-0.08	0.18	4.4E-02	0.13	RPUSD4
chr19	54839410	54839998	+	-0.18	0.21	4.4E-02	0.13	SCAF1
chr12	56294287	56294746	+	-0.20	0.21	4.5E-02	0.13	ARHGEF25
chr18	8777822	8778278	+	-0.18	0.10	4.5E-02	0.13	CCDC165
chr12	56310028	56310610	-	-0.13	0.06	4.5E-02	0.13	B4GALNT1
chr3	154034189	154034681	+	-0.25	0.16	4.5E-02	0.13	P2RY1
chr7	82831446	82831935	-	-0.16	0.11	4.6E-02	0.13	SEMA3E
chr12	50715779	50716235	+	-0.17	0.10	4.6E-02	0.13	NR4A1
chr15	99839721	99840282	-	-0.11	0.12	4.6E-02	0.13	PCSK6
chr19	15420185	15420671	+	-0.12	0.05	4.6E-02	0.13	MIR1470
chr19	15420185	15420671	-	-0.12	0.05	4.6E-02	0.13	RASAL3
chr19	15420185	15420671	-	-0.12	0.05	4.6E-02	0.13	WIZ
chr12	47008744	47009236	+	-0.06	0.22	4.6E-02	0.13	H1FNT
chr5	177946841	177947366	-	-0.19	0.07	4.6E-02	0.13	COL23A1
chr15	29409641	29410133	+	-0.21	0.09	4.6E-02	0.13	KLF13
chr6	26138210	26138738	-	-0.21	0.23	4.6E-02	0.13	HIST1H2AB
chr6	26138210	26138738	-	-0.21	0.23	4.6E-02	0.13	HIST1H3B
chr14	67156961	67157483	+	-0.13	0.03	4.6E-02	0.13	ARG2
chr2	105867156	105867576	+	-0.17	0.16	4.6E-02	0.13	NCK2

chr16	8963040	8963490	-	-0.15	0.07	4.7E-02	0.13	USP7
chr20	60055875	60056406	-	0.12	-0.10	4.7E-02	0.13	TAF4
chr6	33155034	33155583	-	-0.21	0.06	4.7E-02	0.13	HLA-DPA1
chr6	33155034	33155583	+	-0.21	0.06	4.7E-02	0.13	HLA-DPB1
chr7	126677088	126677508	-	-0.16	0.05	4.7E-02	0.13	GRM8
chr21	15357216	15357666	-	-0.08	0.01	4.7E-02	0.13	NRIP1
chr9	98655007	98655466	-	-0.16	0.05	4.7E-02	0.13	ZNF782
chr11	2672645	2673170	+	-0.14	0.12	4.7E-02	0.13	KCNQ1
chr11	2672645	2673170	-	-0.14	0.12	4.7E-02	0.13	KCNQ1OT1
chr8	79739505	79739991	+	-0.21	0.21	4.7E-02	0.13	FAM164A
chr5	139262484	139262937	-	-0.18	0.19	4.7E-02	0.13	NRG2
chr19	16060922	16061372	+	-0.26	0.11	4.7E-02	0.13	TPM4
chr5	179212218	179212826	-	-0.28	0.17	4.7E-02	0.13	C5orf45
chr1	113061023	113061548	+	-0.16	0.18	4.8E-02	0.13	FAM19A3
chr13	112682119	112682575	+	0.17	-0.12	4.8E-02	0.13	MCF2L
chr11	2801295	2801823	+	-0.26	0.22	4.8E-02	0.13	KCNQ1
chr16	15654429	15654921	+	-0.17	0.10	4.9E-02	0.13	NDE1
chr2	175056895	175057420	-	-0.13	0.22	4.9E-02	0.13	GPR155
chr10	31342256	31342766	-	-0.14	0.12	4.9E-02	0.13	ZNF438
chr3	46908328	46908745	+	-0.21	0.06	4.9E-02	0.13	PTH1R
chr12	47635774	47636197	-	-0.18	0.05	4.9E-02	0.13	ARF3
chr18	44981829	44982285	-	-0.23	0.21	4.9E-02	0.13	DYM
chr11	64859347	64862294	+	-0.14	0.07	5.0E-02	0.13	DPF2
chr8	1911335	1911899	+	-0.14	0.08	5.0E-02	0.13	KBTBD11
chr1	110001637	110002177	+	-0.15	0.17	5.0E-02	0.13	GSTM4
chr16	4404218	4404674	-	-0.17	0.06	5.0E-02	0.13	CORO7-PAM16
chr16	4404218	4404674	-	-0.17	0.06	5.0E-02	0.13	CORO7
chr16	30695692	30696079	-	-0.21	0.13	5.0E-02	0.13	ZNF629
chr11	111095622	111096114	+	-0.07	0.14	5.0E-02	0.13	SIK2