Table S1 Differentially methylated sites among three phenotypic groups; obese non-diabetic group, the obese type 2 diabetic and non-obese

Total number of sites detected after multigroup comparison: 5834 sites with 3129 unique sites
Total number of sites detected in obese non-diabetic group (ND) versus non-obese (non) : 5682 sites with 3058 unique genes
Total number of sites detected obese type 2 diabetic group (T2D) versus non-obese (non) : 2255 sites with 1388 unique genes

										ND-obese vs non-obese			T2D-obese vs non-obese		
Probe ID	CHR	ADDRESSA_ID	MAPINFO_start	Mapinfo_end	RELATION_TO_UCSC_CPG_ISLAND	SOURCESEQ	STRAND	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	Avg ND	Avg non	ND-non	Avg T2D	Avg non	T2D-non
cg00000924	11	23801481	2720463	2720513	Island	CGCTGTCCATAAGGTGCAGATGGGAGCGCACTGCCCAGGCCAGGCTGCAC	F	Body;Body;Body	KCNQ1	0.5285971	0.5810729	-0.052475714	0.5555025	0.5810729	-0.02557
cg00003173	3	24682311	14166750	14166800	Island	CGCCCTGGGGCTTTTCCCCGGGGTCCTCTAGGTCCATTTCGCCGCCTGGA	F	TSS1500;Body;TSS1500	CHCHD4	0.1142709	0.1729171	-0.058646286	0.1379053	0.1729171	-0.035012
cg00006459	4	13754355	148635716	148635766	N/A	CGGTTGCTTAAGCTGACACTGCAGAGCATTGCAAGAAGTGTTGATTAAAA	F	N/A	N/A	0.86598	0.91541	-0.04943			
cg00008671	10	52659362	86087961	86088011	N_Shore	CGCACCTGCCTACCGCATCAAAACACAGGATCTTGCTAAAGCTGAGGGGGA	R	TSS1500	FAM190B	0.79135	0.8582586	-0.066908571			
cg00011203	1	60804456	9259066	9259116	S_Shore	GGAGGGCCTGCTGCAGCTTGGGTTCTAACTGCCCCTGCGCAAGGAGACCG	R	N/A	N/A	0.2125514	0.2437143	-0.031162857	0.2942825	0.2437143	0.0505682
cg00011513	1	68601308	152484386	152484436	N_Shelf	TGCTGCCACAGCTCTGGAGGCTGCTGCTGACCTGGGCCATGAGGAGCACG	R	3'UTR	LCE5A	0.5754543	0.6271857	-0.051731429			
cg00012036	17	64765463	73775612	73775662	Island	AAAAGGCGGGGACACAGTTCCGGAACAAAGCCCCAAGGGGAAACCTCCCG	R	5'UTR	H3F3B	0.0898697	0.1172057	-0.027336	0.0930665	0.1172057	-0.024139
cg00012576	13	36605459	94568320	94568370	N/A	CGGGAGTAGGCAGCCTTCAGAGGGACCTGCTCAGTTTCTTGGTGGCTCAC	F	Body	GPC6	0.7637386	0.8287471	-0.065008571			
cg00017842	2	62757312	119528421	119528471	N_Shelf	CGTCCTGGCCACGTCCAGAATTGTTAGAGGGCATGATACAACCTGGGGGTT	R	N/A	N/A	0.6428329	0.7314729	-0.08864	0.677335	0.7314729	-0.054138
cg00029831	8	70617329	145653349	145653399	Island	CGGGCCTCTCCACCGAGAGCTTCCTGCGCCTGCCCGCCAGGCCCGCTCCT	R	5'UTR;5'UTR	VPS28	0.1786514	0.1527871	0.025864286			
cg00034154	19	58688413	10337163	10337213	S_Shore	AGCTAATAACATTTGGCAGTATTTGTTGAGTGCTTACTATGAGCTAAACG	F	5'UTR	S1PR2	0.5227371	0.6343529	-0.111615714			
cg00053536	1	31791481	17291209	17291259	N_Shore	AGCCACTGCTCCCAGTCTTTTCTTTCTTCTTTTTTTGAGACGGAGTCTCG	R	Body	CROCC	0.6221671	0.6763386	-0.054171429			
cg00058026	12	33679472	53172158	53172208	N/A	ATTTAGAATGGGCAGGACTCAAGCCTTGCCCTCAAGAAGCTCAGGGACCG	F	TSS1500	KRT76	0.6286029	0.7397	-0.111097143	0.6857063	0.7397	-0.053994
cg00061635	17	18616494	8311836	8311886	N/A	GCACAAGCTTGGGCCATGACTCAGCCCCTTTCTGCTCACCTGGTGTCCCG	F	N/A	N/A	0.7950343	0.8432643	-0.04823			
cg00061792	10	21784388	51542259	51542309	N/A	CGTCCTTGAGTTTGTCATTCAGAAACCTGGACCTCCATGTGGACCCCCAC	R	N/A	N/A	0.6363743	0.7353171	-0.098942857			
cg00066750	6	43623366	126080132	126080182	N_Shore	CGTTCCACTTCAGTCTTCTGAAGGACAGAGTGGAACATCAGTGGGTGGTT	F	Body	HEY2	0.7938486	0.8696214	-0.075772857			
cg00072407	19	10655427	12887524	12887574	N_Shore	CCTCCCACCTCAGCCTCTGTAGAGCTAGGAGCTAGGACCACAGAAACACG	F	TSS1500;TSS1500	HOOK2	0.5996757	0.6638257	-0.06415	0.6319563	0.6638257	-0.031869
cg00074771	15	30667312	44120341	44120391	S_Shore	TGGAGGTATAATCCTTCTGCAAGTTTTCTTTATTTTAGTCTTCTTACACG	F	Body;Body	WDR76	0.6981857	0.8188214	-0.120635714	0.7565538	0.8188214	-0.062268
cg00082384	3	30711404	52516316	52516366	N/A	CGGGCCTGCCTGAAGGGGGCGCTGTCCAGACAACACCCAGCCTCCCGTCG	F	Body	NISCH	0.5293629	0.4911	0.038262857			
cg00085199	8	36733333	141106596	141106646	N_Shore	CTATCTCTAAAATGTATTTGGAAGCAGCTACTTCTTACCTTCTTTTCACG	F	Body;Body	TRAPPC9	0.89587	0.9304643	-0.034594286			
cg00087073	2	26768455	71225672	71225722	S_Shelf	CGTGGCTCATGCCTGTATTACCAAAGTACTACTTTGGGAGGCTGTGGCAG	R	N/A	N/A	0.7515071	0.8385943	-0.087087143			
cg00092383	7	39681343	157075207	157075257	S_Shelf	ACCGACAGCCGAGTGGAAGGGGTCAGGCGGGTTATCCGCCATGGCCCACG	F	N/A	N/A	0.8337029	0.9235171	-0.089814286			
cg00093542	8	39715350	27144453	27144503	N_Shore	CGGGGCCAGGTATCAGACAAAAAGGGCAGCCCCTATCCTGAGAGCCACTG	F	3'UTR	TRIM35	0.7775029	0.84467	-0.067167143			
cg00094244	5	13694438	131280217	131280267	N_Shore	CGTGTCTTTAGACAGGGCCTTGAATTTCTGACTTGGGTAGATTCATAGTC	R	N/A	N/A	0.8669243	0.9182057	-0.051281429			
cg00095728	2	33607418	176976081	176976131	N_Shore	CGGCTTGCCTTGGGTGGTGGGCACACAAGCTTGCTACGTTTAGATGCAGT	R	N/A	N/A	0.2241671	0.2863329	-0.062165714			
cg00096307	2	38643464	106761754	106761804	N/A	CGGTCACCTCGTGGCCGTCCATCATGAGTTTGTCAGTTAGATGGGAGCCC	F	Body	UXS1	0.8458043	0.902	-0.056195714			
cg00096447	5	16793410	137576708	137576758	N_Shore	CATTTCCCAGGCTCCCTTGTCAGCTGGCTTTTGGCTGGGTTTGGACAACG	F	N/A	N/A	0.5512857	0.6576757	-0.10639			
cg00098182	15	47651469	22993172	22993222	N/A	TCCTCTTCTGCCTGCTCATCGAGCAGAGCCTGGTGAGTGGCCCCCCAACG	R	Body;Body	CYFIP1	0.7429086	0.7901214	-0.047212857	0.7530825	0.7901214	-0.037039
cg00115567	6	28627451	44279361	44279411	N_Shore	CGGGAGCTAAACTCATGTGGCTTGATTACTTCAGTGGGGTCTCCCTCTCA	R	Body	AARS2	0.8719486	0.9007143	-0.028765714			
cg00121374	1	23798408	3392638	3392688	N_Shelf	CGGGGCCACCTACCTTGACCTTGCTGAAGTCCAGCTGTGTGTGCAGCGTG	R	Body	ARHGEF16	0.8592729	0.8924386	-0.033165714			
cg00121389	8	66626506	17555302	17555352	N/A	TTACAGAACAACCAATAATGTCACAGATCCTGTAACCACTTGAAAGATCG	R	Body;TSS200;Body;Body;Bod	MTUS1	0.5364071	0.7084771	-0.17207	0.6623688	0.7084771	-0.046108
cg00128100	6	68734412	30656094	30656144	S_Shore	CGCCTCAGGGGTCCCCTTCTGCACCGCTGGCTTCCACTCCAAGAAGGTGG	R	TSS1500;3'UTR;TSS1500	KIAA1949	0.85448	0.8941714	-0.039691429	0.8738775	0.8941714	-0.020294
cg00136477	1	67806337	22970339	22970389	N_Shelf	GAGCCTCACCATGGATGGATGGTGGGGCCTTTTCTTCAGCCCAGGCCCCG	F	5'UTR;5'UTR	C1QC	0.6882143	0.7594457	-0.071231429	0.719805	0.7594457	-0.039641
cg00138804	7	72756405	57706707	57706757	N/A	CGGAGGCTCAGGCCTTGCGCATGCGCACTGGCAAGGCCGACTCCCAGCTT	F	N/A	N/A	0.5209914	0.5524514	-0.03146	0.5180888	0.5524514	-0.034363
cg00141447	13	73619370	113544658	113544708	N_Shelf	TCTGCCGGCCAAGCCATCGGGGCAGCAGAAGAGTCTCAAACAGAAACCCG	R	N/A	N/A	0.75306	0.7943786	-0.041318571			
cg00146928	12	74736460	9269671	9269721	N/A	ATCTGTCATTCGTTATGCTTAGAAAGCTCTTTTCATCTCTTTGTTCTTCG	F	TSS1500	A2M	0.8279057	0.8573986	-0.029492857			
cg00151728	3	44725506	169478456	169478506	N_Shelf	CGGGCTAGTATCATGGGGCCCAAAGCCCCAACACTCTAATCACATGGCTG	F	N/A	N/A	0.7734171	0.8392486	-0.065831429			
cg00152047	1	24788417	166893354	166893404	S_Shelf	CGTGGTAAACGCTCTGCCCCTGGTGAAACAGAACTAGGAGGCTGTGTTGG	R	Body	ILDR2	0.8862014	0.9167486	-0.030547143			
cg00152948	21	57795449	43197205	43197255	N_Shore	CGTATCTAGTTGGGTGTATTAGTTTCTAGTGGCTGCCACAGCAAAGTGAC	R	N/A	N/A	0.8699029	0.9106357	-0.040732857	0.8791263	0.9106357	-0.031509
cg00153693	15	58611470	93249643	93249693	N/A	CGCTTTGTGGCTTCTTAAAAGCCCTGTTCGTTAATGAGGTTTCCTAATTT	F	N/A	N/A	0.7552371	0.8356314	-0.080394286			
cg00154119	15	66673318	68174054	68174104	N_Shelf	TTTCACCTCAATTTTAACAGATACCAGGAACCAAGATCACCACACACACG	R	N/A	N/A	0.72159	0.7820386	-0.060448571			
cg00157319	8	43656324	74360923	74360973	N_Shore	CGGGGCTGGAAGATGACCCACCTGGCCTTGAACCCTGGTTATCTGTTTCC	F	Body;Body;Body;Body	STAU2	0.8238257	0.8673714	-0.043545714			
cg00159908	10	60642369	134184627	134184677	N/A	CGGGAGAATGAGACCCTCTGCTTCTAGAGGTGCAGTGTGAACTTAGATGG	R	Body;Body	LRRC27	0.8771029	0.9111286	-0.034025714			
cg00160359	12	13707329	49178192	49178242	S_Shore	CGTGGTTCTCTCACTTATGTGGCTGCTGGATCTTTGGGCAACTCTTTCTT	R	5'UTR;TSS1500	ADCY6	0.7960157	0.85623	-0.060214286	0.8315288	0.85623	-0.024701
cg00171281	7	28607319	79914719	79914769	N/A	CCTCCCCTTACTTTTTCTCTCTAAAAGATTAACATTAAAGGAAAGCATCG	R	N/A	N/A				0.5774113	0.6344757	-0.057064
cg00172672	20	39734423	34895136	34895186	Island	GCTGGGCTGACCCGGGCACCTGGGCTGGGGGGGCACTCACATGGCTACCG	R	N/A	N/A				0.2234713	0.1594829	0.0639884
cg00173659	7	30766492	156871088	156871138	Island	CGGGGACTCCAGGCGTCCTTGTGTTTCAGCTCCCGGCTCTTGCCCGCGC	F	N/A	N/A				0.2696963	0.2108543	0.058842
cg00176043	1	22690368	67900465	67900515	S_Shelf	CACAATTTAACAGTCCCACCAACAATTATGTGAGTTCCAAGTTCTCCACG	R	N/A	N/A	0.4425586	0.5798443	-0.137285714			
cg00177237	21	14790439	43658316	43658366	S_Shelf	CGCAGGGTTGCTGTGAAGACAGAGTAAGTTACTGCTCACAGACTAATAAA	R	Body;Body;Body;Body;Body;B	ABCG1	0.8279629	0.8839286	-0.055965714			
cg00178359	16	49660494	56659460	56659510	Island	AGGCAACCTCGGGGAAACTGGGAAAGGCGGCCTGGACTTCGGGAACACCG	R	TSS200	MT1E	0.32522	0.3759243	-0.050704286			
cg00186701	8	10607449	98290510	98290560	S_Shore	CGCCCGAGCACTTTCTTCATGACAGATGCCACAAGAGATAACTGGAGGAG	R	TSS1500	TSPYL5	0.6603057	0.7674929	-0.107187143	0.7199388	0.7674929	-0.047554
cg00188032	5	11768493	96141721	96141771	N_Shore	CGAGGATGCAGTGCATGAGTGGGGCTTGGTAAAAACTCCATGTAGTGAAT	F	5'UTR;5'UTR	ERAP1	0.9280029	0.94729	-0.019287143	0.95763	0.94729	0.01034
cg00192773	16	29642427	30131641	30131691	N_Shelf	CGGAGATTTCCTGTCCACAGTTTGTGGTGGGGGTTGCAGACACCTCAGTA	F	Body;Body;Body	MAPK3	0.7403843	0.8099543	-0.06957			
cg00199753	12	25631505	113519288	113519338	S_Shelf	GGTGTGTATTCACAGAGCTGAACAAGACAAACAAGGCCTGTGTCCTCCCG	R	Body	DTX1	0.76642	0.8527457	-0.086325714	0.7903563	0.8527457	-0.062389
cg00202819	12	65634310	102134014	102134064	S_Shore	CGGCTTAGTTTCGTTCGCGTTTGGCATTACAAAAAATTGTCCCATAGTCT	F	TSS1500	SYCP3	0.7679471	0.8493114	-0.081364286			
cg00204802	13	64623441	113496682	113496732	N_Shore	CGCTCCACTCTGGCTCGGATCTGGTCAACTTTGCCTTCTATCACTCGGGG	R	Body;Body	ATP11A	0.6664614	0.7814786	-0.115017143			
cg00206233	21	65685362	44011158	44011208	S_Shore	CGGCATTCTGGCCCCGGGGGTTTTAACTGACTTTACCTGGTGGGCCATGT	F	N/A	N/A	0.7139629	0.7791771	-0.065214286			
cg00206779	8	18774435	105341338	105341388	N_Shore	CGGGGAAATTGCATTATATATGTCTGTAGCATTGAAGATGCACCAATGTG	R	N/A	N/A	0.9045371	0.9408086	-0.036271429			
cg00208830	1	18714379	183154778	183154828	N/A	CGATACTCAGTCTTTATAGGGAGGTTGGCCAGTCAATAGGTTACTTTATG	F	TSS1500;TSS1500	LAMC2				0.7321138	0.7843757	-0.052262
cg00210016	17	60744457	18919146	18919196	S_Shore	CGGGGAGGTCTCTTGGCCTGTAATGGCCACATGTGCTGTGGGAAGAATCT	R	Body;Body	SLC5A10	0.8545471	0.8928029	-0.038255714	0.86833	0.8928029	-0.024473
cg00210186	9	37751382	37905641	37905691	S_Shore	ATAACCTCTCCATTCTAATCTGAAATTAATTATTTATGCTTATGAACACG	F	TSS1500;TSS1500;TSS1500	MCART1	0.9063557	0.9515429	-0.045187143			
cg00215851	4	40731397	46427528	46427578	N/A	CGGTATGTACTTGATTCCCAGGAAGGGACTTCAGATATTTGTTAGAAGCA	R	N/A	N/A	0.7951043	0.85179	-0.056685714	0.8159375	0.85179	-0.035853
cg00223877	3	32612303	53290290	53290340	S_Shore	CGAGTCAGGAGCCCAGACTCGAATCCTGAGTTGTTCGTTATGTTATTATT	R	TSS1500;TSS1500;TSS1500	TKT				0.2163025	0.1702857	0.0460168
cg00224929	2	16794347	171705463	171705513	N/A	CGGGTGGCTCTGGAAGCTGCTCAAAAAACTGAGGCCTGCTGTCTGGTTCT	R	Body	GAD1	0.8462986	0.8850714	-0.038772857			
cg00226615	6	17712355	31853565	31853615	N_Shelf	CGCTGCTTCTAGGACTTTTGAGTGGGCAGACTTAGGAAATTTTTGTTCGT	R	Body;Body	EHMT2	0.8260129	0.8704257	-0.044412857			
cg00228708	10	28781501	135048062	135048112	N_Shore	TAGGAAGTGGGGCTGGTCTGGTGCATGGCCGATAAAGAAACGCTAAGCCG	F	N/A	N/A				0.8069863	0.8737529	-0.066767
cg00232105	14	24705379	100752338	100752388	Island	CGGGGGCTCCTACCATCACCCTGCCTGTAGGTTCTGGAGCCACTCCGGCC	F	N/A	N/A	0.7148414	0.7869171	-0.072075714	0.7538138	0.7869171	-0.033103
cg00232952	18	50717363	30047736	30047786	N_Shelf	TGCCTTTTCCCCAGTTTTAGTACTGCAGGTACATTTTACATCTGCACACG	F	Body	FAM59A	0.7271271	0.8379529	-0.110825714			
cg00235460	2	18768400	175867417	175867467	N_Shelf	GATTTGTCAGAGCTCAGCAGAGTTTATACCTGAGGCTCCCCAGAGTAACG	F	Body;Body	CHN1	0.8100743	0.8701443	-0.06007	0.8307875	0.8701443	-0.039357
cg00235754	15	28719502	22904606	22904656	N/A	AGGCTGGCAAGTCCAGCGTTTGCAAGGCAGGCCCATAGGCTAAAGACCCG	R	5'UTR	CYFIP1	0.5548786	0.69715	-0.142271429			
cg00240653	12	22698510	55378411	55378461	N/A	CGACAACTGCTTTGCCTCAAACTCAGCTTTCTACCAGCAGACAGGTAAGC	R	1stExon;5'UTR	KIAA0748	0.7641371	0.8469457	-0.082808571			
cg00242020	8	67688488	37797632	37797682	N/A	CGGCCCAGCCTTGGAGGAAGACTTCTGGGCAGAAGCGGAACACAGGAGCA	R	5'UTR;1stExon	GOT1L1	0.7930371	0.8358729	-0.042835714	0.8055988	0.8358729	-0.030274
cg00244001	10	11697381	126336805	126336855	N/A	GACACATCGAGGATCCAAGGCTCTGGGAGCGTCTGTTGGAAAACCCCCACG	R	Body	FAM53B	0.6420386	0.7262043	-0.084165714			
cg00247614	20	21603476	689300	689350	N_Shore	CCTCAGGCAAATCATTTAACCCTCTCTGTAAAATGAGAGCAATGATAACG	F	N/A	N/A	0.9177829	0.9484114	-0.030628571			
cg00247631	6	68788423	35479350	35479400	N_Shore	CGGCCCAGAGAGGCAGAAAACAACTGTAGTCAAATAGCCCCCACTTTTCT	R	Body	TULP1	0.5928	0.6373114	-0.044511429			
cg00248856	11	42669438	69464272	69464322	S_Shelf	CGGTTTTTCTGAGTCTGGGCTCAGCTACGTTGGTCACTAGCTGATCAGGC	R	Body	CCND1	0.7113671	0.7626171	-0.05125	0.7333738	0.7626171	-0.029243
cg00253735	1	60729344	150779776	150779826	N/A	CGCCTCGAAGAAATGATCAGGAGGCAAAACTTAGACGGAAATCTCTCCTT	R	5'UTR	CTSK	0.68437	0.79558	-0.11121			
cg00256060	6	26794409	33385365	33385415	N_Shore	CGGAGGGCTTCCAGAGGCCATGGTCAGCAAGACTCGGGGTAGCAACAAAA	F	Body;Body;Body;1stExon;Bod	CUTA	0.0617874	0.0878316	-0.026044143			
cg00266604	6	63705386	30178343	30178393	N_Shelf	CGGATGGGGGGTGCTACTGTATGAAGCACTGTGATAGTGCTATTGTAGAA	R	5'UTR	TRIM26	0.89179	0.91662	-0.02483	0.8941488	0.91662	-0.022471
cg00266647	12	74752329	976027	976077	N/A	GATGTCAGAATCAGAAAATTCATGGTTACGGCCGGGCTCAGTGGCTCACG	R	Body;TSS1500	WNK1	0.50076	0.5752129	-0.074452857			
cg00267142	6	58700307	167104601	167104651	N/A	AATGAAAAACTGTAGGTTCTAGAAGATTCAAGCGTTGCCAACTCATGCCG	R	Body	RPS6KA2	0.92624	0.9562929	-0.030052857	0.9434288	0.9562929	-0.012864
cg00269659	16	59660359	27729685	27729735	N/A	CGCTCTGCCTCCTGCCCTGGCACCGAGGGGTTTTCCCAGCATGTGCCAGG	F	Body	KIAA0556	0.7730514	0.8233871	-0.050335714	0.8017188	0.8233871	-0.021668
cg00269996	6	42681300	42979961	42980011	N_Shore	CGGCTTTTGGCTGTGTACATAGGGTGCTTTATTCTCCACAGAGTGATACA	F	3'UTR;3'UTR;3'UTR	PPP2R5D	0.7917071	0.8419257	-0.050218571			
cg00273464	11	51724475	2170412	2170462	N/A	CGGGGAGTCACTGGTGCCCAAGGCTCTCTGCCGAAACTGCCTGGACGATG	F	Body;Body;1stExon;5'UTR	INS-IGF2	0.7413757	0.8140471	-0.072671429			
cg00277714	13	69704367	30459305	30459355	N/A	TAATCACTTATAATCAATCATAGGCTTTCCTCTCTTGCCACGTGTAGACG	F	N/A	N/A	0.7720143	0.82468	-0.052665714			
cg00284179	2	72708318	155314028	155314078	N/A	CGGGGGAAAAAATTCATGATGTCAGAAAATGAGTGAGTCAACAGAAAGCC	R	N/A	N/A	0.8645971	0.8992671	-0.03467	0.8726025	0.8992671	-0.026665
cg00294267	16	46765334	49572227	49572277	N/A	TGTGATGAGATGTGAGCAGTGCCAGGCCCACACACCATAGCAGGAAAACG	R	Body	ZNF423	0.6800814	0.7313871	-0.051305714	0.7059363	0.7313871	-0.025451
cg00295308	10	16669351	5995028	5995078	N/A	ACTGCTCTCACCACCTATGAAACTCGGGGAAACCAGCCCAGCTAAGTCCG	F	3'UTR;3'UTR	IL15RA	0.8076929	0.8465843	-0.038891429			
cg00296018	5	27682480	141205206	141205256	N/A	CCTTCAGAGGCAGCTTAGCCAGAAACGCCAGCGGCAGAGACAACTGTGCG	R	N/A	N/A	0.7892843	0.8502229	-0.060938571			
cg00299511	11	50663343	76858648	76858698	N_Shore	CGGTCCTTGAGGGGTAGAGGTGGCTGGTACCATCCTGACTGAACCCTGTT	F	Body;Body;Body	MYO7A	0.7910529	0.8382886	-0.047235714			
cg00302340	12	53739472	113773809	113773859	S_Shore	TCTGCCTCCCAAAGTGTCAGAGCTGTGTAAACCAGAGCAACTCCATCTCG	R	TSS1500	SLC24A6	0.6231	0.71069	-0.08759			
cg00303210	7	72631304	138745709	138745759	N/A	CGAGTGACTTGATGAGCCCAGGGCATGAACATCTCAAGCATCTGTCAGCA	F	Body;3'UTR	ZC3HAV1	0.71104	0.8218471	-0.110807143	0.7637563	0.8218471	-0.058091
cg00303876	5	16622466	177630081	177630131	N_Shore	ACAAAACTCCTTTATATTATCTCCTTGACCACAAAATTTTAAAGGCCTCG	F	TSS1500;TSS1500	HNRNPAB	0.7343071	0.7875214	-0.053214286			
cg00305585	16	39771510	1610898	1610948	N/A	GAAACATGGAAGCTTCTCTCCTGTTACACACTCCGTCAGCAAACAACACG	F	Body	IFT140	0.70733	0.7640914	-0.056761429			
cg00308841	5	67690473	90790737	90790787	N/A	CGGAGAATTTCAAAGGGATTTCGTATTCTGTGGCTTTCTCCATGCCTGAA	F	N/A	N/A	0.8379986	0.88423	-0.046231429	0.8415375	0.88423	-0.042692
cg00321901	8	29731504	10512459	10512509	N/A	CGTCCCCCTGAGGCTTAGGGGCTGAGCCATGCCCTTGTGCTCCCTGGAGG	R	1stExon;5'UTR	RP1L1	0.5567857	0.6448029	-0.088017143	0.5946875	0.6448029	-0.050115
cg00326902	6	58761510	117747649	117747699	N/A	TCCTCTCTCTCTCTCTCTCTCTTTCTTTGAGACTGAATTTCTGTCTGTCG	R	TSS1500	ROS1	0.68732	0.7551229	-0.067802857			
cg00329101	3	69752479	14338921	14338971	N_Shore	TATTTTTTCTACCCTCTTTACAGTCAAGGTGGCTCACAGCAGCCTCACCG	R	N/A	N/A	0.8866586	0.9135257	-0.026867143			
cg00340855	6	49703319	30458586	30458636	S_Shore	CGGGGGAGTTTCTCTCGTGCCTGATTCTCAGCCCCACACCAAGAGTTTTTT	F	Body	HLA-E	0.7019671	0.7690914	-0.067124286	0.7239125	0.7690914	-0.045179
cg00343092	22	15787442	43547974	43548024	Island	TCAAGAGCCCCGAGGTCTCCCAGATATTCTGAGACCCTCAAGGGAGTTCCG	F	5'UTR;5'UTR	TSPO	0.2912414	0.4482643	-0.157022857	0.353595	0.4482643	-0.094669
cg00353330	4	40785347	101715708	101715758	N/A	CGTAGATCATGAGTGAGAAATAAACTTCAGTTACTTTAGGAGACTGAGAT	R	N/A	N/A	0.6328886	0.7310829	-0.098194286	0.66673	0.7310829	-0.064353
cg00357988	12	38658342	122990019	122990069	N/A	CGTCCTTGTTCACCAAACAGCTAGCACTCTAGCTTGCATGGGTGTTGCAT	R	3'UTR;3'UTR;3'UTR	RSRC2	0.8538186	0.9135929	-0.059774286			
cg00358023	7	45757342	157217482	157217532	S_Shore	AACAAACAAAGATGCACACTGATGCCTGTTCTCCACTTCTCTCCACAACG	R	N/A	N/A	0.7772671	0.8228671	-0.0456	0.8089375	0.8228671	-0.01393
cg00362381	16	60781489	665320	665370	S_Shore	CGGTCTCTCTGCCTACGGTGCCCTTCTTCAGGCATCAGCGCTTCCACCCA	R	Body	RAB40C	0.6881571	0.7589071	-0.07075			
cg00363737	10	33701394	116031419	116031469	N/A	CCCTAACTATAGTCATTTTTCTAATGAGAAAACATCCAACTGACAAGACG	F	Body	VWA2	0.8999086	0.9413229	-0.041414286			
cg00365692	19	57648324	51670423	51670473	N/A	CATGCTTCAGATGTCCCCAGAGGTCCTGGTCCAGGCTCTGGCATTGGACG	R	TSS200	SIGLECP3	0.3542	0.4418143	-0.087614286	0.3665738	0.4418143	-0.075241
cg00366435	12	25643351	6896105	6896155	N/A	CGCTTAACTACGTACATGAATGAATGGAGCAGGGCTCAAAACATCAATGC	F	N/A	N/A	0.9034557	0.9444129	-0.040957143	0.9212313	0.9444129	-0.023182
cg00369142	3	22704317	135864939	135864989	N/A	CGTTGAGGCCTTTACTATTAGCTAGTCTAATACTCCTGGGAGGAAGGAAT	R	3'UTR;3'UTR	PPP2R3A	0.7318443	0.8229614	-0.091117143			
cg00373422	7	49726437	150739712	150739762	N_Shore	ACTGGATGGGCCCCAGGAGAGGGCTCTGGTGGTTCTGAACTAGGAACACG	R	Body	ABCB8	0.84947	0.9127514	-0.063281429			
cg00374546	16	28775404	1574590	1574640	Island	CGGGCACAGGCCTTCAAGAATGCCATCCGCCTGTGCAAGGTACCACGGGC	R	Body	IFT140	0.8523614	0.8894229	-0.037061429			
cg00384653	22	14732500	20237197	20237247	N/A	CGCATCCCAGCAACCCTCTACTGCTCAGTGGACTCTGCCTGAGCCCTGAC	R	Body;TSS1500	RTN4R	0.8845529	0.9196771	-0.035124286	0.9032325	0.9196771	-0.016445
cg00386035	6	29729381	166238706	166238756	N_Shore	CTTGTGTGAGGAAATTTGAGCAAGGCAGAGCCCTGCTCACATCAGGAACG	F	N/A	N/A	0.8149514	0.8653929	-0.050441429	0.828065	0.8653929	-0.037328
cg00390484	22	19671353	20019695	20019745	N/A	CGCAAAACCTGGCTGCCAGGGCGGGTCAACCCCAACCGGAAGGAGGCTG	R	5'UTR;TSS1500	C22orf25	0.8434429	0.8838171	-0.040374286			
cg00390784	6	52783342	2682491	2682541	N_Shelf	CCAACAACCCTGATCAAGTCCCATATTGGGACTAAGTATCATAAAGTACG	F	Body	MYLK4	0.9063186	0.9352657	-0.028947143	0.9156813	0.9352657	-0.019584
cg00393247	1	54664323	36234276	36234326	N_Shore	AGAGGATCATCAGTGCATACATATTAATTCTCAGCAATCCCAGCACTTCG	F	Body	CLSPN	0.7660786	0.83581	-0.069731429			
cg00395929	15	22652397	57181938	57181988	S_Shelf	GCTGGGGCAAGAGCTTGAAATTCAGTCAGGGCTAGGCACAGTGGCTCACG	F	Body	LOC145783	0.4958914	0.5763586	-0.080467143			
cg00395990	11	24764460	119054921	119054971	N/A	CGCTGCTAATAAAGACATACCCAAGACAGGGTAAGTAATTTATAAAGGAG	F	TSS1500;TSS1500	PDZD3	0.5962671	0.6613186	-0.065051429			
cg00398268	18	32787313	47017166	47017216	N_Shore	CGCAGGTGAGAATTCTTAGTTGCCATTTGAAAAGACAGATTTTAATGGAA	R	Body;TSS1500;TSS1500;Body	RPL17	0.8885214	0.9307271	-0.042205714	0.9166288	0.9307271	-0.014098
cg00399591	16	65671346	18802159	18802209	S_Shore	CGCGGGCCTTAATTTTTATTTTAGTTTACTTTTGATAAGGAGTCTCGCTC	F	TSS1500;TSS1500	RPS15A				0.570905	0.7097414	-0.138836
cg00404025	10	70718467	49892741	49892791	N/A	CGGTGCTGGTTGGGGCCAAGGACAAAATGGAAAGTACAGCCCAGCCCTAG	R	TSS1500	WDFY4	0.70739	0.78665	-0.07926			
cg00406010	8	60735327	2178551	2178601	N/A	CGAGTCCAGGAAAACCTGCCAGCTGTGGAACACTTTCATTAACACGAGAT	F	N/A	N/A	0.4457257	0.5852157	-0.13949			
cg00416130	1	51763402	35257924	35257974	N_Shore	CTATGGATGTCCCCCACACCACCCAGCCACCATTTAGAGGCATAAGAACG	R	TSS1500	GJA4	0.7487571	0.8224314	-0.073674286			
cg00423597	1	54661377	33235531	33235581	Island	CTGAGGAATGAGCGTGAGGCACCAGGCACGCCCCGGGCTCCTGGTGCACG	R	Body	KIAA1522	0.9144371	0.9491343	-0.034697143			
cg00423969	2	66620406	97359879	97359929	N/A	CGGGGGCCAACTCCACCCTGTCAGGAAATGCCTGGGGCCCAGGATCCCGA	F	Body;TSS1500	FER1L5	0.73157	0.8039314	-0.072361429	0.7562775	0.8039314	-0.047654
cg00443516	1	72766411	2061836	2061886	N_Shore	CGCCAGGAGCCCCTGGCCCTGGGGACCCTGGTTGGGCAGGACACCCAATA	R	5'UTR;Body;5'UTR	PRKCZ	0.8519	0.8837143	-0.031814286			
cg00447208	17	61667436	76126301	76126351	N_Shore	CGCCAATGACAGGGGCTGGAAGTACAGCAGTAACACCAAGAGTATCTGGA	F	TSS1500;5'UTR;TSS1500	TMC8	0.5684757	0.6750929	-0.106617143	0.61699	0.6750929	-0.058103
cg00448707	1	45650334	68512928	68512978	Island	GGTAACGCCAGCTTTGGCTCCAAGGAACAGAAGCTGCTGAAGCGGTTGCG	F	Body	DIRAS3	0.8003271	0.85392	-0.053592857			
cg00452266	2	44628332	220431399	220431449	N_Shore	ATAACAAGGGGTGCCCTGGATGTTGCATGTGGGTTGAAATTGGCCTTCCG	R	Body	OBSL1	0.8837643	0.9186214	-0.034857143			
cg00468670	3	33688401	69371195	69371245	N/A	CGCTTTGGATTGTGCTCTGTCTGTTTAAATCATTTGTGAGCCAGACGCAA	R	Body	FRMD4B	0.8382314	0.8800286	-0.041797143			
cg00472136	12	22721323	57410604	57410654	N/A	ACTGCTGGGGCTTAGAGGACAATACTCCAAAATGAAGGCCTCAATAGCCG	R	TSS1500	TAC3	0.8056129	0.8511914	-0.045578571			
cg00479347	14	57760318	105851951	105852001	Island	GCTCTCCCACGCAGGAGCCCCAGTGAGATGGGAGCCACTGAGTGCCCTCG	R	Body;Body	PACS2	0.8539871	0.8849243	-0.030937143			
cg00484083	2	20690425	95876354	95876404	S_Shelf	CGTGTGCATGGGAACAGAAGTGGGGAGGAGAACAGAAGCCTATTAAACAT	R	N/A	N/A	0.7431714	0.8465957	-0.103424286			
cg00484484	15	55647428	70936009	70936059	N/A	GATGGAAAGACTGTATGCAGGCTATCCAGCCAAACCGTCAGAAGGGCTCG	F	N/A	N/A	0.7937586	0.8460643	-0.052305714			
cg00495811	16	13631494	55619692	55619742	N/A	CGCTTTTAGAAGACATCTGGTCTGCTCTCTGCATGAGGCACAGCAGTAAA	F	3'UTR	LPCAT2	0.6954943	0.7933257	-0.097831429			
cg00498010	7	46617477	4805943	4805993	N_Shore	CGCTGGTGTGGGGTCCCCATGTAGAGACCCTCAGGTCCCTATCCAGAGAC	F	3'UTR	FOXK1	0.6913429	0.7559014	-0.064558571			
cg00500227	10	30774352	70169555	70169605	S_Shelf	CGTGGGTTCTGGCAATGACTTGCCATGGGTCACATGCTAACACAGACTAT	F	N/A	N/A	0.8046114	0.8887743	-0.084162857			
cg00501787	19	12781427	36128493	36128543	S_Shore	CGCCCGGCCAGGTGGGAGCGGGTGCCTGGCCACAGACCCTATCTCAGGCC	R	3'UTR	RBM42	0.8618257	0.8869	-0.025074286			
cg00502241	19	54731474	18642658	18642708	N/A	GGAACCTGGACAGGGGGCGGCAGGCGGGGTGGGGGGCTGGCACTCAGGCG	R	3'UTR	FKBP8	0.8743757	0.9047486	-0.030372857	0.8815775	0.9047486	-0.023171
cg00503866	1	55690508	39546656	39546706	N_Shore	CGCTCTCTCAGGCTGCCGGGCTGTCCTTCTGCCTGGCCCCTGGTTCTCAA	R	TSS1500	MACF1	0.3651043	0.4292943	-0.06419			
cg00504599	17	25642384	79428036	79428086	Island	CAGCTTCTTGCTGCTGCCGTTGAGCTGGAAGAGGTTCTGCAGCACCCCCG	F	Body	BAHCC1	0.81424	0.8710157	-0.056775714			
cg00511027	7	18603321	1062887	1062937	Island	CGCTCAGCCCGTGTCGCGGCTGCAGGAGCCACCAGACCTTGTAAATACTC	R	Body;Body;TSS1500;Body	C7orf50	0.88456	0.9150471	-0.030487143	0.8940563	0.9150471	-0.020991
cg00511577	7	23751321	131751077	131751127	N/A	ACATAGTGCATGCCATGAGCCAGGCACCATGGGGATCAGACTGGAATTCG	R	N/A	N/A	0.7735057	0.8437957	-0.07029			
cg00512103	19	39623343	1486989	1487039	Island	GGGTGGTGCTGCCCACGGAAAGCGTGTGGATGCTGTTGGTGTAGCCGTCG	R	Body	PCSK4	0.8695657	0.9196343	-0.050068571	0.90319	0.9196343	-0.016444
cg00512872	7	17735463	6268584	6268634	N/A	CTGTATCCTGTTCGTATGTGCCCTAGGAGCCTTCAGAATAAAGGGGCTCG	F	Body	CYTH3	0.5040714	0.7070586	-0.202987143	0.6252325	0.7070586	-0.081826
cg00528490	2	34753356	102394306	102394356	N/A	CGGTCATGATTCTGAGGCCAACATTCTGATATACAAGACACTGGTCTAGA	R	Body;Body;Body	MAP4K4	0.8894386	0.9343743	-0.044935714	0.9128988	0.9343743	-0.021476
cg00531924	6	60784350	111279890	111279940	Island	CAATTTGCGCGGCGAGGAGCGGAGCGGCAGGAACCCAATAAGCTGCTTCG	R	1stExon;5'UTR	GTF3C6	0.1599143	0.1274514	0.032462857	0.1480338	0.1274514	0.0205823
cg00534343	11	59798424	34182335	34182385	N/A	GGACACACAGGCAGACACGTGGACAGACACAGGGACCCCCTCACCCAACG	F	Body	ABTB2	0.7426957	0.7815314	-0.038835714	0.7606513	0.7815314	-0.02088
cg00535248	16	11732310	50588226	50588276	N/A	CGATGGACAGTGTTGTTGTTTGTACCAGGAAGCTCAGGTACACTCTGGGA	F	Body	NKD1	0.8202871	0.8584457	-0.038158571	0.8075563	0.8584457	-0.050889
cg00539955	22	65799441	44395433	44395483	S_Shelf	CGTGGGTGTTCCTGCAGCTGGGGCCTGTGCTCCCAGGCACTCATGGCTTC	F	Body	PARVB	0.7493543	0.7951514	-0.045797143			
cg00543769	5	12807459	70749126	70749176	N_Shelf	GATAAAACTGAGATACTGTTCCTTTTCCAGAGTATTGCAGGGAGCCCACG	R	N/A	N/A	0.7796943	0.8326271	-0.052932857			
cg00543869	22	46699481	21387497	21387547	S_Shore	TGATAAACACAAGTGGGGATCTGCTATTGGGGTCCCATAGGGCCCTCCCG	F	TSS1500	SLC7A4	0.8251657	0.89088	-0.065714286	0.8579138	0.89088	-0.032966
cg00554352	15	21726446	90200115	90200165	S_Shore	TTCTAAATCAATTGGGGTCCTGAACAAGAACAACACAGAGCAGCCTGCCG	R	TSS1500	KIF7	0.8759814	0.9105857	-0.034604286			
cg00556514	3	71646307	38066524	38066574	Island	GAAGCAAATCTGTGTCGAAGCCTGGGGGCGGGGCCAGAGCCAAGGCAGCG	R	TSS1500;TSS1500;Body	PLCD1	0.2118729	0.2713714	-0.059498571	0.239905	0.2713714	-0.031466
cg00559234	1	74643418	9885909	9885959	S_Shore	CAGCACAGGCAGCAGATTATAAAGCTGAACTGTTTGGTTAGAGCAGCTCG	F	TSS1500;TSS1500	CLSTN1	0.32687	0.47771	-0.15084			
cg00579868	7	64774318	5271516	5271566	S_Shelf	CGACCTCTCACACAGGTAGGAAGCCCCTGCGGACAGCGGGGCCAGCGAAA	R	3'UTR;3'UTR;3'UTR;3'UTR;3'U	WIPI2	0.6504857	0.74429	-0.093804286			
cg00584089	2	47637417	202776922	202776972	N/A	GGCTCACAGTATCTTATTGCCTGGGCGTTGCTCCAAGCCACCAGGAACCG	F	N/A	N/A	0.8080657	0.8636257	-0.05556	0.82381	0.8636257	-0.039816
cg00585776	16	32727358	30790892	30790942	N_Shelf	CGGAGAACCATGTTGCCATCTGCATAACGCCCCAGCCTATCCAAGTGCCA	R	3'UTR	ZNF629	0.8819843	0.91791	-0.035925714	0.8997463	0.91791	-0.018164
cg00588297	2	49802486	74753691	74753741	N_Shelf	AGGAGGTGATTTTAGACAGTTGCAGTCTGACTACCCCCTTCAAATGTACG	R	TSS1500	DQX1	0.7723186	0.8516814	-0.079362857			
cg00589617	1	63636378	230415343	230415393	Island	CGAAACTAATATACCTCAGTATTCCATCATGGTCTGAAAGTCAAACTTCG	R	3'UTR	GALNT2	0.9184371	0.9484071	-0.02997	0.93538	0.9484071	-0.013027
cg00590039	6	50795374	111888683	111888733	N/A	CGGCTTCCAACAAGGGAGGCTTTGTTGGGGCTTTCTCAGCTTCAGACTTA	F	Body;Body;Body;TSS200;Bod	TRAF3IP2	0.6632986	0.7394686	-0.07617			
cg00595828	4	10754465	141658925	141658975	N/A	CAATTTATAGTAATCCTGCTGCAAGCACAATACTAAATCCCTGAAAATCG	R	Body	TBC1D9	0.8222829	0.89405	-0.071767143			
cg00615919	2	40661322	240043915	240043965	N_Shelf	TCTTCCCATGGTTTCTGGACTCTGCACAAGAACCTGCCTCCTGCAGAGCG	F	Body	HDAC4	0.88041	0.9111486	-0.030738571			
cg00622375	10	48773318	29892014	29892064	N/A	CAGGAAGATGATAATGAAGGACTTCTTACCATCCTGACGACTGAAACTCG	R	5'UTR;TSS1500;5'UTR	SVIL	0.70311	0.83597	-0.13286			
cg00628277	17	14744317	80875739	80875789	N/A	CGGCTGACTCCAGGGGGCGCCACAAGAACCAGAAACCCCCAACAGTGCAT	R	Body	TBCD	0.4942786	0.5843829	-0.090104286			
cg00637695	5	45635393	121759771	121759821	N/A	ATCTCAATGTCTTTCTTTTTGCTTTTCAAATGGTTCCCAGTGCTCTCACG	R	Body	SNCAIP	0.8207243	0.9012843	-0.08056	0.857525	0.9012843	-0.043759
cg00642501	4	26642382	2963261	2963311	N_Shore	TGTTTACTTCTAAGGGACTAACCCACATGAAAAGACCCAGGCCTCCTGCG	R	Body	NOP14	0.7937	0.8403171	-0.046617143	0.80862	0.8403171	-0.031697
cg00647262	6	27741488	157746584	157746634	S_Shore	GCAGAGACAGGGCTTAAAAGCAGGTCCTTCCTTATCCACTGTGCCAGTCG	R	TSS1500	C6orf35	0.6783757	0.7388571	-0.060481429			
cg00651912	1	32661319	44447575	44447625	S_Shore	CGGCGTCTATGTCATCAACCAGGTGCCCATGCGGGGGTCCATGTGCCTGT	F	Body;Body	B4GALT2	0.8681229	0.9120086	-0.043885714			
cg00654448	8	25714496	142365315	142365365	N_Shore	TCACCAACCCCAGCTGTGGCCATGTGGAGCAGCTGGGGTGGGGGGCACCG	F	N/A	N/A	0.6047243	0.6931229	-0.088398571	0.6401513	0.6931229	-0.052972
cg00655094	16	33745441	89104756	89104806	N/A	GGTGGAGGCAGCCGGCCAGTCCTGGGTCTGTGCACGGCTGGCCAGAGGCG	R	N/A	N/A	0.8463971	0.8984514	-0.052054286			
cg00658652	16	51790506	71500215	71500265	S_Shelf	CGTGGGTACACTTTCCTGTGAGTTAAGTATTTAAAATGATGTCGAATATT	R	N/A	N/A	0.6996971	0.7772	-0.077502857			
cg00660384	10	31600434	43746736	43746786	N/A	AGCCAGCGGCAGCCGCCTGGGGCCCTCATGAAAAGCACCCTGTGGGTTCG	R	5'UTR	RASGEF1A	0.7781457	0.8304	-0.052254286	0.8003713	0.8304	-0.030029
cg00664723	5	72685404	15927184	15927234	N_Shore	GAACAAATCCCATCAGGTCATAGTTTGACAACTTCCAGTCTACATGAACG	F	Body	FBXL7	0.8762343	0.9027857	-0.026551429			
cg00666280	12	58605401	2902480	2902530	N_Shore	TCCACTACTTTTATGCAGAAGTAACAGTGCCAGGGGTCACCCAAACTCCG	F	N/A	N/A	0.7181729	0.7746971	-0.056524286			
cg00668034	1	47665376	28098848	28098898	N_Shore	TCCCAAGCCGGGATATCTTGGAGAACTAGATTCCTAAAATTTAAAAATCG	F	TSS1500	STX12	0.30106	0.3763043	-0.075244286	0.2406188	0.3763043	-0.135686
cg00668592	8	41678414	143386385	143386435	N/A	CGGGCACACCAGCCGGGCTGCCCCGGGGACCTCTTACCTCAAAAGTTTGT	R	Body	TSNARE1	0.8927914	0.9238043	-0.031012857			
cg00671823	16	60667488	27558770	27558820	N_Shelf	CGCTGTTCTTCCGTGTTCCCAGCCTCAGAGATGAGAATCAGGGTTCGCTC	F	Body	GTF3C1	0.6654057	0.7585457	-0.09314	0.7069013	0.7585457	-0.051644
cg00674003	17	57609414	66832096	66832146	N/A	CGGGCTTCCCAGTTCGTTTCTCAGCAGAACCCGTTCAGTCATCCAGCCCC	F	N/A	N/A	0.8252386	0.8580014	-0.032762857			
cg00675940	5	29784369	42923550	42923600	N_Shore	CGCCTGTAATCCCAACACTTTGGGAATTAATCTTTAGAACTGGGCCATTT	F	N/A	N/A	0.5461486	0.6059529	-0.059804286	0.562555	0.6059529	-0.043398
cg00676728	10	29628304	124213760	124213810	N/A	AAACTCTCATTGACCCTTATCTCAGATTTCCCGAATGCTTACCACCCTCG	R	TSS1500	ARMS2	0.9123471	0.9553	-0.042952857	0.9380013	0.9553	-0.017299
cg00683665	15	68741482	75968876	75968926	N/A	ACCACCTCGCCCTGGTCTATCTGGAATTGGCTGAAGGCCGAGGTGGGCCG	R	Body	CSPG4	0.8804671	0.9182014	-0.037734286	0.9038388	0.9182014	-0.014363
cg00691266	17	19708302	74015089	74015139	N_Shelf	CGGCGAAGCCGGGATGTGGCCCCTCTGCCACAGCGAAGAAACCCCCCTCA	R	Body	EVPL	0.8955557	0.9315343	-0.035978571	0.9156438	0.9315343	-0.015891
cg00698906	17	12610332	48619308	48619358	Island	CGGGCCTGTGGGGCGCCCCTGGGCTCCATGACCTACAGCGCCTCTCTGC	F	Body	EPN3	0.0934421	0.1353071	-0.041865	0.1099925	0.1353071	-0.025315
cg00704970	17	31631316	78865368	78865418	S_Shore	CGGTTCGAAAAGGGATGGTCCCTGTTTCTGATGCCAATTGCACGGTTTTG	F	Body;Body	RPTOR	0.6035286	0.6671514	-0.063622857			
cg00711274	2	18728441	75870921	75870971	N_Shelf	CGGAGGATTTGCTAAAGCACAGATCACTGGGTTCTGTGCCCAGAGTTTTA	F	N/A	N/A	0.71991	0.7837557	-0.063845714	0.73473	0.7837557	-0.049026
cg00712146	3	38752378	65340538	65340588	N_Shore	TTTTTTTTCCCAACAGGCTCTATTAATTACAATTTTTAGCTCTGTACACG	R	3'UTR;3'UTR	MAGI1	0.8286357	0.8916771	-0.063041429			
cg00714725	10	53618494	94825576	94825626	Island	CGCCGCGACTGTGTGTACGGTTTTGAAGTCGATTAAATCTCAAGTCCACC	R	Body	CYP26C1	0.1632786	0.1023913	0.060887286			
cg00718518	5	36668494	171766029	171766079	N_Shore	CAAGTCCTTGTTGGATGGGGAGGGCCCCCAGGCAGTAGGGGGCCAAGACG	F	Body	SH3PXD2B	0.7308443	0.8015271	-0.070682857			

cg00721016	11	25800320	76745087	76745137	N/A	CGGCCCTCATGTGGAGGCCCCCTGCAAGTTGCCTGGAAAAGTGTATTGTG	R	TSS1500	B3GNT6	0.7790343	0.83854	-0.059505714			
cg00725472	7	62735370	47554427	47554477	N/A	CGGCCCCAAAAGTTACAAGTTTTGTGGGACTTGGTCCCTGGAAGAAGGTA	R	5'UTR	TNS3	0.8836486	0.9235586	-0.03991			
cg00734436	14	25724411	53331182	53331232	N/A	AGATGCAGCATTTAAACCCAGATCCTCAGTTAATACCAGAGCAGATCACG	F	Body;Body;Body	FERMT2	0.8775929	0.9018957	-0.024302857			
cg00737556	14	40717406	76013302	76013352	S_Shore	TAAGAAAGATGCTCAAGTCCCATGGCACAGAGCAAGGCGGGCAGGGAACG	R	3'UTR	BATF	0.6518271	0.7066614	-0.054834286			
cg00744495	9	11666360	138710327	138710377	Island	CGGCTTTGACTTGGGCTTGCCGAGCCCCTGCTCCTCTAGGATCTGCTGCT	F	Body	CAMSAP1	0.8438114	0.8739486	-0.030137143	0.8535988	0.8739486	-0.02035
cg00746949	7	10722493	141437889	141437939	N_Shore	TTGCTTTTTTTTCCCTCCAGGCAGAGCTAGTCTCTGTTTTGCCTACCTCG	R	TSS1500;Body	SSBP1	0.0877177	0.1115439	-0.023826143	0.0837444	0.1115439	-0.027799
cg00755588	9	51744447	139737793	139737843	N_Shore	GGATCACAGAGGGGTTGGCAGCCCACATCTGAACCCAGGCCAGCCTGCCG	R	TSS1500	C9orf172	0.2877414	0.3617886	-0.074047143			
cg00757822	3	38743425	155304922	155304972	N/A	CGAAGAACTCTAACCTTGTGAATGAGAACTAATAGGGACACAAGATTTGT	R	Body;Body;Body	PLCH1	0.7819671	0.84138	-0.059412857	0.8052813	0.84138	-0.036099
cg00758701	13	38607445	49879718	49879768	N/A	CGGCCCTCCCTGCAGCGGGAATCTCTCGCTCTGGTGACGGGGCTAATGTG	F	N/A	N/A	0.7698886	0.81147	-0.041581429			
cg00762550	17	18620342	33306307	33306357	N_Shore	CTTATAGCACATCTCAATTCCATGCAACATTCAAGTGCTCAATAGTCACG	R	TSS1500;TSS1500	LIG3	0.8395157	0.8959957	-0.05648	0.8455288	0.8959957	-0.050467
cg00768993	2	20772459	200335874	200335924	Island	CGCACAACCCTCCCCAGCTCCGGATGCCCTGGGATACCCGGACCCAGGAG	R	Body	FLJ32063	0.1461743	0.106436	0.039738286	0.1331036	0.106436	0.0266676
cg00771722	5	11631433	131396253	131396303	N/A	GTCTGTGGTTTTCTATGGAGGTTCCATGTCAGATAAAGATCCTTCCGACG	R	TSS200	IL3	0.7836914	0.82797	-0.044278571	0.7966913	0.82797	-0.031279
cg00772257	7	31804400	115891	115941	N_Shore	CTGAGGAGCCCTGCATGGCCATGGAGTTTGCTGGATGAGGGATATGGACG	R	N/A	N/A	0.7744871	0.84391	-0.069422857			
cg00773142	16	19611315	81898406	81898456	N/A	TGTCACGGGGCTGCCATCCTTAATGGTTTGGTGATGGCTGCCTGGGTGCG	R	Body	PLCG2	0.6814371	0.81461	-0.133172857	0.7357375	0.81461	-0.078873
cg00774102	6	72622408	31590870	31590920	S_Shore	TTATTTTCCTCCAATTCTTACGTGTCCAAAGACAGGGAACCACAGACACG	F	Body;Body	BAT2	0.6733986	0.7521557	-0.078757143			
cg00779858	3	30627356	167370529	167370579	N/A	CGTCCCTCATAAGGGATCTTGGGACAACAAAGTGCCAGAATCAGCTTAGA	F	5'UTR	WDR49	0.2555343	0.3629314	-0.107397143	0.2970938	0.3629314	-0.065838
cg00783000	14	61800494	101007650	101007700	S_Shore	CCTTGCCAGGAGCAGCCATGGGGCAGCTCAGGTGGGTCACTGGGCCTCCG	F	Body;Body	BEGAIN	0.8575686	0.89421	-0.036641429			
cg00785042	16	73742400	58538323	58538373	S_Shelf	CTCCATGGAGCAGCTGGCTGCCATGCTCCCCAGCGTGGTGCAGCATTTCG	R	Body;Body;Body	NDRG4	0.8884886	0.9112357	-0.022747143			
cg00789792	2	45657372	179245704	179245754	N/A	CGTGGTTTCCTATAGGTGATGGGCTGATGGGTAATTTTCATACTCATCTG	F	TSS1500;Body;Body	MIR548N	0.8199829	0.8888243	-0.068841429			
cg00791190	22	13752372	50223573	50223623	S_Shore	CGGCGGTGAAGACACCTTTATTTTGCTGTCTCACTGGAACGCTAGTTTCA	R	N/A	N/A	0.8748143	0.9230029	-0.048188571	0.8924263	0.9230029	-0.030577
cg00791548	2	57701378	30966534	30966584	N/A	CGGTCTAGAAGGTGGTGGGTCTTTCTTGGTGACTGGGGTCCATGCACAGA	R	Body	CAPN13	0.7489943	0.8083929	-0.059398571	0.7653063	0.8083929	-0.043087
cg00799658	19	70792428	33625468	33625518	Island	CGCCCCTGCAGGGTTTGGGTTATCTCTCTCATTAGGAAAACCCAACTATC	R	Body	WDR88	0.5036	0.5623914	-0.058791429			
cg00808175	12	61786321	6949119	6949169	N/A	GAGGGGAGCAGGTGGCTGAGATTTCCCTGACAAATCACAGGCTCCAGGCG	F	TSS1500	GNB3	0.8216257	0.8542914	-0.032665714			
cg00809094	6	12604376	170744358	170744408	N/A	GATATCTTTAGATTTTTTTCCCTGCCCACTAAAGGCCTCAGCGTGAAGCG	R	N/A	N/A	0.8735314	0.9152657	-0.041734286	0.8928525	0.9152657	-0.022413
cg00809477	1	47649364	10898189	10898239	S_Shelf	TTGGGATGGGACTATGCCCCAGGACCCAGCCTAGCCCGGGCACAGGGTCG	R	N/A	N/A	0.8316186	0.87491	-0.043291429	0.8407863	0.87491	-0.034124
cg00809729	10	54631450	117969992	117970042	N/A	CGTGACTGTTCGTGTAATGAAAGTGCTGCTGTCAGGGCCTGTTGCTGCAG	R	Body;Body;Body	GFRA1	0.8875614	0.92646	-0.038898571	0.9107	0.92646	-0.01576
cg00812770	1	30779445	1073510	1073560	S_Shore	CGCACAGCCCTGTCCTGAAGGCCTCCATGGGCTCCTGGGATGGGAAGACA	R	N/A	N/A	0.7685857	0.8328271	-0.064241429			
cg00813890	19	61727355	54927291	54927341	N_Shore	GAATATGTCCCAGATAAGGTGGGACCCAGGAGACAGCGGACCTGATAACG	R	Body;Body	TTYH1	0.2279743	0.15004	0.077934286			
cg00814597	6	55724367	144386148	144386198	S_Shore	GCAGTTTGAGACGTGAAGCTAATGAAGCTTAAGCTTCGGGCCCCCTCACG	F	TSS1500;TSS1500	PLAGL1	0.2378	0.3045771	-0.066777143			
cg00819619	7	49803409	93205163	93205213	S_Shore	AATGATTGCTATTATTTCTTTTGCCAAGGAGACAGTGTTTAGTAACCTCG	F	TSS1500;TSS1500	CALCR				0.1337213	0.100509	0.0332123
cg00825690	1	68664425	64960202	64960252	N/A	AATTCTCGAGCTCCCCAACAACATCCCAAAGCTTTGGGATGGTTCTAACG	R	Body	CACHD1	0.8465786	0.9046771	-0.058098571			
cg00827895	6	10751464	36805384	36805434	N_Shore	CTCAGTATGTGAGTGACCCTGTGGCCCAGGCTGAGTACCTAGGGCCCACG	R	Body	CPNE5	0.7463943	0.7959371	-0.049542857			
cg00830029	12	56716401	2943902	2943952	N/A	CGCCGGCTCAAACAGGCCACCCAGTTCCTGCACAAGGACTCGGCCGACCT	R	1stExon	NRIP2	0.4925714	0.5661057	-0.073534286			
cg00831127	1	64804363	23038925	23038975	S_Shore	CGCCCCACAACCCTAAAGTGGCCTGAGAGGTGCACACAGACATCATCCCT	R	Body;Body	EPHB2	0.7155557	0.80089	-0.085334286			
cg00836007	8	10619499	52801982	52802032	N/A	CGAAGGAAAGGGATTAAATAACTTCCTTAAGCTTTTACAGCTAGTAGGAG	F	5'UTR	PCMTD1	0.7396114	0.8094043	-0.069792857			
cg00844155	12	10602491	6576111	6576161	N_Shelf	CGGTGCTATTCTGGTGATAGTGACGAAGTCTCATGAGATCTGATGGGTTT	F	Body;Body;Body	VAMP1	0.79744	0.8435529	-0.046112857	0.8160475	0.8435529	-0.027505
cg00849052	8	26620444	23570444	23570494	N_Shore	CGGCAGACAAAGGTGAGCTGGTGACATTCTACAATAAAAGTTATTGTGTC	R	N/A	N/A	0.6905129	0.7639214	-0.073408571			
cg00851394	19	47797337	40730425	40730475	Island	CGCCACAAACAGGCAAGCCACGCCCAGCAGCTGCAGGCGATGTAGACGCA	F	Body	CNTD2	0.8776743	0.9149357	-0.037261429	0.8485638	0.9149357	-0.066372
cg00858483	12	51755340	123238275	123238325	S_Shore	TCCTTGCTTACAGGTTTGTGAAATGGCTGCTGACATTTCTGAATCCAGCG	R	Body	DENR	0.69661	0.8073657	-0.110755714			
cg00859147	19	11673447	8841460	8841510	N/A	GTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACTCAGGATCACG	R	1stExon	OR2Z1				0.660735	0.7044743	-0.043739
cg00859858	1	49795499	37944257	37944307	S_Shelf	CGCAAGCCCAGGGCCTATGCTTATCACTACCCTGTACGTCAATGCTCAGG	R	Body	ZC3H12A	0.7710414	0.8598957	-0.088854286	0.8082188	0.8598957	-0.051677
cg00867406	16	36617342	89997889	89997939	N_Shelf	CGCAGCGGCCTCGGCCATCAGAGCGTGTCCCACGATGAGGTGGCAACTTC	F	Body	TUBB3	0.9108643	0.9379457	-0.027081429			
cg00870242	8	52713361	10530148	10530198	N/A	CCTGGGGTGTTAAGAGTGCCATGGCCCCTGCATCTGGTTGCCAGGAGACG	F	1stExon;5'UTR	C8orf74	0.6804386	0.7730586	-0.09262			
cg00887508	13	60709394	22425573	22425623	N/A	CGACTATTGGGGTGCTTCCAGCATTGAGGACTCCTGCTTGGCAAGGTAGA	F	N/A	N/A	0.6555514	0.7340343	-0.078482857			
cg00890049	6	16604472	115892863	115892913	N/A	CGCCAAATTTTGTTAAGTCCTGGGTATTAAGGCATCTACCTTGTAGTTGG	F	N/A	N/A	0.8061329	0.8728129	-0.06668			
cg00890054	1	10798412	9405823	9405873	N/A	CGGTCCAGAGCTCTAGTCCCTGACCTCAAAAGACCCAAAATGCACCTGCT	R	5'UTR	SPSB1	0.8327314	0.8874829	-0.054751429	0.8352113	0.8874829	-0.052272
cg00890649	6	26705402	42987318	42987368	N_Shore	CGGCAGCATCACTTTCTGAGACCTAAGCTTATACAGTTATTTTTGTGACC	F	Body	KLHDC3	0.8108743	0.8983071	-0.087432857			
cg00895174	16	33603317	14729433	14729483	S_Shelf	AGAGGGCAGGCTCCAGCGAGAGCCAGGATAGCCTTCTCAGCCCGCCTTCG	R	5'UTR	BFAR	0.7515157	0.8212857	-0.06977			
cg00898920	2	53725359	241504756	241504806	N_Shore	CGAGTCATGCCACCAGGTGAAGGCCATAAGCAGCTTAGGCACTGGCTGAG	R	N/A	N/A	0.7718143	0.85739	-0.085575714	0.81293	0.85739	-0.04446
cg00902815	13	36743507	76313846	76313896	N/A	CGGCAAAATAGTGTGACCTGCTCTATGTGGTGATCACTGCTGACACATCG	R	Body	LMO7	0.8667229	0.9248629	-0.05814	0.90135	0.9248629	-0.023513
cg00911370	20	66619367	1472098	1472148	N/A	TGTGTTGCTGCAATGAAAACACTTCCCCAAGCAGCTGTGGCCAAGAGACG	F	1stExon;1stExon;5'UTR;5'UTR	SIRPB2	0.5216843	0.5805629	-0.058878571	0.54243	0.5805629	-0.038133
cg00916439	6	23773366	31509424	31509474	N_Shore	CGCCGAGCGCCGCCTCTCATTGATGCTGAGGCCTCCAATATGAGAAGAAC	F	5'UTR;TSS1500;5'UTR	BAT1				0.0398396	0.0673807	-0.027541
cg00919591	22	58629460	23524136	23524186	Island	GGAGAAGTCCTCCTCGCTGGAGGTGAGGTTCTCATTGGAGCTGCAGTCCG	F	1stExon;1stExon	BCR	0.6463857	0.7233857	-0.077			
cg00923873	20	33729438	3650247	3650297	N_Shelf	GCCAGGGCTGTCCAGTGGCTGTGGGGCCCAACTCCATGGGGTGAACGCCG	R	Body;Body	ADAM33	0.7601329	0.8013086	-0.041175714			
cg00924575	5	27739336	76474673	76474723	N_Shore	CGGTCCAACAAACTGAAAGGAGGTAAATTCTGCCAAAAATCAGGAGAGCC	R	N/A	N/A	0.8831557	0.9141586	-0.031002857			
cg00925020	19	22686461	2543877	2543927	Island	CGTGAGAACAGAAGCAACCTTCATCTGGCTCTAAAACTTCCAGAACCAGT	F	5'UTR	GNG7				0.0528243	0.147887	-0.095063
cg00925831	9	33741475	113340796	113340846	N_Shore	CGGACTTTTGTAAAGTGTGTCTGTTTTTCTGATTACAAATTAATCCATAT	R	Body	SVEP1	0.5667271	0.72008	-0.153352857	0.6550375	0.72008	-0.065043
cg00929860	10	52644415	73846448	73846498	N_Shore	CGCCTTCGCCCCACATGCGACCTGTCCAGCCGCAGGAGCCTGGAGCCCCG	R	3'UTR;Body	SPOCK2	0.8544429	0.9139743	-0.059531429	0.87731	0.9139743	-0.036664
cg00930618	18	56704328	74088820	74088870	N_Shelf	GTCCGGTGGATCAAGTGGGCGTCAAACTCCCCTTGCTCTGCTGGGAGGCG	R	Body	ZNF516	0.9008457	0.9335471	-0.032701429			
cg00936348	7	24665374	43577034	43577084	N/A	TTGCCTGTGGGGAAGTTGATTACATTAGCTGTTAACACAGGTCACAAACG	F	Body	HECW1	0.7077343	0.7868729	-0.079138571			
cg00944599	7	32673377	98479808	98479858	S_Shelf	TCCTCAACATGGTATGGGGTTCGCTATCACCAGCGTGAAGATGGAAAACG	F	Body	TRRAP	0.7011286	0.7960457	-0.094917143	0.7371075	0.7960457	-0.058938
cg00949661	20	65617359	50214496	50214546	N/A	AAAGTTGGAGCAGACCTCCCTTTTCCAGCCCCTGGGGCCATTAGACCACG	F	3'UTR	ATP9A	0.7199714	0.7780843	-0.058112857			
cg00952050	20	70697349	33585040	33585090	Island	CGTGGGGCAGCTGTCACCTCTGTGGGCCTCTGACCCCAGGCCTCACCCAC	R	Body	MYH7B	0.6568743	0.7445614	-0.087687143			
cg00961252	4	19685443	26319518	26319568	N_Shore	CGCTGGGGCTCTCAGAAGGCCATGATTCCAAATTAGATCAGTGGTCTGGA	F	N/A	N/A	0.8345857	0.8855886	-0.051002857	0.8379625	0.8855886	-0.047626
cg00963496	6	33763366	32154023	32154073	N/A	CGAGACTCTCTGTGCTGGGGGTGCTAATTACATGGCAGGAAGAATGGGGC	R	3'UTR	PBX2	0.3691414	0.4917014	-0.12256	0.4424325	0.4917014	-0.049269
cg00968167	1	41790387	19810215	19810265	N_Shore	AACTCCTTGTTTGGGGAGGTGGGCCTGGCCCCAGGCCTTGATGGAGAACG	F	Body	CAPZB	0.6189629	0.7411186	-0.122155714			
cg00969893	15	33716463	63133069	63133119	N/A	GAGAACAACATAATACTGACTTTTCTTTGTTGGTAACAGTCCATGAAACG	F	3'UTR	TLN2	0.8138114	0.8882271	-0.074415714	0.8468838	0.8882271	-0.041343
cg00970757	3	21708427	71167804	71167854	N/A	CGGGCTATAGTTTGCTGACCCGTGACTAGAAACTTTCCAGTTAGTCATAT	R	Body	FOXP1	0.7536486	0.8138143	-0.060165714			
cg00980698	14	14697303	21250509	21250559	N/A	CGAGAGAAGGGAATAGGGAAGACAGCAAAGAAAGATTCAGATTTCTAACC	F	3'UTR	RNASE6	0.2904671	0.4156786	-0.125211429	0.339035	0.4156786	-0.076644
cg00986580	14	57642348	22951241	22951291	N/A	CGCTGGCAGTTTCTGTAAAGCCTCGTGCTGTGGTGTAATTCAGGGAGCCC	F	N/A	N/A	0.6881114	0.7473329	-0.059221429			
cg00988179	6	50673451	55314478	55314528	N/A	CGTTCAATTAGCAGAAGAGAAGGCAGAAAAGAGGAAAAAAATTAAAAGTG	R	Body;Body	HMGCLL1				0.6418525	0.7304571	-0.088605
cg00991400	7	35635504	126883137	126883187	N/A	CTCACAATGATGCAAAGAACTCACAGCCAGGAGTATGCCCATTCCATACG	F	1stExon;Body;Body	GRM8	0.8333557	0.8963843	-0.063028571	0.871275	0.8963843	-0.025109
cg00994601	6	12620367	31628797	31628847	S_Shore	CGCATCCAAGACTTCATGAAAGGCTTTCCCAGAAAAGAAAAAATGAGGAG	F	TSS1500	C6orf47	0.18758	0.3062786	-0.118698571	0.2353013	0.3062786	-0.070977
cg00994629	14	65779506	22694547	22694597	N/A	CTTTTCTTTTTGAACCATCACACTCTACCCCTAGCGTCTGCCTGTGTGCG	F	N/A	N/A	0.7858429	0.8504043	-0.064561429	0.8130738	0.8504043	-0.037331
cg00998124	12	43787427	115138766	115138816	S_Shore	CGCCTACACACGCAGCCTGGCACACCTGCATGGCAGAGTCCCACCAAGCT	R	N/A	N/A	0.5623857	0.6783971	-0.116011429			
cg01003815	9	24726402	5184060	5184110	N_Shore	CGGTTTGAAAATGATCATGAATCAGTCTCATGGTTTCTGTCTTTAAAAGT	F	Body	INSL6	0.7976986	0.8640771	-0.066378571			
cg01007737	16	37749346	2787413	2787463	N/A	CGGGCCCTGCACTGCCCTAGGGACCCCCAGCCAGGCCCTCCCCAGCTGAG	F	Body;Body	LOC100128788	0.71984	0.7877314	-0.067891429			
cg01008256	7	16806430	100463985	100464035	Island	GACTTTGTGAACAGTGGGCGGGGAGACGCAGAGGCAGAGGCCCTGGCACG	R	Body;TSS1500	SLC12A9	0.6120914	0.6901543	-0.078062857	0.641205	0.6901543	-0.048949
cg01008263	16	34620463	70605696	70605746	N/A	GAACTGGACCGAACCCCACCCGAAGTGTCCAAGAAACTCGAGGATATCCG	R	Body	SF3B3	0.8296357	0.8752571	-0.045621429			
cg01008405	5	13607458	139039026	139039076	N_Shore	GAGCATGGGGGGTGCATTCCAGCCCTCCTGCAGTGTGCGGGGCACACCCG	F	5'UTR	CXXC5	0.5074629	0.5511543	-0.043691429			
cg01016119	3	27756307	56835282	56835332	N_Shore	GCTGCCAAAGGGCTGCAAGGCCAAGTCTGACAGGTGAGAGGGCTGGTACG	R	Body;Body	ARHGEF3	0.5451457	0.6543843	-0.109238571			
cg01019246	16	72765475	56400961	56401011	S_Shelf	CGGCTCCCTGGAGAGCTTGCCCTAGGCCATCCCCATCTGAGTTTAGATGG	F	Body	AMFR	0.86072	0.8907971	-0.030077143	0.86787	0.8907971	-0.022927
cg01023827	8	66647415	144387696	144387746	N_Shore	CGCTCTGTTCTTGTGATCATGGCTGAGTGGGATCCAGTGTGAGTCTCCAC	F	N/A	N/A	0.8903714	0.92266	-0.032288571	0.8989725	0.92266	-0.023688
cg01025894	6	30665484	30291451	30291501	N_Shelf	CGTCGTGCCATTATATTAGTAGGATAAATTTCTGGAAGTTTGGCTGCTGG	R	Body;Body	HCG18	0.8886314	0.9302257	-0.041594286			
cg01030213	5	28752319	179563745	179563795	Island	CACATTTCTGGGCAGGGCCATCTCTTGCTCTGGCCTTTCTGCGGTTGACG	R	Body	RASGEF1C	0.8768471	0.9001043	-0.023257143			
cg01033299	12	43756402	53601015	53601065	N/A	CTGGTGCCCTGGTACTCACAGGTGCGTGCAGAGCAGTCCTTCCTCTGGCG	R	TSS200	ITGB7	0.6346543	0.7209571	-0.086302857			
cg01037768	19	20637455	56612425	56612475	Island	CGCACGTAAGTGGGACCCCACATGCTATGGCCAGGCCAACCCCCGCCTAC	F	Body	ZNF787	0.7654729	0.8063086	-0.040835714			
cg01037823	16	17666301	2879998	2880048	N/A	CGCAGCCTGATGGCTTCCACCTGAGGGTGGCGGGTCAAGGGTCCACAGAA	R	TSS200	ZG16B	0.6285629	0.7155086	-0.086945714	0.6540625	0.7155086	-0.061446
cg01039092	10	16794418	129245398	129245448	N/A	ATAGCAAGTATCACACGAACACTAAAACTGGAGTGTGAAGCAAGGCATCG	F	Body	DOCK1	0.92059	0.9462357	-0.025645714			
cg01041455	3	10797415	160879983	160880033	S_Shore	CGTAGCTCATAGCCAGAGATGGCTGTAAGGGAAGCTGGAAAATATAAATC	F	N/A	N/A	0.5363529	0.6180114	-0.081658571			
cg01053681	10	50681494	80931119	80931169	N/A	CAGGGCCTAGAACTTAGGGACTGGCCTGGGCTGTCGCTCAGAGGATGCCG	R	5'UTR	ZMIZ1	0.8611829	0.8901614	-0.028978571			
cg01056004	10	20664335	98948259	98948309	S_Shelf	CGGGTGGGGAGGAGGCAGGCCTGGCACATTGCTTCTGCCAGGAATACTCC	F	N/A	N/A	0.5253871	0.6428586	-0.117471429			
cg01058902	1	30767440	201707751	201707801	N_Shore	CGCTCTCACTGCCTTTAAAGAGGTCTGGGTGGTGCTTTGAGTCCTAGGAA	R	TSS1500;Body	NAV1	0.8680171	0.90804	-0.040022857			
cg01059818	17	60788456	26370690	26370740	S_Shore	CGTGTGTTTGATTCAGTGGCCCTGTGGCATTAAGTGTTAGCACCTGATCC	F	Body	NLK	0.8768271	0.9018057	-0.024978571			
cg01060188	1	56627342	54620626	54620676	N/A	CGGGGTCTTCGTGTGAAGGAACTCAACCCAAAACAGTGGCTCCAGCCCTT	R	TSS1500	CDCP2	0.8744743	0.9042443	-0.02977			
cg01066494	14	49675421	102231419	102231469	S_Shelf	AGTGGGGCATCATACTCAGGCACTGCAGGCCACACCGCAGGTCTCACACG	F	Body;Body	PPP2R5C	0.8843671	0.9206943	-0.036327143			
cg01071493	11	26677458	65363954	65364004	N_Shelf	CGCCTACAGTAGCCCAGCGTAGGTCTCCCTGGACCACATTTATCCTCAAG	R	TSS1500;TSS1500;TSS1500;	KCNK7	0.8476529	0.9009671	-0.053314286	0.8799813	0.9009671	-0.020986
cg01071534	21	58728376	46385572	46385622	N_Shore	TCTTGCCTCTTGAGTGGCCACTGTGGAGGGTCACCCTGAGGCATTTCCCG	R	Body	C21orf70	0.8967743	0.9343843	-0.03761			
cg01076217	6	63667403	137364811	137364861	N/A	CGGTGAATCTGGAGTCCTTGGTAGTTAAAGAAAAAGTTAAATTCAATATA	R	Body	IL20RA	0.5979171	0.7072443	-0.109327143	0.627585	0.7072443	-0.079659
cg01080456	7	42789327	156177920	156177970	N/A	TCCATCTCAGGACCAGAAGAGCTGGGGTGCACTACATTTTGCTTGCCTCG	R	N/A	N/A	0.9049314	0.9298914	-0.02496	0.90113	0.9298914	-0.028761
cg01081096	7	41794491	150721518	150721568	N_Shelf	CGGCTTCTCCAGAAAGGTTGGAAGGATGGGAGCTGTTGTTGCTTCCACAA	F	1stExon;5'UTR	ATG9B	0.7426986	0.7877529	-0.045054286			
cg01089060	10	74665467	97050836	97050886	Island	CGCCCCCGCCCTGGCCCTCGCGGTTGCCCTGCCCCCGCCAGCCCCAGGCT	R	TSS200	PDLIM1	0.19435	0.16901	0.02534	0.1897163	0.16901	0.0207063
cg01089579	7	19690313	155914371	155914421	N_Shore	CAGGCTGGGCCCCCTTGGCCAGCAGGGCCCCTGTGAGGAGCTGCCAGACG	R	N/A	N/A	0.7089586	0.7784643	-0.069505714			
cg01093202	3	27791424	15384168	15384218	N/A	TCCTCTTGCCTGGCTTCCCCTCCAAGTCTCAATCTCTAAATGTTGGGACG	F	TSS1500	SH3BP5	0.8460929	0.9138457	-0.067752857			
cg01109707	11	43678356	47166816	47166866	N/A	CCCAGCCAGAATAAGAATGCAGGCAATACAGCCGGGTGCGGTGGCCCACG	F	Body;Body;Body;Body	C11orf49	0.7432829	0.7910471	-0.047764286			
cg01111006	6	43788367	11161658	11161708	N/A	CGAATGTCTGTCTGTGCCCTTAGCATTCATGGTTTCTGCCATGGAACTGA	F	N/A	N/A	0.8687114	0.9030329	-0.034321429	0.8860925	0.9030329	-0.01694
cg01114085	11	48749376	69803503	69803553	N/A	CGGGTGTTATTCAGCCACAAAAAAGGAATAATGCACTGGCATGGGGCACA	R	N/A	N/A	0.8718814	0.9102243	-0.038342857			
cg01116137	20	18633387	25034263	25034313	N_Shelf	CCTCTAATCGTTCAGAAGGCAGGACACTGACAGCGGCAAGACGCTGTGCG	F	Body	ACSS1	0.6283243	0.7589129	-0.130588571			
cg01119585	2	59610435	10571959	10572009	N_Shore	CGGCCTCCTTCAGGGCCCCTGGTGTCTAGAGAAATGAAGGAGTTTCTCCC	F	N/A	N/A	0.6813943	0.7484029	-0.067008571			
cg01122318	9	49637484	107525114	107525164	N_Shore	TTCCTTCTGTGGCAGATGAGGATTTAGGTCTCACAGAAGCCACTCCCCCG	F	TSS1500	NIPSNAP3B	0.8644571	0.9244586	-0.060001429	0.8941625	0.9244586	-0.030296
cg01123946	16	52788507	89163343	89163393	N_Shelf	CGCTGCCTGTGGGTGGGCACTCCTGCCACCAGCCCCTGGGAGGTGACAGA	R	Body;5'UTR;5'UTR	ACSF3	0.8539957	0.89719	-0.043194286			
cg01129847	19	70604347	2281919	2281969	S_Shelf	CGGGGGAGACAGTGTCCAGGGACCCAGGGATCCACACTCAGGCCTCATCC	F	5'UTR	C19orf35	0.6773729	0.7355414	-0.058168571			
cg01130273	22	19774449	20776864	20776914	N_Shelf	CGCAGACATGCACACACAAAGCCAGCAGAATCTCAGAAACACAGAGACGG	R	N/A	N/A	0.70964	0.8408914	-0.131251429			
cg01142676	11	26777376	117695591	117695641	N/A	CGCACGTCCTCACCCTGCAGAAGGAGCCCCTCCATCCACACTGCAGCTTT	R	Body;TSS200;TSS200	FXYD2	0.1958357	0.135124	0.060711714			
cg01148092	6	51788334	40509971	40510021	N/A	CCTGCATCCCATGGAAAGGCAATTCACCCAGGGGCCCAGAAAGCTCATCG	F	5'UTR	LRFN2	0.7225286	0.7614057	-0.038877143			
cg01148741	2	55617316	96811453	96811503	Island	GGGAAGGTGTTACCCGGAGTCGGAGGGACTAGCACCCCTCCGTTTTTGCG	R	TSS1500	DUSP2	0.68365	0.7319371	-0.048287143			
cg01150105	3	43757436	175139160	175139210	N/A	CGATTCACAAGGTCTGGAGTGGAGACTGAGAAATCACATTTTGATTAAGT	R	Body	NAALADL2	0.80509	0.8567514	-0.051661429	0.8357313	0.8567514	-0.02102
cg01151584	11	30693376	64627528	64627578	N/A	GTCCTGCTCCTCGGCCTCAAAGAGCTTGCGGTTGTCGGGGATGAGGAGCG	R	Body	EHD1	0.7254614	0.7892071	-0.063745714			
cg01153613	6	50735459	139928856	139928906	N/A	ACCCCACCCCTTAGTTGGGCAAACAACCTAAACCCTCAGGAGAAACTTCG	R	N/A	N/A	0.8412829	0.88527	-0.043987143			
cg01154505	2	51726470	112940409	112940459	S_Shore	GTGCAACGGTAAGAGCCCGGGGTGTTCACGCAGGCGTGCATGCAGAGCCG	F	Body;Body	FBLN7	0.8717529	0.9364429	-0.06469	0.90005	0.9364429	-0.036393
cg01157004	3	16611477	177256538	177256588	N/A	CATATGGGAAAATCTCTCACATTCAAAAGCATGCAAGCAGCTAGCTAACG	R	N/A	N/A	0.8151786	0.88052	-0.065341429	0.8427613	0.88052	-0.037759
cg01158469	16	49716386	69832831	69832881	N/A	CGGAGGTGCCACAGGGAATCTGTACCTCCCACAACCCCCTCGGAGCACCC	R	Body;Body	WWP2	0.8093086	0.8754371	-0.066128571			
cg01160311	17	60729362	42838541	42838591	S_Shore	CGGGGTGCACAGTTCACAGGTAGGGAGTGACACCAGGCAAGACAGCCAGA	R	Body	ADAM11						
cg01167556	12	23744487	56323639	56323689	N_Shelf	AGACACAAAGAAGTCTAGAGTAAGACTGATTCCACCTTATTCCTTATTCG	R	TSS1500	DGKA	0.7099914	0.8073171	-0.097325714	0.7509575	0.8073171	-0.05636
cg01171858	16	42757326	31494347	31494397	N/A	AGCCTTCAGCCTTGATATGACCTGATTCAGCTAAACAAAGCTGGGGAGCG	R	TSS200	SLC5A2	0.9127929	0.9365786	-0.023785714	0.9139563	0.9365786	-0.022622
cg01180831	14	70616315	89361469	89361519	N/A	CGGCTTTGGGCATAGTGAGCCTTGATGGAAAAAGTATTTCAATAAAAGAG	F	N/A	N/A	0.9186171	0.9457943	-0.027177143	0.9312513	0.9457943	-0.014543
cg01181259	5	62613375	1856259	1856309	N_Shore	CGACGTTGCTTTCTGATCTTTCTCAGGCCAGAGGAAGTTTGTGGGCCAAG	R	N/A	N/A	0.6489243	0.7190043	-0.07008			
cg01183991	4	14635324	16256356	16256406	N_Shore	CGGCAGGCAGATCTCAGAGACAGAAAGGAGGGACAAATAATCTGAGAAGC	R	Body;Body	FLJ39653	0.9085957	0.93762	-0.029024286			
cg01185080	15	54651444	90543813	90543863	Island	TTAAACAGCTGTTAGCAGAGCCCTGGACGGCCTGACTCGAGGGAGCGGCG	F	TSS1500	ZNF710	0.5874457	0.6691971	-0.081751429			
cg01185573	3	20770307	135432551	135432601	N/A	GCCCATGTGTCCCTGAGTTTGGAATCCTGACCTGGCCCAGAGAACTCTCG	R	N/A	N/A	0.6181714	0.6988929	-0.080721429			
cg01186595	11	21702476	89954679	89954729	N_Shore	GCACTGCACCAATTCACACATGGATACAGACTTCCAACAAATGACTATCG	R	Body;Body	CHORDC1	0.8648157	0.9177671	-0.052951429	0.8922513	0.9177671	-0.025516
cg01190323	16	49682501	2498952	2499002	N/A	CGTCTCCGCCTTGGAAGGGAAGATTCGAGTAAGCAGCGGTTCCATTTTCC	F	Body	CCNF	0.9043571	0.9408786	-0.036521429			
cg01190666	20	14736403	62204908	62204958	N_Shore	GTGACTGCTTGTGGAGCCCTGGAGGGGGCAGAGCCCTTGGCACAGTGCCG	R	5'UTR	PRIC285	0.4900557	0.5859671	-0.095911429			
cg01192748	3	59626507	183145151	183145201	N_Shore	CGGGGATCATCAGGGGTGTGCTTAACCCTCCAGGCAGCACAGTAAAACAG	F	Body	MCF2L2	0.6989614	0.7858443	-0.086882857			
cg01197294	12	13760356	111358627	111358677	N/A	CGGTGCTTGGGCCGGGGACACTTGTGCTTGTCAATTTTGAGAAAAAAAAT	F	TSS1500	MYL2	0.8830943	0.90557	-0.022475714	0.8765438	0.90557	-0.029026
cg01197763	1	48635471	858362	858412	N_Shore	CAGGGGCCAGGGTCAGAACAGGAGGCCCCTTTCTAGTGGATGCAACACCG	R	N/A	N/A	0.8669614	0.9014014	-0.03444			
cg01199494	20	52714324	39994320	39994370	N_Shore	GTTCCCTTACTCTCAGAGCAGTTCTTGTACCACCTCCTCCAGGAGGCTCG	R	Body	EMILIN3	0.6798743	0.7521071	-0.072232857			
cg01200651	4	30742404	8087343	8087393	Island	CGCTGCAGCCCTGTCCACTCACGCAGGTCTGGGGGTGCCCACGCTGCAGC	F	Body;Body;Body;Body;Body;B	ABLIM2	0.8661943	0.9062186	-0.040024286	0.8742363	0.9062186	-0.031982
cg01201818	2	19697402	231906828	231906878	S_Shelf	GGAGTGGCTCCGGGTGAGTTTTCTCCCCTCCATTCCCACTGCCCAGGTCG	F	Body	C2orf72	0.7860529	0.8327543	-0.046701429			
cg01210084	21	72775394	46717495	46717545	S_Shelf	CGCGAGAACTCACTATTGCGAGAACAGTACCAAGAGGAAGGTACTAAACC	R	N/A	N/A	0.7053086	0.7681986	-0.06289	0.71344	0.7681986	-0.054759
cg01210589	14	51651361	89895742	89895792	N/A	CGCACTGGCTTGCTTTTTGCTTTTGAGTAGCTTGAATATCAAACCAAGCA	F	5'UTR	FOXN3	0.6198729	0.7227129	-0.10284			
cg01215211	2	47636474	173598421	173598471	N_Shore	CGGGGCCCCATCTCCTGTAGCTGGGTTATGGACCCTTCCTGAGTTCAGTG	F	Body	LOC91149	0.8995914	0.9236314	-0.02404			
cg01217329	10	19676443	99192404	99192454	N/A	CATGTCACACTGACCACATCTGTAGACATCTTGAGTTGTAGCTGCAGACG	R	3'UTR	PGAM1	0.5658657	0.6506786	-0.084812857			
cg01223135	16	41787485	15826468	15826518	N/A	AGAGACGCGGTCCCATGAGGCTCAGGTCCAGGAGATGAGGCAGAAACACG	F	Body;Body;Body;Body	MYH11	0.6958043	0.7479829	-0.052178571			
cg01229421	16	10625311	11370688	11370738	S_Shore	CTGCTGTTGCCATCTTAACAGTAAGCTGTGTGCACAGAGATCCAAGCACG	F	TSS1500	PRM2	0.8554986	0.8943271	-0.038828571	0.8661025	0.8943271	-0.028225
cg01229943	6	18799352	40904807	40904857	N/A	GGGGAAACGACTCAAGCTGTAACTATTCTACCCACTCATGCTGAGACTCG	F	N/A	N/A	0.8598286	0.9127886	-0.05296	0.880085	0.9127886	-0.032704
cg01240566	11	47765398	117232202	117232252	N/A	CGGCTCTGCCTCCCAAAGTGGTAGGATTACAGGACTGAGCCACCGAGCCC	F	Body	CEP164	0.7159514	0.7599857	-0.044034286			
cg01241450	1	21785455	3110867	3110917	N_Shore	CGCCCTGCACAGGGAGGTACCAGTGAACACCTCTGCAGGACCTGAGATGA	R	Body;Body	PRDM16	0.7957257	0.8498786	-0.054152857	0.8157238	0.8498786	-0.034155
cg01242602	6	16685367	99871510	99871560	N_Shore	CGGACTATATCAGGGGAAGATCACAGAGGTAAGATGCCCTTTTCAACACA	R	5'UTR;5'UTR	SFRS18	0.8867214	0.9156243	-0.028902857			
cg01244346	2	29679385	74272962	74273012	N/A	CAACCAAGCCTGTGTGTACACACGTGCTCTAAGTGTGAAGTGTGGGTTCG	F	TSS1500	TET3	0.9241214	0.9558257	-0.031704286			
cg01246398	3	55768388	123165872	123165922	N_Shore	ACCAACCCTCTATCCAGGGCTGGATTAACAAAGCAGCAGTGGCACTCACG	R	Body	ADCY5	0.6541886	0.7146186	-0.06043			
cg01246665	15	21691367	93258479	93258529	S_Shore	CGACTTGGGAGACAGAAAGAAAGAAAAATGAACGTTTAAAATTTTATCAG	F	N/A	N/A	0.4375457	0.5475257	-0.10998			
cg01258050	10	74761374	135010532	135010582	N/A	ATGGGGACCCAGTGACACGGGGACGGTGCAGCCGTGGCTGAGGCCTGTCG	R	Body	KNDC1	0.7500329	0.8080886	-0.058055714			
cg01258793	7	23747343	1987132	1987182	N/A	CGGGCTGTGCCTGTTGGGCCAGGGCATTGCAGAACCAGGCCCACCAAGAG	F	Body;Body;Body	MAD1L1	0.8557114	0.8921143	-0.036402857	0.8716375	0.8921143	-0.020477
cg01276323	1	30621466	41282145	41282195	N_Shore	CGCCCAGTGTGCCCAGGACAGAGCTGAGATTAGAGCCAGGGTTCCCAACC	R	Body;Body	KCNQ4	0.8518686	0.8827186	-0.03085			
cg01281175	5	49652325	175109114	175109164	N/A	CGTGCCGACAGAAGAGCGTGGCTGCACTCCAACAAAACTTCAGTAATGAA	R	5'UTR;5'UTR;1stExon	HRH2	0.6543371	0.7426314	-0.088294286			
cg01284415	19	16795338	49457725	49457775	N_Shore	CGCCCAGGCTTGTCTCTAACTTGTGAGCCCAAGAGATAACCCCGTCTCAG	R	TSS1500;TSS1500;TSS1500;	BAX	0.3312914	0.39612	-0.064828571			
cg01286319	19	27713479	2695343	2695393	N/A	TCTGGGTCAGAGGGGCCTGAGCCCAGGGTGGCACAGAGGTGGGGGCCTCG	F	5'UTR	GNG7	0.4629129	0.5882014	-0.125288571			
cg01287088	5	50654509	176827392	176827442	Island	AGGAGGTGGGCGTGCTCACGGGGCCGGACAGGCACACCTTCCTGCAGGCG	F	1stExon	PFN3	0.4523714	0.5466129	-0.094241429			
cg01287788	2	16786462	86362935	86362985	N/A	AAGTGTGTGCCAAACTGCCTGCGCTAACAACCAAATGCAAATGTCATACG	F	TSS200;Body	SNORD94	0.5818014	0.6681471	-0.086345714			
cg01288337	14	42685323	92991035	92991085	N/A	GCAAGCAGGGGCTGGATGAAGAGTTTCCAGAGTGGCACGAAGCTCTGACG	F	Body	RIN3	0.7821614	0.8412257	-0.059064286			
cg01290287	6	25793468	134376081	134376131	N/A	GTCTGTCAGCCAGCAAATACTTACTGAGTATTTGCTGAGTGCCAGACACG	F	N/A	N/A	0.7363486	0.7986371	-0.062288571	0.7457375	0.7986371	-0.0529
cg01298000	6	17662503	168120635	168120685	Island	GTTTAGTCGCTGCCTTTCTCCTCTTTCTGAAGGATGAGCTGAGAGTTTCG	R	N/A	N/A	0.8857829	0.9305543	-0.044771429	0.8937663	0.9305543	-0.036788
cg01298120	11	24717413	2499341	2499391	N/A	CGGTAGCAGAACTCCTGCCAAAGACACAGCTGTCCAGGGTCGAATCATCC	F	Body;Body	KCNQ1	0.8152686	0.8779057	-0.062637143	0.8485863	0.8779057	-0.029319
cg01299119	19	53706444	13070604	13070654	S_Shelf	ACAGGCGCAAGCCACCAAGCCTGGCTGATTTTCATATTTTACTAGAGACG	R	N/A	N/A	0.5766457	0.64701	-0.070364286			
cg01307483	7	28698392	129254604	129254654	S_Shelf	CATAATTATCGTTTAATAAAACAAAAAACCTACAATTTGGGGTCCTAACG	F	5'UTR	NRF1	0.8543057	0.89941	-0.045104286	0.8757513	0.89941	-0.023659
cg01311470	5	67613336	39365733	39365783	N/A	GATGCAGGGTCTCATCACAAGTCAATTAACTTAGAGCTGAGCAGACAGCG	F	TSS1500	C9	0.9100557	0.93897	-0.028914286			
cg01315919	20	43788449	22401404	22401454	N/A	TGGAGTGGAAGGCCTGCAGGAGGGCCTGCCTGCTCACAGCAAACACGACG	F	TSS200;TSS200	LOC284788	0.8595214	0.8899143	-0.030392857			
cg01316152	10	72670322	116168351	116168401	S_Shelf	TGGGTCTGAGCCCTGGAGCTCAGCCCCTTACATCAGCACCCTGTTCCACG	R	N/A	N/A	0.70099	0.7556186	-0.054628571			
cg01323672	3	57698314	49700451	49700501	N/A	CTGGGCCACCCTCATCATGAGGCCACAGGCCCTCCTCAGGGGGTTCATCG	F	Body	BSN	0.8929257	0.9234786	-0.030552857			
cg01336878	19	62725482	54963396	54963446	S_Shelf	GGAGAAGGCCCGTCAGGCCCTGGCCAGCATCAGCAAGTCAGGAGCTGCCG	R	Body	LENG8	0.8877714	0.9113271	-0.023555714			
cg01345586	4	18796402	2435944	2435994	S_Shelf	ATGTGATGTCCGCCCCAGTATCCGGGAAAGGCCCAGCGGCAGCAGGATCG	R	N/A	N/A	0.59056	0.6606514	-0.070091429			
cg01352472	12	23643307	51154575	51154625	N_Shelf	GAAAGTGAAACAAAGAAACTTAGAGCCATGGCCGGGCAGGGTGGCTCACG	F	N/A	N/A	0.5660629	0.6423757	-0.076312857			
cg01353486	6	30753451	88117432	88117482	N_Shore	CGGAAGGGCTGTATCCTGGGCAAATAGAGTTCTTGTAAAAGTATCTAGTT	R	TSS1500;TSS1500	C6orf165	0.0475823	0.0791356	-0.031553286	0.05747	0.0791356	-0.021666
cg01358513	22	36675453	25595705	25595755	N/A	CGGGTCCACGGAGGCCCCCAGTGCCTGTCTCCTCAGCCACCGTCTCTGAT	R	TSS200	CRYBB3	0.8246386	0.8711143	-0.046475714	0.8462013	0.8711143	-0.024913
cg01359200	3	33759436	194763212	194763262	N/A	CGCTCCTGCAGCCAGAGGGACCATCCAAAGCTTCCATGAGATCTTCTCTC	F	N/A	N/A	0.8537286	0.9029886	-0.04926	0.8699563	0.9029886	-0.033032
cg01359469	15	60694417	64679265	64679315	N_Shore	CGAGGGTAAAAAACAGTAAAACAGGAGTTGGAATTTGGCTTTGAGGACTT	R	TSS1500	TRIP4	0.8701086	0.9035157	-0.033407143	0.8893325	0.9035157	-0.014183
cg01359809	17	72725375	38628452	38628502	N/A	CACATAGTCCTCCCAAGCTCAGAGGGAACCAGGGACCCAGGCCTGGATCG	R	N/A	N/A	0.78555	0.8169529	-0.031402857			
cg01359999	7	46673500	151828356	151828406	Island	GAAAGTGAGAAATGCTCTGATAGACTCACGTACCAAGAAAACACAGAACG	R	N/A	N/A	0.8531357	0.8974814	-0.044345714			
cg01360627	6	71759449	31544931	31544981	N_Shelf	CGCCGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCA	F	Body	TNF	0.7701643	0.8434714	-0.073307143	0.7942125	0.8434714	-0.049259
cg01363572	16	65677475	9203216	9203266	N/A	GAAAGTGGGGCTTTGAATAAACATACCGAGTGAAGTCTGACTTGGCATCG	F	Body	C16orf72	0.8584514	0.9139986	-0.055547143			
cg01363620	7	22603391	45144116	45144166	N/A	TGTGCTCTTGGACGTGGCCTATGCCTATGGTGAGCCCTTTGGACAGAACG	F	Body;TSS200;Body;Body	TBRG4	0.9029257	0.9343043	-0.031378571	0.912965	0.9343043	-0.021339
cg01364621	1	37806399	2389638	2389688	S_Shore	GTGGCCGGCTGGGTGGGGACTCAGGGCAGGACACCGGGCTGCCTGGGGCG	R	N/A	N/A	0.82762	0.8577357	-0.030115714			
cg01367992	1	21652464	160766535	160766585	N/A	CGGGAAACTCATCTCCTTGCCAGAAATTACTTTGCATGTGTGCATATTCG	R	Body;Body	LY9	0.7941543	0.8456257	-0.051471429	0.792695	0.8456257	-0.052931
cg01369413	11	18743393	5530544	5530594	N/A	ATGGCACGGTGCTGCCTCTTGATGACCAGGTGGACAGTGAGGCCATCTCG	R	Body	UBQLN3	0.8491814	0.8863957	-0.037214286			
cg01374580	15	41797369	62521056	62521106	N/A	CGGGGCTGTCTTAGTCAATTCTTGTTGCTATGAAGAAATAACTGAGACTT	F	N/A	N/A	0.8562443	0.9020557	-0.045811429	0.8692563	0.9020557	-0.032799
cg01379969	12	48795403	48166813	48166863	N_Shore	TGGGGGAATGCTGCTAAAAAGGCGGATTCCTGGGCCCATCCCCAGACCCG	F	TSS200	SLC48A1	0.0725844	0.1071084	-0.034524	0.0814564	0.1071084	-0.025652
cg01381846	7	66637365	27204785	27204835	Island	CGGGCGCCTGGGGGTGCACGTAGGGGTGGTGGTGATGGTGGTGGTACACC	F	1stExon	HOXA9	0.2002457	0.2324914	-0.032245714			
cg01384495	8	49734373	10536539	10536589	N/A	AACCGGGTCCCCAGAAACATGTAGGGCTCAGCCTGGGCCTGGAGGTGACG	F	Body	C8orf74	0.9007186	0.9257871	-0.025068571			
cg01386831	17	26674348	79906364	79906414	N/A	CGTGTCCTAGGGCTCGTTTTGTCCCTGGTCCTGCAGGACAGCATGGCAGC	F	TSS1500	MYADML2	0.7369557	0.7873371	-0.050381429	0.766815	0.7873371	-0.020522
cg01391681	7	28702305	141540905	141540955	N/A	ATAGCCACTGAGTCTACCAGGTGTTCCTGAGAAGACAACTAAGCCAACCG	F	1stExon;5'UTR	PRSS37	0.8832986	0.9102414	-0.026942857	0.8912725	0.9102414	-0.018969
cg01395047	3	33638507	52260349	52260399	N/A	AGTTCTTCCCACTCTCCTTCTGATCTAGGTGAGGAGACTCAGATTCCTCG	R	TSS200	TLR9	0.5963371	0.7026657	-0.106328571			
cg01400924	12	24656404	124947742	124947792	N_Shelf	CGCACTTGGAATCTGGATAAAACATACACAGAGGCAGCGCTAGCGATGTG	R	Body;Body	NCOR2	0.8813629	0.9082429	-0.02688			
cg01404893	16	41781427	89043547	89043597	N/A	GAAGGCCCGCGCAGGGCAGGGCCCCAGATGGTTCCTGTCAGGGAAGTGGCG	F	TSS200	CBFA2T3	0.5308114	0.6168486	-0.086037143	0.5927275	0.6168486	-0.024121
cg01408476	16	59600461	58330382	58330432	N/A	TAAACCTCCCAAAGCATTAGCCATTATATAGATATGAGCCACTGCACCCG	R	TSS1500	KLKBL4	0.5813086	0.6731371	-0.091828571	0.6316725	0.6731371	-0.041465
cg01416043	2	13605486	11053694	11053744	Island	CGCTGGGCAAGCTCAACGCGGCCATCAGCTTCTTGTGTGGTGTCATCGCC	F	1stExon	KCNF1				0.8698288	0.89714	-0.027311
cg01416168	1	56799494	48687359	48687409	N/A	CGCACTTAGATATCTGCTCACATGGTCCTTCCAAAGTAGCTGCATTTGGA	R	TSS1500;TSS1500	SLC5A9	0.9152343	0.94677	-0.031535714	0.933365	0.94677	-0.013405

cg01425293	1	33632376	155150019	155150069	S_Shelf	GCTCAGGAGAGTGCTCGAAAAACCCCATGCATAGCTCAAAAAACCCCACG	R	Body	TRIM46	0.85257	0.8822529	-0.029682857	0.8642963	0.8822529	-0.017957
cg01433332	16	72685482	85407575	85407625	Island	CGGTGGCTGCATGTGCGTATGTGTGTGGGTGTCCACATGTGTCAGGTTCA	F	N/A	N/A	0.7467414	0.7937686	-0.047027143			
cg01436254	3	54677432	121796580	121796630	N/A	CGGAGCATGAGTGTAAAGCCCTGGGAAACCCCCAAAGGGAGCCCCATCCA	R	TSS200;Body	CD86	0.7102886	0.76203	-0.051741429			
cg01437781	10	69618400	118563568	118563618	N/A	CGGCCCCTCTGTGCAGCTCCCTACGGTCGACAGGCACATACGCATTTATA	F	N/A	N/A	0.6600471	0.7384143	-0.078367143			
cg01438090	11	12790460	30502936	30502986	N/A	CGCTGATTGCACTGTCAAGAAGGAAAATACTGTTTGAAAAGACAACAGGA	R	Body;Body	MPPED2	0.8451186	0.8988186	-0.0537	0.8788188	0.8988186	-0.02
cg01441865	4	49655375	2275880	2275930	N_Shore	CGCATGCTGCCCCACAGGCCACAAGAGAGAAGATCCGGTCCAGGTTCCAC	R	Body	ZFYVE28	0.9092886	0.9383614	-0.029072857	0.9088963	0.9383614	-0.029465
cg01446731	15	66758462	80770633	80770683	N/A	CGCTTCCCTGGCAGCTTCCCCAGCTGGGTCTCCAGACTGGGTTTCCAAAA	R	Body	ARNT2	0.6690514	0.7328786	-0.063827143			
cg01446989	1	61771359	222566256	222566306	N/A	CATTATTACATAGTATTTTCCCCTGCCCTATTCATTTTCCTGAACACACG	R	N/A	N/A	0.7751214	0.8222514	-0.04713			
cg01449674	10	40600481	31531682	31531732	N/A	CGGGAGATTGGTCATAAGCACAAAGCAGAAGCTGGTCACTCTATCTGAGG	F	N/A	N/A	0.8926043	0.9320114	-0.039407143			
cg01453388	17	28653450	55312649	55312699	N/A	CTCAGGAATGAATGACATACATGCAAATGCTTAGAACAATCCCTGGAACG	F	N/A	N/A	0.8911286	0.9256043	-0.034475714			
cg01457418	15	38635422	75094936	75094986	N_Shore	CGGGCCCAGTGAGCAGGGGCACCAGGTCCATGATCTTCCAGGTTCAGTCC	R	3'UTR;3'UTR	CSK	0.8375929	0.8703257	-0.032732857			
cg01461514	7	69631317	55177182	55177232	N/A	CGGCTTTGTGCTTTGTAGCAGGTCCTTGATTTTTTTGGAGAGGGCCATG	R	Body;Body;Body;Body	EGFR	0.7124757	0.7864071	-0.073931429			
cg01466133	20	44664313	36149022	36149072	Island	CGCAGTGCTCTGGCTCAGCTCCCTACAGTAGCGACCTCCACCGCAGATTC	F	5'UTR;5'UTR;5'UTR;5'UTR;TS	BLCAP	0.8557071	0.9024486	-0.046741429			
cg01467417	2	38705311	113874068	113874118	N/A	AGGAAGTGAAGGCCCCATGGGAAGTCCCTGCGGTCGGGAGCACCCAGGCG	R	TSS1500;TSS1500;TSS1500	IL1RN	0.7275757	0.80208	-0.074504286			
cg01476789	11	16727474	71146764	71146814	Island	GTGGGCTACTACATCTTCCGGGTGGCCAACCACCAGAAGGACCTGTTCCG	F	Body;Body	DHCR7	0.8029343	0.8725529	-0.069618571	0.83466	0.8725529	-0.037893
cg01477971	2	28687307	103405951	103406001	N/A	CGGGTTTTCATTTGCAAGCAAAACCAGTTTGTTCTGTTAAGATATTTAAA	R	Body	TMEM182	0.8516957	0.9129557	-0.06126			
cg01485797	11	44705331	810820	810870	S_Shore	CGAGGCAAAATCGTGATTAACAAGCTTTGGAAGTTTAATACCAGTGAGCT	F	TSS1500;Body	SNORA52	0.1528914	0.2387671	-0.085875714			
cg01486818	1	45635376	2409335	2409385	N_Shore	GGGCTTTCCTGGAGATGCCCCAGGCAGGGGCACAGGCACTCAGGAATTCG	R	Body	PLCH2	0.7562829	0.83579	-0.079507143	0.7939013	0.83579	-0.041889
cg01497589	20	12633342	3640605	3640655	N_Shore	TTGGCTCCCACCCCCAAGGTGTCCTCCACAGGCAGGGCCCTGGAGAGACG	F	Body;Body	GFRA4	0.5775086	0.6444786	-0.06697			
cg01502320	17	52749380	16875558	16875608	N/A	CGCCAGGAGCCTGGGCCGCAGCCACCCACCTGGGCTCCTGAGACCCAATG	R	TSS200	TNFRSF13B	0.7977386	0.8390029	-0.041264286			
cg01502653	20	19674430	6031196	6031246	N_Shore	CCAGCCATCTAGCCTTGCAACTCAGTCCAGTTCAGAGTAGCATTAGAACG	F	Body	LRRN4	0.7748743	0.8564029	-0.081528571			
cg01503299	4	47704335	2963264	2963314	N_Shore	TCGTCCAGTTGACTCCAAGCTTGATAACGCGTGTAGGGGCCGTGAGGCCG	F	Body	NOP14	0.7519686	0.83817	-0.086201429			
cg01503740	16	23649459	1445865	1445915	N_Shelf	CGCGCATCATGCTTTCTGGGTGTCGGTGACCACACACTCAATGGTGTCAC	R	N/A	N/A	0.85787	0.8886	-0.03073			
cg01505111	6	51674457	125621795	125621845	N_Shore	CGTGGGACTCTCTGATAAATATGAAGAAGAAAAAGAAGTTTTAAAGAACA	F	Body	HDDC2	0.6324214	0.7451729	-0.112751429			
cg01512760	22	47792473	43267011	43267061	S_Shore	GTCAATGGTGGGTTACACTGATCTTGTTCCACTGATTACTCTCTCTGACG	F	3'UTR	PACSIN2	0.8876514	0.9429371	-0.055285714			
cg01517571	1	11646346	55089959	55090009	N/A	CAGAGAGATCTGGAATGTGAGGCTGTGATAGGCCACCCGAGGCAGAGCCG	R	Body;TSS1500	ACOT11	0.5795929	0.7242729	-0.14468			
cg01518398	2	26808476	74406523	74406573	S_Shore	GCAACACAGTGAGACGCTCGTCTCTGCAAAAACTTTGAGAAAATTAGCCG	F	TSS1500	MOBKL1B	0.4525486	0.5235429	-0.070994286			
cg01523027	19	27757452	12508210	12508260	N_Shelf	ACTTTGAGTCCACACTCGGCAACACAATGAGACTCTGTCTCTAGGAAACG	R	Body	ZNF799	0.6263271	0.7158029	-0.089475714			
cg01528832	10	67602333	65225240	65225290	Island	TGTCACACAGGGACAGCCGCAATCCGGACCTGGCGGTAAGAGAGTCAGCG	F	Body;Body	JMJD1C				0.1798913	0.0531831	0.1267081
cg01535838	1	13794417	7102397	7102447	N/A	TGGCACCATAGCCTGGGTACCCAGTGTACCATGGAGTGTGGGCAGAAACG	R	Body	CAMTA1	0.8605729	0.9032686	-0.042695714	0.8726563	0.9032686	-0.030612
cg01537713	3	48651475	142606818	142606868	N_Shore	TAGCTCCTAGAATATTTAAATTATAGCCTGACAAAGCATTCAGTCCAGCG	R	Body	PCOLCE2	0.8684514	0.9108271	-0.042375714			
cg01554357	1	70722397	164750454	164750504	N/A	AGGACACTGGGTCTATTTATGGGTGCCCCAGGTCCATTTCAAAACACACG	F	Body	PBX1	0.8950557	0.92867	-0.033614286	0.9146375	0.92867	-0.014033
cg01564943	16	71661455	27853505	27853555	N/A	CTGATATGAAATTTAACACGCGCAACAACGTGCTACTGATGTGAAATTCG	F	Body;Body	GSG1L	0.89512	0.9374743	-0.042354286			
cg01572434	5	48735375	130219926	130219976	N/A	TGATTTACACACATTGACTGCCCTCTGACTCTGTCTTTATTGTCTCTTCG	F	N/A	N/A	0.7833729	0.82445	-0.041077143	0.7966713	0.82445	-0.027779
cg01578764	7	44785446	1024749	1024799	Island	CGGCCCCCTGCTCACCTCTGTAGCCATCCAGCTGCCCAGAGAGGCATTTC	R	Body	CYP2W1	0.8055929	0.8636829	-0.05809	0.8265	0.8636829	-0.037183
cg01581526	7	71779418	100294393	100294443	S_Shelf	CGAGAACAGCCCAGGCAACATAGTGATACTTCAGTCTGTACAAAAATTTA	R	N/A	N/A	0.7794771	0.8538529	-0.074375714			
cg01583595	4	65605372	106525	106575	N_Shore	ACAAGGTTCCTTATCCCTGTGAATTAAAGACATTGAATGAATATACCTCG	R	Body	ZNF718	0.8897086	0.9247957	-0.035087143	0.8859088	0.9247957	-0.038887
cg01588592	1	57702426	157069325	157069375	N/A	GTTGGCTGGGATGCCCTCAGCCAAGCAGCTGCAGTGCATGGTCCACTCCG	R	1stExon;5'UTR	ETV3L	0.8278086	0.8803643	-0.052555714			
cg01589461	1	28738307	1558622	1558672	Island	CGGCCTCCCTGGTGCCAGACTGCGGGCCTCCTTGGGCCCTAGGGCTTGAA	F	Body;Body;Body;5'UTR;Body;	MIB2	0.7927243	0.8430943	-0.05037			
cg01591487	7	42730412	151298634	151298684	N_Shore	CGTGACCCTGGAGTGAAGCTATGAGGGAGGATGCTCTGAGGCTGTACAGA	F	Body;Body;Body	PRKAG2	0.7799829	0.8583929	-0.07841	0.831265	0.8583929	-0.027128
cg01595262	12	21665474	106630712	106630762	N_Shelf	CGAAGTGGCAGGGCTAAGCTTTGGACCTCATCCTTGCTCTAACTGGGACA	R	N/A	N/A	0.88018	0.9203771	-0.040197143	0.8966663	0.9203771	-0.023711
cg01597685	6	12772379	11591981	11592031	N/A	AATTCTTTCTCTTAAGAGCCTCTCCCGGGTGCCGGGCGTGGAGGCTCACG	F	N/A	N/A	0.8305914	0.86019	-0.029598571			
cg01597891	10	21780461	105037796	105037846	Island	TGGCAAACTTGGACTTGTACCATTCTTCCGCGGACTGCAGGTTCTTAGCG	F	1stExon	INA				0.1898288	0.1395716	0.0502572
cg01604404	2	43714439	237460590	237460640	N/A	CCGGCAGATCAAGTAGCCACGGCCTCTGCTCAGAGGCTCAGCTCTGGTCG	R	N/A	N/A	0.7758543	0.8252814	-0.049427143	0.7845825	0.8252814	-0.040699
cg01605921	6	44676396	28545895	28545945	N/A	CGGGTTCACTTGCCTGGCACAGGAAAGCCAAACATCCACATCAACAGGAG	R	Body	SCAND3	0.6760486	0.7840071	-0.107958571	0.73478	0.7840071	-0.049227
cg01606029	1	59601380	2228238	2228288	N/A	GTGTTTTCTCTCTGTTCCTTGTGCTTTGGTGTCATGGAAGCACTTCTGCG	R	Body	SKI	0.9324614	0.9589614	-0.0265			
cg01607321	8	24665433	1872335	1872385	N/A	CGGCCAGGCTCCACGGGCTTCCTCTGTGTTCAGCTGCCTCAACTGATATT	R	Body	ARHGEF10	0.6566843	0.7271043	-0.07042			
cg01614102	12	66709389	115134918	115134968	N_Shore	CAAAGGAAATCGCAGGCGTCTTTGCAAAGCTGGTGGGAAGTAACCCAGCG	F	N/A	N/A	0.5148314	0.6033786	-0.088547143			
cg01615453	7	61659456	2598506	2598556	N_Shore	CTCAATTGAATCTCCTGCCTTAGGCTCCCATAGTGTTGGGATTACAGACG	R	TSS200;TSS200	IQCE	0.2284943	0.2564057	-0.027911429			
cg01617139	19	74621313	2543861	2543911	Island	TTAGAGCCAGATGAAGGTTGCTTCTGTTCTCACGTTGCTGCTGCAGGCCG	F	5'UTR	GNG7				0.068164	0.2041479	-0.135984
cg01617920	13	10642450	49925538	49925588	N/A	CTTCCTCTACAATCGAATCACACAGGCTTTATTCCTCCTTCTCTGTTTCG	F	Body;Body	CAB39L	0.92511	0.9487043	-0.023594286			
cg01618719	12	24735421	131366711	131366761	N/A	CGGGAGTACCTAGAGGTGAGAAATCCGTATAAAAAGGAAAGCAAGAAAGA	R	N/A	N/A	0.8934786	0.9335786	-0.0401			
cg01619562	14	27637394	93500118	93500168	N/A	TGGTCCCCAGGGCCTCAGGAACCAGGGAGGGTTTCTCCTGGAAGAGAACG	R	Body;Body;Body	ITPK1	0.7135971	0.7673871	-0.05379	0.7441388	0.7673871	-0.023248
cg01621943	17	58803420	53531409	53531459	N/A	CGCTGGAGAGAAGAGGAAGTGGGCTTGGCTCTAACTTGCCCTGATCCCCT	R	N/A	N/A	0.6351829	0.7265957	-0.091412857			
cg01627594	6	51782480	159241461	159241511	S_Shore	CGTGCTAGCCTCATAGTAATTGATGCTTAACCTGTCTTCCTAGGGACACA	F	TSS1500	EZR				0.9053825	0.86375	0.0416325
cg01631215	3	67681508	67706047	67706097	S_Shore	AAAGCAACCACAACCTGGAAGGAGACCCCAACTAGGGGCCACTACTGGCG	F	TSS1500	SUCLG2	0.63716	0.7293371	-0.092177143			
cg01639892	6	27793410	22079302	22079352	N/A	AAGAGTGGTTCTTTTAAGTCGGATCACGTCTTTGCTCTGCTCAAACTTCG	F	Body	FLJ22536	0.8681986	0.9182514	-0.050052857			
cg01644798	8	29784305	11617305	11617355	N/A	TTCTCAGCAGAGCTGTAGCTGACTGTGGCATTACTACGCCTCCCCACACG	R	3'UTR	GATA4	0.7318	0.7926214	-0.060821429			
cg01653727	7	51711319	5527669	5527719	N_Shore	TGCTCCACAGCTCTTTGGTGTTTTGTGTCCTCAGGCACAAGCTGAGCCCG	F	Body	FBXL18	0.6661829	0.7430529	-0.07687			
cg01657796	14	39602493	91766373	91766423	N_Shelf	TCCAACAGGCACGGTGACATGCTGAAGCGCAAGGCGGAGCTGGAGGAGCG	F	Body	CCDC88C	0.81207	0.8368414	-0.024771429			
cg01674405	9	65690462	138871595	138871645	N_Shore	CGCCTGCAGCTGAGTCCCTGCTGGCCCCCAGGGTCTAGGTTCTCCCAGAC	R	N/A	N/A	0.7332686	0.7991471	-0.065878571	0.757505	0.7991471	-0.041642
cg01684175	13	29786352	41185353	41185403	N/A	ATGAGTTTTGTTCTACCCTGTTACATAAACAAGTTCTATGTGACCTCACG	R	Body	FOXO1	0.8964386	0.9266129	-0.030174286			
cg01693193	11	33737466	2705153	2705203	N/A	CGTGTCACAGAGCATGCACCTTTGGCCATCTTTTGCATTTATGATTTGGA	R	Body;Body;Body	KCNQ1	0.7219743	0.8088186	-0.086844286	0.7617963	0.8088186	-0.047022
cg01704739	3	53601501	149103190	149103240	N/A	CGATGAATGATTTCAAGGTTAACCTGATGTCTCAAAATTAAAGCTACAGC	F	N/A	N/A	0.7729229	0.8471971	-0.074274286			
cg01706544	21	44743334	46075673	46075723	N/A	CTGAGAGATGGCTCATCCCCCACCGTGTGACACCACCGTAGAATAAAGCG	F	TSS1500;Body	KRTAP12-4	0.9073314	0.9227329	-0.015401429			
cg01713613	20	13783369	60775743	60775793	Island	CGGCCACTGCAGGGAAGACAGGGGCACACGAGGTGACCACTTGGCACACC	R	Body	GTPBP5	0.9148286	0.9450771	-0.030248571			
cg01718742	16	59600455	62070184	62070234	Island	CGGACACCCAGAGCCCAGCGCGCCCGCCCTGCGTCTCCGCACCAAGCCCT	R	TSS200	CDH8	0.1483443	0.0685857	0.079758571			
cg01730064	1	31794432	235362916	235362966	N/A	ACTAAACTTACTCTGAATAGGGCCTGGAATGCCCCCTACCGTTATTTTCG	F	Body;Body	ARID4B	0.4794071	0.5650514	-0.085644286			
cg01732465	11	42711413	2243935	2243985	N/A	CGGCTGAGCTTTGTTCTGGGATGCAGTTAAGATACTTTGGAACAACTTGT	R	N/A	N/A	0.72398	0.7779829	-0.054002857	0.716495	0.7779829	-0.061488
cg01736278	10	37663393	931793	931843	N/A	CGTGTGTCCTGGAAAACTTGAGGATTTTAATTTTATTTAAATAATCATAC	R	TSS200	LARP4B	0.8462129	0.8797229	-0.03351			
cg01743658	14	58745488	31859505	31859555	N/A	TCTCTCAACACAGCAGCAGCATGACATATTATATCACTCGTCTGCTCACG	F	TSS1500	HEATR5A	0.8595471	0.9090971	-0.04955	0.890235	0.9090971	-0.018862
cg01753176	7	69716449	1950147	1950197	N_Shore	CGCTGGGCACTGCCCTGGGGGCTGAGCAGCTGTCTCCATTGGTCATTCAG	F	Body;Body;Body	MAD1L1	0.8771	0.9003271	-0.023227143			
cg01754967	15	71676312	54049269	54049319	N_Shelf	CGTGACACATGTAAATAAAGAAACTCCTGGGTCCCCAAAGTTGATTAGGA	F	5'UTR	WDR72	0.7516329	0.8367414	-0.085108571			
cg01757206	17	36667376	7183913	7183963	N_Shore	CGAACACCTGGATCTGCAGCTCCAGAGAAGGGCCTGGGTCAGATGTCACT	F	TSS1500	SLC2A4	0.0489397	0.0272877	0.021652			
cg01762921	1	28622386	6673618	6673668	Island	ATACTGCGCACAAAGGAAACCTTGGGGACTCCAACCCCCATGAGGCTCCG	F	TSS200	PHF13	0.1007319	0.128505	-0.027773143	0.0930041	0.128505	-0.035501
cg01763602	7	57688392	101559810	101559860	S_Shore	CGAGGGTCTGAGACACCCACACACCTGCCCACGTGTTCTTACAGACCAAG	R	Body;Body;Body	CUX1	0.9332157	0.9512271	-0.018011429			
cg01763692	4	54664462	128064781	128064831	N/A	CGCCTGTCAGTGGGCTTGATAACTACCAGAATTAGGGCTCGAAAGCTGCC	F	N/A	N/A	0.5814643	0.6563757	-0.074911429	0.6014638	0.6563757	-0.054912
cg01767230	6	41721322	88414961	88415011	S_Shelf	CCACCACCTTTAAGTACAACAACACTTTGCTGACTGGGTGCAGTGGCTCG	F	N/A	N/A	0.77979	0.8697714	-0.089981429			
cg01769243	17	24724371	42992917	42992967	S_Shelf	CACCCCCTCAGGCTATGCCAGGGGGTGTTGCCAGGGGCACCCGGGCATCG	F	TSS200;TSS200	GFAP	0.7986229	0.8452757	-0.046652857	0.8292963	0.8452757	-0.015979
cg01772700	19	47740472	56904442	56904492	N_Shore	CGGTTCTAAGTCTTCTGGGGTCTTGTAACTCTCTGAGAACCTCATGAAAC	F	5'UTR	ZNF582	0.3846386	0.4628143	-0.078175714	0.407515	0.4628143	-0.055299
cg01774027	19	22743505	947712	947762	Island	CACCCACGGGGCGGATATTAATAACACTCTCCAGAAATGACAATGAAGCG	F	Body	ARID3A	0.7527214	0.8292057	-0.076484286			
cg01774475	12	39618500	132895447	132895497	N_Shore	CGCCCTCTGCCAGTGGCTGGCTAGGTGCTCAGAGATGACAGTCCTAACGG	F	Body	GALNT9	0.7252	0.7792543	-0.054054286	0.7494125	0.7792543	-0.029842
cg01783650	1	48784457	3310911	3310961	Island	AGAGGGCTGGGTGGGCGGACGGGGGCTGGGCGGCCCTCCTGGATCCTCCG	F	Body;Body	PRDM16	0.6748529	0.7504157	-0.075562857	0.7190363	0.7504157	-0.031379
cg01789743	1	60712334	236159467	236159517	S_Shelf	CGAAAACCCAAAAAACCAAGAAGTACCTACTTGACTGTGCTGGGGGATGC	F	Body	NID1	0.8549914	0.9117429	-0.056751429			
cg01792592	1	34713422	3412973	3413023	N/A	ACCTCTGTGCCTGGCTGTGCTCAAGCCCCTGGCAGACATGGCGCAGGTCG	R	Body	MEGF6	0.7003757	0.7601029	-0.059727143	0.71912	0.7601029	-0.040983
cg01795959	1	23721499	47486850	47486900	N_Shelf	ACTTGCTACAACTCAAAAATATGATTCTGGAGGCCAAAAACAGAGCAGCG	F	N/A	N/A	0.6900514	0.7977271	-0.107675714	0.751655	0.7977271	-0.046072
cg01816880	1	15661304	228404896	228404946	Island	CGGCTGGTGGCAGCCACAGTCACCAGGCAGGATGAAGGCACCTACTCCTG	F	Body;Body	OBSCN	0.8748371	0.9017386	-0.026901429			
cg01819995	20	45634327	30537979	30538029	N_Shore	AGGAGGTCACAGCTGTATAACTCAGCCTTGTGGGAAATTGAAACAGTCCG	F	Body	PDRG1	0.7886914	0.8558286	-0.067137143			
cg01821426	8	29714469	528139	528189	N/A	GAAAGTGTTTTGACGACACATGAAACATGTTCCTAGCCACATGTCTCCCG	F	N/A	N/A	0.8719414	0.91105	-0.039108571	0.8728613	0.91105	-0.038189
cg01824948	14	24682487	102057263	102057313	S_Shelf	CGTGGTGCCCGGCAGCAGCCTCAGTCCTGCCGTCCACACACCGCCTGTGC	R	N/A	N/A	0.8693486	0.8993257	-0.029977143	0.8838863	0.8993257	-0.015439
cg01829002	5	27651401	50259133	50259183	N/A	CCGACGGATAATTCGTGTAAACAACAATATCCCTCAAGATGAGCTCTTCG	R	N/A	N/A	0.094758	0.0726461	0.022111857	0.1055228	0.0726461	0.0328766
cg01831771	13	45743454	113428172	113428222	N_Shore	TGACGCGCATCACGGGGTGTGGAGAGGTGCACCTGTGCGGGATTTCCACG	R	Body;Body	ATP11A	0.8863343	0.93937	-0.053035714			
cg01833470	1	69675483	36270210	36270260	N_Shelf	CGCACATGCCTCCAGGACAGGGTAGGGCATGAGTAAAGAATTGACAACAT	R	N/A	N/A	0.6016014	0.7231843	-0.121582857			
cg01835319	2	70721381	236900893	236900943	N/A	CGGCTCCTCCGCTGCGCTCCTAACCACGCAACATGGACCCAGGAAGACCG	R	Body;Body	AGAP1	0.8749343	0.90651	-0.031575714	0.8886138	0.90651	-0.017896
cg01836096	8	49670426	145578603	145578653	S_Shore	CGCGGTCCACCCTGGGCCGCTCCCTGGCCTCGCTGCCCTGTCAGTCGCCT	R	TSS200	C8ORFK29	0.7391671	0.7729171	-0.03375	0.7398425	0.7729171	-0.033075
cg01838443	21	52609486	15752932	15752982	N_Shelf	AACCTTTCTGGTGAGCAAACCAGAAAAATAAATCAAAAGCCTTAAAAACG	R	Body	HSPA13	0.7079714	0.7894629	-0.081491429			
cg01838544	16	27775352	57576594	57576644	N/A	CTTCTTCCTGCAGAAGCTACAAGACAGCAGCCGAGACAGCAGCTGAGACG	R	TSS200	GPR114	0.6423	0.7227671	-0.080467143			
cg01852186	12	28806510	81192282	81192332	N/A	CGGTTTTCAATCCACTCAGTAGGCCCCAGGGGAGGTTGGGCACATCTCTT	R	3'UTR	LIN7A	0.7975214	0.84687	-0.049348571			
cg01852244	16	24718414	47494711	47494761	Island	AGGACCGGCCATTGGGCAATGGGTTTGGGGAACACCGGGAGAGGCACACG	R	TSS1500;Body;TSS1500	PHKB	0.1805371	0.2086486	-0.028111429	0.1731388	0.2086486	-0.03551
cg01859360	17	29754508	26990458	26990508	S_Shore	CGGTACCACTTTCTGATGTAATTAATCTCCTGATGAAGTTAAAACCTCCT	R	5'UTR	SUPT6H	0.6284743	0.7611029	-0.132628571			
cg01863290	14	35651389	96730669	96730719	N/A	CGCAGCCAGTGGTAGGAGGAAACCCAGAATATTTAACTCCACAATCCTTG	R	Body	BDKRB1	0.8521386	0.9034614	-0.051322857			
cg01870665	14	17657482	24475053	24475103	N_Shore	CGGGTCTGCCTCCCTCACCTGGGACACGGGGAGTTAAATTTGCTTAATCA	R	3'UTR	DHRS4L2	0.7351743	0.79386	-0.058685714			
cg01871722	12	51649440	32120103	32120153	N/A	CGGGATGACACCAAGCCAGATGAGAACACCAAACTGTGGCCATTTTATAG	R	5'UTR	C12orf35	0.7942329	0.8708657	-0.076632857	0.8297425	0.8708657	-0.041123
cg01873637	6	62752358	32180305	32180355	N/A	CGGGCCTCTCTGCAACCTTCCACTGTCCTCCTGCCAGAAGGCTGCACTGA	R	Body	NOTCH4	0.7893643	0.8469	-0.057535714	0.7965013	0.8469	-0.050399
cg01874152	12	15628489	55375859	55375909	N/A	CGGGAAATCCCAGAGTAGCTAACATTTCTCTGTTCATGAACTGGACAAAC	F	5'UTR;TSS1500	KIAA0748	0.8701	0.9351029	-0.065002857	0.91183	0.9351029	-0.023273
cg01875118	14	67741456	105288878	105288928	N/A	CGGCCTTGCCACGCCTCTGCAGTCCTTACACAGAGTGGCCGTGACAGCTA	R	Body	MGC23270	0.82755	0.8745986	-0.047048571			
cg01877700	19	28789398	50452390	50452440	N/A	GGTTCAACCAATTCTCTGCCTAGTCTCCCGAGTAGCTGGGATTTTAGGCG	R	3'UTR;3'UTR	SIGLEC11	0.7826029	0.83033	-0.047727143			
cg01878366	15	35689420	42411135	42411185	N/A	ACAGCTTCTCCTTAAAGAGTCTTGCTTCTGGGATTTGTCAGTCAGCCCCG	F	N/A	N/A	0.5149129	0.6473786	-0.132465714	0.5165438	0.6473786	-0.130835
cg01881182	16	64809506	8806531	8806581	N/A	CGTCAGCCCCCAGCCCCCAGCCCCCAAATCGGGGCAGAACAAGGGCCAAA	R	5'UTR;TSS1500	ABAT	0.6541357	0.7560043	-0.101868571			
cg01881474	1	36602329	48242657	48242707	N/A	ACCTGTGGCCGATGATGGCTTTTATTGTTGGAGCCTCCTCAGCATTCCCG	R	N/A	N/A	0.8087229	0.8629143	-0.054191429	0.8436188	0.8629143	-0.019296
cg01887138	6	21793357	151687264	151687314	N/A	CGGCTTCAGGCACTTCCATGGCATCTTTCCCGAGGTCAGCTGCATTGCTA	R	Body	ZBTB2	0.8784129	0.9121657	-0.033752857			
cg01897944	17	40673448	67633729	67633779	N/A	CAGCCACGAGGGAGCACATCCATGTGAGAATCTGAGGAAACAGTGCAACG	R	N/A	N/A				0.8039563	0.8660729	-0.062117
cg01903374	1	50796326	151129844	151129894	N/A	CGGTCACAGCCACATCCTGCAGAGCAGAGGAGGGGGAAGTAAGAAGCAAA	F	5'UTR	TNFAIP8L2	0.72727	0.8092643	-0.081994286			
cg01904296	11	45777383	45713046	45713096	N/A	GCCTCAGGAGCTCCACTGCCTTCAGAACCTAATTTCTCAGGACAAAGACG	R	N/A	N/A	0.7115271	0.7698086	-0.058281429	0.7469713	0.7698086	-0.022837
cg01906055	2	74706437	97000811	97000861	N_Shore	CGGTCCAGGTGGGGAAGAACTGATGCAGAAATGCTATGTATACATTAAAT	R	TSS1500	NCAPH	0.8119443	0.8891443	-0.0772	0.8524713	0.8891443	-0.036673
cg01909364	17	17611326	41739926	41739976	N/A	CATTCTCACTTTCTCAGTAACTTAAAAAAACAATCAGATTCTTCCTTCCG	R	TSS1500;TSS1500;TSS1500	MEOX1	0.7967443	0.8861743	-0.08943			
cg01909681	1	10708413	42550741	42550791	N/A	CGGAAAAATCAGCAACTCAAAATCTGTCAGAGAAATGAGGTCACAGGACA	R	N/A	N/A	0.8006829	0.8489871	-0.048304286			
cg01913970	1	56660456	45308593	45308643	Island	CGCCGCCCCTCAGAGAGCTGCCCCCGAGTTACACACCCCCAGCTCGAACC	R	1stExon;1stExon	PTCH2	0.1619271	0.0997323	0.062194857	0.1462559	0.0997323	0.0465236
cg01916058	7	61612337	99016932	99016982	N_Shore	GGAAGGGTTTCTGAGGTGTGTCCCTATATGGCATGGTGGCAGGTCCTTCG	R	Body;3'UTR	BUD31	0.7837929	0.6473543	0.136438571	0.7321513	0.6473543	0.084797
cg01918001	12	53621350	13687295	13687345	N/A	CGGTTGGTTACAGAATAAATACGCCAGTAGCTCATGCAGCCTTTTCTTAA	F	N/A	N/A	0.82715	0.8920129	-0.064862857	0.8554675	0.8920129	-0.036545
cg01918081	7	14791370	98988510	98988560	N_Shore	GTGCCGGCCGTTCCTCCACCTCCTTGATGTAGGCTGAAAAGATCCTACCG	F	Body	ARPC1B	0.8613314	0.8955471	-0.034215714			
cg01935122	15	40673368	41234390	41234440	Island	CGGGCAAAATGGGGAGAACCCAGTGCGGGGCTTTCCCCCAAATATCCTCC	F	N/A	N/A	0.087342	0.1316743	-0.044332286	0.098813	0.1316743	-0.032861
cg01935149	14	69604403	33403900	33403950	Island	GGCGGCAGCAGCGGAGCCAGGCACCAGCCTGCAATCCCATTAGTGAGCCG	F	N/A	N/A	0.126202	0.0840903	0.042111714	0.1047626	0.0840903	0.0206723
cg01936220	13	55791389	114906016	114906066	N/A	ATTGTCTCCCAATTTCTTCGTCTGTAAAATGGGGCTGGCAGCAGTGCCCG	R	N/A	N/A	0.7707343	0.8237429	-0.053008571			
cg01937212	6	18616404	32295097	32295147	N/A	CGGAAGGAACACAAAATGGAGAAATCAACATGTGTAGAACCAAGTGAATT	F	Body	C6orf10	0.67614	0.7295714	-0.053431429	0.675215	0.7295714	-0.054356
cg01941663	1	31755494	38476345	38476395	N_Shore	CGCATTTCTCATGACAGGGGTCACTCCTCCAGCTCAGGAGCTCCAGGGAA	R	N/A	N/A	0.8229343	0.87921	-0.056275714	0.8432063	0.87921	-0.036004
cg01945625	16	35758394	1437845	1437895	N_Shelf	CGGGGTCTGCCCAGGTCCGTGCTCTGGGGCACGGTCCCTACACACAAGCT	F	N/A	N/A	0.7579857	0.8024329	-0.044447143			
cg01945913	5	43779453	1469001	1469051	S_Shore	CGAGACTGCTCCGTGGAAGCCCTTCCTGCTACATGCAGTCCCCCCAAAAT	F	Body	LPCAT1	0.8908914	0.9135986	-0.022707143			
cg01947066	15	58678303	74289586	74289636	N_Shore	CGCAACTCTCCATGCCTCAGTAACAAAAGGAAGAGAGGCTACTCTCTTTG	R	Body;Body;Body;Body;Body;B	PML	0.5009714	0.6919743	-0.191002857			
cg01950077	6	54765367	109610932	109610982	N_Shore	CCTCAACCAATTTAGCAACATTAAGAACAGTCTGGCCTTGAAGAAAATCG	F	N/A	N/A	0.6349957	0.7039171	-0.068921429	0.6288725	0.7039171	-0.075045
cg01973390	7	59789509	112030679	112030729	N_Shore	TTGCTGCTTTTCAAGGCACTGTCCACATATTATTTTATGAGGCCTTCACG	F	N/A	N/A	0.93103	0.9579157	-0.026885714	0.9459588	0.9579157	-0.011957
cg01980928	19	21702498	1952821	1952871	N_Shore	CACGAGGGCTGCAGAGTGAAGGGCACAGCAGGGTTCGGCCTAACTCCCCG	F	3'UTR;5'UTR	C19orf34	0.8698643	0.9018057	-0.031941429			
cg01986630	16	52751348	53946263	53946313	N/A	GACGCATGTCAGTGCATCTCTGAAGTTAACACATAAAACCACAAAACACG	F	Body	FTO	0.7487043	0.8325771	-0.083872857			
cg01987702	2	56635390	74264707	74264757	N/A	TAGCAGGGTGGGGTGTTGCCACCACTATCTTGGAGTCCCATGAGAATTCG	R	N/A	N/A	0.6940386	0.81012	-0.116081429	0.7515513	0.81012	-0.058569
cg02002207	16	11679350	89913618	89913668	N_Shelf	CGCCCCGAGGTTCTCCACGGTGGCAGGTGCCTTATCACTGAATTGTTAAG	R	Body	SPIRE2	0.8724686	0.9062171	-0.033748571			
cg02003612	16	45722496	8622412	8622462	S_Shelf	CGTGCAAGGCTGTGTGCTTTGTTCTTGTTGTTTGTTTTGTTTTTGAGACA	F	TSS200	TMEM114	0.5998743	0.6443271	-0.044452857			
cg02006421	1	19790369	27707622	27707672	N_Shore	CGGGAGCTGGGACCACTGTTTGCCCTTCATATTGTCAGACTCCTTCCACC	R	Body	CD164L2	0.9140686	0.9351643	-0.021095714	0.9039925	0.9351643	-0.031172
cg02006426	2	24780366	72012453	72012503	N_Shore	CGGGCAGGACACTGCAAACAGCTTTTAGCTGGGTGAAGATGAAGGAGAAC	F	N/A	N/A	0.7818229	0.8379943	-0.056171429	0.8163213	0.8379943	-0.021673
cg02006915	5	32685473	175991129	175991179	N/A	AACATAGAGCATACAGACAACTTTCTAGACAGACAGCAAGAAACAAAACG	R	5'UTR	PCDH24	0.5511871	0.6571829	-0.105995714			
cg02009395	16	11695383	20702744	20702794	N/A	TTTTGGTGGGGATTTATCTTCCCAGCTGAGGAACCACATGGCAGAAAACG	R	TSS200	ACSM1	0.6648957	0.7507886	-0.085892857	0.70878	0.7507886	-0.042009
cg02014853	6	29671434	29595335	29595385	Island	CGCCATCTCCACCGCGGGCTGGCAGGCCTGGCCCCCTGGCCAGCCCCCGC	F	Body;1stExon;Body	GABBR1	0.3049671	0.2324343	0.072532857	0.2741688	0.2324343	0.0417345
cg02016094	7	20793439	44345367	44345417	N_Shelf	AGACAGGGGCGAGAGGCCTTGGGTGCCGTCTTGGCTCACTCCATCACTCG	R	Body;Body;Body;Body;Body;B	CAMK2B	0.8593871	0.9024114	-0.043024286	0.86664	0.9024114	-0.035771
cg02021288	16	39674398	11435867	11435917	N_Shelf	AGTTTCCCAACCTCAGCCCTACTGACACTGGGGCTGGATAATCTTTGTCG	F	N/A	N/A	0.7982	0.8825329	-0.084332857			
cg02021641	17	14737436	7758692	7758742	Island	GGTGTGTGGTGATGCTGGCGGTGGGGTCTATGGGCCACAACTTCAACCCG	R	Body	TMEM88	0.6571971	0.7376529	-0.080455714			
cg02022488	14	25755365	102702045	102702095	N/A	AAATGGATGTAAAGAACAATAGTTCCTTCCCGGGAGGCGGGATCGACACG	F	Body	RAGE	0.8344957	0.9008129	-0.066317143			
cg02025879	16	65658504	22326203	22326253	N/A	CGTGCCTGCCCAGCCCAGAGGCTTGAGGGGGATTAGAGTCCCAGGCGCCA	R	Body	POLR3E	0.8264686	0.8714457	-0.044977143			
cg02026611	16	69755335	2826048	2826098	N_Shore	CGGCTGGCTGGTAGTTGAGCCTTTTGATGCAAAGTTTCCTCATCTGTAAA	F	Body;Body	TCEB2	0.7210671	0.7926171	-0.07155			
cg02028524	14	52717303	92573410	92573460	S_Shore	ACCCAGCACTTGTATAAAAATGATAGCTAGGCCGGGCGAGGTGCTTCACG	R	TSS1500;TSS1500;TSS1500;	ATXN3	0.7472743	0.8180157	-0.070741429			
cg02033124	14	41671339	54553150	54553200	N/A	AGCAGATGCCTGCAGAACACTTTGTCATCATAAGACCAGGAGGATCCACG	F	N/A	N/A	0.8512314	0.8968371	-0.045605714			
cg02042623	12	41710428	104227548	104227598	N/A	GGCCTGTCCTGTTAGGTACAGAATGGAAGCCTTCCTACTCCTCCAAGACG	R	Body	NT5DC3	0.8769314	0.9164757	-0.039544286			
cg02044621	11	57728432	62452831	62452881	N_Shelf	CGCCTTGTTTGCCAGGCTGGTCTTGAACTGACATCAGGTGATCCGCCCTC	F	N/A	N/A	0.5366243	0.6129786	-0.076354286			
cg02051688	11	37719346	111568985	111569035	N/A	CTTTCTTTGTGCTAGATTTGTAAAGCAGAGGTTGAAACTGGGCTACCACG	R	Body	SIK2	0.8841043	0.9331986	-0.049094286			
cg02059928	15	59603301	57731108	57731158	N/A	GGCACATTCCTGATCATCCAGTAAAAACCTGTACAAAGAGTTGGCTGACG	F	Body	CGNL1	0.9383029	0.96723	-0.028927143	0.9558525	0.96723	-0.011377
cg02061553	1	49788308	3370110	3370160	N_Shore	CGCCCTCCACCCACTAGTCCCCCAATGTCTGCCCTGTGGCTGGGGCTGCCTG	R	TSS1500	ARHGEF16	0.7607271	0.83804	-0.077312857			
cg02061660	5	56741407	110088130	110088180	N/A	CGCGAGGTAGGAGTTCCTGTAACCAAGGCTACCTGTGTGGTTCAGTCTCT	F	Body	SLC25A46	0.7756857	0.8488357	-0.07315			
cg02063827	6	46727304	33878127	33878177	N/A	CTCAGTTCCATTGCAAGCTGCAAGACACAGTGGGGCTCTGAGACCAAACG	F	N/A	N/A	0.81416	0.8595829	-0.045422857			
cg02066590	22	35733405	47016623	47016673	N_Shore	CGGCCTTGGGAGGGAGCCTGCCTTTCAAGATCAAGATGGCTCCAGAAGAG	R	N/A	N/A	0.8410386	0.8699914	-0.028952857			
cg02067239	16	61652310	22776055	22776105	N/A	CGTGCTTCCAGGGGCCTGTGAACCTGTCCAGAACCGGCCTCAACTTTAAT	R	N/A	N/A	0.6524343	0.7332671	-0.080832857	0.6865925	0.7332671	-0.046675
cg02068923	14	11630439	61547469	61547519	N/A	CCAGTCGGGTGGGTGTGATTTGAATGTTCTCTGCTACAGCTGCTGCACCG	R	N/A	N/A	0.8525471	0.8972143	-0.044667143	0.8796838	0.8972143	-0.017531
cg02072940	6	27787351	31656126	31656176	N/A	CGGGTGACAACTGGCCCACCCCTATCCCTGCACTGGTAGCATTCTTACCC	F	Body	BAT5	0.75595	0.80015	-0.0442			
cg02074930	14	26633389	75423089	75423139	S_Shore	ACTCAGGCATCTCCTCCTGGTCCCTGGCCGAGGAGGAACTGTACGCTGCG	R	TSS1500	PGF	0.85336	0.91078	-0.05742			
cg02088237	6	48600314	39304008	39304058	N/A	GATGGTGCTATTTCACATTCTCAAAAGCTTATAAAGATCTACACAAAACG	R	3'UTR	KIF6	0.3068814	0.4049929	-0.098111429			
cg02091607	16	54637498	30760815	30760865	S_Shore	CGCGCCACCACGCCGGCTAATTTATATTTTTAGTAGAGGCGGGCGTTTCA	F	Body	PHKG2	0.8345457	0.8787286	-0.044182857	0.8546738	0.8787286	-0.024055
cg02094042	3	38602466	38223776	38223826	N/A	CGTGCGGCAATGTCAAGCCAATCTGCCCTTAGCAGCAGCAAAGCCAGGGC	R	Body	OXSR1	0.89645	0.94371	-0.04726			
cg02095334	6	21626391	33138108	33138158	N/A	CCAGACACATTGGTCTCAAGGGACAGGGGCTGAGATGACTCACATCAGCG	R	Body;Body;Body	COL11A2	0.8957843	0.9288143	-0.03303	0.9119813	0.9288143	-0.016833
cg02096229	6	34751471	28555929	28555979	S_Shore	AGGCACACAGACAAAAATTTTATACAGAATTTTACTCAAGACCATTCACG	F	TSS1500	SCAND3	0.7529843	0.8552914	-0.102307143	0.796005	0.8552914	-0.059286
cg02098313	6	44717357	128222378	128222428	N/A	CGTGCTAAGTAGCGCATTCTGTCCTTTGTTAATCCAGGTGTGCATCTACT	F	5'UTR;TSS200;TSS200	THEMIS	0.6844957	0.7632214	-0.078725714	0.7052525	0.7632214	-0.057969
cg02104648	15	54721306	44121440	44121490	S_Shelf	CGGCGCTCCTGGTAGGCAGCAGAAGCCAAAAGAATTACAGACCAGGCTGG	R	Body;Body	WDR76	0.8934414	0.9324286	-0.038987143	0.8961738	0.9324286	-0.036255
cg02108033	4	57650393	17783294	17783344	Island	CAAGGGGAGAGCTTCCGCGGCTAGGAGCTGCCGGCCTTGGGGGGTTTGCG	R	TSS200	FAM184B	0.0868731	0.0469096	0.039963571	0.0717654	0.0469096	0.0248558
cg02114909	17	43691432	1294652	1294702	N/A	CGTTGTCCAGCTTTTTATCACAGAGATAGCTTAGATCTACGTCTCTAGGA	R	Body;Body	YWHAE	0.2025771	0.3390457	-0.136468571			
cg02116131	17	74799327	1175360	1175410	S_Shore	CGGGGCCTGGGAGTCTAAGGATGGGGTCAGCCCCGTCTCTGGACCTCCCT	F	N/A	N/A	0.73613	0.78928	-0.05315			
cg02117416	1	68683503	205897545	205897595	N/A	CGCTTGTCCTGCAGGGTTGGAACAGGCAAGGGAGGGAAGACCACATAGCA	R	Body;Body;TSS200	SLC26A9	0.85975	0.8819129	-0.022162857			
cg02120735	16	19674499	89032995	89033045	N_Shore	ACTCAGTAGTGGAAGCAGTAGAAGCACCCGGTGCCAGGCCCTGCCCAGCG	R	Body	CBFA2T3	0.7832857	0.8151657	-0.03188			
cg02123534	7	48647378	965485	965535	N_Shore	CGCCCTCCGTTGACTCACTCCGTGAACCCACTCAGCAGAGGGCCCACCCCC	R	Body	ADAP1	0.7527557	0.8349814	-0.082225714	0.78722	0.8349814	-0.047761
cg02124149	1	31709445	92413007	92413057	N_Shore	CGGAGGAAGGATGAAAGAGCCAATTGTAGAAGCCCAGAGACAAAGGATAG	F	N/A	N/A	0.7444071	0.8072743	-0.062867143			
cg02127509	6	17800429	135516936	135516986	N/A	CTCCCAAACAGGAAACAGGTGCACTGTCTCCATGAGGTCTGGTGTGGTCG	F	Body;Body;Body;Body;Body;B	MYB	0.8040086	0.8553486	-0.05134			
cg02127888	16	33756468	1665900	1665950	S_Shore	TAATATATTTCCTTGTCAAAACTACCAGGACCATTCACTAAATGTAAACG	F	Body	CRAMP1L	0.7034257	0.7638814	-0.060455714			
cg02131512	16	70769412	29882803	29882853	N/A	CGAGGGGCCTGCCCCCCGCCCTACCGGCTTTTGGATTCTGGGAGGGGGAAC	R	3'UTR;3'UTR;3'UTR;3'UTR	SEZ6L2						
cg02137984	6	55709509	31545898	31545948	N_Shelf	CGGAGCTGAACAATAGGCTGTTCCCATGTAGCCCCCTGGCCTCTGTGCCT	F	3'UTR	TNF	0.9140329	0.9507071	-0.036674286	0.928835	0.9507071	-0.021872
cg02143988	8	17733468	32785240	32785290	N/A	CGGGCCCTCTTCCAGGTGCTTTGCATGGATTAACATTTTAGTAGATGGCT	R	N/A	N/A	0.7255743	0.7713886	-0.045814286			
cg02150218	6	60801338	157341044	157341094	N_Shore	CGTCCAGATACACCCAGATTTTCTTTTGGCTTGGTGGGAAGAATGAATGG	R	Body;Body;Body	ARID1B	0.6872871	0.75743	-0.070142857	0.72717	0.75743	-0.03026
cg02156570	1	17701503	208196481	208196531	N/A	GAAAATGCAAAGTGGCTTCACAGACACAGGGCTGTGGGAGCAGATCGACG	F	3'UTR	PLXNA2	0.8587214	0.8833643	-0.024642857			
cg02156952	1	13600426	201193569	201193619	N_Shelf	TGTAGAGGTGTGACGTGGAGGGCACTTTGCATTTTTGCCGAACCTCTTCG	R	Body	IGFN1	0.8529957	0.8973543	-0.044358571			
cg02167713	17	41746394	79630115	79630165	N_Shelf	CAACCTGAGCCGGTGAATGAATTCCTCTCTGCTGGGCGGCCTTGCCGACG	F	N/A	N/A	0.81594	0.9068171	-0.090877143	0.8595638	0.9068171	-0.047253
cg02178957	16	38696405	85964200	85964250	N/A	CGACCTGTCATCTATTCTGGTCTCTGAAGGGCCTTTGTGCGCCTCTTCTG	F	N/A	N/A	0.8385671	0.8898429	-0.051275714			
cg02179478	3	12677344	35785377	35785427	N/A	AGATGCCTGTATATTATTACCCATCTGGTCAGTACCCTACCTCAACCACG	R	TSS1500;Body	MIR128-2	0.8851371	0.9180671	-0.03293			
cg02180633	4	50739304	680114	680164	Island	CGGGTCAGGAACGCTGCCACCAGCCCAAGTGCCTGCCCCGTCCCCCGAGC	F	Body	MFSD7	0.9030629	0.9223957	-0.019332857			
cg02196805	5	45635451	131409637	131409687	N/A	CTCTCACTTACCATCTCAGCAGCAGTGTCTCTACTCAGGTTCAGGAGACG	F	1stExon	CSF2	0.8004571	0.86641	-0.065952857			
cg02208432	11	63604368	76571458	76571508	N_Shore	GACACTTACACCTTTATCAGAAAATCACGGTTTATTTCCTGAGAATCACG	R	TSS1500	ACER3	0.6328843	0.7197957	-0.086911429			
cg02212934	16	63713346	90072563	90072613	S_Shore	CGGGTCTTCGCCTCACTTGGAGACCAGCCGGCTTTCCTGGGGGACACACG	R	3'UTR;3'UTR	DBNDD1	0.8285114	0.8684686	-0.039957143	0.8481663	0.8684686	-0.020302
cg02213045	6	65691346	43967803	43967853	N_Shelf	CGGTTACAATCTAGGCAATGTATGCTCCACTGCACTGTACCCACATGTGC	R	TSS1500	C6orf223	0.91626	0.9423386	-0.026078571			
cg02213214	7	52761313	7170845	7170895	N/A	GGGTGCTGGCGGAGCTTCCTCAGAGAACCTTCATTGCAGCCTTTCCACCG	R	N/A	N/A	0.8921829	0.92733	-0.035147143			
cg02216481	17	28795450	7942137	7942187	N/A	CGTGGTGGGCACAAATCTACCCCCACCCCAACTGGGTCCCAACTCTAGGC	F	TSS1500;TSS1500;TSS1500	ALOX15B	0.6027857	0.6937614	-0.090975714	0.6515888	0.6937614	-0.042173
cg02219476	15	42630317	63115816	63115866	N/A	TCATCAAAGACCATGAGCCATTCTCCTTTAAAAACAGGCAACCTGAGACG	F	TSS1500;Body	MIR190	0.8855857	0.9208814	-0.035295714	0.9030825	0.9208814	-0.017799
cg02220365	11	72729346	67211717	67211767	N/A	CTGCTGTTGTTTTCTTTACATTGTTAACCAAGAGCATGAAATTTAGGCCG	F	TSS1500;TSS1500	CORO1B	0.4649586	0.5998229	-0.134864286	0.5597188	0.5998229	-0.040104
cg02223905	3	17804318	46720206	46720256	N/A	CGCCTGAGGAGGGCGGTGTCTTGCCACATGAGGCTGTCCCATTCATAGCA	F	TSS1500;Body	ALS2CL	0.8218457	0.8719771	-0.050131429	0.8367475	0.8719771	-0.03523
cg02229382	22	52628362	49765138	49765188	Island	CAGTTCTGTGGCCACAGCCTGGCTGTGTGGCGATTCTCAGCTGAGGACCG	F	N/A	N/A	0.5384429	0.6427443	-0.104291429			

cg02229607	7	48600485	2759813	2759863	S_Shore	CGGCTCCTCTGCTGACATGGACCGGTTCATCTACCCACGCGGACGCCCAT	F	N/A	N/A	0.8692057	0.8998143	-0.030608571	0.8854425	0.8998143	-0.014372
cg02234120	2	47608508	234626351	234626401	N/A	CATCAGCAATCTTGCGAGCACATGTAGGAGTGACTTTCTGGAGCAGGACG	R	Bodv:Bodv:Bodv:Bodv:Bodv:T	UGT1A10	0.8381657	0.90206	-0.063894286	0.86869	0.90206	-0.03337
cg02234847	16	57773401	30674533	30674583	S_Shelf	AAGAGCGCTGGCTTTGGTGTCAGACCCAGATTCAAATTCTTGCTCTGACG	R	TSS1500	FBRS	0.7398643	0.8360229	-0.096158571			
cg02243630	4	59795312	154386540	154386590	N_Shore	CGCTGGTAAAGGCAGGATGTTAACTTAAAGAGATGCCAGATTTTGGACTT	F	TSS1500;TSS1500	KIAA0922	0.6795371	0.7755729	-0.096035714			
cg02245191	17	57808374	77816139	77816189	Island	CCCAGCAGAAGGCTCTGGGAATCCCAGGTGTAGGGCTAGTTTCTCCTGCG	F	N/A	N/A	0.2144857	0.2852471	-0.070761429			
cg02255510	2	27642466	37310396	37310446	N_Shore	CGTGAAGAGATTATGTGGTCATGATTCTTAAGAAAACACATGTTATGTTT	R	Body;TSS1500	HEATR5B	0.7586929	0.8569714	-0.098278571	0.816005	0.8569714	-0.040966
cg02255914	17	47809464	8700574	8700624	N_Shore	AAAACTCAGCCTGCTGAGGACAGAAACCTGCCCTGGACTGCTGGGAGCCG	F	1stExon;3'UTR	MFSD6L	0.7347186	0.7993129	-0.064594286			
cg02259047	14	13787500	104175555	104175605	N/A	CGCCGTTCTGATTCGCACATGCTCTGCCCCCTGCCCTGACTGCCCTGCGC	R	Body;Body;Body	XRCC3	0.8917129	0.9154686	-0.023755714	0.8919438	0.9154686	-0.023525
cg02274103	17	72768459	78078650	78078700	N_Shore	GCCTCGCACTGTTCCTGGGTGATGGCCTTGTCAGGGGCGCAATCGAAGCG	F	Body;Body;Body	GAA	0.8726971	0.9203714	-0.047674286	0.9055788	0.9203714	-0.014793
cg02278319	16	15646493	596009	596059	Island	CGGGCTTCTGTGAAAGCCCAAGCAATCTGCCCGTAGACAGCCAGGCCTCT	R	5'UTR	SOLH	0.8328029	0.8626714	-0.029868571	0.8441238	0.8626714	-0.018548
cg02278646	12	59795334	45608691	45608741	N_Shore	CGGAGCACACCACCATGTGGGGCTTATTCTTAAATTTTTTTGTAGAGATG	R	TSS1500;TSS1500;5'UTR;TS!	ANO6	0.6270986	0.7586171	-0.131518571	0.7181863	0.7586171	-0.040431
cg02299465	6	25704350	33247509	33247559	S_Shore	CGGGCCTGGGCATTCAGGGGCCTGCTCCATACCAGCCTCTCTATCTGCTC	F	Body;Body	WDR46	0.8200871	0.8641186	-0.044031429			
cg02302730	8	36771417	142526477	142526527	N_Shore	CGGGTTTTAATTTCCAGTGCTTCACTAAAGCAGCTCTAGCAAAAGTCATC	F	N/A	N/A	0.8883871	0.92918	-0.040792857			
cg02304614	6	29612358	33131336	33131386	S_Shore	CGCCCTGGCCCAGGGCTCCCTAGATAGTGAGGAGCCCTCTTGGGAGGTGG	F	3'UTR;3'UTR;3'UTR	COL11A2	0.7681571	0.8195657	-0.051408571	0.7985688	0.8195657	-0.020997
cg02310103	3	29795494	50391305	50391355	S_Shelf	CGGGCCTCCAAATGCCCAACTGTCCCAGTGCCTGAGGTGTCCCCTGACTC	R	3'UTR	CYB561D2	0.4555557	0.5427929	-0.087237143			
cg02319549	19	39651403	10463037	10463087	N_Shore	CGCGCCTGGCCCAGCCTATGCCTTTCTAATTGCTCTAGCAAACTCCCGGT	F	Body	TYK2	0.8462	0.8843829	-0.038182857			
cg02321903	11	16807383	60926056	60926106	N_Shelf	TTCCGCTGATTTATCTGGTCCCACCTCAAGCAGGATTACAACTAGTCACG	F	5'UTR	VPS37C	0.8652771	0.9158471	-0.05057			
cg02323277	12	27760306	115109504	115109554	Island	CATATAAACCACGCCAAGAAGACAGGGGCTGTCTCTAGCACATTCTCTCG	R	3'UTR;3'UTR	TBX3	0.6083557	0.6761229	-0.067767143			
cg02326386	19	71664352	2085286	2085336	N/A	TTCTCTAGAAGTTTCCAAGGGTCACTTGTGTCTCGTCCGTGGGAAGACCG	F	5'UTR	MOBKL2A	0.7206971	0.8130443	-0.092347143	0.73464	0.8130443	-0.078404
cg02327773	7	16744320	70258726	70258776	S_Shelf	CGCCCTGGACTGACTTTTCCAGTGCCTTGGATGCACTTCTCAGATGCCCC	R	N/A	N/A	0.8970857	0.9434543	-0.046368571	0.9141838	0.9434543	-0.029271
cg02328239	5	53778470	37837463	37837513	Island	ACCAAGCTCTGCTCCTCAAGTGACGGGGGCTCTGCTCTGCCAGGTGACCG	R	5'UTR	GDNF				0.2734975	0.2053429	0.0681546
cg02329140	1	38772311	232668750	232668800	N/A	CGGGATTTAAAGATCTGTACAGCTAATGTCATTATGGAGCATTGTACCAC	R	N/A	N/A	0.8705457	0.9338714	-0.063325714	0.9073713	0.9338714	-0.0265
cg02330726	10	44602425	14664149	14664199	N/A	ATAAAGTCCATCTTTCAATATTCATTCAATAAACATCCATGCATCCAACG	R	Body	FAM107B	0.7517114	0.80242	-0.050708571			
cg02332206	3	33666483	47933600	47933650	N/A	CGGAGGTCTTCTGGTGTACCGAGTTCCCCTCCAAGGGATGGCAGGTCTCT	F	Body;Body;Body;Body	MAP4	0.8602529	0.8887957	-0.028542857			
cg02335306	11	62713488	2559880	2559930	N/A	CGGTTCCAGCCCAGGATTCCTATGTACTCGGGGAACGTTCCGGTTCCAGC	R	Body;Body	KCNQ1	0.8516071	0.8922014	-0.040594286	0.8660775	0.8922014	-0.026124
cg02338162	10	19622508	43844651	43844701	N_Shore	AGGAAGAGCTCTTCCCTTCCCCATCATGTGGTGTCTAGACAGTCTTCCCG	R	N/A	N/A	0.7687643	0.8335857	-0.064821429			
cg02341480	1	32743417	235267474	235267524	N_Shore	CGTGAATTAAAATTCTAGATGGGAAACTACCAGACAGGAGAAGATAATTG	R	N/A	N/A						
cg02346997	19	11633307	7733883	7733933	N_Shore	CGGTCCCACATCCGGGGCCAAGAGGAAGCCCCTGAGCAGACAGTAAGGGC	R	TSS200	RETN	0.7117229	0.7710114	-0.059288571	0.7164213	0.7710114	-0.05459
cg02347074	2	57713329	223155925	223155975	Island	AGACTGGAGCAGAGGCAGCCGGGGGAGCCAAGTCCTGGCCGAGGCATCCG	F	Bodv:Bodv:Bodv:Bodv:Bodv:B	PAX3	0.2328429	0.1841414	0.048701429	0.2463913	0.1841414	0.0622498
cg02349669	5	16696319	115155524	115155574	S_Shelf	CGCCTGTAGTCCCTGCCACTCAGTAGGCGTAGGCAGTAGGCTTGCCTGAG	R	N/A	N/A	0.1002294	0.1585829	-0.058353429	0.1201578	0.1585829	-0.038425
cg02357714	5	25653399	176936563	176936613	N/A	CGGCCCTGCTCCTGGCCGTGACCATGGACCCTCTGGAGACCCCTATCAAG	R	Body;5'UTR;5'UTR	DOK3	0.5626586	0.6242786	-0.06162			
cg02362859	5	56677503	13473755	13473805	N/A	CGTGAATTTGTTTCTAATCTTAAGGTATTCTGAAAGCAACTGATTGAATG	F	N/A	N/A	0.6985614	0.7815743	-0.083012857			
cg02378063	4	24702441	22913868	22913918	N/A	GTTTCACATCTAAAATACTAGTTTTTCTGTGTCCCAGTGGAACTCACTCG	F	N/A	N/A	0.8776829	0.9208743	-0.043191429	0.894305	0.9208743	-0.026569
cg02380983	19	31618341	48568071	48568121	S_Shelf	CGAGGATATGAGAAGGTGGCTGTCTGCAAATCACAGAGAGAGTCCTCAGA	F	Body;Body;Body	PLA2G4C	0.6116943	0.7093614	-0.097667143			
cg02382795	7	10634319	73021225	73021275	N_Shore	GGCATCCCTTTGCCCCCCAAGTAGATGGGAGGCAGAGTTGACAGTTTCCG	F	Body;Body;Body;Body	MLXIPL	0.7104629	0.8314743	-0.121011429	0.749305	0.8314743	-0.082169
cg02386957	13	48649435	111838481	111838531	N/A	CGCAGCCCCAACAGGCAGGGGAAAGGAAGGACACCTCCCTGCTTAGGACC	R	Bodv:TSS1500:5'UTR:Bodv:B	ARHGEF7	0.9276529	0.9544843	-0.026831429			
cg02388849	10	56797425	71509218	71509268	N/A	CGGACCTTGCCTGGGCCTCTCCATCTAGATGGACCTAAAGCAACCTCTAC	F	N/A	N/A	0.6864514	0.7709014	-0.08445	0.70119	0.7709014	-0.069711
cg02393097	8	20633414	27473422	27473472	S_Shore	CAGGACTATGGAGGCACAACATGGAGGCCCAGTCCCTTGCTTGCCCAACG	R	TSS1500	CLU	0.8603829	0.8944771	-0.034094286			
cg02394126	11	27622480	13379029	13379079	N/A	CGCAGTGCAATAGGGGCCCCTGACAGAGGCAAGTCCCAGCCCAGGAACCA	R	Body;Body;Body	ARNTL	0.8684114	0.9066529	-0.038241429			
cg02394395	10	42750503	94825257	94825307	N_Shore	CGGCCGCCAACCCCAGTGGAACAGCCTGACAATGGCTGCAGTGCAACAAA	R	Body	CYP26C1	0.8599614	0.8907571	-0.030795714			
cg02403412	22	39725473	19894638	19894688	Island	CGGCTCTCAGGAGAGTGTGGGCACCATGGGTAGCACTGACCGCTCTCAGG	F	Body	TXNRD2	0.8047329	0.8482886	-0.043555714	0.8094813	0.8482886	-0.038807
cg02403931	17	57724371	8154898	8154948	S_Shelf	GACTCCACCAGCTCAAAGACTCCCACAGAAGCCAGGAGCAGTGGCTCACG	F	5'UTR	PFAS	0.56732	0.64387	-0.07655	0.6027713	0.64387	-0.041099
cg02407493	16	13784466	2068942	2068992	N_Shore	CGCCCGGCCAAGGATCTGGGCCATTTAAGTGGAGTCTTGAAGGATGAGTA	F	TSS1500	NPW	0.8629429	0.8872843	-0.024341429			
cg02409364	20	11687335	35199934	35199984	N_Shore	CGGGAAAATTGCAAACAACTAAATACCCCTCACCAGGAGCTGGCCCATTA	R	N/A	N/A	0.5385871	0.6975671	-0.15898			
cg02415341	10	25793410	135146439	135146489	N_Shore	AATTCTTTCACAGTTCTGGAGTCAAGAAGTCCAAAATGAAGGTGTTCACG	F	5'UTR	CALY	0.7102414	0.7942086	-0.083967143	0.738045	0.7942086	-0.056164
cg02427511	16	17736307	15524851	15524901	N_Shelf	GTCTTTTTTTATTTCTTTCTTTTTTATTTTGAGACAGTCTCACTCTGTCG	R	N/A	N/A	0.4556386	0.4992443	-0.043605714	0.4494913	0.4992443	-0.049753
cg02434314	17	70767391	26577760	26577810	Island	CGCGGCCCAAGCTGGGCTCTGGGAGCAGCCTCATGACCGCTGCAAAGACG	F	N/A	N/A	0.6656557	0.7438843	-0.078228571			
cg02436272	11	70749459	32010528	32010578	S_Shore	TCATATTGTTTAGCACCCTAAGCACCATGGAGTATGGCAGGTGACCTTCG	F	N/A	N/A	0.9028686	0.9184657	-0.015597143	0.891485	0.9184657	-0.026981
cg02438481	6	71655432	168199400	168199450	S_Shore	CGAGTTCCGGGTGCCTGCGTGACCCATTTGTAACATGGAAATAGCAAAAG	F	N/A	N/A	0.8116743	0.8650443	-0.05337			
cg02440396	17	42605312	12366545	12366595	N/A	CGGCTTGGAAAATGCAGCCTCCTTGCTTGGATAATTCACCAGTGGAGGGG	R	N/A	N/A	0.4033129	0.4752429	-0.07193	0.4092238	0.4752429	-0.066019
cg02442436	9	61744441	112402882	112402932	Island	ATAATGTTGTTCGCTGGGCGCTAGACAAGACACCCCACTTCAGGGTTTCG	F	TSS200;TSS200	PALM2	0.1716029	0.1265543	0.045048571	0.1813988	0.1265543	0.0548445
cg02453013	16	25640318	1297491	1297541	N/A	TGAGAACTTGGCTAGTTACAGGGTGTCAAGGAATCTCCCCACAAAACACG	F	N/A	N/A	0.6287886	0.7162157	-0.087427143	0.6647588	0.7162157	-0.051457
cg02461739	17	30613397	72860448	72860498	S_Shelf	GCCTGGAGACATTCTACGTTGCTGACAGAGGTCCCCCGCCCGAGGAAGCG	F	Body;Body	FDXR	0.8962129	0.9243271	-0.028114286			
cg02462396	16	63626350	1676214	1676264	Island	AGGTGAGTAGGCTGTGGAGGCACGGCCAGGCAGCCTGGGCGTCCCTCTCG	R	Body	CRAMP1L	0.8878614	0.9256414	-0.03778			
cg02470043	11	71623354	72467029	72467079	S_Shore	CGTGGAAGAAAACCACAGGGTCCTAGGTAAGCACAGGCTATACATGGGTG	F	Body	STARD10	0.8983886	0.9296686	-0.03128	0.91127	0.9296686	-0.018399
cg02477658	6	42610501	30157133	30157183	N/A	GAGCGCACAAAGGGTGGGAGTCAGAGCAGGGCTACCTCGTAGAAAGAGCG	F	Body	TRIM26	0.8099671	0.86023	-0.050262857	0.8339113	0.86023	-0.026319
cg02488887	5	34681381	176830915	176830965	Island	GCAGGCAGTGAGCGGCCGTCAGCACCCAGCAGGGGGCGATGAGGCTGCCG	R	Body	F12	0.3804571	0.5008714	-0.120414286			
cg02489189	2	69797376	157049585	157049635	N/A	CGAACCAGGCAGCCAAATGATATGCTGTATTATTGCATGGGAGCTGTTTT	R	N/A	N/A	0.8712143	0.9139043	-0.04269			
cg02508251	2	31704350	153508150	153508200	N/A	CGTGGGCCTCCAGCAACTCTCACAGCATAGAGCTTGCTGCCTGAGTGGTG	F	3'UTR	PRPF40A	0.68796	0.8025486	-0.114588571			
cg02519625	13	17756477	114191747	114191797	N_Shelf	CGTCCTCCAGGCCTGGCCGCGTCGCCGTGCGCACCAGCACTTCGCCCCTT	F	Body	TMCO3	0.80825	0.8477614	-0.039511429	0.8071513	0.8477614	-0.04061
cg02527190	5	28683335	128302248	128302298	S_Shore	GGCCTCGCCAAGCTGGGCTGCGTGGTGGCCTTTCTCAACACCAACATTCG	R	1stExon;Body	SLC27A6	0.8370557	0.7570643	0.079991429			
cg02527375	3	42792311	41724686	41724736	N/A	CGGTTAAACATTTTGAGAGCTCAGTGGAACAATATAGCATGACTAAAGCC	R	Body	ULK4	0.91368	0.9402029	-0.026522857	0.9141038	0.9402029	-0.026099
cg02535060	10	35656315	134150690	134150740	N/A	CCCAGACCAGACATGGCTCTGGCTATTTGCTCAGTAAGCAGGCGATTTCG	R	Body;Body;Body;Body;Body	LRRC27	0.4594857	0.5808471	-0.121361429	0.4955925	0.5808471	-0.085255
cg02538280	7	43729480	157956927	157956977	Island	CCCGGTGCATAAGAAAGGCACACAGAACAGGAGCGCGCAGGAAGGGCTCG	R	Body;Body;Body	PTPRN2	0.5910686	0.6627814	-0.071712857	0.6068775	0.6627814	-0.055904
cg02550741	11	30772350	119554281	119554331	N/A	CTGACTGGGTGTCAGGTGATAGGTCAGAAACAGGGGCTTTGGGGATCCCG	R	Body;Body;Body	PVRL1	0.7795286	0.8284786	-0.04895			
cg02551646	2	27667356	216478293	216478343	N/A	CTGAAGCTCAGCAAAAACGTTACAAAGACCCTCTGAGGTGCAGAAACTCG	F	N/A	N/A	0.6065629	0.6740871	-0.067524286			
cg02554361	16	45656413	11001757	11001807	Island	CGCCCGCAGTGTCCCCGGCTGCAGCCGCTTCAGGTACCTCGCAAGCACCT	R	Body	CIITA	0.9174986	0.94634	-0.028841429	0.9345725	0.94634	-0.011767
cg02560408	10	54683330	62757486	62757536	N_Shelf	TTAGTATGTATAACCTATTTTTAAATTTCTTCTGGTCTCTATAAACTTCG	F	Body;Body	RHOBTB1	0.8149543	0.8740043	-0.05905			
cg02564302	3	58644499	98612083	98612133	N/A	CGAGGGCTGGGATTGAATCTGGGTAGCAAGTAAATTTTTGTTCAATGAAT	R	Body	DCBLD2	0.8670171	0.91824	-0.051222857	0.8800588	0.91824	-0.038181
cg02576092	1	13650315	27668556	27668606	N/A	GGGGCAGCTGCTGGCTGGGCTGCCTGTTGAGTCAGCCTTCTTCCCTCACG	R	1stExon;5'UTR	SYTL1	0.1671629	0.24753	-0.080367143	0.1908275	0.24753	-0.056703
cg02576394	6	10707321	30707038	30707088	N_Shelf	CGGCCCATGCCCCTCTAATCAAGCAGTGCATTCTGACATGGGTCTGCATC	R	Body	FLOT1	0.92028	0.9451829	-0.024902857			
cg02588532	6	54621461	166922931	166922981	N/A	AGCCAGCCTCTGCAGCCTCCTCTGCCGGGAGGTAGAGGTTTGCAACTGCG	R	Body;TSS200;Body	RPS6KA2	0.9088786	0.9357029	-0.026824286			
cg02591356	2	72804456	20442088	20442138	N/A	CGTCTAAATTACTTGGAGTTGATCTTTCTAAACAGGATTGCTCAGACACA	R	N/A	N/A	0.4536543	0.5376414	-0.083987143			
cg02596645	4	46801308	187628413	187628463	N/A	CGTGTCCGTTGGGCCCCAGGTCTTTATCTGTGGCTTCAACCTGGATGATT	F	Body	FAT1	0.8344014	0.8589957	-0.024594286			
cg02598564	10	61621457	72822634	72822684	N/A	GCGCTGCACTTGGGAGGGTCACCGTGCTGGAGGTCTTGATAGAAGGCCCG	R	N/A	N/A	0.7979886	0.8554729	-0.057484286	0.8248063	0.8554729	-0.030667
cg02600411	8	34681335	11832039	11832089	N/A	TTTAAGCATCTCAATCTTTGGGAACACCCACTTTTATGTTCAGACTCACG	R	Body	DEFB136	0.8338229	0.8956829	-0.06186	0.87184	0.8956829	-0.023843
cg02603876	16	57727447	30689847	30689897	N/A	CGCCTGGATTCCAATCTGCAGGCTTTGGGAAATGTTTATTGACAAGTAGA	R	N/A	N/A	0.7953529	0.8670386	-0.071685714			
cg02616565	3	63741377	30303691	30303741	N/A	TGGTCAATCATAGGCGACCAACTATTCAAATTGTGTTAAAGGCACACACG	F	N/A	N/A	0.88902	0.9226129	-0.033592857			
cg02623469	3	14727445	51702509	51702559	N_Shelf	ATAAATACGTCATAGAAACAGCCAGTTGCCCAGTCTCTGGGGCAGGAGCG	F	N/A	N/A	0.8811829	0.9153629	-0.03418	0.893755	0.9153629	-0.021608
cg02623718	1	60621371	240565704	240565754	N_Shelf	CCGCCTTACTTTCCAGGAGAACTGCAGAGTTCAGTTAAACCATTTATTCG	F	Body	FMN2	0.7761643	0.8702943	-0.09413	0.8134725	0.8702943	-0.056822
cg02626854	17	69636357	80315917	80315967	N/A	CGTGAGCCACCTTGCATGGCCAGCTCACTTATTTTTTAACACTGAATGGT	R	TSS1500	TEX19	0.8720957	0.9171371	-0.045041429	0.8837838	0.9171371	-0.033353
cg02628107	5	32779456	10279354	10279404	N/A	CGGTGGGCTAGAGTTGTCACCCAGCTGTTGTCTCCTAAGCAGTGGATTTC	R	3'UTR	CMBL	0.8938486	0.9297271	-0.035878571	0.9141138	0.9297271	-0.015613
cg02636348	10	18685460	78923827	78923877	N/A	CGGCATTCTGCAATTTGTCATGTCCTGAGAGCTGGACTCATCTGGCTTTC	F	Body;Body;Body;Body	KCNMA1	0.63902	0.7744857	-0.135465714			
cg02641917	2	29722354	198127245	198127295	N/A	CCCTTTCTGAAGCCTTTTCTCATTTTAAGGCATATGGATTTGTGCTAACG	R	N/A	N/A	0.8256171	0.8828643	-0.057247143			
cg02641941	12	16787391	40410965	40411015	N/A	CTGACGTTAGCAAGGCACTTCATAAATGTTTCTTTGACTTTCTGTTTACG	F	Body	SLC2A13	0.6687529	0.7704171	-0.101664286			
cg02666566	6	51801381	2510173	2510223	N/A	TGTCATCAAGCTAGGCGGCAACGCTCGGCTGGTAACTCAGGCGGCGAACG	F	N/A	N/A	0.9104043	0.9459771	-0.035572857			
cg02668218	20	56672326	2191729	2191779	S_Shelf	GCTCTAGTAGCAGTGAATTTCACATTGCCCTGACTAATAGCAGCTCTGCG	R	N/A	N/A	0.8195771	0.8831114	-0.063534286			
cg02673453	16	15672400	15814806	15814856	N/A	CGCCAAACTGCGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCG	R	Bodv:Bodv:Bodv:Bodv:Bodv:B	MYH11	0.9229943	0.9585243	-0.03553			
cg02675969	11	58711382	83526604	83526654	N/A	GACACAGATTTATCCTGGGGCCAAGAAAATTTACTCCCATAGTGCCTACG	R	Body;Body;Body	DLG2	0.8706114	0.9086243	-0.038012857			
cg02676476	1	48660404	9323181	9323231	N_Shore	GACCCTGACTCTTAGGTATTTGAGGGGTCAGGGGGTCCTACAGAGAAACG	F	Body	H6PD	0.7127557	0.7765229	-0.063767143			
cg02678768	17	14641394	74002944	74002994	N_Shore	CGAATTCTGTCTCCCCGTGCCATGTGGTGTCCCATTCATTCACATTTGAG	R	3'UTR	EVPL	0.47558	0.6127543	-0.137174286			
cg02680909	6	56779349	39899321	39899371	N_Shelf	AGTGTGAGGTCTTTACACCTATAGCTTCTGAGGAGGACAGTCACATTTCG	R	Body;Body	MOCS1	0.8198429	0.8807514	-0.060908571	0.8456413	0.8807514	-0.03511
cg02690491	19	57694437	12075772	12075822	N_Shore	CGGGGCCTAGCATTCCATCCAATCAGAGGTGCCGGGGCAGGGCCCTGCCC	F	TSS200	ZNF763	0.1547944	0.2162471	-0.061452714			
cg02694732	17	26679409	46087057	46087107	N_Shelf	GCAGCCATAACCATGCCCGGCCAATTTTTTATTTGTAGAGACAGGTCTCG	R	N/A	N/A	0.8631686	0.88788	-0.024711429			
cg02696428	13	73614480	46743535	46743585	N/A	CGTGACCTAGAAGATGCCAGTGTACACAATATTTGTATGTGATTTGGCAC	R	5'UTR	LCP1	0.73353	0.82104	-0.08751	0.780775	0.82104	-0.040265
cg02701137	20	58703306	34994743	34994793	N/A	TGCCTGGATCTTTAAATCAGCAGGAACCAGGCTGGGTGCGGTGGCTCACG	F	TSS1500	DLGAP4	0.5191686	0.5774057	-0.058237143			
cg02702041	9	51640370	91996229	91996279	Island	CTGTCTCATACACGCAGGGCAACAGGTTTGTCTATGCTGGCTCTAACTCG	F	Body;Body	SEMA4D	0.8981886	0.92401	-0.025821429	0.9137538	0.92401	-0.010256
cg02703701	11	20767388	489666	489716	Island	CTGAAGTTTGTGCTGTGGATGCCCCCGGAGCACTACCTGGTCCTCCTGCG	R	Body	PTDSS2	0.8924429	0.9085786	-0.016135714			
cg02706104	11	54760505	5009489	5009539	N/A	CATGCAGCTCGTCATCTTAAGAGTTACTATCTTCTTGCCCTGGTGTTTCG	R	1stExon	MMP26	0.9199871	0.9480457	-0.028058571			
cg02709032	19	58605455	33699683	33699733	S_Shore	CGACTCTCAGAAGCCTGTTTAAGGAAGCCCTAAAATGTGGACTGGGTTTC	R	3'UTR;3'UTR	SLC7A10	0.6436457	0.7130271	-0.069381429			
cg02710699	16	34627359	30575324	30575374	S_Shelf	GGATGGGTGACAAACGCTTCACAAAGGGTCCCCTGTAGCATCTCTCACCG	R	N/A	N/A	0.9193257	0.9561857	-0.03686			
cg02711147	10	64650498	131260729	131260779	N/A	CGGAGGGAAGAGCTATATAAGGTTTGCAATGATCTTTGTCCACCAGTTAC	F	N/A	N/A	0.91239	0.9467329	-0.034342857			
cg02721394	3	15605425	195914017	195914067	N/A	CCTAATTCTAATTTGAGATCAGAGCCTGACAGCTGGGCAGGTGGCAGGCG	R	N/A	N/A	0.6696657	0.7877029	-0.118037143	0.7454	0.7877029	-0.042303
cg02721693	1	65705482	182922705	182922755	S_Shore	CGTTTCAGGGTGATTATGAGTCACCTTCCAGGTCATCAGGACCTAAAAAA	F	TSS200	C1orf14	0.70326	0.7806257	-0.077365714			
cg02723458	7	60791360	138391286	138391336	N/A	TACACAGTTTCATGCTTCAGGTGAGCCAAGAACAACCTTCCCATTGAGCG	R	3'UTR;3'UTR;3'UTR	ATP6V0A4	0.9094457	0.9377143	-0.028268571			
cg02727566	19	21630393	40718426	40718476	N_Shore	CGGGCTGCCTGCGCTTCTGGTCTCCAGCTCTGGGTAGTTAGTTCCCTGGG	R	Body	MAP3K10	0.7149243	0.7618486	-0.046924286			
cg02732653	20	31622327	62172589	62172639	S_Shelf	CACCTTCATAGGGACACTGGCCATAGGTGAAAACCTCGTGCAGCAGGACG	R	Body	SRMS	0.8512814	0.9004243	-0.049142857			
cg02737335	1	40644397	3379884	3379934	N/A	CACAGCCAGGCTCTTAGGGATCAGCTGTTGGGTGCCCAGCTTGAGGGCCG	F	Body	ARHGEF16	0.8585571	0.9123686	-0.053811429			
cg02747254	16	38639369	29938183	29938233	S_Shore	CGCTTCCCAGCTTCAGCTCGGCATCACCTCCTCAGAGAGGCCTTCCATCC	R	TSS1500	KCTD13	0.2616071	0.1881629	0.073444286	0.2214563	0.1881629	0.0332934
cg02750883	2	22644496	60808820	60808870	Island	CGCCTGCGTGGGGACGACCCCAAAGGCCTGCCCAGGAAGCTTTCCTCCAC	R	N/A	N/A	0.1141197	0.0855281	0.028591571			
cg02753511	11	57806414	69468378	69468428	N_Shore	AGAGGGACACAGCCTGGTCTCTGGGGACACCGGCGCGGTTCTCACGCACG	F	3'UTR	CCND1	0.8832686	0.9166014	-0.033332857			
cg02756168	10	34794471	15055005	15055055	N/A	TGGAATGTCATCCTGTGCTTCCCTGGATATGATGAACAGTAAGTATCACG	F	N/A	N/A	0.7270943	0.81011	-0.083015714			
cg02756281	16	55791469	2812333	2812383	Island	CGCCTGGTGGGAGTTCTGGATCGTGATCTCCGCCTGGCAGGTGTTCTAGA	R	Body	SRRM2	0.8695029	0.8968686	-0.027365714			
cg02761866	12	54777349	48542726	48542776	N/A	CGTGAGCCACCATGGCTGGCCTAAAATGCTTTCTAGAAGGGATTCTTCTG	F	3'UTR	ASB8	0.7897214	0.8562157	-0.066494286			
cg02771117	8	30787304	11279352	11279402	N/A	CGGAGGTTAGGCCAATGTTGCTGCTGACTCATAGACCCACAGAGAGCAGG	F	3'UTR;Body	FAM167A	0.6721414	0.7603414	-0.0882			
cg02771744	7	46752379	7995879	7995929	N/A	TGTCCTCTCTTGCATATACTATTAGCTCACAGGTCTTTCAGAGACCAACG	R	N/A	N/A	0.6598571	0.7512871	-0.09143			
cg02773671	13	74712310	24566085	24566135	N/A	CGGTGATGAAGATCATGGGGTTATTGTAATGATTGGCACTGCCATTGTTG	F	N/A	N/A	0.90442	0.9296314	-0.025211429			
cg02774282	6	40727316	109615419	109615469	S_Shelf	CGCCCCAGGGCAGCAGCCCTTTTCATGCCACTCCCAGGTGGCCAGTTTAT	R	TSS200	CCDC162	0.7542286	0.8416557	-0.087427143	0.781825	0.8416557	-0.059831
cg02775243	10	23804400	102831287	102831337	S_Shelf	CGCAGCCAGTTCTGCTTTTTAAGTGCGTACATTGGGTAGGTTTCTTAACC	F	N/A	N/A	0.7197314	0.8001886	-0.080457143	0.7562375	0.8001886	-0.043951
cg02776177	19	22626403	47774873	47774923	N_Shore	AAAGGCCAGGCCTCACCCGGGGAGAGGGCGCCAGCCAGGTGAGTGGTCCG	F	Body	CCDC9	0.8262629	0.8697743	-0.043511429			
cg02776313	22	25786389	50965782	50965832	Island	ATAATAAGGGACTTGACCCTCAATGCTCAGGGCCCCTGACCCCAAAGTCG	F	Bodv:TSS1500:Bodv:Bodv:TS	TYMP	0.6271686	0.6732186	-0.04605			
cg02786378	8	41625390	17396844	17396894	N/A	ATGATTTTCATGAGCCTAATGATACATGTGAGATCTTTCTTAGCCCCACG	F	Body;Body;5'UTR	SLC7A2	0.8222514	0.8872557	-0.065004286			
cg02787120	7	19683457	111200944	111200994	N_Shore	CCTCTGTGATAGGCTGCCTATTCTGATACTGGCTGCCTGTGTCCTGAACG	F	5'UTR	IMMP2L	0.5487229	0.6487571	-0.100034286	0.59297	0.6487571	-0.055787
cg02795981	10	16685492	81045119	81045169	N/A	CGGGACTCTGGGCCTCATACATGTTAGGCACTTACACTTAACCCTCACGG	F	Body	ZMIZ1	0.7760129	0.8650671	-0.089054286	0.813245	0.8650671	-0.051822
cg02803139	10	21660325	106113391	106113441	N/A	CGCCCCATTGGGATATATTTGCATATTTCTCTGAGGAACCCTGCCCAGGT	F	TSS200	CCDC147	0.0728947	0.1063516	-0.033456857			
cg02803141	16	55798342	85244771	85244821	S_Shelf	GTACCCCCCTAGAAGTGAGGCCCTAAGGAACTCCCAGAGGGGTGGTGTCG	F	N/A	N/A	0.90561	0.93903	-0.03342			
cg02804999	1	32619359	2119992	2120042	N_Shore	GGAGCAAGGGAACTCCCCAGGGTCTCCATTATGGGGCACTAATCCCATCG	R	Body	C1orf86	0.89528	0.9202529	-0.024972857	0.9038888	0.9202529	-0.016364
cg02822108	12	32724307	126718414	126718464	N/A	CGACACTTTGTGAGAACAATAGGCTCCCACCCCAGGGTTCTGTCTTAGTC	R	N/A	N/A	0.6563386	0.7326271	-0.076288571			
cg02824817	4	70633350	170265309	170265359	N/A	AACCCTGAGCTTAGGGAACCTACATTTTAGGTGGACAACAAGCATACCCG	R	N/A	N/A	0.9111386	0.9433471	-0.032208571	0.9279813	0.9433471	-0.015366
cg02825211	19	36720441	8808663	8808713	Island	CGCCACCTGCTGGAGCACGACCTCCGAGTGGCCACCCACGACCACCCGCT	R	1stExon	ACTL9	0.2164229	0.128029	0.088393857			
cg02829992	2	69632341	10710499	10710549	N/A	GCTTGGGACATGGAACTGGCCTCAGGAACACCTAGATCCATGGCTCCACG	F	N/A	N/A	0.8952129	0.9112943	-0.016081429			
cg02835301	3	57739406	11609216	11609266	N_Shore	CGGGACTTGGTTCCTGAATACTCAGTTCATCAGTGTCACCACACATCCTC	F	Body;Body;Body;Body	VGLL4	0.8314914	0.8800086	-0.048517143			
cg02837456	11	63780300	94500612	94500662	N_Shore	CGGCCTTCAGGGACTCCTCCCTGGATTGTGGCAGTTCCCTAACTAGACTG	R	TSS1500	AMOTL1	0.7514843	0.7996457	-0.048161429			
cg02839202	11	64654475	73117693	73117743	N/A	CGGAAGTGCAAGGGTCACTTTATGCATCTTTAATGGTTTTGATTTTTATT	R	3'UTR	FAM168A	0.9141229	0.9436771	-0.029554286			
cg02839622	20	30691489	55904289	55904339	N_Shore	GGAAAGGTCAGCTCAGAGCAGGCAGGCCTGGGTTAAAATCCCAGCCCTCG	F	TSS1500;TSS1500	SPO11	0.7567771	0.8158414	-0.059064286			
cg02839811	19	36679505	51607208	51607258	Island	CGCCGCCTTCTGGAGCATGCGCCTGAATCCCCTTTCAGGTCCCGCCTCCT	F	Body	CTU1	0.8580443	0.89119	-0.033145714			
cg02841692	8	33648476	145987889	145987939	N/A	GTACCAGGGTTTGTGTGCGTCTCAGTGCGGGATGTGAAGTGGTCACTCCG	F	N/A	N/A	0.4401829	0.5253929	-0.08521			
cg02841912	6	11626449	152955983	152956033	N_Shore	CGAGAACTAATGTTTGGCAAGGTGTGCAATATACTGTAGCAAGGGAAAAA	R	5'UTR;5'UTR	SYNE1	0.76036	0.8411529	-0.080792857			
cg02844051	19	37762354	36004233	36004283	N/A	CGCTCAGGGCGTCTCCCAGGCCATGTCCAAGGGCCTCCCCAATATTTGTC	F	1stExon:1stExon:1stExon:1stE	DMKN	0.8927929	0.9222143	-0.029421429	0.8893575	0.9222143	-0.032857
cg02855045	3	43681484	72777245	72777295	N/A	AGGGCTCTCCAGTGGGACTGTGGTCTAGTTGTCCACGATGGCAACACACG	R	N/A	N/A	0.6848886	0.72426	-0.039371429			
cg02860543	7	21735497	23510648	23510698	S_Shore	TTTCAAAATAGGTTATTAACAACAAAACCAGAGTCACAATCCCGAACTCG	R	TSS1500	IGF2BP3	0.1987214	0.2395857	-0.040864286	0.2120638	0.2395857	-0.027522
cg02864690	11	68619502	2023450	2023500	N_Shelf	CCCATCCAGGGAGGGCTTGGGCTGTGATGTGTGAGCCTGCACTGCCGCCG	R	N/A	N/A	0.5332143	0.5737214	-0.040507143			
cg02867735	14	48771307	22975384	22975434	N/A	CGGCTCTGCTGGGGCCAACCCTCAGCAAAGATTCCCTCAGGCCCTGAGCC	R	N/A	N/A	0.7688771	0.8221429	-0.053265714			
cg02871554	18	56678406	21170124	21170174	S_Shelf	CGCCATTGCACTGCAGTCTGGGCAACAAGAAATTAGGCTGGGCGTGATGG	F	N/A	N/A	0.6141957	0.6577986	-0.043602857			
cg02878739	2	43724389	236840858	236840908	N/A	CGGGGCTTCAGCTGCAGCACACACAGGGCTGATGAAAGGCTGACTACCAG	R	Body;Body	AGAP1	0.8085871	0.8661414	-0.057554286	0.8381675	0.8661414	-0.027974
cg02879776	10	52667416	80407110	80407160	N/A	CGAGTCAGCAGCAGCCCTAGGACTGGAGACATGTTTACATGTAATCCCAT	F	N/A	N/A	0.8104571	0.8664557	-0.055998571			
cg02882375	11	12688459	34517751	34517801	N/A	GCTCTGTGGGTGAGCTTCAAAGCAGAGCGCCGAGGAGCAGGGAGCCAGCG	F	Body;Body	ELF5	0.6934443	0.7498886	-0.056444286			
cg02893490	16	23614362	68014110	68014160	Island	GGTGCCTGGCGTAGTGAGGCCTGGGGTAGTGAGGGCGCTGGGGACACCCG	R	1stExon;1stExon	DPEP3	0.8557171	0.8909529	-0.035235714	0.8734163	0.8909529	-0.017537
cg02902854	17	33748301	3474736	3474786	Island	TTGGCTGGTGGCCTGATGTTGGGCAGGGGGAGCTTTGCAGGTTCCCCACG	F	Body;Body;Body;Body	TRPV1	0.8767514	0.9145	-0.037748571			
cg02903929	2	23808349	216602247	216602297	N/A	CGATTGGCTTCCTGTTAGGTTCAGGCAATTGTAAGCACTTAGAGACGTAT	F	N/A	N/A	0.6193729	0.71675	-0.097377143			
cg02906823	1	18802477	32927696	32927746	N_Shelf	GGCCTTATGATCTCTAGATCTGTTGTGGTCTGCTGTGGGACTTACTCTCG	F	N/A	N/A	0.8457429	0.8943357	-0.048592857			
cg02907402	6	58802346	30079425	30079475	N/A	CGGTAAGAAAAACTCCATCCCACGATCTCTGGAAGCAGAAACATCTCTGC	R	Body	TRIM31	0.5187157	0.6669729	-0.148257143	0.604475	0.6669729	-0.062498
cg02908282	8	67664387	145502297	145502347	Island	GAGGCCACGCAGGGTTCAGGGACTACAGCAGCCTTTCCTTGGCCCCAGCG	F	Body	BOP1	0.8466029	0.8736986	-0.027095714			
cg02914667	11	61718438	63894453	63894503	N/A	CGGCCCGGCTTCTCAGGGCCCAGACCAGCCTGGCCTCGTGCCCACCTGCT	F	Body	MACROD1	0.8753486	0.9107814	-0.035432857	0.8980788	0.9107814	-0.012703
cg02919794	17	21681311	80203112	80203162	Island	AGTTCCTGTCAACACATTTCCAGAGTGTGCACAGTGTGAAAACTGCAGCG	R	Body;3'UTR	CSNK1D	0.9161314	0.9466243	-0.030492857			
cg02920178	16	15613427	1364965	1365015	S_Shore	GATCTCTCCTTCCTTCAGAGTCCACGAGCATGAACCTTATGTGCAAGCCG	F	Body;Body;Body;Body	UBE2I	0.7995229	0.85295	-0.053427143			
cg02920396	11	48778339	68782211	68782261	S_Shelf	GGAGGCCTTGATCTTGGCCTTCCAGCCCCCGGAGCCATGGGAAACAAACG	F	TSS1500;TSS1500	MRGPRF	0.6356986	0.7095114	-0.073812857			
cg02926266	2	71790315	205847300	205847350	N/A	CCCCACTAATCCACATAACAATATGTTGTCCATATTGCTTTGCAGCATCG	R	Body;Body;Body	PARD3B	0.7440329	0.8286743	-0.084641429			
cg02930200	1	59793330	38022384	38022434	N_Shore	CGGTGAGCAGAAGGCCTAAGAAGTCAGGCACAAGAGGTTTCTGCCCAGGA	F	TSS200	DNALI1	0.1475614	0.1013541	0.046207286	0.1262526	0.1013541	0.0248985
cg02935052	7	61807418	73751804	73751854	N_Shore	GACCACTTGCACAACACCTAGGTCCCACATAGGGGCCACAGGGGGGTCTCG	R	Body;Body	CLIP2	0.7734529	0.8532514	-0.079798571			
cg02935562	16	45741464	19834374	19834424	N/A	CGGTCTCACCCTTTGGGGACTGTGTTTGTGTCCTAAGATGGTGGATGTGT	F	Body	IQCK	0.8159857	0.8500814	-0.034095714			
cg02936315	7	23758442	1250239	1250289	N_Shore	CGTGGCCGCCAGGAAGCCCAGGGCAATGATTTGTCTGTCAAAGCTTGAAA	R	N/A	N/A	0.3949757	0.4974714	-0.102495714			
cg02936752	19	39617449	54963326	54963376	S_Shelf	CGGCGTCTCCATGCCATTCTCTCGGCCTGCCCCAGCCACCATGCTGTACT	R	Body	LENG8	0.8669729	0.9003829	-0.03341			
cg02936931	6	10689472	134856977	134857027	N/A	GACTGAAACTTGCACCAGTTCTGAATGCCTCTAACCTTGGTTGTATAACG	F	N/A	N/A	0.8744557	0.9033914	-0.028935714			
cg02940147	11	47709354	124747263	124747313	S_Shore	CGCCCCGCTGACGCCCCAGGTGGAGGGAGCATGGCCACCTCCCACCCCAA	F	Body	ROBO3	0.6342386	0.7189071	-0.084668571			
cg02947214	14	14765494	105998115	105998165	S_Shore	CGCTGCCTGTCTGTTCCCATGGGATTTGCTGCAGGTGCCAGAGCCAAGAT	R	N/A	N/A	0.85732	0.8967229	-0.039402857			
cg02947276	14	10683490	24731242	24731292	N/A	CGGATGGTGCCATCTCCAGCTGCATTGACACCGCTGCCCCGGGATACAGG	F	Body	TGM1	0.8610586	0.8898714	-0.028812857			
cg02965351	19	30779332	50823066	50823116	N_Shelf	GTTGAACTCCCCATGCCCAGTACCTGGGATGCGTGGGTGCTGTCTAAGCG	R	3'UTR	KCNC3	0.8680029	0.9172843	-0.049281429			
cg02970663	2	15602449	238542536	238542586	N/A	CGTCCCCCACTGACCTGTGAACCACCAGGGGTGACATTTCAGGAGAGAGA	F	Body	LRRFIP1	0.9123857	0.9452314	-0.032845714			
cg02971555	7	48797342	13935467	13935517	N/A	CGCCCTGCTTGACTGTCACTTGTGTTAATACACGTAGCCTTCGTTGTAGG	F	3'UTR;3'UTR;3'UTR;3'UTR;3'L	ETV1	0.8983814	0.9270486	-0.028667143			
cg02973735	17	29787435	80362014	80362064	Island	CGCTCGTGGGTCCCAACCCGTGGGTGGCAGGAAAGGAACCAGCCTTCGTA	F	Body;Body	C17orf101	0.80918	0.83796	-0.02878			
cg02975091	10	50765451	99164260	99164310	S_Shelf	CGCACTAAGATTACAGGTGTGAACCAGTGCATCCAGCCTCATTCTACGGT	R	N/A	N/A	0.9157157	0.9455429	-0.029827143	0.9245788	0.9455429	-0.020964
cg02978150	11	66744336	125702592	125702642	N/A	CGCTTGAACTACCAGAGCAAGAACTCACTCATTACAATGAGGATGGCACC	F	TSS1500	PATE4	0.8471143	0.8944114	-0.047297143			
cg02981003	10	51644481	134917911	134917961	N_Shore	CGGCTGCCAGCCTGGTCTTCAAAACCAGGCAGCTCTTCCATCAATTACAG	R	Body	GPR123	0.6170143	0.7366043	-0.11959	0.6742863	0.7366043	-0.062318
cg02982237	14	31749409	100492002	100492052	N/A	CAAGGATAGGTTTTTAAAAATACACAGTTGGCGGGGCGTGGTGGCTCACG	R	N/A	N/A	0.8405429	0.8672586	-0.026715714			
cg02989244	10	28626377	28657270	28657320	N/A	CGGTTTGGGTACTTTCTTTAAGTATGTGCCTGAGTAGACAAGTCATCGTA	R	N/A	N/A	0.6964071	0.7775586	-0.081151429	0.7424688	0.7775586	-0.03509
cg02991753	4	74614406	119961172	119961222	N/A	CCAGGCCTGCCTCCTGCTGGTTGGGAGACTTTAAACAAAGGATTCAGTCG	R	Body	SYNPO2	0.7651543	0.8139814	-0.048827143			
cg02992311	19	16671323	39523626	39523676	S_Shore	CGGTTTTACTGCCAGCCAGGGTGGCAACCCCATGAAGTAGGTGCTGTTAT	F	TSS1500	FBXO27	0.4330029	0.3594357	0.073567143			
cg02993606	19	36768504	38803369	38803419	N_Shelf	CGGAGTTAACTGTCCCACCTTGCAGAGCTGTTGTGACACTCATAAACTCC	F	Bodv:5'UTR:Bodv:Bodv:Bodv:	YIF1B	0.8374257	0.9093457	-0.07192	0.8688275	0.9093457	-0.040518
cg03001305	17	46662397	40439492	40439542	N_Shore	GAGGCCCCTTCCCACGAGGCCCAAGGGGTTTGGTAAGGTCGGGCTGGACG	F	TSS200	STAT5A	0.6145914	0.73039	-0.115798571			
cg03010972	7	32713312	130920239	130920289	N/A	CGGCTGTCACCTTCGTGAACAGACTTCTGGTGAGTTTTTGGCTTGTTTCC	F	Body	MKLN1	0.6912943	0.7462786	-0.054984286			
cg03020424	3	41654345	148581801	148581851	N/A	TTCTCAGAGTCACGCTTATGTACTATCAAAATAGTGTGGTTGGAGACACG	F	TSS1500	CPA3	0.8348957	0.8819029	-0.047007143	0.8512725	0.8819029	-0.03063
cg03021297	16	18753346	88986307	88986357	N/A	ATTCTCATCAATTCTCATGCTGCTTCCCAAGGTAACTCTCCAGGGAGACG	F	5'UTR;Body	CBFA2T3	0.8945971	0.9106786	-0.016081429			
cg03024246	11	44726402	96124628	96124678	S_Shore	CACAGCCTTTTCCTGCAAGCCTTTAGATCTTAAATACTCTCGAACTTGCG	F	1stExon	JRKL	0.9177543	0.9381757	-0.020421429			
cg03029146	15	12786388	77265894	77265944	N/A	CTCTAGGAGGCGCTGTTCCTCCAGCATCCAAGAATCAGCCTGAACCAACG	R	N/A	N/A	0.3604743	0.42248	-0.062005714			
cg03031281	6	53800412	31941422	31941472	S_Shore	GACCCTATTAACTTCCACTCTAAACCTGGAGTCCTTAACCACGGACCTCG	F	Body;Body;TSS1500;Body	STK19	0.8884343	0.92046	-0.032025714			
cg03032122	11	42629369	9337659	9337709	S_Shore	AACAAATTCATTGAATGGCCACTTAGGTATTGGCACTCTGTCAGCTACCG	F	TSS1500;TSS1500;TSS1500	TMEM41B	0.8732329	0.9377714	-0.064538571	0.9005575	0.9377714	-0.037214
cg03035162	14	35680419	22993190	22993240	N/A	TAGGGGACAGGCAGGCCAGGCTCTTAATCTAGCTCTGCCCCTCATCTGCG	F	N/A	N/A	0.8170129	0.8679771	-0.050964286			
cg03051777	12	52654382	115131789	115131839	S_Shore	CGTTAGGAAGATCTAAACTGAAGCACTAGAAAGGTCTGTGACTCTGTTCT	R	N/A	N/A	0.6281743	0.7549557	-0.126781429	0.6881688	0.7549557	-0.066787
cg03052182	6	59633450	30653530	30653580	N_Shore	CGGTTCTGGTGCACTGGCCCGATGGCCTCCAGAAGGACCGCAGACTCATC	F	Body;1stExon	KIAA1949	0.5289814	0.6365871	-0.107605714	0.5944475	0.6365871	-0.04214
cg03058346	1	41680381	91275170	91275220	N/A	CGCCCAAATTGCCCTGTGAAGCTGAGCCCAACCAGCTTGAGGTCAATTTG	R	N/A	N/A	0.72389	0.8078957	-0.084005714	0.7847713	0.8078957	-0.023124
cg03065503	4	33756447	4442273	4442323	N/A	TATAGTGAAACACCTTTCTAGCTTTGACTCAGCTTTCTCAGACTGATTCG	F	Body	STX18	0.8707214	0.9123571	-0.041635714			
cg03066788	8	26721421	28175285	28175335	N/A	CGGTGCGCAGGCTGCTTCTCCGCCTATCACTGAACTTGATGCCATCCAGA	F	5'UTR	PNOC	0.5949286	0.6844886	-0.08956			
cg03068068	19	57742418	36203512	36203562	N_Shelf	CGGGGACCTTGACCCCTTGGGCAGGAAGTGAAAGAAACCCAAGTCCTGAT	F	TSS1500	ZBTB32	0.5643229	0.6924343	-0.128111429	0.609365	0.6924343	-0.083069
cg03071245	13	43624483	37463034	37463084	N/A	CGCACATGAAACTGACCACATTTGTTGCCTTTGGAAAGGGAACATGGCCA	F	5'UTR;5'UTR	SMAD9	0.8004257	0.85397	-0.053544286			
cg03078819	7	58624403	140218338	140218388	N/A	CGGCTCCCAGGTCCTCATCCAGGGAAGAGCCCAGCCTCGGCCAGAAGCCA	F	3'UTR	DENND2A	0.8320586	0.9102371	-0.078178571			
cg03078854	6	26808482	32810001	32810051	N_Shore	CCTCACCCAGGCTGTACTATCTGCGAAATGGAGAACGTATTTCAGTGTCG	F	Body;Body	PSMB8	0.9154171	0.9434057	-0.027988571			

cg03094723	7	64724509	150035787	150035837	N_Shore	TGGCAGGAGGCTGAGGAGCACCAGGAGACCCAGTGCCTCAGGGTGCAGCG	F	Body	RARRES2	0.8824386	0.9099043	-0.027465714			
cg03095778	7	28744314	182203	182253	S_Shelf	CGCCTCCTGTCGCCTCCACTCCTGACCCCCATCCAGAGTGTGGGATGCTG	R	N/A	N/A	0.8095014	0.8490771	-0.039575714			
cg03103944	7	30672437	1601985	1602035	N/A	CAATTCCATTCCCAGGCACTCAACAAGATAGCCGAGGCCAGCTCACTCCG	R	N/A	N/A	0.5519186	0.5868886	-0.03497			
cg03109729	10	58793450	78939740	78939790	N/A	CGGCATATGATTGCGTGTTGTATAGTACAGAATATATTCATTGTGCAGAT	R	Body;Body;Body;Body	KCNMA1	0.9266714	0.9542871	-0.027615714			
cg03117379	20	59782316	17943971	17944021	N/A	GACAAGCCTGGGCAACACAGCAAAGCCTTAAAAAAAATCACCTAGGCTCG	R	TSS1500;Body;Body	SNORD17	0.7279114	0.7995343	-0.071622857	0.7698613	0.7995343	-0.029673
cg03117697	4	71787399	148491949	148491999	N/A	CGGCCCTGTTTCTGCAAGAACAGTTTTTATCCATTATGTTTGTCTGAACA	R	N/A	N/A	0.4074514	0.5049686	-0.097517143	0.441325	0.5049686	-0.063644
cg03119435	16	58707361	71570193	71570243	N/A	GCAGGAATCACAAGCCATTCCTCCAAGACTTGAGTCAGACTGAGGTGACG	R	5'UTR;5'UTR	CHST4	0.88484	0.9172986	-0.032458571	0.87979	0.9172986	-0.037509
cg03122427	10	14621453	97552565	97552615	N/A	CAGTGGCCTCCTATAATTTTTGTTGAACACCCATAAATGAAGGCAGCACG	R	Body;Body;Body;5'UTR;5'UTR	ENTPD1	0.6515514	0.74633	-0.094778571			
cg03126561	11	53708386	12434050	12434100	N/A	CGGCCTGGGCTGGTGAACTGCATCCCGGAGCCCCCTGGTGGTCCTTTCCA	R	Body	PARVA	0.4617314	0.58696	-0.125228571			
cg03127349	10	33629486	31101116	31101166	N/A	ACTGTTACATTCTGCCTCCACATTCAAGGCCTGGCTGTGGTCAGAGGTCG	R	N/A	N/A	0.3762457	0.4921114	-0.115865714			
cg03133987	16	69664346	2053563	2053613	N_Shore	GCAGGGCCTCTCCCTGGGTCCTGGCCTCCCTGTGGTTGTGGCCCTTCACG	F	Body	ZNF598	0.6859857	0.7454471	-0.059461429	0.7224875	0.7454471	-0.02296
cg03141944	2	14749508	206595862	206595912	N/A	CGGGCCCACCCTGTATGAGAATCATAGGTTCCATATTTATGGCATGTGGA	R	Body;Body;Body;Body;Body;B	NRP2	0.8868043	0.9174157	-0.030611429	0.8963075	0.9174157	-0.021108
cg03143333	18	15783361	47793599	47793649	N_Shore	TAGTATTACTTGCTATTCTATCAACCCTGTAAGATATTTGCGGCCACGCG	F	TSS1500	CCDC11	0.8917171	0.9329014	-0.041184286			
cg03148693	2	29744471	205130924	205130974	N/A	GGGCCTGGGAATAAGCCACTTTGTCATTACCCATCCTGTAGCACCGTTCG	R	N/A	N/A	0.9062857	0.9319071	-0.025621429	0.91563	0.9319071	-0.016277
cg03159191	6	20623414	161285451	161285501	N/A	GCCTGGCAAGGCCTCTCCAGTTCCTGCAGTCCTGAACCGCAGGGGTGGCG	F	N/A	N/A	0.8174886	0.86227	-0.044781429	0.8341675	0.86227	-0.028103
cg03160378	21	27658446	44880700	44880750	S_Shelf	GTGGGCCTGGGGAGTCGAGCTAGGTGTGCGTGCAGGTGCCTCACCTGCCG	F	N/A	N/A	0.8850543	0.9106514	-0.025597143			
cg03169836	19	39806369	16284256	16284306	N/A	CTGGGCTGTGGTTCACACCATGGGCAACAAGCAGACAGTCTTCACACACG	F	1stExon	CIB3	0.4515643	0.5316443	-0.08008			
cg03171770	10	63753414	43393728	43393778	Island	CGCCCTCCGTCCCACGGTTCTGCTCCGCAGGGAGGCTCGGCCCCATCTCT	R	N/A	N/A	0.1999943	0.137966	0.062028286	0.1744013	0.137966	0.0364353
cg03176203	16	32745442	14580863	14580913	N/A	CGGCTTCACTGTGCCCAAGAACAGCACGGTCCGGGGTGGTCCAGTCTGAT	F	Body;Body	PARN	0.3446414	0.2839186	0.060722857	0.3154175	0.2839186	0.0314989
cg03177972	11	63611342	78480035	78480085	N/A	GGAGAGAATCAATGAGCCTTGTTCTATAACCTACGCTTGTATGTATACCG	R	Body	ODZ4	0.9067429	0.9458343	-0.039091429	0.9220988	0.9458343	-0.023736
cg03178781	7	58635433	75650855	75650905	N/A	GACATCAGCTGGTCTGACGGGCCCCACAGGAGCTGACTCACCAAAGAACG	R	Body	STYXL1	0.5248843	0.6357071	-0.110822857			
cg03178887	6	73720322	32027402	32027452	N/A	CGGGGGTAAGCTGTCCTGGTCCACGTTCAGTTTTGTGTTCCTGTCTCCAC	R	Body	TNXB	0.9097371	0.9311371	-0.0214	0.9104263	0.9311371	-0.020711
cg03188390	8	40618341	43131535	43131585	N_Shore	GTGGAGGAAAGTGCAATGCTTCTGGTCCTCAGTCTCCTGCTGCACCACCG	R	N/A	N/A	0.4935314	0.36829	0.125241429			
cg03193847	4	45609481	169637496	169637546	N/A	ACAATCATTTCATTATTATTTTCCCAGGCAAAAGGACACAGACTTTCACG	F	Body;Body;Body	PALLD	0.68844	0.7499257	-0.061485714	0.7139038	0.7499257	-0.036022
cg03194064	16	14643327	57509786	57509836	N/A	CCTCCAGCAAGGGGCCCCAGCGGCTGGAGAAGTATCCAGATGAGAAGTCG	F	Body	DOK4	0.6049471	0.7094743	-0.104527143	0.667985	0.7094743	-0.041489
cg03197193	11	58768346	68190428	68190478	N_Shore	CGGCCCCCAAACTGTCTGTCCTGGTGCCCTGCAGAGAAAACAGTACGTGA	F	Body	LRP5	0.8540271	0.8908914	-0.036864286			
cg03202732	11	73773411	63655087	63655137	N/A	GCTTTGCCCTTCCCTAGAGGGTTAATGGCTACCAACGTGAGAAGGTCACG	R	TSS1500;Body;Body;Body;Bo	MARK2	0.7154957	0.8073157	-0.09182			
cg03205764	15	44673349	39626450	39626500	N/A	GCAGCAGGACGACTCCTGCAGTGAACACAAAGGGCACTGAACTCCTAACG	R	N/A	N/A	0.8582629	0.8971057	-0.038842857			
cg03224126	15	47749392	72491032	72491082	S_Shore	CGCTAATGCAGGAAGACCAAAGTGGAAGAACCATGGCCAAGGCCACTTTG	F	TSS1500	GRAMD2	0.8642571	0.9013386	-0.037081429	0.8796538	0.9013386	-0.021685
cg03225093	5	57647500	2008713	2008763	S_Shore	CGGGCTGAATCCTTTGCGTTTCTTTGTAATTGGAAAAGGATGTTTTTACA	F	N/A	N/A	0.5054157	0.6040271	-0.098611429	0.5352388	0.6040271	-0.068788
cg03229767	7	65648381	14415317	14415367	N/A	GGTAGGATTTCTTGAGTGCTCTATTTAAAATTATAAATAGATGCCTCACG	R	Body;Body	DGKB	0.6092271	0.7119671	-0.10274			
cg03233490	17	23654349	59018422	59018472	N/A	CACAAAAGCCTTAATGTTCAGTCTCCAGCTACCTCAGATTTTGGAGAACG	R	Body;Body	BCAS3	0.6698971	0.7580057	-0.088108571			
cg03233918	4	62764360	84991657	84991707	N/A	CGGGAACCTCGTATCTGTGTGGTAATGTCAGAGATAATGTTATGATTCGC	F	N/A	N/A	0.4636643	0.59558	-0.131915714			
cg03234405	4	27726336	25680103	25680153	S_Shore	CGGGCAGGGGCTGTGGCCGTCTTTGTACTCTGGTGATTTTTAAAAATTGA	F	3'UTR	SLC34A2	0.65782	0.7475171	-0.089697143			
cg03243902	8	20800413	140748972	140749022	N/A	CGGTCACATGTTCTCATTGCAAGGCAGCTGCGAGCATCGCCGCCATCATC	R	Body;Body	TRAPPC9	0.87696	0.9151843	-0.038224286			
cg03258749	1	23785321	151040405	151040455	N_Shelf	CGGAAGTTTTAATTTGAGGTTATCTGCTACGAAACAGTATTTCTAAAAGG	F	3'UTR	MLLT11	0.6067757	0.7275757	-0.1208	0.6571763	0.7275757	-0.070399
cg03263979	19	22728467	33860337	33860387	N_Shelf	CGGTCTCCCAAAGTACTGGGTGTGATGGGTGGCATGTGCCTATGGTCCCA	R	N/A	N/A	0.7829129	0.83155	-0.048637143			
cg03274456	11	37743471	62273116	62273166	N/A	AGGGCGGCGGCTTGCAATGAGCGGCAGGGAGCGTTGAAGGGCGTGGAGCG	F	Body	AHNAK	0.6114571	0.7005529	-0.089095714			
cg03274794	9	25787333	117374075	117374125	Island	GGATGGGGGATCTCCTTCTCCCCATAAATCAGTCTGGCCCTCCCCAACCG	F	5'UTR	C9orf91	0.3450657	0.4336771	-0.088611429	0.398475	0.4336771	-0.035202
cg03275758	11	74610389	128692159	128692209	N_Shore	CGATGCTGAAGACTTCTCATCGAGGAAGAAAGCCACATTCTTCATGGAGA	F	N/A	N/A	0.8318357	0.89387	-0.062034286			
cg03281929	6	13726432	22920242	22920292	N/A	CGCCTGACCTCAATGGAGATTTTCTGACAGATTATTTTTTGATAGTCCTT	R	N/A	N/A	0.9010129	0.9416743	-0.040661429	0.9210088	0.9416743	-0.020666
cg03284670	16	52725315	55909732	55909782	N/A	CGGTGGCAACTATGAAGGGCCAGAGGGGAAATAATATAATCGAAGAAGCC	R	TSS1500;TSS1500	CES7	0.8641443	0.8957686	-0.031624286			
cg03287207	2	53609324	132233561	132233611	N_Shore	GCCGGATCCCAGTTCTGATTGGCCATTGCTCAACATGTGTACTGGGGACG	F	TSS200	TUBA3D	0.9297829	0.9588643	-0.029081429	0.9459013	0.9588643	-0.012963
cg03287579	10	56672439	21187442	21187492	N/A	CGTGATGACTGTGTAGAATGTTTTTCTTGTCAGGATTTTCAGTTTAGGTA	R	Body;TSS1500	NEBL	0.89332	0.9311729	-0.037852857	0.899005	0.9311729	-0.032168
cg03290281	6	59798425	2632607	2632657	N_Shore	CGTTGCTATGCACCCATTCAGGGCTTAGCCTCACAGCCAAACTGAGATCC	F	5'UTR	C6orf195	0.7251429	0.80533	-0.080187143	0.7595013	0.80533	-0.045829
cg03293647	15	21751461	89849450	89849500	N/A	ACACTTACAGCCCTTGTCAGATATGTGAGTATTTGAGACAAGCAGATTCG	R	Body;Body	FANCI	0.9103	0.9493457	-0.039045714	0.9275625	0.9493457	-0.021783
cg03300649	16	31731304	28504949	28504999	S_Shore	CGAGAGGGCACATTTCCAACTGCATTCTGAAGGCCTGGTGGTGAGAAAGA	R	TSS1500;TSS1500	APOB48R	0.8191571	0.8722986	-0.053141429			
cg03301116	4	23720508	74065349	74065399	N/A	TAAATGTGTCACTCCTAAGTCCTTATGAATACCTCCTCCCCTCAGTCACG	R	Body;Body	ANKRD17	0.9177543	0.9478929	-0.030138571	0.9273988	0.9478929	-0.020494
cg03302951	12	59737426	122230972	122231022	Island	CGCCCTGCAGCCTTGGCAGGGCCTTGGCCGGCTCTTCACTCCTGGAGGCC	R	Body	RHOF	0.6446643	0.7359229	-0.091258571	0.680615	0.7359229	-0.055308
cg03303475	6	58742318	31130398	31130448	S_Shelf	CGTCTGGTTCCATGTGGCCTGTGTTGGCTGCAGCATCCAGGCTGCCAGGG	F	Body;Body	TCF19	0.81896	0.8650486	-0.046088571			
cg03303633	2	48665363	145196972	145197022	N/A	CGAGGCTGAGAGGACGCACCAGGCCGTCTCACCTGGGCAATGAGCAAAAG	R	Body;Body	ZEB2	0.8757486	0.9033986	-0.02765			
cg03303857	11	11660392	120619307	120619357	N/A	CGTGCCTGTGTTTTGCTGACTCTGGCATTTGCACTTGGTTTTTCCCCACA	F	Body	GRIK4	0.5367814	0.6457071	-0.108925714	0.592195	0.6457071	-0.053512
cg03304437	4	61794384	159092536	159092586	N/A	CGGCAGAGAAATGACCTGTCCAGACAAGCCGGGGCAGCTCATAAACTGGT	R	5'UTR;5'UTR;5'UTR	FAM198B	0.4790843	0.5675971	-0.088512857			
cg03311252	11	64640400	67209355	67209405	N/A	GGGTGTGGCCGAAGGGGGCCAGCAATAGGACCAGCAGAGGACTGAGCTCG	F	Body;Body	CORO1B	0.78907	0.83902	-0.04995			
cg03318906	8	67743445	37755254	37755304	N_Shore	CGGGCTCCTTCCAACCTGGAGAAATCTTTACTAACATGGGGCCCAGGGCA	F	Body;Body	RAB11FIP1	0.7474057	0.8274971	-0.080091429	0.7905188	0.8274971	-0.036978
cg03325664	8	23801464	11534225	11534275	N_Shelf	CGCCGTTCATGGGGAGAAATGCTCAGTTCACCGTATGTGCTTCCTGCACC	R	N/A	N/A	0.45956	0.5759643	-0.116404286			
cg03330920	16	68644500	1610308	1610358	N/A	CGTGTTCCTGGTCACCATGTAGAGCCAGGCTGCACAGCCAGCAGAGGCCG	F	Body	IFT140	0.7865157	0.8341057	-0.04759			
cg03331035	8	69745473	135813886	135813936	N/A	CGGTTGTAATAGAAGTAGTTAAAACAGAAAAGCAGTATGGTTGTAGAGTG	R	TSS1500	MIR30B	0.86251	0.9002757	-0.037765714			
cg03333377	11	20600358	93277841	93277891	S_Shore	CGCAGCAGGAAGGACACTTCCTGTAAAAATGAAAAAAAAAGCCTTAAGTT	R	TSS1500	C11orf75	0.7339286	0.7971214	-0.063192857			
cg03334660	4	40616364	39050551	39050601	S_Shelf	CGCGCCTGGTGTACATTGGCTCTTCAGGGCTTCTGTCTGGAAGTGACACT	F	5'UTR;5'UTR	KLHL5	0.8596829	0.8933086	-0.033625714			
cg03344105	20	23606503	57426131	57426181	N_Shore	CGGCTTAACCACTTGAGCATCCACTGAATGGCCCAACTGGGTCCCAACAC	R	TSS200;3'UTR	GNASAS	0.47975	0.5482686	-0.068518571			
cg03347739	6	39665350	53787668	53787718	N/A	CGTGCTCCTTGTCCTAACCAGCCCCCGCGCGCCATCTTCCCGTGGAGTGT	F	3'UTR	LRRC1	0.87546	0.9008814	-0.025421429	0.8816263	0.9008814	-0.019255
cg03355370	10	65622338	30046142	30046192	N/A	CGGCAGAGGAAAGCCTGTTTTGCAGATTGAGATTTCCCATAAATTGTTAC	R	N/A	N/A	0.8971243	0.9433657	-0.046241429			
cg03357664	1	19693374	29446693	29446743	N_Shore	GTCATTTTCTAAAGTAAGTTACCCACATTGACCAAAATGCAGCTTCAACG	R	3'UTR	TMEM200B	0.6618829	0.7512029	-0.08932			
cg03360907	11	33648423	62688748	62688798	N_Shelf	AAGAGGGGTCTGTAGGGTCCTCAGCCCCACTGCCTCCCTGGGGGCCTGCG	R	5'UTR;1stExon	CHRM1	0.68184	0.7666229	-0.084782857	0.7206013	0.7666229	-0.046022
cg03367275	10	25637449	93649798	93649848	S_Shelf	AAAAGTCTCAAAGGTAGTATGTCGTACTGAGCAGGGATCCCCAACCTCCG	F	N/A	N/A	0.73428	0.8150043	-0.080724286	0.7533288	0.8150043	-0.061676
cg03369965	3	54615484	169531731	169531781	S_Shore	GGAGCATGCAGACGGGCAGGTTGTGGGGCACGTGGGCTCCGAACTCACCG	R	TSS1500	LRRC34				0.337875	0.2650443	0.0728307
cg03384175	7	64706467	94286343	94286393	Island	GCTTCATTGCGCTATAAACTGATGGGCGCTTTATGTGCCACAAACTGACG	R	TSS1500;5'UTR;TSS1500;5'U	SGCE	0.5429557	0.5917486	-0.048792857	0.562575	0.5917486	-0.029174
cg03386373	2	69625332	231860456	231860506	N/A	CGCATTCATCTTCAGGTCAGCTTCCTGAAGATTTGGAGCTTCTTCGAAGG	R	TSS1500	SPATA3	0.8223571	0.8774257	-0.055068571			
cg03388247	2	34701423	242165505	242165555	N/A	CGTCGGGTGATGTGGAACTTGCCTTTTACCCACGTGCTGGTTACAACAGT	R	N/A	N/A				0.929995	0.9091686	0.0208264
cg03399210	8	45724501	37616064	37616114	N_Shelf	CTTCTTCTATGTGCTATCCCATTTGTAATCTTATTCCATTTTTTTTCACG	F	N/A	N/A	0.89814	0.92877	-0.03063	0.9071275	0.92877	-0.021643
cg03405789	8	27727491	67088895	67088945	N_Shore	CGGAAACTAAACGTAGACAAAACGAATAACATTGTGTTGCTGCTGCACGT	F	3'UTR	CRH	0.3568986	0.4706214	-0.113722857			
cg03410806	4	64644331	811641	811691	N_Shore	CGGCTGGTGGGAACAATGCACCCTCCAATGGGCACCTGGGGAGGGTCTCT	R	Body	CPLX1	0.5352514	0.6011	-0.065848571	0.5637038	0.6011	-0.037396
cg03417055	8	30622487	144501878	144501928	N_Shore	CGCCCTGTCCAGGGCCCCAGAGTTTCTGAACTCAGCTTAAGTCAGCTCCC	F	N/A	N/A	0.6415757	0.7223471	-0.080771429			
cg03421926	17	71663421	34057601	34057651	N_Shore	GATCCCAACTCCTCATCCTGTCAATCAGGGCCTTTGTGACCAACCTCTCG	R	TSS1500	RASL10B	0.8650129	0.8978	-0.032787143			
cg03434509	8	34648315	82543424	82543474	Island	CGGGGCGGGGCCCAGCAAAGCAACCACGCCCCCTCATTGATGGGCTTAAG	R	N/A	N/A	0.3781029	0.5295057	-0.151402857	0.4625925	0.5295057	-0.066913
cg03441171	8	23752367	144965352	144965402	N_Shore	GGCTGGCAGGTGTGGCCTCTTGGGCAGGAAGAGTTTGCTAACATCTGACG	F	N/A	N/A	0.6283143	0.7243871	-0.096072857			
cg03446289	10	20659462	106075560	106075610	Island	TCATCAGGAAGAGGATCATGCAGAGGGTGCTCCAGAGGTCCCAGGCCACG	R	Body	ITPRIP	0.8573971	0.8875314	-0.030134286			
cg03447361	16	50713509	58972525	58972575	N/A	CGGTGGATTCTGCCTTGAGCTTTGAAAGTGAGTCAAGGAGAGAATTAAGC	R	N/A	N/A	0.5017643	0.6038571	-0.102092857			
cg03450635	4	29726319	159094213	159094263	N/A	CGTGGATTCTCTCTGATTGGAGGTTTTTTGAAAAAACAGGTTAGGGATTG	F	TSS200;TSS1500;TSS200	FAM198B	0.2905771	0.3900029	-0.099425714	0.3404013	0.3900029	-0.049602
cg03456771	7	32747494	56242072	56242122	N_Shore	CGCGGGCTCACCACCCCGCCCCAGCTACCACCACTGCCCACCCCGCCCAC	R	N/A	N/A	0.5618086	0.6508443	-0.089035714	0.6002725	0.6508443	-0.050572
cg03460315	4	50760353	111010391	111010441	N/A	CGGTAGTGTATAAAAACGTGCATTCAGCTTAATATAACTACAGTTGGCCT	F	Body;Body	ELOVL6	0.9309257	0.9688829	-0.037957143			
cg03461851	15	74639425	62457883	62457933	S_Shore	CGTCCAGGTTACATGCAGGGTGAGTGACGGTTTATCTCCTAGCCAAATTA	R	TSS1500	C2CD4B	0.6454071	0.72921	-0.083802857			
cg03463948	11	74704392	122612858	122612908	N/A	CCAGGCTTGAATAATCCCTGAGGTCAGAGGTTAAGACCAAGGCAGTCTCG	F	Body	UBASH3B	0.6552443	0.7009843	-0.04574	0.7203138	0.7009843	0.0193295
cg03469233	1	30732335	230527641	230527691	N/A	CGGGCCACTGCTGAGCATGGAAGAAAGAAATGCAGCATGGGGCTCGTTTT	R	N/A	N/A	0.7294086	0.8106357	-0.081227143			
cg03472898	14	20687404	29240992	29241042	N_Shelf	TGGGCTTCAGGAAGCCTTTACAAAGTTCTCTCTCCATATATCCACCTTCG	F	TSS1500;TSS1500	C14orf23	0.1696757	0.2529457	-0.08327	0.1959963	0.2529457	-0.056949
cg03472954	7	39719441	597596	597646	N_Shore	CGCAGCAGGGGAATCACAAAGGATTCATTTTCCTTGCGACTATTTTGATT	F	Body;Body;Body;Body;Body;B	PRKAR1B	0.8158443	0.9015757	-0.085731429	0.877585	0.9015757	-0.023991
cg03476212	16	16635318	85301802	85301852	N_Shelf	AACCCTTGTGCCACACCTTGTGCCAGTACCAGGGCCTCAGAGAGTAGACG	F	N/A	N/A	0.7785343	0.8337857	-0.055251429	0.8035625	0.8337857	-0.030223
cg03480067	7	69631487	148286320	148286370	N/A	GGAAGAAGTTATTCCTAGACAACGAATGAATCCCCTGGATTTGGGTTGCG	F	TSS1500	C7orf33	0.7150843	0.7796286	-0.064544286	0.7376963	0.7796286	-0.041932
cg03481488	10	47715320	81091172	81091222	N/A	CGGCCTCACAGGCTCACCTGTGTCAGCCTCCTGTGATGCTCCCTGACTCG	F	N/A	N/A	0.8581729	0.8978857	-0.039712857			
cg03481774	11	13716401	45959600	45959650	N/A	CGGACTGGGAGAGAGAAGAGACTGCCATTTCCCCGGGAAAGGAATTCCTC	F	Body;Body	PHF21A	0.9156586	0.94003	-0.024371429			
cg03481855	8	23808494	129089293	129089343	N/A	TTTGAGGCTCAGGACCACAGAGGTCACAGGATCTGATTCAGATGCCAGCG	R	Body	PVT1	0.82373	0.8746357	-0.050905714			
cg03482617	11	19780337	70936781	70936831	N/A	GTGAGGCTTTCTGTTATTTCATCTGTTTCTAGCATGTTCCTAATTGTTCG	F	TSS1500	SHANK2	0.8816086	0.9387443	-0.057135714			
cg03498588	3	50624374	66015536	66015586	N/A	AATGACTTGGCTAAGTAAGGGATGCTGTGCACAGACCTATCCCTAACTCG	R	Body;Body;Body	MAGI1	0.8961943	0.9262114	-0.030017143			
cg03500617	16	40783417	74812570	74812620	S_Shelf	ATGGGAAGCCTGGCCCAGATGCCTCAGGGGTCCCCAGGTCAGAAGAGCCG	R	N/A	N/A	0.7133057	0.7571929	-0.043887143	0.7209788	0.7571929	-0.036214
cg03502982	14	65650394	25043625	25043675	N/A	TGAACCCAGTGGCTCTGCCTAGAGCCCAGGAGGGACTGAGACCCGGGACG	F	Body	CTSG	0.6028171	0.6672529	-0.064435714	0.6065563	0.6672529	-0.060697
cg03511628	18	45799415	77280586	77280636	S_Shore	GGGAGGGTGCATCCACCACTAATGTGTGTCCGTGTGTGTGGGGGCATCCG	R	Body;Body;Body;Body	NFATC1	0.6229514	0.7310114	-0.10806			
cg03511735	8	14679406	142405227	142405277	S_Shelf	CTACGGCAGCTGAGAGCTGCGCTCTTTAGCCGAGCGGGATCAGGGCTACG	R	N/A	N/A	0.8273929	0.8909814	-0.063588571	0.8607538	0.8909814	-0.030228
cg03511806	5	36768484	66124801	66124851	N/A	CGTGCCCAGTAAAGGAATGACAAGGGAACTTTGAAATCCTCAATGGCTGG	R	Body;Body;Body	MAST4	0.0881294	0.1279831	-0.039853714	0.088435	0.1279831	-0.039548
cg03524755	1	60605457	78277588	78277638	Island	CGCCACCTGCCGAGGAGCCGCCCAAGCCCATTTTGCATAAATGTTTTATG	F	Body	FAM73A	0.6211857	0.7673629	-0.146177143			
cg03528519	1	34704309	53513817	53513867	N/A	CGCTCAGGGCATCCACAGATGTGTAAAAGAGTCAGTGCAGCCAGAGATCC	F	3'UTR;Body;Body;Body	SCP2	0.8511871	0.8990514	-0.047864286			
cg03531984	17	14716407	3500374	3500424	N/A	CGCTGTGGACGCCCTTCGGCACTCAAGGAAAAAACGCTTCCAGCGATGCA	F	TSS1500;5'UTR;TSS200	TRPV1	0.8080286	0.8745543	-0.066525714			
cg03534655	7	35714397	3082233	3082283	N/A	CGCAGAAGTGGACACTTACGGAGAAATTCCTGTCCTCATATCAATTCCCG	R	5'UTR	CARD11	0.8602286	0.9108929	-0.050664286			
cg03535079	8	33794458	48523498	48523548	N/A	TATTAAACATTGCACTGATACTTGTCATTGCCTTCAAAATAAGCTCTACG	R	Body	KIAA0146	0.8986586	0.9427986	-0.04414	0.9249113	0.9427986	-0.017887
cg03544474	3	62601338	126206070	126206120	N/A	GCAATGATAATGGATCCTGGGGAACCTGGGGTCAGACCGTGGCTCCATCG	R	Body;Body	UROC1	0.6313829	0.7002943	-0.068911429			
cg03546360	1	72690400	12675968	12676018	N_Shore	GGAGCCTGAACTATCAGCCAAAGCCGATCCGATTAACTCTTCCCTAGCCG	F	Body	DHRS3	0.21117	0.1448671	0.066302857	0.18919	0.1448671	0.0443229
cg03548415	11	53731425	111991342	111991392	N/A	GAGAAGTGAGTCATAGGCCCAATGAAACTTATGAACCAAGATTAGTCACG	R	N/A	N/A	0.6061929	0.7246671	-0.118474286			
cg03551378	6	18724457	36309528	36309578	N/A	CGCTATGTTGTCCAGGCTGGATTAGAATTTCTAAGCTGGAGAGATCCTCC	R	N/A	N/A	0.6276414	0.6820471	-0.054405714	0.6574763	0.6820471	-0.024571
cg03551497	5	32607378	4866009	4866059	N_Shore	TAAGACAGTAATTTATTTCCCCAAACCTTTCCAGCTAACATGGGCTTTCG	F	N/A	N/A	0.7649543	0.8477557	-0.082801429			
cg03552086	16	34655445	979188	979238	N_Shore	CGTTGTTCTGGGACTGAGACCAGGGCCGGTCCCCAGTGCTTCTGGAGACG	F	Body	LMF1	0.8872929	0.91832	-0.031027143			
cg03559389	10	47606508	679322	679372	Island	CGGACTCCCCCCGTCTGCTCTATGGCACCGCCGGAATGTGAACGCTGTTG	R	Body	DIP2C	0.9021314	0.9273314	-0.0252	0.9154113	0.9273314	-0.01192
cg03562117	8	14688335	85461487	85461537	N/A	TCACACTATCACAGTAAGTGATTAAAGGGTTGACTGTTATCTTCATTTCG	F	Body;Body;Body;Body	RALYL	0.7007229	0.8173671	-0.116644286	0.7396613	0.8173671	-0.077706
cg03562528	14	67614313	94423943	94423993	N/A	GTGCCTTAGTCCCCGCTCCTGCAAGGTGGCATGAAAACAGCCTGTGCTCG	R	TSS200	ASB2	0.8330229	0.8789357	-0.045912857			
cg03563169	6	50685407	85445250	85445300	N/A	CGGTGAGGAATTTCAGTAGGTTATCTCCAGCAATCTGTCTTTTGGGAGCT	R	3'UTR	TBX18	0.4819914	0.6066657	-0.124674286			
cg03573824	2	66764402	175547126	175547176	Island	CGGCGATGCCCTGGGGCTGCACCTACACCCCAGCTAGGACAGAGGGGGAC	R	5'UTR	WIPF1	0.19769	0.2538143	-0.056124286	0.202195	0.2538143	-0.051619
cg03586847	1	29791304	40726012	40726062	S_Shelf	ATCAGGTCTGTGAGAAAAGACCAATTTTCAGCCGGGCACGGTGGGTCACG	F	Body	ZMPSTE24	0.7228114	0.7766043	-0.053792857	0.7503388	0.7766043	-0.026266
cg03588812	22	69627321	19777109	19777159	S_Shore	CGGGGACGTTGCCCCCACCAGGCAAGGTACACTGTGTGGCTCCTGCCGCC	R	Body	GNB1L	0.8931971	0.9211214	-0.027924286			
cg03591912	6	73808410	160258242	160258292	N/A	CCCAAGGGGACCACATCAGCTCTGGGGGACCAAGATGCAGCAGGGGAGCG	R	N/A	N/A	0.79393	0.8329214	-0.038991429			
cg03600094	11	39795348	2481475	2481525	N/A	CGGCCTGCCCACAGAGAATCAGGTCACGCAGGGACTCACCCTGCCCCGGA	R	TSS1500;Body	KCNQ1	0.8423529	0.8908229	-0.04847			
cg03610280	10	38644422	97592418	97592468	N/A	CGCTGCCTCTTCTGTGAATGCAGGCTCAGGGACCAGACCACTTTGATTTT	F	Body;Body;Body;5'UTR;5'UTR	ENTPD1	0.6409843	0.7571414	-0.116157143			
cg03614954	1	22704509	24439418	24439468	N/A	AGGGCCTCAATCCCCTGTATGGCCAGCGTTCCACCAGAAGGGACGGGACG	F	TSS1500	MYOM3	0.8123014	0.8436743	-0.031372857			
cg03616722	13	38770466	112602415	112602465	N/A	CCGGAAAACAGCCGTAAAACGTGTCGGGGAGAACGCGTTTTCAGTCAGCG	F	N/A	N/A	0.8823471	0.9212443	-0.038897143	0.9041163	0.9212443	-0.017128
cg03625918	3	20665317	62468713	62468763	N/A	CGGTGCCAGCTTGAGGAGCCGTGTATGACACCGTCCTTCCAAAGAAATAC	R	Body;Body;Body	CADPS	0.8065329	0.8640114	-0.057478571	0.8201238	0.8640114	-0.043888
cg03626186	10	18777438	5882466	5882516	Island	TCAGGTCTGACCCTGAAACGGAGACCCACCTCCGTGGGGAGAAGCACACG	R	N/A	N/A	0.6122957	0.6758986	-0.063602857	0.64973	0.6758986	-0.026169
cg03632782	16	60693436	82781365	82781415	N/A	ATACTCTGCTATTCCTAAATCCCAAGAGTTGACATACTTCACAACATTCG	F	Body	CDH13				0.79856	0.8427786	-0.044219
cg03633706	6	59767455	47754443	47754493	N/A	TTTGTGGGTTTAAACTACTCCCCATTCTAAAGTACTCACTGTCTCAAACG	R	Body;TSS1500	OPN5	0.8017614	0.86715	-0.065388571			
cg03636939	6	39801301	4221388	4221438	N/A	TGATTCAGTCTCTCCTAAGATTTTCATTTCAAATCATCTTTCTTGACTCG	F	N/A	N/A	0.85216	0.9093386	-0.057178571			
cg03639249	6	36643382	29574225	29574275	N/A	CGTCTCTATTCTGCCCCAGCTGGAGCATTGCAGCTCCAGGAAGATGAATA	R	Body;Body;Body	GABBR1	0.6698686	0.72425	-0.054381429	0.6716113	0.72425	-0.052639
cg03639429	7	57665379	55070311	55070361	N_Shore	AGTTGCTGTTCAAAACCTTGGAGTCACCCTTGGCTTGTCTGTCCCTCACG	R	N/A	N/A	0.7737029	0.83188	-0.058177143			
cg03648611	16	39610479	31091702	31091752	Island	AACCGCATGGCCCTGAAGGACCACCAGAGGCTGCACTCAGAGAATCGGCG	R	Body	ZNF646	0.89318	0.9195443	-0.026364286	0.9019563	0.9195443	-0.017588
cg03649060	19	11657480	11665451	11665501	N/A	CGAGGAAACTGTGGCACAAAGAGCTTAAATAACCTGCCCAGGTCACGCAG	R	5'UTR	ELOF1	0.6869486	0.7552914	-0.068342857			
cg03657678	17	42603352	80960511	80960561	Island	GCCAAGGGCCCCACAGAGGATGGCAGGGACAAGCCACCCATGTGGCAACG	R	Body	B3GNTL1	0.8843371	0.9084557	-0.024118571			
cg03660788	5	34625390	115782914	115782964	N_Shore	CAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACG	F	Body	SEMA6A	0.8445	0.8801257	-0.035625714			
cg03661054	2	56677308	3281330	3281380	N/A	CGGGTAAGTGAGTTCTTATTTGTAAAGCACGTAGGTGAAGGCCACACAGG	R	Body	TSSC1	0.8737029	0.8998557	-0.026152857			
cg03661567	16	40783506	50978181	50978231	N/A	CTATCCCAGAGAGAAACACTCATGTGCTCGTGCGTTAATTCATCCCTTCG	R	N/A	N/A	0.86418	0.8952171	-0.031037143	0.8681713	0.8952171	-0.027046
cg03667871	1	54733464	198125222	198125272	N_Shore	CGTGCTCATTAAATTGTTGCTGTTGTTCATAGGTCTCTCACTAGTTTAAC	R	TSS1500	NEK7	0.8316571	0.9129429	-0.081285714	0.8818613	0.9129429	-0.031082
cg03668470	12	57740478	57588180	57588230	N/A	AGCTGGGTGCGTAGCAGAGTGAGGTCCGCTCGCAGGGCTGGAAGAGCACG	F	Body;TSS200	LRP1	0.8537757	0.9042771	-0.050501429	0.8793838	0.9042771	-0.024893
cg03680663	3	19651387	140071429	140071479	N/A	CGGAATGCAAATGTATTTGCTAACCCAAGCAGCTCTACTGTAACGTACAT	R	Body	CLSTN2	0.8940286	0.9287557	-0.034727143			
cg03691338	10	71766472	50344050	50344100	S_Shelf	CGGTGCTCTACTGAGCCATGAAAGTCACGCCTGACCTAAACAGAAGACTA	F	N/A	N/A	0.6569143	0.8014286	-0.144514286			
cg03691530	8	30741374	128834932	128834982	N/A	GGACAAATCAGGGGGCATTCCCACTGAGGCAGGACTTGAGATGAATCTCG	R	Body	PVT1	0.5957286	0.6740814	-0.078352857			
cg03692651	19	13803361	22444593	22444643	Island	GGTGCGGGCGGGGCGGGCGGGGCGGGCGGGGCGGGGGTGTCGGGGGCTCG	R	N/A	N/A	0.1640806	0.1134567	0.050623857			
cg03698948	6	53654450	39760092	39760142	Island	GAGTAACCTTGCCATAAATATCCCGCTCCAAGACGCCTGACGTCAGAGCG	R	TSS1500	DAAM2	0.1264471	0.0973474	0.029099714	0.121989	0.0973474	0.0246416
cg03708045	8	31687399	48595620	48595670	N/A	GGGAATTGTTAATGCTTAGCCTACACAGTTCAAACAGAATCTCTCAGACG	F	Body	KIAA0146	0.7611771	0.8436829	-0.082505714			
cg03715070	17	20720362	46124684	46124734	N_Shore	AGGAACGCATTGCAAACGCCAACCCAATGATTCCCTAAATGGGGTCTTCG	R	TSS1500	NFE2L1	0.3395071	0.4749343	-0.135427143			
cg03716908	5	38807413	81149002	81149052	N/A	AAGAATGTGGCTGCACCCACAGGTGGACAGATACTGAACTCTCTCAGCCG	F	N/A	N/A	0.9122	0.9408886	-0.028688571	0.92762	0.9408886	-0.013269
cg03718883	11	11687384	2098414	2098464	N/A	AAGAAGACTCACTGTATATTTCCATATATACAGTGAAACTCAGAAATGCG	F	N/A	N/A	0.7501071	0.8399986	-0.089891429	0.7762	0.8399986	-0.063799
cg03730703	1	32743455	160173841	160173891	N_Shore	GAATCTCAGAAGAACCCTCAGAAATAGACATTGGCACCCTGATCTGACCG	R	TSS1500	PEA15	0.8894271	0.9145671	-0.02514			
cg03731740	1	57651494	29062689	29062739	N_Shore	TTAATTTCCTTGCTTCCCTCTTGAGGTCCTTAAGATTCATAGGTTCTCCG	R	TSS1500	YTHDF2	0.6888243	0.5698429	0.118981429	0.6668788	0.5698429	0.0970359
cg03734229	1	16769317	41236997	41237047	N/A	TCTGCCCTCAGATGGAATTAGGTGAATGTGTGTAGCTGCTTTTTCACTCG	R	3'UTR;3'UTR;3'UTR;3'UTR;3'U	NFYC	0.8315757	0.8805786	-0.049002857			
cg03734896	14	58804307	105286870	105286920	S_Shelf	TCATATGTTGAAGTCCTAACCCCTATCCCTCAAAATGTGACTGTATTTCG	F	TSS1500	MGC23270	0.73063	0.8369786	-0.106348571			
cg03736062	4	31708493	113208476	113208526	S_Shore	CGGGCAACCTAGATCCCTCCCATGTGCAGGGTTCCTGCTCCTATAAGAAT	F	TSS1500	TIFA	0.8802071	0.9157214	-0.035514286			
cg03736977	20	55809473	55684764	55684814	N_Shore	CGCCCAGCCCAGCAATGAGAAAGCTTGTGTTCTAGTTCCAGTTCTGGTAC	F	N/A	N/A	0.9100786	0.9381386	-0.02806			
cg03738656	21	44779352	45581008	45581058	N_Shore	CCAGGGAGTTTTACAGATGCTGGATCACAGGGGTGGGCCCATGAGAAGCG	F	N/A	N/A	0.8276443	0.8878043	-0.06016			
cg03742132	12	15714397	81227142	81227192	N/A	CGGGACTATAAACAAGAACTGGTGATTGACTGGATATGCAAGGTGAAGAA	R	Body;TSS1500	LIN7A	0.9099486	0.9480543	-0.038105714	0.93366	0.9480543	-0.014394
cg03748259	19	73735401	11773378	11773428	Island	CGGCCTCGCCTTCGGCTGCATCATCTCGGGGATGTTTCACTTGTCTCTTC	F	N/A	N/A	0.8549357	0.8989329	-0.043997143			
cg03752203	8	21774433	103874399	103874449	N_Shore	ATTCACATCAGTATAAACCCACAAGTCTTAAGTATGCAATTTGATGAACG	F	5'UTR;5'UTR	AZIN1	0.7971529	0.86534	-0.068187143			
cg03758633	16	33684425	51611768	51611818	N/A	GGCATCTACACATTGAGTCAGAGGACGCCAAGTGTTAAACTGTAATACCG	F	N/A	N/A	0.6881457	0.7932929	-0.105147143	0.748515	0.7932929	-0.044778
cg03761513	6	34610369	168633350	168633400	N_Shore	CGCTCCTGCAGGAGCTCCCTCAGGCTGTTTTCCCTGCAGGACTTTTGAGC	R	N/A	N/A	0.6170043	0.6916529	-0.074648571			
cg03762393	19	24799505	623245	623295	Island	CGGCAGCCAGGCTGAGTTCCTAGGCCCTGCATGACCAGACCAGGGCATGA	F	Body	POLRMT	0.8969671	0.9219157	-0.024948571	0.9011363	0.9219157	-0.020779
cg03766264	12	64748473	27396229	27396279	N_Shore	CTTAGAAATGCCACCTGTCATCTTTAGGTTTCCCAAGAGCAGGTGACACG	F	TSS1500	STK38L	0.8942457	0.9299157	-0.03567	0.8988513	0.9299157	-0.031064
cg03771731	11	50654303	20643929	20643979	N/A	CGGCCCTGCACTTCAGGAACCTGAGAGTGAGCGCCTCTCAATTTTGCACA	R	Body	SLC6A5	0.8399943	0.8823586	-0.042364286	0.843415	0.8823586	-0.038944
cg03773183	17	47682448	79325994	79326044	N/A	GGACGGGAGGCTCAGGCATGGCAGGCTGTAGGTCCCAGCTCTGCCCCACG	R	N/A	N/A	0.5069657	0.6887929	-0.181827143	0.5781488	0.6887929	-0.110644
cg03780486	11	26611440	6817280	6817330	N/A	CGGCTGCCCTAAAATGAGAGTTTGTCTTTGAGTTGGATCATGACTCTGTT	F	TSS200	OR6A2	0.8191571	0.8843329	-0.065175714	0.858475	0.8843329	-0.025858
cg03785456	2	54658475	134255543	134255593	N/A	CGCATGGCTCTGGGGACTGCATTTGCTCATTTTCACCATTGCGGGTTGTG	R	Body;Body	NCKAP5	0.8920914	0.91347	-0.021378571	0.8892788	0.91347	-0.024191
cg03786842	10	54688416	127569751	127569801	N/A	CGGGTTTCTGTCATTTCTGCTGCCTGCTTAAAAGAACAGGAATAATTTAG	F	5'UTR;1stExon	DHX32	0.5903743	0.6809986	-0.090624286			
cg03789372	8	31675338	27125756	27125806	N/A	CGAGAATTGACTCTAAGTGGTCTCAGATCCTATACTATGAGCAGAAAGGA	F	N/A	N/A	0.8339814	0.8852914	-0.05131			
cg03793678	15	25739401	96862225	96862275	N_Shelf	CGGTGATGTGATGTGGTTCTGCCAAGAAATAACCAATGTGACATTTTTCA	F	N/A	N/A	0.5498157	0.6722329	-0.122417143	0.6251213	0.6722329	-0.047112
cg03803861	5	66738365	41511150	41511200	S_Shore	CGGAAAGCCCTGAAACCCAGCATGAGAAGTCTGTTCCTCAGGAGGCAATA	R	TSS1500	PLCXD3	0.2580857	0.3447086	-0.086622857	0.2757688	0.3447086	-0.06894
cg03811905	2	10684386	239070208	239070258	N_Shore	CTCCTGCAAAGTGTCCCACCTGCTTGGTAGGAGCCCAGTGAGGCCAACCG	R	N/A	N/A	0.7532514	0.8012029	-0.047951429			
cg03818767	11	11626487	64338639	64338689	S_Shelf	CGGCTGCCTGGCCTCTGCCATGCCAGGCCCTTGAAGTCGCCCAACTCGCC	R	3'UTR	SLC22A11	0.8426386	0.8720914	-0.029452857			
cg03819227	5	49621403	110252994	110253044	N/A	CGGATGTTTCTGCTTTTGATCCTTAGCCTGTTTCCGACTCTTGGTATCTG	R	N/A	N/A	0.4132271	0.53457	-0.121342857			
cg03819692	16	57798410	89225639	89225689	N_Shore	CGAGGTCACTGGAGGATAAACATCCGTGACTGCACCTCATGATCCATCAC	F	Body	C16orf81	0.4955	0.5828386	-0.087338571			
cg03820837	3	74796439	28431690	28431740	N/A	CGCACTTTTACTCTGTGAAGATGATATTCTTTGTTGTGTTGCCCTCTCTG	R	TSS1500	ZCWPW2	0.9021629	0.9410114	-0.038848571			
cg03834055	10	50809478	134548558	134548608	N_Shore	GGCTTAGAAGTGTTGTCTGCTCCCCAGCCGTGTGGAGCAGGTGCATCTCG	R	Body	INPP5A	0.8831271	0.91833	-0.035202857			
cg03835229	4	62616473	3442311	3442361	N/A	CGGGCTTGTGGTGGGTGGTACACACAGCTGGCACTGGGCTTCATCTTCCA	R	TSS1500	HGFAC	0.8231471	0.8657714	-0.042624286			
cg03836747	7	67671353	64696583	64696633	N_Shelf	TTCCCTCTTTACTCTCTCTTCCTCCTGCTCCATCCATGTAGGATAGGTCG	R	N/A	N/A	0.7842614	0.8387857	-0.054524286			
cg03837526	17	48724304	60886284	60886334	S_Shore	CGGTTCTGGTGCCCTGGCTCCAAAGCTGTAGGGCCTGGTCTAGGCCTCTA	R	TSS1500	MARCH10	0.8085986	0.8545757	-0.045977143	0.8193238	0.8545757	-0.035252
cg03841136	21	20677481	43136835	43136885	N/A	GAAGGTTGGAGTGATGTGGTCTGCTGCGGGGACCCTGAGGCGTGCAGGCG	R	Body;TSS1500	NCRNA00112	0.8468814	0.8975486	-0.050667143			
cg03846076	5	27767378	172743837	172743887	N/A	CGAAATCCTAAGGGAAATTTGTCAAATGTACTCCCCAGGTGTGTATTTTC	F	3'UTR	STC2	0.6989186	0.8115157	-0.112597143	0.7605025	0.8115157	-0.051013
cg03847348	1	33617409	2413705	2413755	N_Shore	CGGCCCCCTCCACAGAGTGGCTATGTGCCAGGGTGAGCCACTCACCACTG	R	Body	PLCH2	0.7950586	0.84256	-0.047501429			
cg03848588	9	41702352	32525008	32525058	N_Shore	AGCACCTGGGCAAACTCACACTGCCTTGCCACCAAATGGTTTGCTGAGCG	R	Body	DDX58	0.8402214	0.8839557	-0.043734286			
cg03854322	2	30733507	128699333	128699383	N/A	CGGAGTCACTTATGACACAGATCAGGTTTAACAGGGGTGCACCCGAACGC	F	3'UTR;3'UTR	SAP130	0.9180857	0.9467771	-0.028691429	0.9374913	0.9467771	-0.009286
cg03856411	16	62751321	23410986	23411036	N/A	TCTGCCTCTGTGTACCGCATACATCCTATGGCCAGCCGCTTCTCTAATCG	F	Body	COG7	0.8824757	0.9193914	-0.036915714			
cg03857617	5	44721440	19854080	19854130	N/A	CGTGGCACAAATGTGATAAGCAAAGTAGGCAAAGTGCTGAAGAATGCCAC	F	5'UTR;5'UTR	CDH18	0.7492014	0.81692	-0.067718571	0.791735	0.81692	-0.025185
cg03870976	4	72759329	530048	530098	Island	TTGCAGTCTGGCCAGGGAGCGATTCTCCCCTTGGAAAGGCTCCATGTCCG	F	Body;Body	PIGG	0.9210914	0.9456171	-0.024525714			
cg03876697	5	43644496	148759078	148759128	N/A	CGGCCAGAGCCCCACCAGACACACAGGGCATTGTCCCTCGGTCAACAGCC	R	TSS1500	IL17B	0.8886714	0.9298943	-0.041222857			
cg03881351	22	27635335	46240067	46240117	N/A	CTCTGCCTTTCCAAAACATTGACAAGACTCATTTCCAGTTAATTAATTCG	R	3'UTR;3'UTR	ATXN10	0.88006	0.9324257	-0.052365714			
cg03883275	10	62665404	49608385	49608435	N/A	AAATGTATCCAAGTCTAATTCCTCATTTGTTTCTAGTTTATTTGTCCTCG	R	TSS1500;TSS1500;TSS1500;	MAPK8	0.6752343	0.7789857	-0.103751429	0.73196	0.7789857	-0.047026
cg03893663	11	31721481	110067118	110067168	N/A	CCAAAAGTAATTCTAACCAGGCTGAGGTCAGAGTGTAGAGTTTGTGGACG	F	N/A	N/A	0.9375443	0.9624814	-0.024937143	0.9492413	0.9624814	-0.01324
cg03893901	6	47634510	106498597	106498647	N/A	CGTGTTTGAAGGTGTAACTGTGTAAGACATCTAGCATACAAAACTACCCA	R	N/A	N/A	0.68148	0.76227	-0.08079			
cg03898010	2	40650317	242716203	242716253	N/A	GTGGGGCAGGTGAACTGGAATCCCCAGAAGCTCACCTGCCTCCTGGGACG	F	TSS200	GAL3ST2	0.7352671	0.8036071	-0.06834	0.7808075	0.8036071	-0.0228
cg03900581	1	44650317	96468567	96468617	N/A	ACTAGTAGACAAATCAGAGGGTCAGGTTCCATCTACTGGTCATCTTTTCG	R	N/A	N/A	0.8941114	0.92033	-0.026218571	0.8930888	0.92033	-0.027241
cg03903705	5	72603486	134094672	134094722	Island	GCAGCATGGGTCGGGAGTCACGGTGAGGCAGAGCGCCGAGCGGGCTAGCG	R	Body	DDX46	0.0930626	0.0716501	0.021412429			
cg03915940	16	10623319	3545106	3545156	N_Shore	CGGGCCTTGGTACTAAGAGTGCTTTCAGGACCTCAAGTCCTTTCTACTAC	F	Body	C16orf90	0.7649129	0.8341857	-0.069272857	0.7994563	0.8341857	-0.034729
cg03921216	6	46791324	31166799	31166849	S_Shore	GGGGAGGTCGCGGCTGCAGTGAGCCATGATTAACCCACAACTGCACTCCG	R	Body	HCG27	0.5625671	0.6714329	-0.108865714	0.6186438	0.6714329	-0.052789
cg03922834	4	51673394	4226530	4226580	N_Shore	CGGACAAGGACCAAAAGAGCTTTACAGAAAGGGGGCCATGGTGGCCCATA	F	Body	OTOP1	0.6953971	0.7397714	-0.044374286	0.7115913	0.7397714	-0.02818
cg03935444	7	21605382	2754314	2754364	N_Shelf	TTAAAATCACCACAGTCTAGCTCATGAATCTGTAACTTGGGCAGAGCTCG	R	3'UTR	AMZ1	0.90551	0.9314557	-0.025945714			

cg03940525	5	52713334	61698089	61698139	N_Shore	GATAAGAGCTCTTAATCTGACTCCATTTTTAGATTTCTTCATGATCTACG	R	Body	DIMT1L	0.8807586	0.9316714	-0.050912857	0.908345	0.9316714	-0.023326
cg03946012	16	53709376	58328209	58328259	N/A	ATGCCTCTGCTGTGGTTTTACCCTTCTAAACTCTGCTGGCTAAAAGAACG	R	5'UTR	KLKBL4	0.7720157	0.8465843	-0.074568571			
cg03948207	1	66650508	114302014	114302064	Island	CGGGGCCTTTGCACCTGTCTTTTCCAGCTGGGCACAAAGCCTTTTGCTGT	R	TSS1500	PHTF1	0.1408857	0.1781686	-0.037282857	0.1509263	0.1781686	-0.027242
cg03953980	16	73657444	460365	460415	Island	ACCAGCGGCACCTTCAATGTGTCTCGTGTGCTCTATGAGAAGTTCTTCCG	R	Body	DECR2	0.8751157	0.9006	-0.025484286	0.9151125	0.9006	0.0145125
cg03960326	8	50779361	42065741	42065791	N/A	CTTCTTTGTAAAGTGCAGGGCTGCAGTAGGTGGCCTCCGGGGACTTTCCG	R	TSS1500;TSS1500	PLAT	0.8690129	0.9139829	-0.04497	0.8917575	0.9139829	-0.022225
cg03961853	1	24642300	230384989	230385039	N/A	CGGCAGGGGAACCCAGTCGCCCCTATAAAGTAAGTGCCAGCATCCTTCAG	F	Body	GALNT2	0.8976086	0.9414443	-0.043835714			
cg03966955	16	46709395	2749496	2749546	S_Shelf	GGGCCCTGCTTGCCAGAGCCTTTCCCGACCGATGAATTCAGGGCTGCACG	R	Body	KCTD5	0.8880871	0.9252814	-0.037194286	0.9065313	0.9252814	-0.01875
cg03969079	10	35732484	63759909	63759959	N/A	GAAGAAACGAACGTGATAGTTCTCAGCTACCCCCAGTACTGCCGGTACCG	R	Body	ARID5B	0.8713843	0.9119543	-0.04057			
cg03982537	11	73612347	64404325	64404375	N_Shore	CCAGTTGGTAACACTAGGCCGGGTTCCCTCAGGTACCTCGGGGTCTCTCG	R	Body;Body;Body	NRXN2	0.8905086	0.9185871	-0.028078571			
cg03983223	2	61718387	175499283	175499333	N/A	AAAGCACTAACCTGTATTGTTTTAATCTGCTGAAAACAACCAACTTCTCG	R	1stExon;5'UTR;5'UTR	WIPF1	0.4937629	0.6377071	-0.143944286			
cg03992191	22	17692350	22312957	22313007	S_Shore	CGAGCTGGTCCTGTGGTCATCAGGCTCTCGGGGCAAGAGCTACCCGCTGT	R	Body	TOP3B	0.8178114	0.8529114	-0.0351	0.8249563	0.8529114	-0.027955
cg03992323	1	19706320	224023297	224023347	N/A	CGGTTGTAGTTAGATCATCACGGATAGATCTTAAAAATGTAGTGCTTAGT	R	Body;5'UTR	TP53BP2	0.7935614	0.8672871	-0.073725714			
cg03993743	21	14724471	38072998	38073048	Island	GCCCAAGCACTGCAGGCTGAGGCCACAGAGCGAACACTTGTGCTGAGCCG	R	Body;Body	SIM2				0.1925125	0.1508114	0.0417011
cg03994820	3	52797342	350682	350732	Island	AGTCCGCTGGGCCCCCTTCTTGTGGCCCGGACGGTGCACAGTGGAGCTCG	R	5'UTR	CHL1	0.3968086	0.3139814	0.082827143	0.393285	0.3139814	0.0793036
cg03999137	11	71713417	64359693	64359743	N/A	CGGCCTCACCCTGTCCTGGCCCTGCTGACCTGTCAGCCGTGACTCCAGGC	F	Body;5'UTR	SLC22A12	0.8292857	0.8795086	-0.050222857			
cg04004345	15	14667393	65590875	65590925	N_Shelf	CAGGAGAATCGCATGAACCCCGGAGGCGGAAGTTGTCGGCCCAGATCACG	R	N/A	N/A	0.8457614	0.8872257	-0.041464286	0.870905	0.8872257	-0.016321
cg04005677	16	26697449	744939	744989	Island	AGGGGCCCCAGACTCTCCCAGGATCTGAGTGGGGCCGGGAGCTCTCCCCG	R	Body	FBXL16	0.2764229	0.37258	-0.096157143	0.3202788	0.37258	-0.052301
cg04011707	16	27635456	88480909	88480959	N/A	CGGGAGGCTGCCACCTTTCAAATCCCGGCGCCACAGCATCCCTGGGCCTC	R	N/A	N/A	0.8437271	0.8800771	-0.03635			
cg04013970	17	18719461	43158427	43158477	N/A	CGCCTGGCTGATTTGGGCATTTCTCATGACTGACCATTTTGGACACAGAT	F	Body	NMT1	0.8203314	0.8767771	-0.056445714			
cg04016527	17	62808429	36707775	36707825	N/A	CGTGGGTATCACATGGCATCCCCATGGGTAGGAATGCCACCCTCATTATA	F	Body	SRCIN1	0.8981686	0.9309643	-0.032795714			
cg04017276	22	17674412	44577135	44577185	N/A	CGGCACCCAATAGCTCTTAAAATAAAATCCAGGCTGTGCGTGGTCTGTCT	R	5'UTR;Body;TSS200;TSS200;	PARVG	0.5868671	0.6565071	-0.06964			
cg04021454	1	56606315	28968404	28968454	N_Shore	AGATTCTAGAAGCATTTAAGGAACATTAACCAAGCATCTCATTTGCTACG	R	5'UTR;5'UTR	TAF12	0.7966914	0.9203157	-0.123624286			
cg04025739	5	50749314	138398087	138398137	N/A	GATTTCTACCCTTGCCTGGAAGCCATGCTGGGTAACTCTTCTAAGACCCG	F	Body;Body	SIL1	0.76939	0.9041743	-0.134784286	0.8319175	0.9041743	-0.072257
cg04047566	21	51797315	42675292	42675342	N_Shore	AAACCTGGGCCTTCCCTCTGTTCTCTGGAGTGCATCTTAATTTTTACACG	R	N/A	N/A	0.8141571	0.8744143	-0.060257143	0.8269025	0.8744143	-0.047512
cg04064254	21	25620318	47409570	47409620	S_Shore	GGAAGACCCGGGGACCTCGGACCTGTTGGGTACCAGGGAATGAAGGTACG	R	Body	COL6A1	0.81607	0.8638929	-0.047822857			
cg04064380	11	29630349	117688259	117688309	N/A	TGAGAAGAGCTACTGAGGCAAAGCCTCTTTCCCCTCCCACCCTACAAACG	R	N/A	N/A	0.2757786	0.3635314	-0.087752857	0.265785	0.3635314	-0.097746
cg04075230	7	26684507	97600632	97600682	N_Shore	CGCTTGTGATTGAGGCTGCAGGTGAGCTGTAATTGGGCCACTGCACTACA	R	Body	MGC72080	0.9008143	0.92897	-0.028155714	0.9166338	0.92897	-0.012336
cg04091563	5	38728469	148034045	148034095	Island	GCACAGGGGAGTGGGCACAGAGGCGGGCTGGAGCGATCTCACCCGTTCCG	R	TSS1500;TSS1500;TSS1500;	HTR4	0.1908857	0.1218527	0.069033	0.1621888	0.1218527	0.040336
cg04093323	15	15739485	78454685	78454735	N/A	CTGAGTTTGCCTTTGAGTATGCCCGGAACAACCACCGGAGCAACGTCACG	R	Body	IDH3A	0.8543057	0.8940857	-0.03978			
cg04098829	5	52747432	92744116	92744166	N/A	CGCTGGGAAAAGCAGCAGTAACAGGGAGCAGTTTGAATGCTATTTGTGGC	F	N/A	N/A	0.7947214	0.8623657	-0.067644286			
cg04104695	5	14736479	139058749	139058799	N_Shore	CCTGCAGAGTAGGGCCTGGGTGGAGGTCTCAGTGAGAACCCAGAGAGCCG	F	5'UTR	CXXC5	0.7674529	0.8017814	-0.034328571			
cg04105547	16	70739324	965857	965907	N_Shore	AGCACCATCACCGGGGGCCGGAGCAGGTGAGATGCAGGGGCCGGAGCACG	R	Body	LMF1	0.8023429	0.8464043	-0.044061429	0.817805	0.8464043	-0.028599
cg04108328	8	42620323	27634490	27634540	S_Shelf	CGTCCCTGGAAAATGAGCCGTCACTGGGACGCACCCAAAAGAGTAAATCA	F	Body	ESCO2	0.9224986	0.9587043	-0.036205714	0.9424163	0.9587043	-0.016288
cg04110105	3	58790436	46395356	46395406	N/A	CCTTGAGTGTGAGTCAGGCAAACCCTGTACATCTGCTCCTGTTTCTAACG	F	5'UTR;1stExon;1stExon;5'UTR	CCR2	0.4410629	0.5516971	-0.110634286	0.4745425	0.5516971	-0.077155
cg04110886	1	42656309	10675575	10675625	N/A	CGCCCACACAATGCACGATTCAAACGCAGAGATTCCTGCCAATACCACAG	R	Body	PEX14	0.7864143	0.8650114	-0.078597143			
cg04113632	11	20723382	67892272	67892322	N_Shelf	CGGGCCTCAGCCCTGCCACCAACTCCAAGGCCTGTTCTGAGAAAGGGCTT	F	N/A	N/A	0.7193786	0.8392443	-0.119865714			
cg04114088	3	41679426	128971491	128971541	S_Shelf	CGCTTCCGTGGTCCCCAGGTGCTCCCCCTGTGTTAATCAAGAAAGAAGTC	R	Body	COPG	0.7814114	0.8215714	-0.04016			
cg04116217	7	54753349	55223664	55223714	N/A	CTTTGGAGGTGGCATGAGAGCCCAGCCTCAGCAGCCGAGAACAAGCCTCG	F	Body;Body;Body;Body	EGFR	0.7856329	0.8313186	-0.045685714	0.81515	0.8313186	-0.016169
cg04118062	12	20640412	132822560	132822610	Island	CGGTGCGTTCCATCCCTCTGAGGGCCTCGGCTTTCTTAGGCCCCTGACTG	F	Body	GALNT9				0.8843713	0.8673971	0.0169741
cg04121624	10	27755332	62760791	62760841	N_Shore	CGGGGGTGGCCAGAGGGATTAGAGAGATAAAGTCACTGTCAGTCAGAAAA	R	Body;TSS200	RHOBTB1	0.3245429	0.3979443	-0.073401429			
cg04121631	1	52703452	875345	875395	N_Shore	TGCAGCGGGCAGGGGGTCCGAGTGCATCCCGGAGGGACCCCTGGAGAACG	F	Body	SAMD11	0.1479886	0.115384	0.032604571			
cg04128880	16	48749355	22198056	22198106	N_Shelf	CGCCTCCATCTGGCCCTGAGACCCATCTGCAGCCTCCCACCGCTGCTCAC	F	N/A	N/A	0.8495143	0.9021486	-0.052634286			
cg04131101	11	61684353	94427846	94427896	N/A	CGGGGCCCAGCTACTTTTAGAAACCATTTCTTGTGGCTTAGTGCTGAGC	F	N/A	N/A	0.8036557	0.8701	-0.066444286	0.8347513	0.8701	-0.035349
cg04131610	3	37787476	46411447	46411497	N/A	CTTCTTAGAGATCACAAGCCAAAGCTTTTTATTCTAGAGCCAAGGTCACG	R	TSS200;TSS200	CCR5	0.7705957	0.8482129	-0.077617143	0.806035	0.8482129	-0.042178
cg04132510	1	26657444	3044741	3044791	N/A	CGGAACCAGACCCAGATCTAGTCTTCAATTTCCGAACACTCAGAATGACT	R	Body;Body	PRDM16	0.85818	0.9069857	-0.048805714			
cg04136321	6	50760415	32093933	32093983	N_Shelf	CGGTTTCAAATGAGGATGTTGGGTCATCTCCCAGGAGACACAGTGGGGGT	F	Body;Body	ATF6B	0.8235257	0.8562243	-0.032698571			
cg04137564	7	22669494	66022277	66022327	Island	GTCCTGCTGGCTGAGGGCCTGGGCCTCAAACAGCTGCTTCATTATGAGCG	F	Body	LOC493754				0.8181825	0.7540857	0.0640968
cg04141261	12	55704475	125308274	125308324	N/A	CGGACTCTTGGGTCGTTTTCGCCCATTGCGAACAGTGCTGCTGTGCACAT	R	Body;Body	SCARB1	0.7324571	0.7867886	-0.054331429	0.7618688	0.7867886	-0.02492
cg04146137	1	11705435	38279984	38280034	N/A	TTGGTTGCCAGGGCTTGCAGATCGCAGTGAATTTTCCTTGGGGAACATCG	F	3'UTR	MTF1	0.8474957	0.9498629	-0.102367143			
cg04150588	3	73604315	107602013	107602063	N/A	GACAATGGGCGGAAATGCCCAGACACTAGTACTCCCACTGTACTTATTCG	R	TSS200	LOC285205	0.9112314	0.9423043	-0.031072857	0.9237825	0.9423043	-0.018522
cg04158018	12	68640386	54696210	54696260	N/A	CGTGGGGGACACTTAGAGGGCTCACAGCAGCTGCCTTTTATCAACTAGGA	R	TSS1500	NFE2	0.64578	0.7294886	-0.083708571	0.6823663	0.7294886	-0.047122
cg04158049	1	50609344	16550535	16550585	N_Shelf	ACAGCAGCCAACATCACACATAAGGTCTCTGCTCTCATGGAGCTCACACG	R	N/A	N/A	0.7945543	0.8611771	-0.066622857	0.8304913	0.8611771	-0.030686
cg04160694	5	70647365	176886312	176886362	S_Shelf	CGGCTCCCCCGCCCTCACTGACCCACCTGGGGTTTGTTCCACAGGCAGCC	R	Body;Body	DBN1	0.7556157	0.7948957	-0.03928			
cg04165508	1	39645470	94167631	94167681	N/A	CGATCCACCCACTGGCGCTGTGGCAATGAAATTCTCACGGGGGAAAGTCT	F	N/A	N/A	0.8561529	0.9173171	-0.061164286	0.8793563	0.9173171	-0.037961
cg04165964	10	49634400	95479029	95479079	N/A	TCAGTATATGCTATGAACTAGCATTGTGCTATGAGCACAGAGGGAACACG	R	N/A	N/A	0.8541014	0.8776843	-0.023582857			
cg04166500	14	41752319	100571607	100571657	N/A	TCTCAGTCATCCCTGCCTCTCTAGAACAAGTACAGAGGCGACACACCACG	R	Body	EVL	0.6704971	0.7240286	-0.053531429	0.6778863	0.7240286	-0.046142
cg04168670	2	38716348	124782817	124782867	Island	GGCTGCTCTTATAGGCGAGCGCGGGGCGGGCCTGGCTGGGGGCGGTGCCG	R	TSS200	CNTNAP5	0.2370857	0.1889671	0.048118571	0.217225	0.1889671	0.0282579
cg04171487	4	16675509	126245530	126245580	N/A	TTCAGCAAACATGTATGGAGCACCTACTATACATCAGGTAATATGCCACG	F	Body	FAT4	0.7630014	0.8397486	-0.076747143	0.8124775	0.8397486	-0.027271
cg04173182	4	69808310	54446035	54446085	N/A	CGTTGCCACATGCCAAATGTTATATTTATCCAATTGTCCTTCTAGTGGAG	R	5'UTR	LNX1	0.83411	0.8979057	-0.063795714	0.86372	0.8979057	-0.034186
cg04176254	16	11752438	67517429	67517479	S_Shelf	CGGGATTCTTGCCTAGAGAGTTCCCGGCCACCCCGTGCCCTTGGCTTATA	F	TSS200;5'UTR;1stExon	AGRP	0.85892	0.8786214	-0.019701429			
cg04179571	14	29691471	68444789	68444839	N/A	CTGATATTATAAATCATCCTAAAACACAAACTTAATGAAATCTGAGATCG	F	Body;Body;Body	RAD51L1	0.8242114	0.88799	-0.063778571	0.8546388	0.88799	-0.033351
cg04189187	10	55635408	6183528	6183578	N_Shelf	CGCCCTGTTCTATCGCCGCATGGATCTGCAGAGGCAGCCGTTCCTGCCGG	F	N/A	N/A				0.3811675	0.4770357	-0.095868
cg04192393	15	45788331	63673286	63673336	N_Shore	TTCTTAATCATTGTTTTTCTCCAGGAGGGCTCTACTATGCTGAATGTACG	F	Body;Body	CA12	0.78257	0.8967957	-0.114225714	0.833035	0.8967957	-0.063761
cg04195774	5	13612473	118677172	118677222	N/A	CGATCCTTGGGCTATAAGCCATCTGACTTCAACTATCACTGCTGTGTTTG	F	Body	TNFAIP8	0.6439457	0.76627	-0.122324286	0.7073138	0.76627	-0.058956
cg04216235	5	22740384	172738061	172738111	N/A	CGGCTCTGTGCCAAGGTTCCTAAGAGTTTGACATTTGGAAAAGATCTGGC	R	N/A	N/A	0.4527457	0.5393986	-0.086652857			
cg04216796	3	29635305	128770015	128770065	S_Shelf	CTTTGTCCACTGAGCTGAAGTCTGAGACGATGTCTCGAGGGAGCAAAACG	R	N/A	N/A	0.8298086	0.8589143	-0.029105714			
cg04225554	10	15709388	135082008	135082058	N_Shore	CGGCCACCAAAACCATGCCCCGCCCCAGCCTCAGGGGAAGGTGGAGTCCA	F	Body;Body;Body	ADAM8	0.8233286	0.8842014	-0.060872857			
cg04233669	5	34780374	135173201	135173251	S_Shelf	CAGTTTCCCTTTCAATTTCAGTCACTAACTGCTGCAACAAGGCTGATACG	R	Body	LOC153328	0.7413443	0.8131671	-0.071822857	0.7711838	0.8131671	-0.041983
cg04252939	12	12725488	69206578	69206628	S_Shelf	CGGGCATGGTTGCATTCCAGTAAAATTTTCCTTACAGAAAGAAAGGCAGC	R	Body;Body;Body;Body;Body;B	MDM2	0.4823229	0.5762743	-0.093951429			
cg04262934	6	13670454	33173581	33173631	N_Shore	CACCTGGGGGGTCTGAGGGAGGTACCAGCATTCAGCCCTCTCCAGAATCG	R	Body	HSD17B8	0.5648471	0.6536471	-0.0888	0.6141788	0.6536471	-0.039468
cg04266474	7	62703473	36318491	36318541	N/A	CGCCCCTGTCAGCAGTGACTCTCTCCACAGCCACTCTGCTCTGGGCTGTG	F	Body	EEPD1	0.7126914	0.8188471	-0.106155714	0.78381	0.8188471	-0.035037
cg04269351	14	32716308	68142533	68142583	S_Shore	ATTACAAGGTCCCTTCTTGCACTCCATGGGTATAAATTCCTGTCTTCACG	R	TSS1500	VTI1B	0.8811957	0.9180914	-0.036895714			
cg04275695	6	25630462	149806273	149806323	N/A	CTGCCCTCACGGAGGGTTTGTTTTGCATGTGGTTGCTGAACTTTGATTCG	F	TSS200	ZC3H12D	0.5408071	0.613	-0.072192857			
cg04278110	2	71725415	198063759	198063809	N/A	AGGATGCCAGCTGACTTCAGAACTTCCGGTCTCAGAGCTAACCAGGCTCG	F	TSS1500	ANKRD44	0.6050343	0.7478357	-0.142801429			
cg04279139	12	12642383	27925367	27925417	N/A	AATGACTCATTCACCTTCTTGACACAAAAATCATCAGCATTCTTTGAACG	R	TSS1500	LOC100133893	0.5852943	0.6999714	-0.114677143			
cg04281898	17	24709309	7011140	7011190	N/A	CAAGCTGGAGAAACAGCAGCAGGACCTGAAAGCAGGTCAGAGAGCCTCCG	F	Body;Body;Body;Body	ASGR2	0.5277814	0.6244886	-0.096707143			
cg04285362	4	59790340	14746310	14746360	N/A	CGCTCCAGGGAGCCCTGTAAGATCAGTGAGGCTCTGGGTCTGCCCAAACC	F	N/A	N/A	0.7108671	0.7967243	-0.085857143	0.7572738	0.7967243	-0.039451
cg04289891	1	15699479	20395440	20395490	N/A	CTGTTGGTATCTGTGCCAATTCTGGGCCTCTTTGTCCTAACTTCCATCCG	F	TSS1500	PLA2G5	0.7549714	0.8109886	-0.056017143	0.7383588	0.8109886	-0.07263
cg04291025	15	35707312	69746140	69746190	S_Shore	AACGAAAAACACCTAGGAGATCCAGCGGCATGTGGGGCGTTATGGCACCG	F	Body;Body	RPLP1	0.31806	0.3964314	-0.078371429			
cg04299274	17	47729355	25798741	25798791	N/A	CGTGCCAGGCACTGTTCTGGAATATAAGAGTGAATGAGAGATGTATTGTG	F	TSS1500	KSR1	0.68758	0.7858429	-0.098262857	0.73953	0.7858429	-0.046313
cg04303879	16	17699427	56899081	56899131	N/A	CGCAGCCTATAAAACCACCCTGTGTGTCCTTGCGGATCCTGGCCCCTCCC	F	TSS200;TSS200;TSS200	SLC12A3	0.9075157	0.93493	-0.027414286			
cg04303901	12	74689403	97886312	97886362	N/A	CGGGGAAATATAATCAGACATGCCCAAAGAAGTCTGCTTAGGGTGAAACA	F	Body	RMST	0.8873143	0.9259886	-0.038674286			
cg04304036	16	15724389	68334619	68334669	N/A	CGGTTGTGAAATTACTGACTGACTTCCTTTGGCAGTGGGGCCAAGAAACA	R	3'UTR;3'UTR;3'UTR	SLC7A6	0.6782457	0.7677757	-0.08953			
cg04308882	22	18681376	32368489	32368539	S_Shore	GGGGGCCCAGACCCGGGCCCTTCCAGGAGGTGCCAGGGCAGTGGGACCCG	R	N/A	N/A	0.80718	0.8541986	-0.047018571			
cg04310063	1	66770319	234342613	234342663	N/A	CGGCCAGCCTGTGCTCAGGAATAACTAAGGAGTGGAGCCGCATCAACCTC	F	Body	SLC35F3				0.810305	0.8626643	-0.052359
cg04321126	6	67673346	39393690	39393740	N/A	CGGTCCGGTTTTCCTGTTGGTTTTAGATGGCTGTTTGATTCTATGTTAGA	F	Body	KIF6	0.6251429	0.6947229	-0.06958			
cg04321396	11	40617388	65480401	65480451	S_Shore	GTCTTTGGCATTCTGTCCTGAGCCATCCCCACTGCTACAGTCAACAAACG	R	Body;Body;Body	KAT5	0.2924043	0.3580229	-0.065618571			
cg04330631	6	56684319	42018203	42018253	Island	CGCCGCCCCGCCCCGCCCCGCCCCGCGACTACAAGTCCCATCGCGCCCCG	F	TSS200	TAF8	0.1580329	0.1252043	0.032828571	0.142625	0.1252043	0.0174207
cg04332442	22	74749450	46770063	46770113	N_Shore	TTTCCACTCAGGAAACCAGGGTGTTTGGTGTAGAGTTCTCCAGCCACACG	F	Body	CELSR1	0.6267386	0.7285571	-0.101818571	0.6768288	0.7285571	-0.051728
cg04343928	16	42617395	85863576	85863626	Island	CGCCTCCCGCTGCGGCGTCCATGGGCTTGTGGTTGCCTCGGCCCCAATCT	R	N/A	N/A	0.6685957	0.7188729	-0.050277143	0.6893913	0.7188729	-0.029482
cg04348689	14	36760490	93765993	93766043	N/A	AATCAGATGATGCTGACTGTCTTAAACTAAAATAAGCTCCAGTGATCACG	R	5'UTR;5'UTR	BTBD7	0.8384171	0.8858143	-0.047397143			
cg04352288	16	46725346	87958407	87958457	N/A	CGGGACCAACAAGCGGGACGCTGCCCCCACGCTCACCTTCATGCCCTCTC	R	Body	CA5A	0.8179671	0.92862	-0.110652857	0.8836888	0.92862	-0.044931
cg04354126	1	43738414	6338812	6338862	N_Shore	CGGTCCCCGAACCCTTGGCTTTGACATGTCCTAACCTGTGGCCCTTCTCT	R	Body;Body;Body;Body	ACOT7	0.8828529	0.9112529	-0.0284	0.89415	0.9112529	-0.017103
cg04356090	12	49615374	129280133	129280183	N_Shore	GAAAGGCACTCAAGAGGGAGTCTGGACGCGGTGAGGGTGCTAGCAACACG	R	Body	SLC15A4	0.8560529	0.9021757	-0.046122857	0.8853888	0.9021757	-0.016787
cg04362211	11	36601386	92577663	92577713	N/A	TTCTAGCATTGGACAGCTTCTGGATCAGGTAGGCTGGCTTGTAGAACTCG	F	Body	FAT3	0.89081	0.9304929	-0.039682857	0.9022325	0.9304929	-0.02826
cg04364752	16	67752305	88906534	88906584	N_Shore	AGCTGCTGTGCCCATCAGCTCTGCCCTGTGCTTTCTGAGAGCTCAGCTCG	R	Body	GALNS	0.7872957	0.84858	-0.061284286			
cg04365102	2	61623366	238769342	238769392	S_Shore	CCAAAGAGGTCTTGTGCGGCAGGTGCCTCTGACCAACATCACTGTTTCCG	F	Body	RAMP1	0.5368829	0.63151	-0.094627143			
cg04372519	19	47739472	48183167	48183217	Island	CGCCCACCTCCCAGCTCCTGGCCAAGCAGGTGCCCGTCAGCGGCTACCTG	F	Body	GLTSCR1	0.8965286	0.9253071	-0.028778571			
cg04379469	7	15785362	98568573	98568623	N/A	CGGCAGCCACTACTTCATGGAGGACAGAAAGCCACCAAGCCTAAGGCATC	R	Body	TRRAP	0.9367071	0.9681771	-0.03147	0.9545488	0.9681771	-0.013628
cg04382077	7	20780382	150935054	150935104	S_Shore	CGGCCACCTTCTCGTGGCCCGTAGACCAGCAACAGGGTGAGCAATGCATG	R	Body;TSS1500	CHPF2	0.8577243	0.8991157	-0.041391429			
cg04389439	16	53735319	69508230	69508280	N/A	CGGAACAAATTAACAGAGGCTTCTTTGTAACATTGAGGGTCCTCATTGGA	F	N/A	N/A	0.9153757	0.9569314	-0.041555714			
cg04396010	3	54641497	176239943	176239993	N/A	GCTCACTTCCTTGTAGCTGGTTGCCACTTACTAGCTAGCCCAGGAAAACG	F	N/A	N/A	0.6199286	0.6863014	-0.066372857	0.6357338	0.6863014	-0.050568
cg04405704	6	66618488	31369119	31369169	N_Shore	CCATGATCCCTAGCCTACACTTTTCTGTGGATGAAAATGTAATGTATTCG	F	N/A	N/A	0.4812386	0.6526057	-0.171367143	0.4713463	0.6526057	-0.181259
cg04406574	8	68641396	41910366	41910416	S_Shore	CGGCTTTGGAATAAGACAAATCTCAGTCCCAGGCTCAGGTGCGCGCCACA	R	TSS1500;TSS1500;TSS1500	MYST3	0.8262129	0.8809314	-0.054718571			
cg04407660	20	60779470	2447742	2447792	N_Shelf	CGGAATTGTAGCAAAGTAGACAATATCTCCAATTGTTTGTATAAATGCCA	F	Body;Body	SNRPB	0.8004329	0.8848043	-0.084371429	0.84241	0.8848043	-0.042394
cg04409427	21	26713474	35736023	35736073	N/A	TTCCTCTTAGGGTAGGCTTGGGGGACAACAGCATTCCCTGCCAGAATACG	F	TSS1500	KCNE2	0.8924114	0.9219971	-0.029585714			
cg04411052	14	47670431	72219061	72219111	N/A	CGCCAGGAGTCTCCACAGAAGAACGTTGATCACTCATGACGTGGGGCGGA	R	N/A	N/A	0.8971686	0.92981	-0.032641429	0.9073875	0.92981	-0.022422
cg04414509	3	55732412	169351419	169351469	N/A	TGACATTGAGTGCTGGGATGCTTGGAGACCACCTTTCCAGTGGTTGATCG	F	Body	MECOM				0.7565888	0.8334514	-0.076863
cg04422084	4	56706502	129436654	129436704	N/A	TTAATAAATAATAATAATAGTCACCCTTCCACCTCCATAGCACAGCTACG	R	N/A	N/A	0.89191	0.9194943	-0.027584286			
cg04431186	13	55706395	113614132	113614182	N/A	GACAACCAAGCTGCACAGTGGCCTGGCATGGTGTGTCCACAGCAGCAACG	R	N/A	N/A	0.78552	0.8497186	-0.064198571			
cg04440811	11	23731381	129817712	129817762	N/A	CGGTCTGTTGCTTACCTATTTGAAGTCTTGGGAGACAGGGCAGGCCTCTC	R	TSS200;TSS200;Body;Body	PRDM10	0.9000186	0.9254514	-0.025432857			
cg04443870	21	23627470	46321415	46321465	Island	CGGCGACCTGCATCATGGCGTCCAGCCCACCCTCGGGTGCATCCAGGTTT	F	Body;Body	ITGB2	0.8211657	0.8545986	-0.033432857	0.843305	0.8545986	-0.011294
cg04454629	12	44603474	32851191	32851241	N/A	TTTCCATCATAGGGGACCTTTCTGGACAACATGAATGAGCCCCTATGTCG	R	Body;Body;Body	DNM1L	0.8656529	0.9331514	-0.067498571			
cg04457114	5	22673487	174159705	174159755	Island	CGGGCTTTAGATATCCTTGCGTCCGATGCCAGAAGCCTGGCACGCAAATT	F	N/A	N/A	0.4988943	0.3841957	0.114698571			
cg04458281	8	15804393	41433172	41433222	N_Shelf	CGCTGTGAATATGGGCTGTCTTTAGATTATTGTTGGCAGTATTTTCACAT	R	N/A	N/A	0.77337	0.8959471	-0.122577143			
cg04458969	2	20715485	183733105	183733155	S_Shore	CGGTGAGAGATGGCTAAATTGAAGCAGAGAAATATTTCAGTGATGCAGAG	R	N/A	N/A	0.5877486	0.6667643	-0.079015714			
cg04467093	5	39766308	133448932	133448982	N_Shore	CGTGCCCATGCCACCCCCCAGCCCCAGCCTGGGGAAAGGAGGAAAAGTGG	F	TSS1500	TCF7	0.7082271	0.7699686	-0.061741429	0.7501313	0.7699686	-0.019837
cg04468380	8	21753315	8601022	8601072	N/A	TTCCAGTCATGGAGGACTTGGCAGAGAGCAGCTCAGGGCCAGGAGCAGCG	F	N/A	N/A	0.6464286	0.7319886	-0.08556	0.6764138	0.7319886	-0.055575
cg04470557	5	36698383	131630995	131631045	S_Shore	CGCAACATCTAGGTTCTTAGGAAACTTCATTTGTTGTGAAAATCGGAAAT	R	Body	SLC22A4	0.56646	0.6527271	-0.086267143			
cg04470754	20	43628376	14904432	14904482	N/A	CGCACCGCCAGCCTAGGAAACCCTGAGGCACAAGGCCTATAATTAAGAGT	R	Body	MACROD2	0.6932714	0.7778914	-0.08462			
cg04471202	7	65743382	123564379	123564429	N/A	GGCTGAAGTGGAGGCTTGGGCCACAACCAGTCAGAGGCATTTCTCGTTCG	R	TSS1500;TSS1500	SPAM1	0.83732	0.8795486	-0.042228571			
cg04476764	4	43635471	122682720	122682770	N_Shelf	CGCTTGCAGGGGTGGAAACTTGGAACTAGGTGAGTAAAAAATATGAAATA	R	Body	TMEM155	0.7338557	0.80802	-0.074164286	0.73395	0.80802	-0.07407
cg04481053	11	72615301	73008839	73008889	N/A	CTTCATTGGTGACTCAAAGCATGGAGCATACCCCTTGATGACAGTACACG	F	3'UTR;3'UTR;3'UTR;3'UTR	P2RY6	0.8559929	0.9080343	-0.052041429			
cg04486885	5	17679472	176823424	176823474	Island	CGGGGGCACTGGGAGAGACGACCTCCATGGGGGTTTGCTCCCACTGCAGT	R	Body	SLC34A1	0.6425457	0.7423729	-0.099827143			
cg04492193	4	31771427	8135668	8135718	N/A	GTGCATTCGTCCATGGGGGGAGCACCTGTCAGGCACCAGAGCAAGGCACG	R	Body;Body;Body;Body;Body;B	ABLIM2	0.7554657	0.8121743	-0.056708571			
cg04499214	1	45633312	3140299	3140349	N/A	CGCGTGACCTCTTGCACCTGGTCTGTGATTGACTGAGAAGTTAGTTCCTA	R	Body;Body	PRDM16	0.8108371	0.8578229	-0.046985714			
cg04517044	7	45642380	150946998	150947048	N_Shore	ACATACCCAGGCAGGGAGTCCTGGGCCTACCCAGGTCCCCAAAGGCCACG	R	Body;Body;TSS1500	SMARCD3	0.4334871	0.5151643	-0.081677143			
cg04517343	3	37686473	153875979	153876029	N/A	TCCAACCCACAGGCTCCTTAAATGTTTCTTTGTCAAAATTCTGACATTCG	F	Body	SGEF	0.9099	0.9400086	-0.030108571	0.9253075	0.9400086	-0.014701
cg04524475	13	32632354	74875971	74876021	N/A	TTAGAGTGTACGCTGCATTGGAATCCAACCAATCGCAGTATTCTTGCCCG	R	N/A	N/A	0.8028486	0.8616571	-0.058808571			
cg04530345	5	59646311	53601057	53601107	N/A	CTAACCTATCAAATCTAATCTTATTAAATCCCAAACACTGGCAGGGCACG	R	Body	ARL15	0.8956343	0.9245314	-0.028897143	0.9136188	0.9245314	-0.010913
cg04541228	8	67796360	11625883	11625933	N_Shore	TGCAGGAGGCATCCCTTGAAGAGCCTCTGGTCCCCCTCTTTCTATGTCCG	F	TSS1500;TSS1500;TSS1500;	NEIL2	0.8980657	0.9293757	-0.03131			
cg04545079	16	41703493	67599924	67599974	S_Shelf	CGTAGATGATGTGGAATGGCTGTGACAGCAGCAGCATCCCTGAAGCAAAA	R	5'UTR	CTCF	0.8569629	0.9073214	-0.050358571	0.88076	0.9073214	-0.026561
cg04548204	12	69750328	9162872	9162922	N/A	CGTGTGAAGAGCTCAGAAGGAGGAAGTACCACCTTGCCCTCACTCATTTC	R	3'UTR	KLRG1	0.8181457	0.8853186	-0.067172857			
cg04550524	5	17652384	161494015	161494065	N/A	GCCCTCCTATTTTGTGATGTGTAATCTTTATTCAAGCAGCTATCCCCACG	R	TSS1500;TSS1500;TSS1500	GABRG2	0.38204	0.4574614	-0.075421429			
cg04555665	20	65617466	30540304	30540354	S_Shore	CGCCTCAGTGTCTCTCCACAGGATCGGAAGGAAGCAGGAATCAGCTGGGC	F	TSS1500	PDRG1	0.66753	0.77247	-0.10494			
cg04561791	16	69742348	85478769	85478819	N/A	CGGGGTGCCACACACCTGACTGCCCTCCCCCATGGGGCCCCTTGCTGCTT	F	N/A	N/A	0.8232457	0.8812329	-0.057987143			
cg04565630	16	64729390	3108373	3108423	Island	AACTGGGGCCCTGCAGGGTGGAGGCCGGGAGGTCAGGGGTGGGCTCCCCG	F	Body	MMP25	0.1175014	0.1568929	-0.039391429			
cg04566826	19	45715494	34289872	34289922	S_Shore	CGCGCTGAGGATAAACTGAACAGGAAGGAATTCTGGCTGAAATTCTATCA	R	5'UTR;5'UTR;5'UTR	KCTD15	0.6121343	0.7405543	-0.12842	0.709625	0.7405543	-0.030929
cg04572258	2	51752445	224402829	224402879	N/A	GAATCTGGCTGATGAGTCACCAATATTAATGGGTTTTTGAATCCTATTCG	R	N/A	N/A	0.4842529	0.6692214	-0.184968571			
cg04579608	7	16727357	129410435	129410485	N/A	GTGGGGTTGGGCCTCCACACCAGGGCGACCCTGCAGGAAGGACCTTGTCG	F	TSS200	MIR182	0.8963414	0.92442	-0.028078571			
cg04581293	3	41745337	156889197	156889247	N_Shelf	CGTGTAACTGAAAATCCCAGCAGTAGAATACAGGGCATGGCTGCAGGGAA	R	N/A	N/A	0.6958371	0.7518514	-0.056014286			
cg04588257	19	51611341	45059935	45059985	N/A	CGTCTTCCTTTCAGTGGGTGTAATTTATTATTGACACACAGGACTTTTAG	R	Body	FLJ41856	0.7362843	0.8244771	-0.088192857			
cg04606053	20	60794397	33815214	33815264	S_Shore	GTCTATCCTACCTCCACCTGACAGCCCTTCAGCTACGAAGACAGTGATCG	F	Body	MMP24	0.4587357	0.4213729	0.037362857	0.45224	0.4213729	0.0308671
cg04623270	16	71685490	58150017	58150067	N/A	CTCTCTACAGCACCACATATATCACATGCCCTGCAGACCCCAAGAAGACG	F	Body	C16orf80	0.5821271	0.6836586	-0.101531429			
cg04642165	7	14725491	150063431	150063481	N_Shore	CTTCTTGGCTAGAATCACTTCATTTATTCTTCCAAACTGACATGGAGCCG	F	N/A	N/A	0.7494271	0.8507614	-0.101334286			
cg04650834	8	63648313	49456262	49456312	N/A	CGCATATTTATTTTGGCCAGACGTCTGCCTTCTAACCTAGAAAACTGCAG	F	N/A	N/A	0.4802214	0.5848143	-0.104592857			
cg04655299	19	11748386	48825620	48825670	S_Shore	CGAGTCTAGGACTCAGAATCAAGTTCCCTGAGTGGGATCGGCGCCAGGCT	R	N/A	N/A	0.0521707	0.0752011	-0.023030429	0.0956434	0.0752011	0.0204422
cg04656171	15	42806479	42211689	42211739	Island	CGTCCTGGCCCCGGAAGGCCTTGATGGCCTCTGAGAATTCATCTGAGATG	F	Body	EHD4	0.7941457	0.8472857	-0.05314			
cg04656831	6	36723426	29282808	29282858	N/A	CGTGATAGCTCTTAAAAGTAGTGTGCTGAGTGAAAAAAAGTAAGAAACTG	R	N/A	N/A	0.6128614	0.6860214	-0.07316	0.6415838	0.6860214	-0.044438
cg04658841	16	40657387	85478651	85478701	N/A	CGGGGGCTGTCTTTTCTGCACGCCTTGCCCTTGATCTTCCCTGGCTTTAT	F	N/A	N/A	0.7966043	0.8404	-0.043795714	0.8133588	0.8404	-0.027041
cg04658856	6	57689437	16242468	16242518	S_Shelf	CGGTGAAAGCTAGACCAGAACTCTTCTCACGGGACTGCTGGGGAAAAAAC	R	Body	GMPR	0.9204971	0.9542257	-0.033728571	0.939925	0.9542257	-0.014301
cg04665604	6	34712427	31696852	31696902	Island	CGGGGGCTGGCCTTCCCGCTCTGGATCTGGCCAAAGCTCAAAGGGAGCAC	R	Body	DDAH2	0.3274429	0.4388957	-0.111452857			
cg04668677	16	46781367	2146389	2146439	N_Shelf	CCTCAGCACACCTGAGCATAGGAGGGCATGGCAGAGCCCGGGGTCACACG	R	Body;Body	PKD1	0.8435557	0.8743157	-0.03076			
cg04676568	5	18684469	141633556	141633606	N/A	AGAGTGGGTACCTTGCCTATCACTCACTGGGTCAGGACCAGAGCCGAGCG	R	N/A	N/A	0.8810486	0.9067229	-0.025674286			
cg04677405	4	53742439	3446682	3446732	N_Shelf	GTGGTGCTGACCGGCAGTAGGCATGGGGGCCCAGGCCCAGCAGGGCCGCG	F	Body	HGFAC	0.6989743	0.74128	-0.042305714	0.7105575	0.74128	-0.030722
cg04685387	10	41679474	34925640	34925690	N/A	TGATTTCCTTCATAATGGGCTCTGTCTCCACGTTAATTTGACTGCATGCG	R	Body	PARD3	0.8552357	0.8888829	-0.033647143			
cg04686230	6	32649378	106428957	106429007	N_Shore	TAACCTCCAGATTTTACCAGAAACCCACAGAATGAGTTGTTATGCTTTCG	R	N/A	N/A	0.3809329	0.5827371	-0.201804286			
cg04691264	10	71605386	29697905	29697955	N_Shore	CGAGGAGGAAGAGTTGGTCTGAGGTTGCACCACAAGAAGTTTATATGCAC	F	TSS1500	LOC387647	0.8601329	0.90609	-0.045957143	0.87593	0.90609	-0.03016
cg04703197	16	39698304	68406272	68406322	Island	CGGAGGCCTACTGCAGACCCTGCAGAGACAAAAGTAGGGGGACTGTTTTT	F	5'UTR	SMPD3	0.8410286	0.8734357	-0.032407143			
cg04703560	6	39664322	25886385	25886435	S_Shelf	CGGACTCACAGTGTTTCACAAAGAGAGTTTCAGAACTACCTTGGTTTTTA	F	N/A	N/A	0.9123286	0.9408586	-0.02853			
cg04721268	16	48717500	112802	112852	Island	CGGGGAAATCAGTTGTGTCCTCCTCCAGAAAGCTAGCTGGAGTGAAGCTT	F	Body	RHBDF1	0.90114	0.9345671	-0.033427143			
cg04723721	9	14802370	139915388	139915438	N_Shore	GGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCG	F	Body;Body	ABCA2	0.79416	0.8422143	-0.048054286			
cg04724143	13	70803477	114185494	114185544	N_Shore	CACCGCAGCGCCCAAGAACCAGGATGGCCGTGGAGTCAGTGTGAGAACCG	R	Body	TMCO3	0.9100814	0.9398857	-0.029804286			
cg04733537	12	61691477	130388748	130388798	Island	CGGTGCCCGGAGCCGGCTGGGGCTTTCGCCTTAAAAATTTGTCTGCTTTT	F	TSS1500	TMEM132D	0.15582	0.1089496	0.046870429	0.1561863	0.1089496	0.0472367
cg04734712	17	47682364	1811474	1811524	Island	CGAAAACCTGGGATGATCATTTAAATGTTTAAAATATGCACATGGTAATT	R	N/A	N/A	0.4439286	0.6071529	-0.163224286			
cg04737150	2	29799394	161077747	161077797	N/A	CGACCAGGGCTCTGGAGTTAAAAGAAAGATCTGAATTCTGACTGGAATCA	R	N/A	N/A	0.8122214	0.8660114	-0.05379			
cg04741516	14	28653386	99786208	99786258	N/A	GGCTTTGTCTAGACGCTAGCAGGGAAAATACGGCAGCGTCTGTGCCCTCG	F	N/A	N/A	0.90578	0.9333371	-0.027557143			
cg04746914	3	44808476	45797767	45797817	N/A	TACGCACCCTGACTGATGACTGATCCCAGGTGGCCCTGAGTTGTAAGACG	R	3'UTR;3'UTR	SLC6A20	0.8608471	0.9128729	-0.052025714			
cg04749316	10	26713482	49893346	49893396	N/A	GAAGTTTGGGAGTCAGGCTGGGCTCCAGCAGCACTCCTCGACCTCTGACG	R	TSS200	WDFY4	0.7386386	0.8499914	-0.111352857			
cg04758026	2	54710452	152159591	152159641	N/A	CGTGATTCTTTCTGTGTATCTCCCAGTAATGTTACTTTGGTTTATGCTCA	R	N/A	N/A	0.5360814	0.6394829	-0.103401429	0.5713525	0.6394829	-0.06813
cg04762129	6	59633472	34105785	34105835	N/A	GCATCCAGGGCCCAAGCCAGAAAGAACCACAAACCACAAAACAACAACCG	R	N/A	N/A	0.4602829	0.5175129	-0.05723			
cg04762815	14	12633339	100996455	100996505	N/A	CGAGCACAGAGGTTGGCTGTGGGTCCTGGGTACCACCTTCTGAGCCTCAG	F	3'UTR;3'UTR	WDR25	0.8834343	0.9083057	-0.024871429			
cg04767522	6	42778353	17980388	17980438	N/A	CGTCCAAAGGATTAGAAACCCAAATAACTTCTCAACAGAAGCACTGAAAG	F	Body;Body;Body;Body	KIF13A	0.7746457	0.85096	-0.076314286			
cg04774132	6	25787462	28482073	28482123	N/A	CGAGTCTGCAGTTTTCGTGGGATTCTGCATCTCATTTCACAGAGTGACAT	R	Body	GPX6	0.8286714	0.8724714	-0.0438			
cg04776489	22	59610371	22597965	22598015	N/A	CGTGCACCCAGGGCCACTTCAGCCTTGATCACAGGCCTGCACAGGTTCCA	F	TSS1500	VPREB1	0.5365657	0.6033886	-0.066822857			
cg04785187	14	60721487	99997549	99997599	N/A	CGCTCCCCAAGCTGGCCCTCTGGTCTAGGGAGAGAGAATATCAGGAGAGC	F	Body	CCDC85C	0.8095514	0.8718386	-0.062287143	0.833115	0.8718386	-0.038724
cg04788444	1	60722500	228584774	228584824	S_Shore	GCTGCAGCTTCACATCCTGGACCCTAGAGGGGACAACCCAGGTGTTGTCG	R	Body	TRIM11	0.9051457	0.9309114	-0.025765714			
cg04791256	9	31750354	126131309	126131359	N_Shore	CGAGGCTGGGCTTCAAACCCTGGTGACTTCTCTGGGCCTGGGTTCCTCCA	F	Body	CRB2	0.7500514	0.8248214	-0.07477			
cg04803930	12	62604453	133159472	133159522	Island	CGGGGCCTCCAGTTTCTGGGTGGCCGGTGACCCCTCAGCACCCACAGCTC	R	Body	FBRSL1	0.7184629	0.7724029	-0.05394			
cg04810287	20	39788436	36149271	36149321	Island	GGGCACCACGTTTTTTGCTCTATGGGGCAGATGACCCCTCCCTAATTTCG	R	5'UTR;5'UTR;5'UTR;5'UTR;TS	BLCAP	0.62893	0.7151686	-0.086238571	0.6695125	0.7151686	-0.045656
cg04811942	8	17645404	143868062	143868112	N/A	CGGGCACCTGCCCCACCCTGCCTGGCCCACGCCCACCAGCCTGGCTGTCG	F	TSS200	LY6D	0.7126429	0.7786786	-0.066035714			
cg04813787	6	58624357	167814397	167814447	N/A	CGGCCCCAGGCATGGGGCTAGGGCCCAACTGAGCTGGGCAAGATCAGTTA	R	N/A	N/A	0.7836314	0.8634529	-0.079821429	0.8184388	0.8634529	-0.045014
cg04813904	5	36751415	66488838	66488888	N/A	CGCAGCAGAAGGATTCAAACTTGCTTAGTTCTGATCGGTTGGTGCAGCTG	R	Body	CD180	0.8501829	0.8921471	-0.041964286	0.8677	0.8921471	-0.024447
cg04817870	17	28605438	79963651	79963701	S_Shore	CGCCTCCGTCCGCCGTGGTCTGGCCCCCAATTCTCTGTGCTGAGTGAGGT	R	Body	ASPSCR1	0.61735	0.6623443	-0.044994286			
cg04825872	6	27750324	149381604	149381654	N/A	GCCGCAGTGACACACATTCATTTCCGCTGGAGGCAGCCCTAGGGAGTCCG	R	Body	UST	0.6970771	0.7739429	-0.076865714	0.7218875	0.7739429	-0.052055
cg04836028	6	63764493	31554263	31554313	N/A	GAGTCTCTGCTCCCCAAAGAAATTAAAGACAATTCATTTCTGTGCCCACG	R	Body;TSS1500;TSS1500;TSS	LST1	0.6659757	0.7470414	-0.081065714			
cg04839683	11	28770428	15737281	15737331	N/A	CTCAGAACTTAGACACTGTTTCTTCTACCAGTACAGAATCATGCCCCACG	F	N/A	N/A	0.82466	0.8835671	-0.058907143			
cg04839991	2	59663473	237880790	237880840	N/A	CGGGTTTTGAGGCAAGAGCTAACTCCAGGACCTCAATGTTGGAACACAAA	R	N/A	N/A	0.7246171	0.7978943	-0.073277143			
cg04847275	14	67693365	95693828	95693878	N/A	CGGGTCTCGCGTTTTCTGCCTCGCATTAACAGGAATAACATTTCCGTAAG	R	Body	CLMN	0.70988	0.7770629	-0.067182857	0.748185	0.7770629	-0.028878
cg04848570	12	17661467	131561270	131561320	N/A	CAGTGGCTATGCCTGTCCCTACCTGAGGTCGCCCAGCTGTAAGGGTCTCG	R	Body	GPR133	0.9090243	0.93855	-0.029525714	0.9124738	0.93855	-0.026076
cg04855107	6	17632361	108971457	108971507	N/A	ACTGACTGCTAATATGGTGGGACCAGTGAGCCCTGGAGCACAGGGACACG	R	Body;Body	FOXO3	0.8704714	0.9016143	-0.031142857	0.884505	0.9016143	-0.017109
cg04855494	3	32777498	9027277	9027327	Island	AGCTGTTGGGGAACATCTTCTCGGTGGGCGTCACGGCCGGGCTGCCCACG	R	Body;Body	SRGAP3	0.9049943	0.9325343	-0.02754			
cg04864179	7	70640414	128579964	128580014	S_Shore	TAGGTCTAATTCAGACCACCCCAATCAAGGCCCATGACTTTGGAAGTTCG	F	5'UTR;TSS1500;5'UTR;5'UTR	IRF5	0.8419014	0.8951771	-0.053275714	0.8535775	0.8951771	-0.0416
cg04864327	7	62754452	111396894	111396944	N/A	GCCAAGCTGTGCTGAGATGAATAGGGCAGAGATCTTGTGACAAGAGCTCG	R	Body	DOCK4	0.8046243	0.86425	-0.059625714			
cg04864441	7	54741360	157670677	157670727	S_Shore	CGCGGGATTTTCCTTGGGGCGCTGTTAATTATGTTACAGAGCTGAATGTT	R	Body;Body;Body	PTPRN2	0.6142186	0.7187629	-0.104544286			
cg04870120	15	19693474	32999748	32999798	N/A	CGGCCTCTACATGGCACTTGGAGTACATAGATGCTCCCAGACCTTTGTTG	R	N/A	N/A	0.8581029	0.8958757	-0.037772857			
cg04871173	7	55704449	1883056	1883106	N_Shore	CCCATCAAGCCCCCTCAGGAGGGGCTGGATGACAGAGGAGGTCTACACCG	F	Body;Body;Body	MAD1L1	0.8923557	0.91566	-0.023304286			

cg04885666	1	17676352	204459579	204459629	N_Shelf	CGGCACGAAACTCCAAAGTGTTGCAGGATAGGTCCTTTCACGGGTCATGT	F	TSS200	PIK3C2B	0.8228229	0.86337	-0.040547143			
cg04887030	7	11681438	1022471	1022521	N_Shore	CGGCCCCAAAGCCCTGTGAATCCCAGTTCTGAGGGGTGGCCAAGGCCAAG	F	TSS1500	CYP2W1	0.8515514	0.90294	-0.051388571	0.8728925	0.90294	-0.030047
cg04889790	1	62710434	2288405	2288455	N/A	GGCTGGGGGGTTCTGCCGGAGCACCTGGGCCTCATCTCCACGAAGAAACG	R	Body	MORN1	0.6391371	0.6972714	-0.058134286			
cg04890576	17	16682456	73032613	73032663	S_Shore	GCTAAATAACAGTGAACAAACAACTGGGAACAGGCTCAGCTAAAGGCACG	F	N/A	N/A	0.4296314	0.53563	-0.105998571	0.43467	0.53563	-0.10096
cg04903429	16	68624467	4043204	4043254	N/A	CGCTGGTTTCCACGTGGGTTGCTGCTGACCCTCCCTCGAGCTCCCTGCCG	F	Body	ADCY9	0.8046629	0.85431	-0.049647143			
cg04910179	1	40709418	57816236	57816286	N/A	CGCCCAGCAAAGTGGATCTAAATACAGAGGGAGCTCATTCCATTCAGCAG	R	5'UTR	DAB1	0.7891429	0.8613986	-0.072255714	0.830265	0.8613986	-0.031134
cg04914290	16	56719404	88845204	88845254	Island	GCTGGATGCCTGGGTGTGTGGGTGGCTCCCAGTGTGTGGGATGGCACACG	F	Body	FAM38A	0.8172643	0.8689329	-0.051668571			
cg04915058	3	55768372	55693741	55693791	N/A	CGGTTGAGACTGAGGTCAGAAAGCCTTTCTGCTAGTTTTTTGAAGAGATT	R	TSS1500;3'UTR	C3orf51	0.80059	0.8599671	-0.059377143	0.8315525	0.8599671	-0.028415
cg04917208	16	32688474	70680104	70680154	N/A	GGACAGGTTAAAAAAGCAGACGAGCTCCCACTCCGAAAACAAGCCGGACG	F	TSS1500	IL34	0.8176514	0.8590986	-0.041447143	0.8338338	0.8590986	-0.025265
cg04918708	1	49795412	204057900	204057950	N/A	CGGCCACCACCTCGCCTCGTCAGGGATCAGGACACCATGCCTGGCACTCA	F	5'UTR	SOX13	0.8966171	0.9383957	-0.041778571	0.9219938	0.9383957	-0.016402
cg04921776	17	72759316	59564657	59564707	N/A	CGCAAATCTATGACAGGTCTCCAAGGCATACGGAACCAATCAGGGACATC	F	N/A	N/A	0.69202	0.7897943	-0.097774286	0.7558763	0.7897943	-0.033918
cg04925220	6	46736500	107807442	107807492	N_Shelf	ACTTAATAGCTTTTCTCTCTCTCTCTCTGAGATGGAGTCTTGCTCTGTCG	R	N/A	N/A	0.7387857	0.7819071	-0.043121429			
cg04928930	14	69785387	20926227	20926277	N_Shelf	ATTAAATAGTTATATACACATCAGTTCCTGTGGTTCTGTACAGAGCAGCG	R	3'UTR;3'UTR	TMEM55B	0.8777086	0.918	-0.040291429	0.8928825	0.918	-0.025118
cg04929932	1	58802460	91195683	91195733	S_Shelf	AAAGGCTAAGTCAAAACTTCAAGCTCTCTCATTATGAGGTATACCTGACG	R	N/A	N/A	0.6043529	0.6808543	-0.076501429			
cg04937851	2	71750451	237993660	237993710	N_Shore	CGGAGCTTCCTTGTTCAAAAAACAGAAAGAAAGTGCCTCTGAGGTCATAA	R	TSS1500;TSS1500	COPS8	0.6158271	0.7026886	-0.086861429			
cg04938830	12	62663411	105710210	105710260	N/A	GACAATAACATGACTACTACTATACTAAAACTGTCACCTGGTGCCTAACG	R	N/A	N/A	0.75741	0.8256357	-0.068225714			
cg04945457	16	19696322	56894587	56894637	N/A	CGGATCTCCTGGCTCTCAGACAGAACAGGAGCAGTGAAGAAACTGAAACT	R	N/A	N/A	0.4673614	0.55841	-0.091048571			
cg04950627	2	28664455	39758157	39758207	N/A	AAGATCTTGGCCAGGCAGCCTGCAAATGAGTAAAAACCAGAGCCTCCACG	R	N/A	N/A	0.82087	0.86327	-0.0424			
cg04958528	16	63703390	28982197	28982247	N_Shelf	GGCATGAGCCACCATGCCTGGCCTTCAGTGAGTTTTGGTAGATGTACACG	R	N/A	N/A	0.64074	0.6960071	-0.055267143			
cg04964220	12	37704475	57396584	57396634	N_Shelf	CGCCTCTTTGGAATGGATGATGTACATGAAGGTCTGCTCGATGGTGAAGT	F	Body	ZBTB39	0.8809529	0.8998829	-0.01893			
cg04973925	15	25669308	49218062	49218112	N/A	CGGGACAGATTCAAGTGACATCATGGAAACAGATACTACAGAATTCGGCA	F	Body	SHC4	0.5765414	0.6576657	-0.081124286	0.62098	0.6576657	-0.036686
cg04981492	19	74760401	15218713	15218763	S_Shore	CGCCTCCAGGGCTCCCGATGCCCCTTGCCCAGCCCGACTGGGCCCCAGTG	R	Body	SYDE1						
cg04983519	6	54675313	31853647	31853697	N_Shelf	ATAGATTGTATTCTCTAAAAAATGCTTCTGGCCGGGCGCTGTGGCTCACG	R	Body;Body	EHMT2	0.68402	0.7436929	-0.059672857			
cg04990210	17	28716448	3558661	3558711	N/A	CGGCCCAGGGGGTTACCTTTTCCGCCTCCAATTCATGATCACCTGAGGGT	R	Body;Body	CTNS	0.8255157	0.8844043	-0.058888571			
cg04992588	3	47645408	58563674	58563724	N/A	CGCTCTTCCGTTGGCTCCTCTGTGAAGTTCCAATGACATTCAAGGTATCA	R	TSS200;TSS200	FAM107A	0.6811	0.7464957	-0.065395714			
cg04997017	3	49632317	65518607	65518657	N/A	CGGTCCTGCTAAACCAGCGACACCCCTAACGTTGTGCCATTTGAGGGGAG	R	Body;Body;Body	MAGI1	0.9164057	0.9439614	-0.027555714	0.9317425	0.9439614	-0.012219
cg05005382	16	43602318	841550	841600	Island	CGACTTCCCCCGAGTTGTTACTGCAACGCTCCAGTTCTAACTCACGCTAA	R	Body	CHTF18	0.5899729	0.7414871	-0.151514286			
cg05005432	11	23619407	6191109	6191159	N/A	CGGCCAGAGCAATCCTCCCCACAACAGGCCATGTTAGCACTGTTGTATAT	F	1stExon	OR52B2	0.9170029	0.9366114	-0.019608571			
cg05012356	4	32675374	95124979	95125029	N_Shelf	CGTCTTCTTGGCCCCAAAGATTCCTTTAGGGCAGGGCATAGCTGGAAAGA	R	N/A	N/A	0.71868	0.7680571	-0.049377143			
cg05020685	4	16703374	40858965	40859015	Island	CCTTTGTTTGCAGGTGCGTTCAGGGGGAACGGGGGTCGAGCCCAAGCTCG	F	Body;5'UTR;5'UTR;5'UTR;Bod	APBB2	0.6419943	0.7305	-0.088505714			
cg05024762	10	73712374	104472143	104472193	N_Shore	ACGACTGACTAAATTCAGTGTTTCACTTCAAGTTTTAAGAACAGCTCACG	R	Body	ARL3	0.8399986	0.9058143	-0.065815714			
cg05026014	4	40664432	1749153	1749203	N/A	CGCAGCCCTGAGTTAACTCAGGCTCCAGGATAAACACCCATTCAGCCACA	R	N/A	N/A				0.5701113	0.7566786	-0.186567
cg05037327	6	21690385	88880599	88880649	S_Shelf	TTCAAACCATATGAGGAGTATGTTCCAACAGATAATAAACAAGCACATCG	R	N/A	N/A	0.7989914	0.8383257	-0.039334286	0.777265	0.8383257	-0.061061
cg05045498	16	39665426	318213	318263	N_Shore	CGTGTGCCTCAGTGCTACACATGCCTCATACGCACACACACCCATGCATG	F	N/A	N/A	0.7089329	0.8031329	-0.0942			
cg05049822	4	37640328	103171630	103171680	N/A	CGCGGGGCTCAATTTCTTGCCAGGCCTTAGCTGCCTCCCTGCCGGGCAGG	R	N/A	N/A	0.8963471	0.7045971	0.19175			
cg05051976	12	11723345	69329653	69329703	S_Shelf	CGTGGACACTATCTGATTTCCTGCAGGGTGCTGTGGCTGGAGACTGGAAG	F	5'UTR	CPM	0.8106757	0.8594857	-0.04881			
cg05052501	8	38613345	69240774	69240824	N_Shelf	GAGACTACTATTTTATTGTTAATAGAGACAAAGTCTCGCTATCCTGCCCG	R	N/A	N/A				0.5044388	0.5385029	-0.034064
cg05058204	3	10680394	173129681	173129731	N/A	TACAATTAAACCTTAATATTTCTGCATTTTAAGTCTTACTGTCAGCTTCG	F	5'UTR	NLGN1	0.1717829	0.2793543	-0.107571429	0.2096388	0.2793543	-0.069716
cg05063097	16	45666356	49861680	49861730	N/A	TTGCCTGGGCTGGTCTCACACTTCAGGCTTCAAACAATCCTACTGCCTCG	R	TSS1500	ZNF423	0.56822	0.6349143	-0.066694286			
cg05064567	17	59716424	78870138	78870188	Island	TTAGGGTCTGAGTGGGGGCTCCATTCTTAGCAGCACCCATCCCATCCACG	R	Body;Body	RPTOR	0.8864557	0.91722	-0.030764286	0.906155	0.91722	-0.011065
cg05067973	20	59713374	360745	360795	N_Shore	GGCCTATGGACTTAAGAGCTGACTCTGGGCTCAAAGGAACCACCGTGGCG	F	TSS1500	TRIB3	0.9026186	0.9331643	-0.030545714			
cg05068866	3	24666459	66633374	66633424	N/A	CGCTCCACTAGTGTGAGAAAGCCACAACACAGCACGGAGGGAACCATTCA	F	N/A	N/A	0.7531329	0.8355886	-0.082455714	0.7606725	0.8355886	-0.074916
cg05070265	3	23620343	55777041	55777091	N/A	GGGAGCAAACCACATTAAGAAGTCTGGGCTGCCAAAGCCTGGCCTTTACG	F	Body	ERC2	0.8511971	0.8909214	-0.039724286	0.8637225	0.8909214	-0.027199
cg05074138	2	33624418	204732687	204732737	N/A	CGGCACAAGGCTCAGCTGAACCTGGCTACCAGGACCTGGCCCTGCACTCT	F	1stExon;1stExon	CTLA4	0.80912	0.8814	-0.07228	0.8339613	0.8814	-0.047439
cg05075562	2	23664479	42123725	42123775	N/A	CGACTGCCCAGGATCCTCTGCTGTGGCAACATATATCACTGGCCACCCCA	F	N/A	N/A	0.7953257	0.8613471	-0.066021429			
cg05093811	3	61800403	58059919	58059969	N/A	CGTAGGTAATGCTGATGTTCTTGGTCTGGGTCATAAGAGTAATTCTGATC	R	Body;Body;Body;Body	FLNB	0.8116757	0.8654357	-0.05376			
cg05097579	3	52792374	136750029	136750079	N_Shore	AGGGTCTTGATATGTCAGGCTGCAGGCTGAAGTATAGTGGCACAATCACG	R	N/A	N/A	0.5747586	0.6835114	-0.108752857	0.622925	0.6835114	-0.060586
cg05101231	3	36640450	51593459	51593509	N/A	CCCAGATATCTTAAATTTAGTAAGTTTGGTGTCTTACACTTGGTAACTCG	R	5'UTR	RAD54L2	0.6313514	0.7673743	-0.136022857			
cg05118364	16	35612438	3533812	3533862	N_Shore	CGAGACCAGCCTGGGCAACATGGTAATATGTGCAACTCGATTTACCCAAA	R	Body;Body;Body	NAT15	0.46617	0.5169571	-0.050787143			
cg05121202	10	26690339	85957323	85957373	S_Shelf	CGGGGTTCTTATAAACTCAGAGACCCAGAGGGTCTGTTGGGGCTCCAACA	R	Body	PCDH21				0.6787738	0.7230214	-0.044248
cg05127995	4	32615412	2735245	2735295	S_Shore	CGGCTGGAGTCCCGGGGGCCTGCACTGGGGTTTCAAGGACACTACTGTTG	R	N/A	N/A	0.6645914	0.7397529	-0.075161429			
cg05128520	16	73683312	84676746	84676796	N/A	TTTTTTCCTTAATCTGATGTTAGGGGCCACCCAAGCACTGGGGCCAGACG	R	N/A	N/A	0.3231171	0.3884971	-0.06538	0.35174	0.3884971	-0.036757
cg05130075	14	66640411	55089473	55089523	N/A	CGCTGCACGACAGACCAGTCAAATCAGAACCATGAGGGCTGAAACCAGAA	R	Body;Body	SAMD4A	0.8979871	0.9379471	-0.03996			
cg05136848	11	69682477	45718281	45718331	N/A	GGATGTCAGCCTTAGTGAGAAATTCCCCAGACAGCTGGCAGTTGGTCCCG	F	N/A	N/A	0.7812886	0.8578343	-0.076545714	0.8310688	0.8578343	-0.026766
cg05138403	14	31755419	93510791	93510841	N/A	ACCAGCTTCACAGCCAAGCAGAGGGATGCCAGTGTTCGGCCTAGGCTTCG	F	Body;Body;Body	ITPK1	0.9075443	0.9419386	-0.034394286			
cg05139861	6	30691340	44007826	44007876	N/A	GAAGTGGTGGGTGAGCCCTGAATATTTTACCTGAACGTGACACAGGGCCG	F	N/A	N/A	0.8654671	0.9125371	-0.04707			
cg05146888	6	66730373	33129060	33129110	N_Shore	CTGTTCGGGGGGCGACCTCTGCGGGTTTGGCTCCAGCTGCAGAAAGAGCG	R	N/A	N/A	0.4672857	0.5690486	-0.101762857	0.5146088	0.5690486	-0.05444
cg05154454	9	11690312	113100053	113100103	N/A	CGGCAAGTATTTATTTGGCTTCACTGAGTATTTCAAATGTGGACATCTTG	R	1stExon	TXNDC8	0.8614271	0.9218343	-0.060407143			
cg05157904	1	46777336	109207578	109207628	S_Shelf	CTGACCGGTGTGGATGTATAAAAGTCCAGCTCCGTGATCTCAGACTTCCG	R	N/A	N/A	0.8741871	0.9119329	-0.037745714			
cg05165553	18	66629348	77171010	77171060	Island	GGGACGCGGGTCTGGAGGAGCGGGCACCCAGCCAGCTCTCCTCAGTGACG	F	Body;5'UTR;Body;Body;Body	NFATC1	0.8269086	0.8655529	-0.038644286			
cg05181927	10	26609479	79798897	79798947	N/A	TAAACCTGGGATTGCCTGCCCAGGACTGTAATCACATTGATGTCCCAGCG	R	Body;Body;Body;3'UTR;Body;:	RPS24	0.9090629	0.9409314	-0.031868571			
cg05185019	2	13786466	179672121	179672171	N/A	CGGGTGTAGGGATTGCATAGAAAAGCAAAACTACACAGTCTTGACTGTGT	R	1stExon;5'UTR;5'UTR;5'UTR;1	TTN	0.8001	0.8766929	-0.076592857	0.8220488	0.8766929	-0.054644
cg05186311	10	18693377	131758454	131758504	Island	GGCGGGAGGCTGGGGCCGGGAGCTCCAAGTTCCCTGCATAAAATTCCACG	R	Body	EBF3	0.2053386	0.1501814	0.055157143			
cg05197133	20	11732438	37005424	37005474	N/A	CACGTCTCAGAGATTCTTGAAGAATGAAGACATTTCTGCTCTCAGCTCCG	R	3'UTR	LBP	0.8040814	0.8512286	-0.047147143			
cg05199904	5	33624432	71251691	71251741	N/A	CGGTCCTGGGACCACCTTCCTCAGTGCTATGCTGAGCAGAAAGATGGCAC	R	N/A	N/A	0.8187743	0.8816029	-0.062828571	0.8455613	0.8816029	-0.036042
cg05200628	1	35752479	160681760	160681810	N/A	CGGAAACTGAGAACAATTTTGTTTGAAGGTACATGAGTGCTTTTTTGTAG	F	TSS200	CD48	0.6863471	0.7815871	-0.09524			
cg05202439	14	57689486	24629534	24629584	N/A	CGGCCACTGAGCGCTACCTGCACGTACGCCCCCAGCCTTTGGCTGGAGAG	F	TSS1500;Body	IRF9	0.8574043	0.90864	-0.051235714			
cg05205299	9	36746392	109848356	109848406	N/A	CCACACCATAATGCATGATTGCCTAAGGCTGAGCCCTCAGCAGGGGCTCG	F	Body	MIR548Q	0.7777914	0.8330586	-0.055267143			
cg05214088	10	39666375	134743551	134743601	S_Shelf	CGTGGCCCTGGGCAGCCTCCACAACTGTGCTGGCCCCGGGAGACTGCTGG	R	Body	C10orf93	0.5602614	0.60215	-0.041888571			
cg05223061	2	30683393	233768377	233768427	S_Shelf	AGGGAGTTTTTCTTGATGCTTTGAGGTGGACGTGGCCATTACCTAAAACG	F	Body;Body	NGEF	0.74719	0.8367671	-0.089577143			
cg05227350	11	59738386	130185670	130185720	S_Shore	TAACTAGGTTGATTGATTTTGCAGTTGACCAAGAACTTCAAAACCCCCCG	F	TSS1500	ZBTB44	0.6096886	0.7015571	-0.091868571			
cg05231226	16	74642420	89171772	89171822	N_Shore	CGCCCTGCATGGACACAGCTGTCCTTGGTGAACGTCTGCTGAGTCAAAGT	F	Body;Body;Body	ACSF3	0.8368271	0.8778014	-0.040974286			
cg05233877	6	63614474	31599162	31599212	N_Shore	CGCGGGCAGGCTTTCGGCCTGCTTCTGGCCCCGTCAGCTGTGCAGTCTCC	R	Body	BAT2	0.8220343	0.8597086	-0.037674286			
cg05235248	10	55738481	35503876	35503926	Island	CGGAGCTCCCCGCACACCCGTGCGCGTGGGATCCACAGCTCTCCCCACAC	F	N/A	N/A	0.85442	0.9077186	-0.053298571			
cg05236720	2	55792436	37893255	37893305	N/A	CGCCTGTGGTTCTCTAACTAAAATGTCCCTGGGTTGCTTCGGCTCTGTAG	F	5'UTR	CDC42EP3	0.7960657	0.8571243	-0.061058571			
cg05245416	2	40643383	105087010	105087060	N/A	TTTGTCTCTTTCAAAGCTGGATAACACAAGAGCTCTGCACATCTGTATCG	R	Body	LOC150568	0.9022057	0.9276843	-0.025478571			
cg05245794	8	70725341	119884332	119884382	N/A	CGGCTGGCTCCTGTGCTAGGTGCAGATTTCGCTCTATGATGAAGAGCACT	R	N/A	N/A	0.8077843	0.8479043	-0.04012	0.8147188	0.8479043	-0.033186
cg05248804	22	58635448	45895926	45895976	N_Shelf	CGGCCACCTGCTCCATTCCCATTGGGACTTCTCAGTCCTGGCTTCACTGA	F	N/A	N/A	0.8924929	0.9355486	-0.043055714			
cg05249026	16	62797468	11031524	11031574	N_Shelf	CGGGACGAATAATCCAACTGAGCTGCCTCTGCACCAGAACTGCTGGGACG	F	3'UTR	DEXI	0.0946323	0.0611039	0.033528429			
cg05251389	22	19622379	43525330	43525380	N/A	CGGGGCTGGCCCCACCCCCATGACCACTGCCCTGGAGGTGGCGGCCTGCT	F	3'UTR	BIK	0.7694286	0.8476943	-0.078265714			
cg05260714	22	41769348	25344500	25344550	N_Shelf	CGCCTGCAGGCGGCTTGGGTCAGTTGCTGCATCTACTTAGCCACCTAGGC	F	N/A	N/A	0.8619614	0.8924157	-0.030454286			
cg05264578	1	36604358	1886865	1886915	Island	CGCCCGTGCTGGGCCTGCTGGGCCAATGCTGGAGGTGCCTTCAAGTCTTC	F	3'UTR	KIAA1751	0.8544286	0.8800529	-0.025624286			
cg05266321	3	66796307	46401927	46401977	N/A	CGCATGACTTCATAATGATACAAAACAAAACACAAAAGGCTTTTGGCAGC	R	3'UTR	CCR2	0.7719057	0.8632057	-0.0913	0.8147625	0.8632057	-0.048443
cg05270224	1	31769381	8212843	8212893	N/A	CGTGTGGTTTCATGGTTTCCTTTGCTAATGTACGAAAAAGAACAAGATGA	R	N/A	N/A	0.6821371	0.79841	-0.116272857			
cg05299486	17	15631346	40609380	40609430	N_Shore	TACACTTGAATTTCAACAGGGTTCCACCACCCAGGAAGACAGAATAACCG	R	TSS1500;TSS1500;TSS1500	ATP6V0A1	0.3132343	0.4517986	-0.138564286	0.3549925	0.4517986	-0.096806
cg05302095	11	21647486	76516376	76516426	N/A	TATTTAAAGCTTGCACTAAGTATGACTTTGCCCACAGTCTGCGGGAAGCG	F	N/A	N/A	0.7052043	0.7882029	-0.082998571	0.7478163	0.7882029	-0.040387
cg05305046	5	38773470	40841315	40841365	N/A	GCCTAGTGTTGGAGAGTGCAGATACAAGCACAGTGGGGCAACCCAGCTCG	F	TSS200	CARD6	0.3590814	0.4635171	-0.104435714			
cg05308645	3	24620367	184107534	184107584	S_Shelf	CGGGGGCCCTTGGTGCTGAGTGAAGATAAATTAAAAATCCCAACAAGCCA	R	3'UTR	CHRD	0.7536671	0.8052314	-0.051564286	0.778355	0.8052314	-0.026876
cg05309399	4	19704376	106552544	106552594	N/A	TTGTAACTTGCCTGGCCCCACGTAGTTCAAGGATTATGTGAGATAACACG	R	3'UTR	FLJ20184	0.7008157	0.8032629	-0.102447143	0.7567963	0.8032629	-0.046467
cg05310309	2	54775363	109257429	109257479	N/A	TCACTCATATGTGAAAGCAAAAATACAATTGAACTCACAGAATTAGAACG	F	5'UTR	LIMS1	0.73677	0.8325971	-0.095827143	0.7823938	0.8325971	-0.050203
cg05312779	15	23651426	90328239	90328289	N/A	CGGCCCCCAGCAAGGCCGTTCATTGTCCATCGAGAGCTTCTGCTCATCTG	F	3'UTR	ANPEP	0.77404	0.83554	-0.0615			
cg05316065	8	17704317	130799007	130799057	N/A	CGAGCCAAAGAAGTTGTTCCAGCTAGAGTTGCTGGGAATCCATGAATCAA	R	1stExon;5'UTR	GSDMC	0.6927029	0.7706371	-0.077934286	0.7354188	0.7706371	-0.035218
cg05318454	19	26618456	46117805	46117855	N_Shore	TGAGCTTCCCACACTGGAGGTAAGCAGTAAGACTCTGGAAACCACCAGCG	R	Body	EML2	0.6676	0.7823286	-0.114728571	0.7405188	0.7823286	-0.04181
cg05320533	16	56658443	89541815	89541865	N/A	CGCTGCACTGTTTCTATAGCAACCAGAAAGAAAATATAAAGCAAGCAGTT	F	5'UTR	ANKRD11	0.6551729	0.8154414	-0.160268571			
cg05330497	16	43660413	58147704	58147754	N/A	CGCTGGAGCTTATTCCGCCGCCTGCCCCAGTGTGGGGGGAGATACCTTTA	R	3'UTR	C16orf80	0.9145614	0.9400843	-0.025522857			
cg05338785	14	44686315	94630892	94630942	N/A	GATCCTAATCCTAACTGGTTAGCCCTGGAACCTGGAACAAGTGGCTCCCG	F	N/A	N/A	0.8598286	0.89711	-0.037281429	0.8627463	0.89711	-0.034364
cg05340882	19	57708345	2543750	2543800	Island	CGGCTGCGCTTTTCCAGTCTGCTCATCAAAGCAGAGCCAGCCTTGTGTGG	F	5'UTR	GNG7	0.2004557	0.2818414	-0.081385714	0.1108265	0.2818414	-0.171015
cg05342136	4	33764417	3528373	3528423	S_Shore	GGGTGTGCCAAACACACAGAATTGGCTTCGTGCGAGTCTTGAAAGAAACG	F	Body	LRPAP1	0.8501414	0.8996243	-0.049482857			
cg05347965	17	51791320	55663256	55663306	N/A	CGACCTCAGCCTCCTCTGCCCCGCTGGGCGCGAGCTGCAGTCCTGGCACC	F	Body;Body	MSI2	0.7816557	0.8352614	-0.053605714			
cg05348668	2	37728458	190686969	190687019	Island	CGCCTGGGTAGGAGCACCGACTGCGGGGCCTCTACCGACCTTACTAGAAA	F	Body;Body;Body	PMS1	0.9099229	0.9386386	-0.028715714			
cg05349242	14	16762508	77255429	77255479	N/A	CGGTTAGACTTTCTCCAGGCCTGGCTGCGTTCTCTGCCTGTGGTCCTTGC	R	3'UTR	ANGEL1	0.7509271	0.8011157	-0.050188571	0.7750288	0.8011157	-0.026087
cg05368595	6	60775438	14755316	14755366	N/A	ACACTAAGGTCACCCAGCAAGTTAGCAGCGCAAAGAGAATTAACAAAACG	R	N/A	N/A	0.8894114	0.9162414	-0.02683			
cg05372113	19	67695435	41595975	41596025	Island	CGCGCCAAGCAGCTCCGGCGCTTCTCCATCGCCACCCTAAGGGGTTTTGG	F	Body	CYP2A13	0.1508707	0.29523	-0.144359286			
cg05375309	6	71733348	79621517	79621567	S_Shore	CGAGGGTAACAGAAGCTACTTCACATGGTAGTACAGTATTCATAACATCT	R	N/A	N/A	0.8022971	0.8500714	-0.047774286			
cg05377733	15	73605362	68645969	68646019	N/A	CGGATTCTGCACTGGGTAAAGGGACTTGGATTTGTTCCTTTGTAAATTAG	F	Body	ITGA11	0.8329329	0.8679514	-0.035018571			
cg05380885	1	74642409	183274661	183274711	N/A	CGAGCTTGAAATAGACTTTATCCAGGAGATAGCTGTTTTTCCTGGGTAAA	F	Body;TSS1500	NMNAT2	0.7225257	0.7808929	-0.058367143	0.7307213	0.7808929	-0.050172
cg05389989	6	48612450	30113995	30114045	N/A	TCCCTGGAACAGCCTGATGTGGGCAGATGGTCGTGGAGGCTGAAAACCCG	R	Body	TRIM40	0.8661871	0.90962	-0.043432857			
cg05391643	1	12626375	27214630	27214680	N_Shore	CTTTTTTTTCTTGATAAATTAGTACTCTCGGCTGGGCGTGGTGGCTCACG	F	Body	GPN2	0.5888343	0.6469	-0.058065714			
cg05401312	6	24700447	33838308	33838358	N/A	TGCTGCCACTGATGCAGTGGGGGGCTCATCCAACAGAGAGCTGGCCCTCG	F	N/A	N/A	0.8144171	0.8588843	-0.044467143			
cg05404091	12	55663300	133182886	133182936	N_Shelf	CGGGTGTGTGGACCTGCAGAGACCCAGGATTGTGTGGGAGTGTGTCCACG	R	N/A	N/A	0.7868129	0.8552514	-0.068438571			
cg05407489	10	30801499	73139576	73139626	S_Shelf	GCCAGTGTGCCCCACTATTTCAGGCCAGCAGTGTCCACAAAGTGCACTCG	F	N/A	N/A	0.7122343	0.76766	-0.055425714	0.7432488	0.76766	-0.024411
cg05410934	13	39692377	41059150	41059200	N/A	CGGAAGGGAGATGTCTTTCGCTACAGCGTGTGAATGTTGCTTTGCTTCCA	F	N/A	N/A	0.8830143	0.9286843	-0.04567	0.9030513	0.9286843	-0.025633
cg05412531	8	32778317	125183758	125183808	N/A	ATGGTTCTATAAATGGCGGTTTCCCCAGCTCGCTCTTGCCTGCTGCTACG	F	N/A	N/A	0.8961114	0.9263043	-0.030192857			
cg05416777	8	52690504	48743625	48743675	N_Shore	CGGCTGCCGGCCTCGTTCTCAGTGAGACTTTCCAGAGATGCAGCTCTCCA	R	Body;Body	PRKDC	0.87429	0.9052686	-0.030978571			
cg05418915	2	71603443	196426178	196426228	N/A	ATTTGCCTAAGATCACATGGCTAGCTAGTAATGGAGCTATGATCCAGACG	F	N/A	N/A	0.7311429	0.8375686	-0.106425714	0.78739	0.8375686	-0.050179
cg05424422	3	35616466	184102870	184102920	N_Shore	AGCAGGAGCCCTGGTGCTACCCCCTGTGAAGAGCCAAGCAGCAGGGCACG	R	Body	CHRD	0.6958886	0.7798514	-0.083962857	0.7314513	0.7798514	-0.0484
cg05425294	16	13796366	1644664	1644714	N/A	TGCTTGGTGCGCTGCGTGCTCAATCTAAAACCATCACAGTCGCAACTGCG	R	Body	IFT140	0.9046857	0.92926	-0.024574286			
cg05444024	19	10602429	5841072	5841122	N_Shelf	CGCCCCGCCCCCAGCTGGGTTGTTTCTTAAGGATTCAAAATCCAAAGGTA	F	TSS1500;TSS1500	FUT6	0.8527171	0.8927186	-0.040001429	0.8721413	0.8927186	-0.020577
cg05450629	15	56748469	90627448	90627498	N/A	CGCCGGCTCAGCCCTGGCCCCTCCACTGCAGCCATGGGTGGCGCCTCCCC	F	3'UTR	IDH2	0.7431757	0.7855371	-0.042361429			
cg05456956	10	14683327	6557542	6557592	N/A	CTTGGGCCAATCCCATTACACACATAAATAGACCATGTAAGAATTTTGCG	F	5'UTR	PRKCQ	0.82548	0.8864171	-0.060937143			
cg05457193	5	43607415	14577586	14577636	N_Shelf	TTGGGGCATGGTGGGCTGCAGGTCCCAAGCCCTGCCCCCGTGGGTAGGCG	F	N/A	N/A	0.5436829	0.6116871	-0.068004286			
cg05457684	11	56778369	2919808	2919858	N_Shelf	CTGGTTGGGGCCTGGGCTGAGAGGGCCAACTGAGGGGGCCTTCAGGTGCG	F	Body;TSS1500	SLC22A18AS	0.7431486	0.8145971	-0.071448571			
cg05465032	16	32713507	4658987	4659037	N_Shore	CGCCTGCCTGCTGGGGCTGCCTGCATGCCTCCCCTGCACCTGGGGGTACC	R	3'UTR	FAM100A	0.7723243	0.8228343	-0.05051			
cg05484458	12	19683474	6949260	6949310	N/A	CGGCCCTAAGTCTCAGCAAAGCTCAGAGAGGGAAGACAGGGCTTACACTT	R	TSS200	GNB3	0.8209271	0.8763071	-0.05538			
cg05487134	17	46624429	40489569	40489619	N/A	CGCTGACAAAAGCCCCGCCAGCTCACTCACGATGCTCTGGTTGGAAACCA	F	Body;Body;Body	STAT3	0.73885	0.8507514	-0.111901429	0.78965	0.8507514	-0.061101
cg05492803	2	53686408	120007876	120007926	S_Shelf	CGCCCCACACCAGCTGAGGCGAGGAGCCAGATGGTCTGTGTCTTTCTTAC	R	Body;Body;Body	STEAP3	0.9118843	0.9358557	-0.023971429	0.9114988	0.9358557	-0.024357
cg05500015	11	49800433	89867819	89867869	N/A	CGGAGGCCACCCAGAGCTCACAGCCTCCTGCCAGCGCGCTCTCTGTTTCT	F	5'UTR;1stExon	NAALAD2				0.14726	0.0849413	0.0623187
cg05500240	16	74766476	89925609	89925659	N/A	CGGGACCGCTCCTTCTCAGAGCATGACCTGGCCCAGCTCCGAAGTGAGGT	F	Body	SPIRE2	0.67523	0.7351657	-0.059935714			
cg05504729	16	59781413	89399490	89399540	N/A	CGCCTGCCCCCTGGTGTGAGGTCACAGACTCAGTGGCCAAGCTCAACAAT	F	5'UTR	ANKRD11	0.3894686	0.4831986	-0.09373			
cg05505763	13	32683422	103020269	103020319	N/A	CGTGCCTAAGTTCCGGGCTGAGGCCTTAAGAACCCATGCACTCTTCTCCT	F	Body	FGF14	0.7845043	0.8231971	-0.038692857	0.79605	0.8231971	-0.027147
cg05505855	4	16723350	30719017	30719067	Island	CCATCAGTCCCAGGCTCCGACCTTTCTGCCAGAGCAGCAAAGAAGTGGCG	F	N/A	N/A	0.0640171	0.1027183	-0.038701143			
cg05514299	17	19661387	74868670	74868720	S_Shelf	CGGGCTCTAGCCTCCAGGCAGAGCTGGTTCATTAACAGCTGCAGTCCTGA	R	Body;TSS200	MGAT5B	0.7047571	0.7812943	-0.076537143	0.7414513	0.7812943	-0.039843
cg05517218	16	64642464	58080289	58080339	S_Shore	GGGAGGAACCCCTCATGCCCAGTGCCTGACACTGTGGGCACCCATTCACG	F	3'UTR	MMP15	0.77207	0.8194557	-0.047385714	0.7863863	0.8194557	-0.033069
cg05519606	6	18726498	143176015	143176065	N/A	TGGAGTGGACCTGAAAGCTGTGCCTGCTTTCATTCTTTTTCCTACATCCG	F	5'UTR	HIVEP2	0.8605786	0.9104457	-0.049867143			
cg05521581	16	34810440	58072094	58072144	N_Shore	CGCCACTTCCGGGCTTCCCAGCCGCCCCTCCTATGACACAGTGGGGATGG	R	Body	MMP15	0.8496229	0.8812	-0.031577143	0.8394925	0.8812	-0.041707
cg05523877	10	11779364	72185663	72185713	N/A	CGGTGCTTGGTACCTGGTCTCTCCAGTCTCAACAGACTCAGGTCAGGTCT	F	3'UTR	EIF4EBP2	0.8242757	0.8833243	-0.059048571			
cg05528339	2	40719366	64064409	64064459	N_Shelf	CGGGCTTAACTGGAAAAAGATATCAAATTATATCTATGAGATGGACTACT	R	N/A	N/A	0.7300257	0.7876657	-0.05764			
cg05533210	7	57711301	36409818	36409868	S_Shelf	TATTCATCCTCATCAAGCTTTCTGCATCTGCTTTGTTAATTACTGATTCG	R	Body	KIAA0895	0.8101629	0.8834086	-0.073245714	0.8491663	0.8834086	-0.034242
cg05539509	22	30762370	30663034	30663084	N/A	CGTTCTTCGAGGTCAGCCCTACGCCCAAGGATGATGTAAAACCGCAGCCT	F	TSS200	OSM	0.5739086	0.6538686	-0.07996			
cg05540569	17	44614312	37093398	37093448	N/A	ATACTCCTCTGTCTACCTAAATCCTCAGAAAGCCTTGCCTTTAGAGAACG	F	3'UTR	FBXO47	0.7747514	0.8663014	-0.09155			
cg05541747	18	27797455	32617356	32617406	N_Shelf	CGATGAGGAAACTAAATGTTAGAGATACAAAGTAACTTGCCAAGGTCATA	F	5'UTR;Body	MAPRE2	0.8804629	0.91695	-0.036487143			
cg05550420	11	11757451	6668214	6668264	N/A	GGAGGAGGCCTGGGTGGTGCCAGCTCCCCCAGCCTGTTTCCCCTTCAGCG	F	5'UTR	DCHS1	0.6058729	0.7058129	-0.09994			
cg05552543	16	29753364	75322715	75322765	N/A	CTCTGTTCTGCTGCCACGAGGCAGCATGGCACCTGGAGAGCCTGTCACCG	R	N/A	N/A	0.7460529	0.8112314	-0.065178571	0.7775613	0.8112314	-0.03367
cg05552569	5	46731488	73980039	73980089	N_Shore	CGCTAGGCAGACCAAAACCACAGATCTGCTATATAAGTATTCTGAAAATG	R	TSS1500	HEXB	0.8849514	0.9288929	-0.043941429			
cg05556038	3	43685429	25427224	25427274	N/A	GATTGTTAGTTTTGCAGCAATAGGTGATCTACATACCAGCCTGCCCTACG	R	N/A	N/A	0.8698171	0.9098557	-0.040038571			
cg05568423	7	56767408	6674031	6674081	N_Shelf	CGGCCTTAGATCCCTCCACCCTGTCAGGCAGGGACCCCGAATCACCCCAG	R	N/A	N/A	0.6709229	0.7374871	-0.066564286	0.6817338	0.7374871	-0.055753
cg05570654	2	60767480	240259075	240259125	N/A	GAGAGAAACTCACACCCTGCATAAGCCACTAACCGGTGGGGACTCCCACG	R	Body	HDAC4	0.7067971	0.7472	-0.040402857			
cg05573378	15	44651352	42876795	42876845	S_Shelf	ACTGAGGAGAACAGCATTATTCACAGAAATGCCTTATCTTATACACTCCG	F	Body	STARD9	0.7232457	0.7690671	-0.045821429			
cg05574357	12	46724344	115134362	115134412	N_Shore	CGCCAACCAGGTCAGTAACGCTGTCTGGGTTTCCAAGGCTCCCAGGAGCA	R	N/A	N/A	0.6383729	0.72281	-0.084437143			
cg05575217	21	61665381	46518030	46518080	N_Shelf	TGACTTGCCAGCTGCTGGACAGCAGGGAGACGTGGAAAGGCAAGCACCCG	F	5'UTR;5'UTR;5'UTR;Body;Bod	ADARB1	0.7313257	0.7750357	-0.04371			
cg05575393	10	22758314	114544316	114544366	N/A	CGCTAAATTGGGCGATAAGTCAGTGTTTCAATGTGGCACAGTCAACCACA	F	Body	VTI1A	0.8885357	0.9360614	-0.047525714			
cg05587232	7	41667373	1154545	1154595	N_Shore	CGTGGGTGGGAGCCATGGTCACTCTGCAGCCTTCCCAGCAACCCCATAAG	F	Body;Body;Body	C7orf50	0.8367757	0.88757	-0.050794286	0.8603163	0.88757	-0.027254
cg05588508	3	62727400	120007636	120007686	S_Shelf	CGGAGCACTGAGAGGGAACACAGCTGCAACTGTGAAGAAACATACAGGAG	F	N/A	N/A	0.6345586	0.7272529	-0.092694286			
cg05589762	12	70608435	10469147	10469197	N/A	CGCACCTGAGTCCCAAGTACTCAGAAGGCTGAGGTGGGAGGATCCCTTGA	R	3'UTR;3'UTR;3'UTR	KLRD1	0.6277671	0.6908043	-0.063037143			
cg05590294	12	63620497	9913395	9913445	N/A	CGTAGCAGAGAACAGCTCTTTGCATCCGGAGAGTGGACAAGAAAGTAAGT	R	1stExon;Body;Body	CD69	0.60404	0.6967943	-0.092754286			
cg05592245	10	24621319	65280473	65280523	N_Shore	CGTGTCTGTAAACAGTCTTTGCAGATGCTCTGATGAAAAGGTGCCCTAAG	F	TSS1500	REEP3	0.7325929	0.8454529	-0.11286	0.81052	0.8454529	-0.034933
cg05598477	16	19784433	66436910	66436960	Island	CGGCTACGAGGGCTCCGAGTCCATAGCCGAGTCCCTCAGCTCCCTGGGCA	F	Body	CDH5				0.8383463	0.9061357	-0.067789
cg05600626	22	41670452	21991401	21991451	N/A	CGAGTGGCTAGTGGGGACTTCATGGTGGGTCACCGTGGCCCACGTCCACG	F	3'UTR	CCDC116	0.89122	0.9227671	-0.031547143			
cg05602360	4	69639457	187192322	187192372	N/A	TGAAACAAAGACTTCAGAGTGATCACTTTCTGACAGCATCTGATGGCTCG	F	Body	F11	0.8949686	0.9368729	-0.041904286			
cg05603367	2	58695464	73511020	73511070	N_Shore	CTGGCCCCTGTTCTCCAAGGTCCAGAGTCCCAGTGGGGTTCTGGAGCCCG	R	N/A	N/A	0.1964114	0.2794129	-0.083001429			
cg05603680	3	42604451	55033444	55033494	N/A	CTTTTCAATTGCAAGTTGAAAGCTGCCCCCAGAGGACACATTTTATAGCG	R	Body	CACNA2D3	0.64443	0.7211071	-0.076677143	0.6642525	0.7211071	-0.056855
cg05607401	19	36683324	39826693	39826743	N/A	ATAAACAGGATGTGGTGTTGGATGAAACCTTCCTCCTACTGCACAGCCCG	F	5'UTR;1stExon	GMFG	0.4813614	0.6026857	-0.121324286			
cg05607935	4	62760344	763393	763443	N/A	TTCAAATGATACCATAATTTGTACGGGACAGGGTGCGGGCAATGGCCACG	R	3'UTR	PCGF3	0.89955	0.9298	-0.03025			
cg05613083	16	22697301	87751605	87751655	N_Shelf	CGGGTCCACAGGTTCCTTCCGGCACACAGCTGGCTGGCCACACCCTCTAA	F	Body	KLHDC4	0.8667929	0.9014286	-0.034635714	0.87566	0.9014286	-0.025769
cg05616969	2	41766383	118982661	118982711	S_Shore	CGCCCTTTGTGTTACATACGGGGCAAGCAAGGTCTGCCAATCACTACCAT	F	N/A	N/A	0.7281086	0.80482	-0.076711429			
cg05618595	7	17739346	7874409	7874459	N/A	CGTTCAATTCATATGTTGAAGCCCTAACTGCCGATGTGATGGTATTTGAA	R	N/A	N/A	0.8721586	0.9110086	-0.03885			
cg05626644	16	35710327	86714721	86714771	N_Shore	CGGTGCGCTTTCCCACCCAGGCTGCAGAGGGGCTTGTAATTGGAAAAGTG	R	N/A	N/A						
cg05629278	2	23726440	225874509	225874559	N/A	CGCTGGAGTCCTACTCTTTATTTAATGATATGGTCAAGTCATGCAGGCTG	F	Body	DOCK10	0.8843271	0.9266586	-0.042331429			
cg05632420	7	73794506	130793732	130793782	N_Shore	AATAATCAGAAAAACATAATTATCCCTAGCCATACCATACTTGCTAGACG	R	TSS1500;TSS200	MKLN1	0.6775857	0.7638486	-0.086262857	0.69802	0.7638486	-0.065829
cg05632908	16	39645396	84880339	84880389	N/A	CGGGAAGCTCACTAACTTCTCCAGACCCCCGAGGCTTCCCTGTCTGGCAG	F	Body	CRISPLD2	0.8399943	0.9027429	-0.062748571	0.8784375	0.9027429	-0.024305
cg05633070	17	24692320	933118	933168	Island	GCTGTGGCGGACGGAGGGACGTCTGCCACAGTGTGTCCGTGTCGTGGACG	F	Body;Body;Body	ABR	0.7862629	0.8815657	-0.095302857	0.8252188	0.8815657	-0.056347
cg05638500	15	60798355	101795550	101795600	S_Shelf	ACAGAGTTCCCTGTTAGAGCTTCTTTAAAGATGAAGCCTCTCCACTCACG	R	N/A	N/A	0.86207	0.90747	-0.0454			
cg05639205	7	26628464	155595693	155595743	Island	GAGCCAGGTGCCTATTTGGTAGAGCAGCTGCGAGTACCAGTGGATGCCCG	R	Body	SHH	0.4381386	0.5475614	-0.109422857			
cg05641849	4	73733397	1748820	1748870	N/A	CGGGTCAGCTCTGCTCTGACAAGGTCTCAGGACACAAGGCGGCTGCCAGG	F	N/A	N/A				0.5735663	0.7188543	-0.145288
cg05642283	11	31799476	63374221	63374271	N/A	GCAAAGGCCCCAGCGGGGCGCGTGTCTGAGCAACAGCAAGGAGGCCAACG	R	Body;Body	PLA2G16	0.7642414	0.8236686	-0.059427143	0.7827638	0.8236686	-0.040905
cg05642789	1	72775495	1564482	1564532	Island	GGAGGCCCGAGGCCTGTAGCTGGGCGGCAGGACAGACGCCGGTGAGGGCG	F	Body;Body;Body;Body;Body;B	MIB2	0.7253829	0.8078614	-0.082478571	0.7493738	0.8078614	-0.058488
cg05643545	17	22649405	20165967	20166017	N/A	CGGTGCTGGAATCTTCCGAAATTTTAGCAAAATATTGTTAAGAATGCAGT	R	Body;Body	CYTSB	0.9061543	0.9456486	-0.039494286			
cg05648614	3	30779447	5180520	5180570	N/A	GAAACAGTAAGCACTGTAAAGCCACTCCATTAGTCCAGTCAGTGCTTTCG	F	Body	ARL8B	0.7055	0.8166286	-0.111128571			
cg05648988	6	42659488	33865492	33865542	N/A	TCCACCACTTGTAGTCCTAGGAATCCATGGACACCCTTATTGTGGCTGCG	F	N/A	N/A	0.8842114	0.9189886	-0.034777143			
cg05651511	17	39737488	78754090	78754140	N/A	CGGCTCCAGTTGTACTTAGGGAAGCTGACGTGCCCAGAACACCATTCTGG	R	Body;Body	RPTOR	0.6766014	0.7620086	-0.085407143	0.73246	0.7620086	-0.029549
cg05689267	6	21766485	32798439	32798489	N/A	CGTCTCCTTTGCATATCCCAATCGCCCTGACAGGCCTGTGCTCAAGGTGC	R	Body;Body	TAP2	0.7971814	0.8432557	-0.046074286	0.8257863	0.8432557	-0.017469
cg05694761	16	19618443	11922606	11922656	N/A	TGGTTGGCTTTCAGTTGACCATTTCATTTGGTTCACCTGCTGAGAATTCG	R	Body;Body	BCAR4	0.8975886	0.94254	-0.044951429			
cg05703659	7	50656323	158494734	158494784	N_Shelf	CGTGGTTGAGGAATTTTCTTGCAGTTCTTGGATGTTAATATCAAATTAAA	R	5'UTR	NCAPG2	0.7847586	0.8383829	-0.053624286			
cg05705549	16	33735470	5094341	5094391	N/A	CGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCAT	R	3'UTR;3'UTR	C16orf89	0.9088629	0.9395929	-0.03073			
cg05706103	16	43618404	970167	970217	N_Shore	GCCGAGCCAACGGGCCAGGGCCAGTGTGGATGTCATGTTGGGGGACGACG	F	Body	LMF1	0.8052743	0.8501357	-0.044861429			
cg05708512	5	62611332	31731391	31731441	N/A	CGCTGGGTACCATGGTTGCCTGGTAAATATGGGAGCCCTATCATTCTGGG	R	N/A	N/A	0.7522157	0.8506643	-0.098448571			
cg05714496	10	39695381	134358685	134358735	N_Shore	AGGTGGAGCAGGGCAGAGGGCCCCGCACGGCTCTGGGATGGCTGTGCTCG	R	Body	INPP5A	0.7575371	0.8262114	-0.068674286			
cg05714778	12	10677315	51236059	51236109	N_Shore	CGGAAGGATGGTATGAGCAAGGCAACTGTCCTTTTATTGACCTCTACGTT	F	TSS1500	TMPRSS12	0.6353729	0.7704	-0.135027143	0.7237725	0.7704	-0.046628
cg05719612	10	33784429	18629545	18629595	N/A	GAGGGTCTTATTCTCCTCTGAATTACGTCAGCTGGCTTGGAAGACAGACG	F	Body;TSS200;Body;Body;Bod	CACNB2	0.5378157	0.6607743	-0.122958571	0.5575913	0.6607743	-0.103183
cg05736768	8	49720396	105479248	105479298	Island	GGCCGCCGGGCTCCGGATTTGCAGCCTGAGGCAGAGCTCGGGGGCTGTCG	F	1stExon;5'UTR	DPYS	0.1603343	0.1211249	0.039209429	0.1428588	0.1211249	0.0217339
cg05736785	22	61726395	50437507	50437557	N_Shore	CAGACAGCCCCTCTTGACAGGCTTGGTTTTCCCAGGTGAGCTGGTCCACG	R	Body	IL17REL	0.8775586	0.9241929	-0.046634286			
cg05740575	8	38744448	104387844	104387894	S_Shelf	CGGGCATGTGGTATGAAGGGATTCTTGACTCCAAGGGCTCAAAATAAATG	F	Body	CTHRC1	0.8841514	0.91919	-0.035038571			
cg05751616	12	41774488	6652601	6652651	S_Shelf	CGGCGGCATTAGATTCTCACAGGATCCTGAACCCTACCTTACGTGAACTG	F	Body;Body;Body	IFFO1	0.6071057	0.6705629	-0.063457143	0.62003	0.6705629	-0.050533
cg05765254	1	59713364	152132853	152132903	N/A	AGTATTAGAAACCTAGGCGCATGTGGAGTCCTCATGGCTGGGCCTGGACG	R	TSS1500	RPTN	0.59932	0.7317314	-0.132411429			
cg05770446	12	37704343	18835631	18835681	N/A	CGAGTGTGTATAAAATTGATTTGCCTGCAAACTGTATTCAGACTCCGTAT	R	N/A	N/A	0.92316	0.9542086	-0.031048571	0.9366313	0.9542086	-0.017577
cg05774290	12	49700450	31811203	31811253	N/A	TTCATCCACTTATGAGCTGCTTTTTTCTTAATTAGTTGCTGATGTAAACG	F	TSS1500;TSS1500;5'UTR	C12orf72	0.83109	0.8911714	-0.060081429			
cg05777976	11	45624318	2163538	2163588	N_Shore	GTCCTCCAAGGACTCTGAGCAACTTCCCTAGATCTTTAGATTCAAAAACG	F	Body;Body;5'UTR;TSS1500;B	IGF2AS	0.51413	0.6057371	-0.091607143			

cg05778424	17	29628500	55169508	55169558	N/A	TTTTCATCCCTCTTCAGCTTCTGTGTCATCACAGTAAAGAATTCTCACCG	F	5'UTR	AKAP1				0.7776663	0.7463329	0.0313334
cg05780228	11	13605459	70713608	70713658	N/A	CGGGCCAAAGCTGCCTGAGCCAGGGATGCCTTCACAACCTCGCTGCCCCA	F	Body	SHANK2	0.7430886	0.8267343	-0.083645714	0.783865	0.8267343	-0.042869
cg05798321	1	69673381	222210486	222210536	N/A	CCCGCTTTTCCTCAACCCTGTGGAGTCCACTTAGGCTCAGGGTCTTCTCG	F	N/A	N/A	0.8866357	0.9217686	-0.035132857			
cg05799811	1	30745373	167487396	167487446	N/A	TTCAGAGCCAGCTGCTAGAATACACAGCTCCTCCAGGTACAGATTTTTCG	F	Body;Body	CD247	0.7266143	0.7992586	-0.072644286	0.7364163	0.7992586	-0.062842
cg05802386	1	26726436	43422920	43422970	N_Shore	CGGCTCACCTAAGATCCTGGGAGCCTTCCCCGGGAACTTCCCCGGGGTCT	F	Body	SLC2A1	0.8280171	0.8840557	-0.056038571	0.8351488	0.8840557	-0.048907
cg05803810	16	69694405	27507356	27507406	N/A	GATCTCATGAGGATGGCACCAAGTCATGAGGGATCACCCATACCCAGACG	F	Body	GTF3C1	0.8800743	0.90926	-0.029185714			
cg05808709	1	36617307	160094954	160095004	N/A	CGGAGCCCCAGACCCGCTCCCCCGAGTTCACCCATGAGAACCCCCTGGAG	F	Body	ATP1A2	0.8568557	0.89072	-0.033864286	0.873235	0.89072	-0.017485
cg05813616	16	40700402	46781713	46781763	N/A	CGTGGCCCCCACCAAAGCGATGGCCCTGTCCACCGCAGCCACCATCCTGA	F	1stExon	MYLK3	0.8897243	0.9225457	-0.032821429			
cg05814100	17	56706417	78899797	78899847	S_Shelf	GCCCTGGCAGAGAGATGAGCACTGGGACTGTGCTGACAAAGCAGCTCCCG	F	Body;Body	RPTOR	0.8881386	0.9243229	-0.036184286			
cg05824757	10	67757484	72574568	72574618	N_Shore	CGGAATGGGGGTGAGGAGGCCTAAAGATAACCTGTTCATAGTCTTTCAGG	F	TSS1500	SGPL1	0.83187	0.8703229	-0.038452857			
cg05837491	7	47678342	6676001	6676051	N_Shore	CGCCCGCCAAGACCTCCCAAAGTGCTAGGATTACAGACACCGTGCCTGGC	F	N/A	N/A	0.8124086	0.8470529	-0.034644286			
cg05841929	15	71736370	59730852	59730902	S_Shore	CCACTACTCAGAGTGAGTGACCTTGGGTAGGTTAACCATCTGCTCTTCCG	R	5'UTR	FAM81A	0.5385971	0.6452	-0.106602857			
cg05843574	15	22784429	38746242	38746292	N_Shore	GTTTTAGGCACTATGAAGTGTTTATTGCCTCGGGGCTGGGAACCTTTGCG	R	TSS200;TSS200	FAM98B	0.0838911	0.1098531	-0.025962	0.0737299	0.1098531	-0.036123
cg05843596	12	66719466	122212949	122212999	N/A	ACCCTGGCTTTCTACGTGGCCGGCCAGGGGAGTCTGGTGGGTGAGCAGCG	R	Body	TMEM120B	0.90373	0.9411057	-0.037375714	0.92429	0.9411057	-0.016816
cg05848579	16	36637466	1308103	1308153	Island	TATGGAGGCCGGTGTGATATTCCGCGTTGCAAAGGTGGTTTTCCACTACG	F	Body	TPSD1	0.7781414	0.8537143	-0.075572857	0.806735	0.8537143	-0.046979
cg05849676	12	52691425	10171151	10171201	N/A	CGGTACCAGAGCCAAACCAGCTTTTAAAATGACTGTGTATTTACATTATC	F	3'UTR	CLEC12B	0.7001729	0.8291086	-0.128935714	0.7669238	0.8291086	-0.062185
cg05860390	17	12751434	31204705	31204755	S_Shore	CGCAGGTCATTTGACTTAGGAGCCGCAGCGTTCAACCACGTCTGACTACC	F	TSS1500	MYO1D	0.0583536	0.074429	-0.016075429	0.0441448	0.074429	-0.030284
cg05866150	14	23621485	21317205	21317255	N/A	CCCTGGAAGGTTCTTTGGGTACTAACCTTCTGTGTGGTAGACAGAGGGGCG	R	N/A	N/A	0.6933786	0.7864114	-0.093032857			
cg05869491	6	52708449	209763	209813	N/A	CGGCAGGCAGCCTTTCCTGCTGGTCCCAGTGCTTCTCGGAGGGCACCATC	R	N/A	N/A	0.76961	0.8271086	-0.057498571			
cg05876864	5	38791303	176831638	176831688	Island	AGGGAGCCCCCTTTCTCCTCAGACACCAAGGCAAGCTGCTATGATGGCCG	F	Body	F12	0.3329757	0.5663386	-0.233362857			
cg05879505	17	28645450	1926210	1926260	N_Shore	CAGAGGCCCAGCTGTGGATGAGCACAGTGCACTGTGGGGGCCGCTCCCCG	F	Body	RTN4RL1	0.6037171	0.6620414	-0.058324286	0.6275238	0.6620414	-0.034518
cg05880810	5	31631352	99875156	99875206	S_Shelf	CGTTGTGTCTTAGCGTATAGGGTTGGGTAAGCATTCAAATTAAATTAATA	R	Body	FAM174A	0.8176571	0.8900571	-0.0724			
cg05885688	8	73806473	41628552	41628602	S_Shelf	CGGGCAGTGCTAAACACAGTGATTACTGACTGGTGTTAGAAGAATGATGT	F	Body;Body;Body;Body;Body	ANK1	0.8705086	0.9223486	-0.05184			
cg05888643	11	72777374	64140424	64140474	S_Shelf	CGCCTGGCACCCGTCTTGGGTCCATAAGGAGAGTCCTCCAGACTGGACCA	R	N/A	N/A	0.8307971	0.8871129	-0.056315714	0.854215	0.8871129	-0.032898
cg05892167	3	51635505	79350387	79350437	N/A	GCGGTCAGCTCTTAAGGTGGCGCTCTGGAGTTTGTTCTTTCTGATGTTCG	F	Body	ROBO1	0.6235843	0.6744871	-0.050902857	0.6544563	0.6744871	-0.020031
cg05897169	17	12764451	33568598	33568648	N_Shore	GAAGAGGCTCCAGCTGTCCTGCACCTTCCTGGGAACTGGCAGTCCCTCCG	F	TSS1500	SLFN5	0.8416714	0.9036029	-0.061931429	0.8728688	0.9036029	-0.030734
cg05898320	3	48681419	55442720	55442770	N/A	CCTGTCAGCTAATGTGCTGCTGTGACTGGATCTCTTGAAGTCATGATTCG	R	N/A	N/A	0.7139814	0.78944	-0.075458571	0.7476763	0.78944	-0.041764
cg05907649	15	71693302	56519080	56519130	N/A	CGGATGGGAGTGGGAGTGGCCAACCATCAAAGAACAAAAGGGAGCTTGCT	F	Body	RFX7	0.5873043	0.6909214	-0.103617143			
cg05920870	7	43604476	100205729	100205779	N_Shelf	GAAGTGCCCCTCTCAACCTGTGCGGGCTGCTGCGTCCCAGGACTGAGACG	R	3'UTR	PCOLCE	0.8535386	0.8802043	-0.026665714			
cg05921581	12	71720349	53098625	53098675	N/A	AGCTATTGCACCCGGCCTTCTGCATTCTTAATTCTTATGAGTTCACAGCG	F	TSS1500	KRT77	0.9226229	0.95156	-0.028937143			
cg05934778	6	54770356	30308355	30308405	N/A	AACTCACCAATTAGCTGTTTAAGGATTTTCCTTAGGGCAAAGTACTGTCG	F	Body;Body	TRIM39	0.8296614	0.9143957	-0.084734286			
cg05936300	1	31752392	3574704	3574754	N/A	GAGAGACCAGGTGGCAGGAAGGGCCCTGCTGGGGCCAGAGCAAGGGCACG	R	5'UTR	TP73	0.6979829	0.74373	-0.045747143	0.7057938	0.74373	-0.037936
cg05949913	6	24764507	132557557	132557607	N/A	CGGGAATGGCAAGCAAATTTATGGGAATATTCAAGAAATTTCACATAGTG	F	N/A	N/A	0.7423829	0.8250086	-0.082625714			
cg05950509	10	54798326	73078578	73078628	N_Shore	CTGGGTCTACTGAAAATAGCTGCCTGGCCTGGGAGGCCCAGTTCAGTCCG	R	TSS1500	SLC29A3	0.82545	0.8825371	-0.057087143			
cg05952498	6	23758347	31545257	31545307	N_Shelf	CAATGATCCCAAAGTAGACCTGCCCAGACTCGGCAAAGTCGAGATAGTCG	F	Body	TNF	0.8305329	0.8790629	-0.04853	0.83612	0.8790629	-0.042943
cg05954830	1	71643314	159838031	159838081	N/A	CGGTCCACACATTGGATACACAGGAAGACATATTGACTCAATATTAAGAA	F	N/A	N/A	0.4079886	0.5065514	-0.098562857	0.4136713	0.5065514	-0.09288
cg05958127	1	27691386	120254177	120254227	N_Shore	GTCTATCATTGTTGGACATTTTCTTTTTGATAGTCGAATTCCCTTCAACG	R	TSS1500	PHGDH	0.4355657	0.5767671	-0.141201429			
cg05962793	16	65670462	84745615	84745665	N/A	CGCGCCCGGTGGCTTTTGCTTTTTAAGGTGGACAGAAACACCTTGCAGCT	F	Body	USP10	0.7594971	0.8060186	-0.046521429	0.7685988	0.8060186	-0.03742
cg05968988	8	54731415	48172318	48172368	N_Shore	GCCCAATCTAGTTGAGGATTTTGGACACCGGGCCTCCCACTGGGACTCCG	F	TSS1500	KIAA0146	0.9019471	0.9288186	-0.026871429			
cg05970116	10	57730445	75351076	75351126	N/A	ATACTTACCAGACAGCACAGTCAACCTCCAGCAAAAGACCTCTAATCACG	R	N/A	N/A	0.5167271	0.6473357	-0.130608571	0.600565	0.6473357	-0.046771
cg05972792	10	23737431	131560421	131560471	N/A	CGCAGCCTTCCGGCTGGGACACTGCTGTCAGCGCCAAAGGGAAACATTCC	R	Body	MGMT	0.8715614	0.9028229	-0.031261429			
cg05977072	8	47761422	29732519	29732569	N/A	AACAATCTTTTTCATCAGAGCGCAGTAGTTACTATTAAAAGCTGCAGTCG	F	N/A	N/A	0.7880057	0.8597971	-0.071791429			
cg05978254	11	37804306	108661896	108661946	N/A	CGGGGCCACAGCTACCATGCTGTGGGAAAAAGCCCACCAATACCTTAGCC	F	Body	DDX10	0.9044543	0.9374414	-0.032987143			
cg05981394	16	26645333	28942152	28942202	N/A	CCCTCCCTACAGGTGGCAGGGCCTCCACTTCCCTTTGGCCAGTTGAGGCG	F	TSS1500	CD19	0.6466629	0.73076	-0.084097143			
cg05985070	7	53672350	2050170	2050220	N_Shelf	CGGGCTCCCGCAGCCGCTTTATTAAATGGAATAAATAACACCGTGCAAGA	F	Body;Body;Body	MAD1L1	0.8429814	0.8716586	-0.028677143			
cg05988358	10	71773494	74082489	74082539	S_Shelf	AGACAGGTAGAGGCAGCCTCAGTGGGCCCCGGGCAGGCCTGGTTCCTACG	R	N/A	N/A	0.7959443	0.8542529	-0.058308571	0.8119088	0.8542529	-0.042344
cg05991092	10	43695415	134731965	134732015	Island	GCGAGGTAGGGACGGCTCGGTGCAGGACACCTGGAGCCAGCCTGAGGTCG	F	N/A	N/A	0.71051	0.7550786	-0.044568571			
cg05998672	11	16617377	986408	986458	N/A	CCACATCCTGAGGAGACAGTAGAGTCAGTGGGGCAGCAGCCGCGCTCCCG	R	Body	AP2A2	0.84545	0.8780857	-0.032635714			
cg06000635	21	57659417	46492095	46492145	N_Shelf	CGGTTTCTATTGTGACGCTCTCCCTGACTTGGAAGAATGGCACTGGGAAC	R	Body	C21orf122	0.8413871	0.8846143	-0.043227143			
cg06002516	12	41726447	57666521	57666571	N/A	CGGGCTTGGTCACCTACCTGCTCAGCAGTCGTGCTACTCATGTGAAATTT	R	Body	R3HDM2	0.7313871	0.8054343	-0.074047143			
cg06008803	6	58754347	20920015	20920065	N/A	AGCACCTTTTGAACACCTTACTATAATCTGGGGGAATTTCCAACCTTACG	R	Body	CDKAL1	0.8847243	0.9263257	-0.041601429			
cg06013113	16	17640345	678127	678177	Island	GGCATCCTGTGAATTCATGCGCTGCGAGTGGCGGGGCTGCCCAGAGGCCG	R	3'UTR	RAB40C	0.8072157	0.8404357	-0.03322	0.82633	0.8404357	-0.014106
cg06038180	17	74763345	7258337	7258387	S_Shelf	TTGGGGGTGCTGTCCCCTCACAACAGAAGCCCTGCTTTCTCTGCCCATCG	R	TSS200	TMEM95	0.8421214	0.8877143	-0.045592857			
cg06040925	2	58722302	103334345	103334395	N/A	ATCAAAATCCTGCAGATTGAAGAAGCTGGTTTATTAGAACCAGCCTGTCG	F	3'UTR	MFSD9	0.9080729	0.9446771	-0.036604286			
cg06043640	2	38745403	196933313	196933363	Island	GAAGTGGTGGAAGCCCCTCCTGCCTAGCGAACTCCCCAGCTGTGACTCCG	F	Body	DNAH7	0.0748374	0.1136664	-0.038829	0.089391	0.1136664	-0.024275
cg06044662	16	74736315	30386144	30386194	N_Shelf	ATTCTCACTCACCATGTCTTCAGTCTCCGGGGGGCAAGGCAGCGGCTCCG	F	5'UTR;1stExon	MYLPF	0.6833529	0.7811786	-0.097825714	0.7142238	0.7811786	-0.066955
cg06062821	5	59737364	120278165	120278215	N/A	CAAGTGGTAACTGCTTATTCCAGACCCTCCACTGCCAAAACTCAAAGTCG	R	N/A	N/A	0.82825	0.8738157	-0.045565714	0.8425675	0.8738157	-0.031248
cg06064964	20	54763407	62199181	62199231	N_Shore	GGACCAGGGAGGTGCAGGTGTCTGCAGTGTCAGAGGAGCCGCTGGGCTCG	F	Body;TSS200	PRIC285	0.6704257	0.77095	-0.100524286			
cg06066587	16	11629433	49448678	49448728	N/A	CGCTGAGTCCTCGCTTCTTAAAGTGCGCCCGTAAGTTACCTTGAAATGTT	R	N/A	N/A	0.7747771	0.8081343	-0.033357143	0.7671225	0.8081343	-0.041012
cg06068991	11	50653491	20140241	20140291	N/A	CGGCTTCCCCTCAGCACAGACCCTCCAGACTGGGTCTCAGAGCCGTGCCA	F	3'UTR;3'UTR;3'UTR;3'UTR	NAV2	0.8265729	0.8813657	-0.054792857	0.8524888	0.8813657	-0.028877
cg06073542	11	36708482	14398601	14398651	N_Shelf	ACAAGAGAATTCCAGAGGGCTAGGCAGCTGGAACTACACTACAGGTCACG	R	N/A	N/A	0.9048786	0.93071	-0.025831429			
cg06081917	16	15688345	14762377	14762427	N/A	CGGGCAGTTCCCATTAGATTTAGTGGCCTTCATGTTATTCAGAATTGTTT	F	3'UTR	BFAR	0.9225214	0.9482057	-0.025684286			
cg06089468	16	34668422	30883978	30884028	N_Shelf	CGGGCACCAGGCTGCCTGAGTTGTTTTGGGTACCTCTTCTAACAAATATT	R	N/A	N/A	0.7880429	0.84958	-0.061537143			
cg06097707	6	48642505	33282175	33282225	N_Shore	CGGGTTATCGGGAAGCCAAGTAAATGACCAATAAATATTTTAATCACTGT	F	TSS200;TSS200;TSS200	TAPBP	0.0557824	0.1364181	-0.080635771	0.08179	0.1364181	-0.054628
cg06100461	13	72685366	52419380	52419430	N/A	CGCCGGCTCATACCCCTGCAGTGTTCCCCAGGCCCGCAGGGGGGGCAGCAG	F	TSS200;TSS200	FLJ37307	0.1022269	0.0729631	0.029263714			
cg06101324	1	28799448	152955543	152955593	N/A	ATCTCCTGGGGGCTTTCCGAGGGTCAGAGCTGTTCCTGCTTAAAGCAACG	F	TSS1500	SPRR1A	0.4165314	0.4903614	-0.07383	0.4479513	0.4903614	-0.04241
cg06103218	4	56809486	2073751	2073801	N/A	CGCATTAACCCTTTGGGGCTGGGGTGGCCCGCCATCCCCTGGAGTAAATG	R	3'UTR	POLN	0.5796614	0.66781	-0.088148571			
cg06105555	6	14668415	22017093	22017143	N/A	CGCTGGGTAGCAAGGGGAGACTCCATCTCCACAATAAATAAATTAACCAG	R	Body	FLJ22536	0.8186857	0.8690829	-0.050397143			
cg06113001	12	72617497	55002180	55002230	N/A	CGCCTCAGAGGGAAAACTTGCCAAACTGGCCCATAAAATCGGGAAGAATC	R	Body	GLYCAM1	0.6743429	0.71801	-0.043667143			
cg06118338	11	57741332	18544818	18544868	N_Shelf	TCAAGTAGATTTTTTCAGAAAGACCTCTCTTTACTATCAGATATAAAACG	R	Body	TSG101	0.8589314	0.9281514	-0.06922			
cg06123942	15	54754496	45722796	45722846	Island	CCGGCCCACCCGGGGCGGTTGTGGTCGCTATATATAAGGTGGGGAGGCCG	R	1stExon;5'UTR;5'UTR;1stExon	C15orf48	0.1100683	0.0843087	0.025759571	0.1033628	0.0843087	0.019054
cg06124876	1	31673428	22721151	22721201	N/A	CGAATTCTCTCACAGAGCCTCCAGAAAGGGATGCAGCCTGCTGATGCCTT	F	N/A	N/A	0.3425914	0.4565771	-0.113985714			
cg06126864	13	70809436	110781645	110781695	N/A	GAGGTTGTGACGACGCATGTACAAGCCTGCAGGAGCATCCGCGAGCACCG	R	N/A	N/A	0.9053943	0.9313643	-0.02597			
cg06133771	16	32723388	57791093	57791143	N_Shelf	TAATAAAATTTGCCTTATAAATTACAGCAGCAGCCCCAGGGCTCAGTTCG	F	3'UTR	KATNB1	0.9034871	0.92946	-0.025972857			
cg06135032	16	58781326	1461221	1461271	N_Shelf	AAGTGATTCTCCCACTTCAGCCTCTGGAGCTATAGACTCTCTACACCACG	F	Body	UNKL	0.9028029	0.9306086	-0.027805714			
cg06139908	7	38774467	54614620	54614670	Island	GTCCGGGTCTCTGTCGGGCAAGAGCTCCACCTGCGGGCAAGGAGCGAACG	F	Body	VSTM2A	0.0972983	0.0610213	0.036277			
cg06146665	17	39809475	76799964	76800014	S_Shore	GACCTGAGGCAGCGCCGTCGAGATGGAGGAGCAGCTCCGTGGTTCTGACG	R	Body	USP36	0.8761057	0.91656	-0.040454286			
cg06148974	4	69724492	1864183	1864233	Island	GAAACAATGTTTCTTTAGCCAAAGCCAGAGTGAGTGGGCAGCAATGGCCG	R	N/A	N/A	0.2961671	0.46839	-0.172222857			
cg06150803	13	63733435	24144257	24144307	N/A	GATCCCTGATGGATGGACGTGCCAAATGACAGCATTTAATTGCCTCTTCG	F	TSS1500	TNFRSF19	0.3080286	0.4431871	-0.135158571			
cg06175927	20	55658462	33563009	33563059	N/A	CGGTTTTGTTTTGTTGTTGCTTTTGAGACTGGGTCTGTTGCCCAGCTGGA	F	TSS200	MYH7B	0.6841229	0.75357	-0.069447143	0.7137338	0.75357	-0.039836
cg06187528	1	56628428	200330607	200330657	N/A	CGTGAGGATTTATTCCAGGGCTTATGGCATGAGCAACTGGAAGGATGGCA	R	N/A	N/A	0.8907657	0.9297557	-0.03899	0.9112575	0.9297557	-0.018498
cg06192141	11	64808462	3865883	3865933	S_Shelf	AGGCCTGCCTCTGTCAGGCCCAGTGGGTGGACACAGAAATGAATCAGACG	F	N/A	N/A	0.9129371	0.9428357	-0.029898571			
cg06193043	1	33745374	11908199	11908249	N/A	CGCTTGGCTGGTGCCCAGCTCCCCTGGTTTGTTTGTGGCTCAGCTGTCAG	F	TSS1500	NPPA	0.7122271	0.7784071	-0.06618	0.7306988	0.7784071	-0.047708
cg06196314	12	54758348	68304774	68304824	N/A	CGAAGCCAATAGGAGACATTTATTTCCAAGGTGGGAAATGTTTATTCTGT	R	N/A	N/A	0.73505	0.8015743	-0.066524286			
cg06196926	12	54761321	108151615	108151665	N_Shelf	CGAAAGACATTTGTAATGGCAGTGCAAGATGGTTTGCATAGAAAAGGTGA	R	Body	PRDM4	0.9354186	0.9624014	-0.026982857			
cg06210989	3	48624446	57440587	57440637	N/A	CGAGAGTGGCCTGGCCAAGTTGTACTTTGTATTTCTCAAATGTTCTGGAC	R	Body	DNAH12	0.7499986	0.8119914	-0.061992857	0.7887938	0.8119914	-0.023198
cg06214253	13	31601467	73438525	73438575	N/A	TGTTTCCTTCATCCACATCATTTCCTTTTGATGCTATTGATGAATAATCG	F	Body	PIBF1	0.92298	0.9579829	-0.035002857	0.9359588	0.9579829	-0.022024
cg06214997	12	55627473	130502468	130502518	N/A	TTAAACACCGTATGAGCCAAGCAAAACACATCTGCAGTTTGTATTCAGCG	R	N/A	N/A	0.7194714	0.7941457	-0.074674286	0.7354488	0.7941457	-0.058697
cg06221449	1	31670384	29102029	29102079	Island	CGCACAGGCGCAGAAGCAAGGGCGGACACCATCTTGAGCCGCAGCTCAAG	R	N/A	N/A	0.3401457	0.2190371	0.121108571			
cg06227019	2	42743376	242479660	242479710	N_Shore	CGACCCAGGGCCACCTCTGCCCCAGGAGCTCACCTGACAACCCAGGGGGGC	R	N/A	N/A	0.8771743	0.9198329	-0.042658571			
cg06228828	13	27739484	50653048	50653098	N_Shelf	CGTGAGTTTTGGGAAGAGTTGGGGGCAAGCTTTAAATTCCACCAGGCTGG	R	Body	DLEU2	0.7965343	0.8621857	-0.065651429			
cg06230418	12	19662327	133129990	133130040	N_Shore	CGGGGACCCAACCACCCAAGGCCCCCACGTGCCACTGAGCCAGCCCTCTC	R	Body	FBRSL1	0.9217271	0.9446871	-0.02296			
cg06233135	6	73720483	42450495	42450545	N/A	CGATCATTTCTGCTGGTATGAGTTGTATAGAGAATACAAGAGTGTCAATT	F	N/A	N/A	0.7566729	0.8236043	-0.066931429	0.779065	0.8236043	-0.044539
cg06233328	15	74686476	28510815	28510865	N/A	CGAGGCCATTCCGATGCTGGTAGCCGGGCTTAAAGGACTGAAGGTCATCG	F	Body	HERC2	0.9275843	0.95223	-0.024645714			
cg06234051	17	13741442	70120541	70120591	S_Shore	TCTCTTTCTTCGGTTATTTTTAGGATCATCTCGGCCATCTTCGCCCTTCG	F	3'UTR	SOX9	0.8409729	0.8825871	-0.041614286			
cg06239064	12	11738324	66697621	66697671	N/A	TATAAAACACTGCCATGATCATGGAAAGTTCTACTGAACAGCACCGGTCG	F	Body	HELB	0.7543743	0.8539057	-0.099531429			
cg06239593	3	57616429	130748639	130748689	S_Shelf	ATCAACAGCCATTTCCACTTATCCAAAGACCTTGATTGCAAGAAGATACG	R	Body;Body;Body	NEK11	0.8628157	0.9169229	-0.054107143			
cg06246199	16	44646373	85458415	85458465	N/A	CGCTGTAAGTGACAGCTGCGCGGGCAGCGCTGGAAACACAGGCTCCAGCG	F	N/A	N/A	0.83126	0.8613186	-0.030058571	0.8347438	0.8613186	-0.026575
cg06285333	16	16691454	67516546	67516596	S_Shore	CGGCTGCAGGGATTCATGGCAGTACCCAGCTTGCGGCAGTAGCAGAAGGC	F	Body;TSS1500;Body	AGRP	0.8376357	0.8851543	-0.047518571			
cg06295856	11	65730305	14993642	14993692	Island	AGTCTCTTCATCAGATAGTCTCTGTTAGTCCGCGATTTATACCAGGCTCG	F	5'UTR;5'UTR;5'UTR	CALCA	0.130069	0.0797526	0.050316429	0.127415	0.0797526	0.0476624
cg06299997	7	40605307	94023557	94023607	N/A	CGCCCTTTCCCGAAGTCATAAGACAAAGAGAGTGCATCACTGCTGAAACA	F	TSS1500	COL1A2	0.1871271	0.1523957	0.034731429	0.2172975	0.1523957	0.0649018
cg06300222	6	43627405	38121432	38121482	N/A	CCACCTGTGCCCCCTCATGTTCACAGAGGATTTCAGCAGCTGCAACTGCG	R	3'UTR	ZFAND3	0.9052529	0.9305129	-0.02526			
cg06302806	20	62633373	43939970	43940020	N_Shore	CACCTTCAAAATATAATATATCCAGAATCCACTGGCTTTTTACCACCTCG	F	Body	RBPJL	0.8828143	0.9050471	-0.022232857			
cg06307212	6	46632392	32134573	32134623	Island	CGCCCCCGGGTGCCGCTTCTTCCAGCCCTGGCAGCACACTGCATGGGTCT	R	Body	EGFL8	0.76995	0.82886	-0.05891			
cg06312813	4	31723418	74964493	74964543	N_Shore	GGACAGGGTTTGGGGCAGCGGGAGAGTCGGGGACCCCAGCAGTGGCAGCG	R	Body	CXCL2	0.1791014	0.1399043	0.039197143			
cg06316897	15	24665446	65602323	65602373	N/A	GAATGTGCATAGCTCCTCGGTGAATTAGTGTTAGCCACGGGAGGAGCACG	F	N/A	N/A	0.7846971	0.8246771	-0.03998			
cg06323049	16	50808312	28943094	28943144	N/A	CGGGAAATGATCTTGTGTGTTTATTTGTTCATTTCTGTTTTCTGCACAAG	R	TSS200	CD19	0.7465771	0.8277029	-0.081125714	0.7779575	0.8277029	-0.049745
cg06330558	11	22717333	9068984	9069034	N/A	CGTGGCTAAAAAGCCTCCCAGAACATCTGAACGCCAGGCAGAGTCCTGTG	R	Body;Body	SCUBE2	0.7673471	0.8241257	-0.056778571			
cg06333085	17	31641453	26850910	26850960	N/A	TCTGCCATGAGAGTGAGGACCAGCATCCAGTGGGACCAACCCAGGTTCG	F	TSS200	FOXN1	0.84755	0.8829886	-0.035438571			
cg06343233	2	43797391	153375639	153375689	N/A	CCTGCCTTTGAGGCTTCCCTTGTTCACTGTGCCCAGTGTGCTTTCGTCCG	R	Body	FMNL2	0.72338	0.76349	-0.04011			
cg06353655	10	50798334	132954294	132954344	N/A	CGGTCTTCTTTGAGTAAGTAGTGCTGAAGAGAAACCAAATGTCACTTCGG	R	Body	TCERG1L	0.6276629	0.7064343	-0.078771429			
cg06358442	6	27743458	33239202	33239252	N_Shore	CGGGACCCTAGTGGCTGAAACTCATGTTCTGGGGCACAAAATTTCAACTT	R	Body;TSS1500	VPS52	0.1334957	0.1753271	-0.041831429	0.1445375	0.1753271	-0.03079
cg06359492	16	69714383	89162377	89162427	S_Shore	CAGACCACTAAGGCACTGGGGCTTCTCGGGAACACACATGCAGCGCAGCG	F	Body;5'UTR;5'UTR	ACSF3	0.8907657	0.9188557	-0.02809			
cg06367135	1	52661361	3077835	3077885	N_Shelf	CGCTCGAAAGTGCTCAGGGAAAAGTTTATTGGAAACTTGGCCCCAGAGCC	F	Body;Body	PRDM16	0.5443429	0.62436	-0.080017143	0.5795338	0.62436	-0.044826
cg06371583	19	69604416	2581343	2581393	S_Shore	GTGAAGGAATTGACTGCTGGTGCTCCAGGCCACCCGAGAGACACCCTCCG	F	5'UTR	GNG7	0.43384	0.5055071	-0.071667143			
cg06383207	16	59697308	75021994	75022044	S_Shelf	TGTTTGCTCACACCTGTTATTTGACAGAATCATTTAAGTCCAGGAGTTCG	R	N/A	N/A	0.6343386	0.7177971	-0.083458571			
cg06394460	13	41762374	28130393	28130443	N/A	GGTAAAATTTTTCAAGATCCCATCTTACCTCTCTTTATTCTGCCATCTCG	R	Body	LNX2	0.8875071	0.9246129	-0.037105714			
cg06399786	2	62803385	26393250	26393300	N_Shelf	CGGTCACCCTAAAGAGAGACCCTACAGGGTAGGGGAAGAAAAGTGAATCT	F	N/A	N/A	0.9435429	0.9686	-0.025057143			
cg06400065	11	26662442	111800554	111800604	S_Shelf	TGTTATTTTGTACATTTCTTATTCTTCCTGTTTTAGATGGCCCTGATTCG	R	N/A	N/A	0.6655029	0.7557271	-0.090224286	0.7026375	0.7557271	-0.05309
cg06405206	17	55648420	47652804	47652854	Island	CGGGCAGCAAGAATCGGCTGCCCTGCCCCCAACTCAGGAGTCCTGGAATT	R	TSS1500	NXPH3	0.4028229	0.4509357	-0.048112857			
cg06412669	17	23741446	78735550	78735600	N/A	CGGGCAGAAGAAAGTGTGTTCTCTGGCAAAGCAGATGTATTTTAGAAGAC	R	Body;Body	RPTOR	0.8006986	0.8702743	-0.069575714			
cg06415302	8	34659422	37591379	37591429	N_Shelf	CATTTGGTTATTATTTAATACCATACAACTTAAAGTTTATCATTCTCTCG	R	N/A	N/A	0.79321	0.8930214	-0.099811429	0.836795	0.8930214	-0.056226
cg06417243	17	51674443	71543112	71543162	N/A	CTGGATCAGTGCCTGGCTCCAGAGTCAAGTCCGGCTTTCCCAGTGTCACG	F	Body	SDK2	0.8210243	0.86718	-0.046155714			
cg06432426	2	38760378	484825	484875	N/A	CGGTTCACTTCCGTGTATGGTCCTACGTGTGGCTCGATTGAACTTGCAAA	R	N/A	N/A				0.8588175	0.8350286	0.0237889
cg06438559	5	27606375	136478693	136478743	N/A	GGCAATGAAGGACTGACATGTCCTGCTAAGCTGTTCAAGCAGCAGAAACG	F	Body	SPOCK1	0.57173	0.6276529	-0.055922857	0.5468825	0.6276529	-0.08077
cg06438577	14	22608401	105796713	105796763	Island	CGGGGACAGGAGCCTCCAAGAAGCCTGGGGTCCGTGTGTCCGTAGGAACG	R	Body;Body	PACS2	0.6526771	0.7906886	-0.138011429	0.7297463	0.7906886	-0.060942
cg06442199	1	17658344	92414344	92414394	N_Shore	CCTTAGGATCAAATAGCAAACAACGCTTCTGAATTCCTAATACTCATTCG	F	TSS1500	BRDT	0.7980657	0.8828786	-0.084812857			
cg06447122	1	42623500	3181532	3181582	N_Shore	TGCTCAGAAATCTGCATCTGTCTGCTTGACCCCTCCTCTGATATCCACCG	F	Body;Body	PRDM16	0.6771029	0.7525257	-0.075422857			
cg06451479	5	55689416	131999237	131999287	N/A	CGCGAGTTTCCGGTGAACTCGGCACCAAACACCTCAGTTTGCTGCTCAGA	F	N/A	N/A	0.6863857	0.7570286	-0.070642857			
cg06456958	17	33636501	80928897	80928947	N_Shore	GATGAATGCCTCCCACAGCGCTGAGTGAGCCCTCGCAGGAACGCACTGCG	F	Body	B3GNTL1	0.91079	0.9361571	-0.025367143			
cg06462291	12	37786415	104235479	104235529	S_Shore	AATGGCCTCTGGCAGTCTAATTAATGGCAGTCTGGACCTCCCCTGGATCG	R	TSS1500	NT5DC3	0.063313	0.0328769	0.030436143			
cg06468106	16	42622356	14419078	14419128	N/A	CACATGCACATCAAGGGTATACCTGTAGAGGCTGGGCTTGGTGGCTCACG	R	N/A	N/A	0.7729014	0.8324171	-0.059515714	0.7871075	0.8324171	-0.04531
cg06469726	2	71766452	242483467	242483517	S_Shore	GCTGTACTCCCTGCTGTGTCAGTGACTCAGCCTCCCTGGTGGAGGGAACG	F	N/A	N/A	0.5383857	0.6851243	-0.146738571	0.625755	0.6851243	-0.059369
cg06471487	5	54679342	143192588	143192638	N/A	CGTCAACCCAGGGCTCCGTGTGTCCTCTTCAAGAGGAGAAAACAAGACAA	R	Body	HMHB1	0.8725729	0.9136957	-0.041122857			
cg06472476	19	61759484	54369471	54369521	Island	GCTTTGAGGCCAAGCCCAGGGGTGGAGGCCGAGTCCAGGAGTGGAAGCCG	F	TSS200	MYADM	0.3566929	0.4931329	-0.13644	0.4094288	0.4931329	-0.083704
cg06476926	17	67694494	80867707	80867757	N_Shelf	CGGGGTTGGGGAGGCCACACCCCTGCCTATGACCAGCAAGTCCTGGGAAC	R	Body	TBCD	0.767	0.8414329	-0.074432857			
cg06477444	19	30677444	50411521	50411571	N/A	GCGGGCCCCAGGGCTGCTGTCGCTCAGTCAAAGGTGATCCGGAAGCTGCG	R	Body;Body;5'UTR;Body;Body	NUP62	0.90053	0.9379129	-0.037382857	0.9238413	0.9379129	-0.014072
cg06484100	17	30600493	41799087	41799137	S_Shore	CGCTTGTTTTGTTGCAAGGAGCTAGTAAGAGCTCAGCCTGGCCTCTCCCA	R	N/A	N/A	0.7513686	0.8162586	-0.06489			
cg06491451	18	70659339	77723518	77723568	N_Shore	CCCCACATGTGAGTCCTAATAAACTCACCTACTCACCAAGCTGGACTCCG	F	TSS1500	HSBP1L1	0.7715657	0.8257286	-0.054162857	0.7920238	0.8257286	-0.033705
cg06491827	4	44674465	138463613	138463663	N/A	CGCCACCCCAGGAAAGAGGCTCCCTGTCTCTGTCTAGGTTAAACAAAAGC	R	N/A	N/A	0.7297814	0.7877671	-0.057985714			
cg06496041	21	62611403	39810840	39810890	N/A	ACCTGGGAGCTTGTTTGAGATGCGGCTTCTTAGGCCCTGCCCTAGAATCG	F	Body;Body;5'UTR;Body	ERG	0.8280071	0.8766686	-0.048661429			
cg06499262	16	14711368	69598417	69598467	N_Shore	CGGAGGTTCAGAAAGCTTTTCAGAGCCACCCCAAGATGGCAAAGCAGAAC	R	TSS1500;TSS1500;TSS1500;	NFAT5	0.6669686	0.7768729	-0.109904286			
cg06508005	19	66725327	17972675	17972725	S_Shore	CGGACACCAACCCAGCCCCAGATGCAGTTCCTGAACTCAAGTCTCCTGGA	R	Body;TSS1500;Body	RPL18AP3	0.7618414	0.8316743	-0.069832857			
cg06508085	11	48802317	45950696	45950746	N/A	GGCCCTCCTGTGACCCCAGCTGGATGTAGCACCTCCCTTGTGCACTGACG	F	N/A	N/A	0.7737871	0.8532243	-0.079437143	0.814845	0.8532243	-0.038379
cg06508738	3	46602310	138763852	138763902	Island	TAGAGGCGGAGGTACACCTGCTGCCCAATAGCGGTGGCTGTGGTTGGTCG	R	TSS200	PRR23C	0.6676514	0.5500857	0.117565714			
cg06512263	6	43649440	20709867	20709917	N/A	CGTGGATTATGTTGCACAACAGGAAGTACAAGAAGGCTTCAGAGTGGGTT	F	Body	CDKAL1	0.7421029	0.8070714	-0.064968571			
cg06520081	5	43787502	134990562	134990612	N/A	TCAGCTGCTGCTGGAGTTTCCAGTTCTTCCACATAGACTGCGAGAACTCG	R	TSS1500	LOC340074	0.7299857	0.8145243	-0.084538571	0.765115	0.8145243	-0.049409
cg06526522	1	63704355	3129005	3129055	N/A	CGGCCGGCTCCAGGCCTGGACTCCCAGAATTCAAAGGTGCCCCCGCTCAG	R	Body;Body	PRDM16	0.7540543	0.8132771	-0.059222857	0.7883063	0.8132771	-0.024971
cg06526721	5	70638383	119799384	119799434	N_Shore	CGGTATTAGCTTTGTGGAATTAGCAGGATTAGGGTACCTCTTTCAAGAAC	F	TSS1500	PRR16	0.5450286	0.66079	-0.115761429	0.608715	0.66079	-0.052075
cg06526741	6	60635309	31549929	31549979	S_Shore	CCCTCTGGTTGTGCCTGTGGTCTTTTGCCCCCTCTGGCTCAGCTGGCTCG	F	Body;Body	LTB	0.6769943	0.7644386	-0.087444286			
cg06531158	13	71775436	36273490	36273540	N/A	CGGCACCCTCGGCCCGGCTGCTTTTGCAAAGTCCACACTGATTCATTATT	F	Body	MIR548F5	0.65515	0.74415	-0.089			
cg06533196	17	42738492	66427630	66427680	N/A	CTGGGGGTGGTGGCTGCTGGGCTCTGCAGCAGGTCTGACTCAGGGGGACG	R	Body	WIPI1	0.8146086	0.8882971	-0.073688571	0.841865	0.8882971	-0.046432
cg06534853	2	61666321	662602	662652	S_Shore	GGTTAACCTCATTCAAATGAACACAGGAAACCGAAGCCCTGTGCTTCCCG	R	N/A	N/A	0.6739157	0.7736486	-0.099732857	0.7205238	0.7736486	-0.053125
cg06535498	6	31743451	32185171	32185221	N/A	CGCTCACCTGCCCCAGGTGTCTTCTCTGGGAAGCTCTGCAAGTTCACCTT	R	Body	NOTCH4	0.8166371	0.8623986	-0.045761429	0.83489	0.8623986	-0.027509
cg06538426	1	65761397	16491125	16491175	N_Shelf	TCCTGGGAGTCAGGTAAGGGCACTTCCTGGGGGCCCCTGGGCACCAGTCG	F	N/A	N/A	0.7813829	0.8375314	-0.056148571	0.77373	0.8375314	-0.063801
cg06538709	8	56617339	48654011	48654061	S_Shelf	CGTTTTTGAGGAGTGCTCTCTAAACGTAAATATGAAATGAAGTTTCAAGA	F	N/A	N/A	0.6441457	0.7065657	-0.06242			
cg06538872	1	70743479	947343	947393	N_Shore	CGTTCAACAGAATTATTGGGAACCCAGCAGTTCCACTTCTAGGCATGTGT	R	N/A	N/A	0.8074171	0.8525286	-0.045111429			
cg06548214	20	38651344	57270552	57270602	S_Shelf	GGCGCTGTGGGCTCGGGGACTGGAGGTGGCAGGCGCAGAGGCTGGGACCG	F	Body	NPEPL1	0.7453457	0.8103586	-0.065012857			
cg06550082	9	29745424	34624160	34624210	N_Shore	CCTCCTGTCCTTCTTGCTAAAACAGAGACCCTGGGGTTCTGTGGGCTCCG	F	Body	ARID3C	0.69617	0.7577057	-0.061535714	0.7276875	0.7577057	-0.030018
cg06552660	7	25717506	11546495	11546545	N/A	CGGTGATGGAGAGTGACAGGTGGGTCATGCAAAGACTCTCTAGGAAGATA	R	Body	THSD7A	0.8837743	0.91643	-0.032655714			
cg06555281	6	48708344	53513754	53513804	N_Shelf	CGGCTGAGTCCTGTGATCAAATAAAAGCATCAGTTCAATATATCAGGGAA	R	3'UTR	KLHL31	0.8224614	0.8869257	-0.064464286			
cg06559111	13	17622446	37495847	37495897	S_Shore	GTTATAATTTCTTTCTCTGCATCTTGTCCTCTGCATTATGCTCATATACG	F	TSS1500;TSS1500	SMAD9	0.8971014	0.92869	-0.031588571			
cg06564473	11	39619414	601660	601710	S_Shelf	TCCGGACCATCCGCAAAAAGTAAGAGCTCAGCGACAAGATCTAAGAAACG	R	Body	PHRF1	0.8282514	0.8807486	-0.052497143	0.8511663	0.8807486	-0.029582
cg06565220	1	48701396	112938731	112938781	Island	CGGGGCTTCTCCAAAGTCATTCAGGCTCCTCCCGGGGCCCCAAGATCCCT	R	TSS200	CTTNBP2NL	0.0925621	0.1285614	-0.035999286	0.103659	0.1285614	-0.024902
cg06566775	5	58670424	134376772	134376822	S_Shore	CGGTGTTCAGGCCCTGCCAGGTGGCCTCTGCACCCTGTCGTGCTGTTCCA	F	N/A	N/A	0.1645271	0.1260181	0.038509	0.1554638	0.1260181	0.0294456
cg06568724	2	70631356	8711120	8711170	N/A	CGCGTTTCATTCAACAAACCAAGTGTGGATTTGATAGCTGTAGTTACTAT	F	N/A	N/A	0.8911814	0.9199014	-0.02872			
cg06569437	6	71730350	130046710	130046760	N/A	GGGACAATCCCAGAGTCTTTCCAGGAGCCCAAAAACCAAGCCAAGGAACG	F	N/A	N/A	0.6018329	0.6794314	-0.077598571			
cg06573709	6	18738384	164057152	164057202	N/A	ATTTGAAAACAGGAGCTGATGCAAATGTCCCCGATGCATCGCGGGGCTCG	F	N/A	N/A	0.69697	0.8115243	-0.114554286			
cg06574809	17	54634350	80351150	80351200	S_Shore	CGTGGGGGAGCCCGGTGTCCTCTGAGTCTCAACGCCCCTTGCTTCCCACT	R	3'UTR;Body	C17orf101	0.8186514	0.8569314	-0.03828			
cg06577241	20	31735316	37354117	37354167	Island	CGGATTCACAGCTGCATTTTTGGGAGGAAAGAAGAAGGGGAAATCGCTGA	F	Body	SLC32A1	0.1437657	0.2063057	-0.06254			
cg06578111	3	12764375	13546418	13546468	N/A	AATTCTCAGTTAACTGCCTGCCTCCCTGGACCTATGGGCTGGTGACTTCG	F	3'UTR;3'UTR	HDAC11	0.7902386	0.8478743	-0.057635714			
cg06582708	17	22739495	21029295	21029345	N_Shore	CGATGCTATTAGCTATGTGTGTCCTTCCAGAGCCAGTTTATTCATAACCA	R	TSS1500	DHRS7B	0.6447543	0.7594243	-0.11467	0.7121288	0.7594243	-0.047296
cg06590119	17	37699350	440029	440079	N/A	AGTGGATGAACCTGCATCAACACGTCATTATCACCCGGACTCTGACGTCG	F	Body;Body	VPS53	0.8916957	0.9227471	-0.031051429			
cg06598461	8	58741344	49890873	49890923	Island	CGGGCCTCTGGGGCCTCAGCTGGCCTCCCAACTTCTGCCCAGCTCGACTC	F	N/A	N/A	0.8088886	0.8381086	-0.02922			
cg06603851	5	60635411	1813772	1813822	N/A	CGTCCTGCTTGTGTGCTGATGCTTTCAGTTACTATCAAAACGGAATGAAA	R	Body	NDUFS6	0.8283886	0.8797429	-0.051354286			
cg06606386	19	30727473	13947469	13947519	S_Shelf	CAATGTGATTTGTGACAGGAAGCAAATCCCATCCCCAGGAACCCCAGCCG	R	TSS200;TSS1500;Body	MIR27A	0.4913214	0.6279371	-0.136615714	0.5690263	0.6279371	-0.058911
cg06613738	16	23711435	15596423	15596473	N/A	CGGGATGCACCAAGTGCCTCGCCTTCTTGCTATAACGTGAATGTAATGGG	R	Body;Body	C16orf45	0.8596643	0.9144757	-0.054811429			
cg06616905	6	64659310	2940957	2941007	N/A	CGCGCCGCCTTAAGAGCTATAGTATTCACTGAGGGTTTGCGGTTTTATTC	F	N/A	N/A	0.8317686	0.87547	-0.043701429			
cg06617449	11	25639346	16763554	16763604	S_Shelf	GACCTTAAAGCAGCACTCCAGGACCAGACTGGCATCAGGGACCAGTTTCG	F	Body;5'UTR	C11orf58	0.8011443	0.8684543	-0.06731			
cg06621080	1	28686303	201631166	201631216	N/A	CAGGTCACTGGAGCCAGACTGCCTGGGGGTCATACCCAGACTCCACTTCG	F	Body	NAV1	0.6195957	0.66559	-0.045994286			
cg06627801	4	54755453	1975624	1975674	N/A	CGGCCCCGGCCTCCACCTGAGGAGCCGCCAGATCCACCGCACAACCGCGT	R	Body;Body;Body;TSS1500;Bo	WHSC1	0.6612529	0.7398914	-0.078638571	0.6845063	0.7398914	-0.055385
cg06628901	6	67616495	134357577	134357627	N/A	GAGATGGACTCTGAACACACATTCTGTGCATAGTGGGCACACACGAGCCG	F	Body	SLC2A12	0.9098229	0.9379457	-0.028122857			
cg06629713	2	71711366	60580559	60580609	N/A	CGGATTATTATTGACCAGGACGGTCTGGAAATTATAGGATCTTTCTAAAT	R	N/A	N/A	0.8087543	0.8775357	-0.068781429	0.8538375	0.8775357	-0.023698
cg06635351	1	58719327	8882925	8882975	N/A	CGCTGATTTTCATTGTCTTGGCCCAATTCCAAGTTTGATAATTAGGAGTC	F	N/A	N/A	0.2574786	0.3755886	-0.11811	0.2844013	0.3755886	-0.091187
cg06638874	6	60717326	168684732	168684782	Island	TAGGAGCGTGTGCCGGGTGCAGGGTGCTCCATGATCACCCGAGGGGCACG	R	N/A	N/A	0.8222986	0.8574929	-0.035194286			
cg06642275	12	47716314	54145184	54145234	Island	AAGGGGTGTGCGTGGGTGTCCTCTCCTTCACTCTTTCCCCAGCCCTGTCG	R	N/A	N/A	0.1121359	0.1490671	-0.036931286			
cg06650664	5	25715353	115870174	115870224	N/A	CACATTCCAGCCTGTCTTTTGAGTCCTCAAATATCCTGGAGCACACTCCG	R	5'UTR	SEMA6A	0.8819457	0.9160043	-0.034058571			
cg06652523	19	27660367	57352723	57352773	S_Shore	AGGAAACATCACGACCTGTTTGCATAAAGAAATGCAAACCTGAAACACCG	R	TSS1500;TSS1500;TSS1500;	PEG3	0.50593	0.5699029	-0.063972857			
cg06654905	9	44723499	14347753	14347803	Island	TGTAAAAGACATTTCCTTAGGAAACAGACAAGGCAGGGCCAGGAGTTCCG	R	N/A	N/A	0.1323643	0.1596186	-0.027254286	0.1422788	0.1596186	-0.01734
cg06654992	3	63675428	122337681	122337731	N/A	CCTCTCCTGCATGGATCCCAGAGCAGCAGACAGGAGGTGCTGCCTGCTCG	R	Body;Body	PARP15	0.7981957	0.8855586	-0.087362857	0.8464138	0.8855586	-0.039145
cg06655349	19	31603352	10332165	10332215	N_Shelf	GGCAAGGAGCCAGTCAGGGGCTTGTTTCCCCTCATAGAGCTCCCCAGACG	F	3'UTR	S1PR2	0.8623443	0.9153	-0.052955714			
cg06658067	16	57697391	29394343	29394393	N/A	CGCTGACGGTGGAAGCGGAACCCGCAGATGCTCAGCAGGTATCTTGATAT	F	N/A	N/A	0.7477429	0.81359	-0.065847143			
cg06667961	6	35667430	31527693	31527743	N/A	CGCCTCTGGGAACACGGGAACATGGGTGGGCATGAGATCCTTGAATAAGA	F	N/A	N/A	0.6946543	0.7724171	-0.077762857			
cg06677021	5	18618396	79490511	79490561	N/A	CGCTGCCTGGGGCCCTCAGCAGCGATCTTAGCTTAGTTACATTTCCCATC	R	Body	SERINC5	0.7842771	0.8468386	-0.062561429			
cg06685949	16	31716436	19721858	19721908	N/A	CGGAAGCTTCTGAAACCAGGAAGTGGACGGTAAGTTTGGGGCTAGGGCTC	R	Body	C16orf88	0.6047386	0.6606971	-0.055958571			
cg06686180	19	30727502	36056027	36056077	N/A	CGCTCACCTGCTCCTGGAGACACGCTCACCCCATAACATACCAAGGTCCC	R	TSS1500	ATP4A	0.8846029	0.9244214	-0.039818571			
cg06688399	17	70784415	18162242	18162292	Island	CGTGGAAGCCTCCAACTCCAGCACAGGGGGGGCCCGCACTCCTTGGTGCC	R	TSS200	FLII	0.0667683	0.0900274	-0.023259143	0.0627289	0.0900274	-0.027299

cg06710672	16	73747383	1133378	1133428	S_Shelf	CGACGGCCCGGCCGCAGTTTCCCTCACTGTGGAGCTAACGACACCTCCTC	R	N/A	N/A	0.6226243	0.6976371	-0.075012857	0.6444038	0.6976371	-0.053233
cg06711078	1	51775509	1358094	1358144	N_Shelf	CGGAGGGGCAGAGGCCGCAGCCCCTTTGCCATGAATCCAAAGAACCTGGA	F	TSS1500;TSS1500	LOC441869	0.7918429	0.85256	-0.060717143			
cg06711175	5	11644306	55543927	55543977	N/A	TAGAGTTGTTCTGTTTTGTGACCAGACTGTACCCCTACCAGCCAAAAAACG	R	N/A	N/A	0.3766457	0.4967843	-0.120138571	0.432395	0.4967843	-0.064389
cg06714655	16	61635364	671171	671221	N_Shore	CGGGGCAAGGAAGCACCTGGCACCCTCAACCCAGGACCAACATGTGCACC	R	Body	RAB40C	0.9080843	0.9387571	-0.030672857			
cg06715885	12	70652485	57595392	57595442	N_Shore	CGGGCTCATCACTGCCATCCACACAGTCATTGTCCCGGTCGCAGACCCAG	R	Body	LRP1	0.85113	0.9002886	-0.049158571			
cg06721975	19	59705431	49425687	49425737	N/A	CGGGACCCCAGCCCTCAGGATTCCTGATGCTCCAAGGCGACTGATGGGCG	F	3'UTR	NUCB1	0.8157543	0.8543086	-0.038554286			
cg06729555	3	70725396	125458042	125458092	N/A	CAAAATCACCGGGTGGTGGATGCACACCCAGTGCTATATTGGGAGTAACG	R	N/A	N/A	0.68218	0.7157243	-0.033544286			
cg06730285	5	12772374	139945107	139945157	S_Shore	GGTCCATCAGGAAACCACTACTGACTCCATTATGAGCTCCTTGAAAGTCG	F	TSS1500:TSS1500:5'UTR:TS	APBB3	0.5581971	0.6346543	-0.076457143			
cg06731886	7	56602506	73284078	73284128	N/A	CGCCCAGGATGGGGGGACTGGACAGAAAAGGAAATGAGGGGATACATAAT	F	N/A	N/A	0.7327829	0.8307457	-0.097962857			
cg06732241	12	24630314	124626058	124626108	N/A	CGGCTCAGGAAGCAGCAAAACACCACCGTCAATGGATATGACCATCAGAA	R	N/A	N/A	0.5887957	0.65853	-0.069734286			
cg06736312	1	25770349	2238334	2238384	Island	AGTAGAAAATTTTGCAGTGGGTTCCAAAACTACATGGTTACAAACACTCG	F	3'UTR	SKI	0.92601	0.96335	-0.03734			
cg06740142	17	49647488	47583281	47583331	N_Shore	CAGCATGATTAAGGAATAATCTGAACGTGGTTCCCACCCAGCCCTCCCCG	F	Body	NGFR	0.6774543	0.7673871	-0.089932857			
cg06750410	5	69685457	55412925	55412975	N/A	CGGAAGGCAGTTTGGCACTATGTATAAAGAACCTCAAAACTGTTCATACC	R	TSS200;Body	ANKRD55	0.6180586	0.7526043	-0.134545714			
cg06752594	1	28722482	109825964	109826014	Island	CAGAAGACTGCATCCCGGTGGCGGAGCCGAGGGTTGAGGCTGCGAGTGCG	R	TSS200:TSS200:TSS200:TSS	PSRC1	0.1249186	0.0991479	0.025770714			
cg06760169	7	73711443	73081893	73081943	Island	GGCGCCCGGCCAAAGTCAGAAATTTGTTGTTGCCATCCGAGGGGAAAACG	R	TSS1500	VPS37D	0.1877386	0.15244	0.035298571			
cg06761584	7	13767464	128469799	128469849	N_Shore	TAGAAAAGCCTCATGTAGGGCCCAAATCCAGAGGCCCAGGAGTAAGACCG	F	TSS1500;TSS1500	FLNC	0.6960371	0.7619771	-0.06594			
cg06764736	12	26800317	23998997	23999047	N/A	CGACAGAGTGGCGAGTCCTTGTCTAGTACAGCCCTGGGAACTCCTGAACG	F	Body;Body	SOX5	0.8816743	0.9188071	-0.037132857			
cg06775420	16	14747454	1742245	1742295	N/A	GAAGCTCTTCTGTGCTGGTGGCGGACGCCCACTGCAGACGGGCTGTGGCG	R	Body	HN1L	0.93611	0.9610643	-0.024954286			
cg06777522	3	62682467	145969007	145969057	Island	CTTTTAGGTTTCAGCGGACTTCAGGGTGCCCCACCTCTTCCAGGAAGACG	F	TSS200;TSS1500;TSS200;TS	PLSCR4	0.1500014	0.2111257	-0.061124286			
cg06780259	15	22689429	43094585	43094635	N/A	AGGCTGTTAAAGGCCTGGGGGCCAGAGGTGGACACCTTGTAGGACTTCCG	R	Body	TTBK2	0.8041457	0.86464	-0.060494286			
cg06780308	1	66791485	39265808	39265858	N_Shelf	CGCCAACTTTCTGTGTGTCAGCAATAAGGCTGATTTATCATTCATGGAGT	F	N/A	N/A	0.8759657	0.9293043	-0.053338571	0.8991075	0.9293043	-0.030197
cg06786238	1	20709312	33231190	33231240	N/A	CGCCACTGATCCCGCCCATCTGCCGACCCCACCCCTTAAATGGGGTGCAG	R	Body	KIAA1522	0.5897171	0.7295857	-0.139868571	0.6498838	0.7295857	-0.079702
cg06795768	7	59706506	34941831	34941881	N/A	CAGATGCAACGACTTCCAACGCAGAGATAGGAGAGCCCAGAGAGACTTCG	F	N/A	N/A	0.8148086	0.8499529	-0.035144286	0.8266213	0.8499529	-0.023332
cg06798878	1	48629317	204083504	204083554	N/A	CGGAGGCTGCCTCTGGAAGCCAGGAGAAGCTGGACTTCAACCGAAATTTG	F	Body	SOX13	0.8848729	0.9108743	-0.026001429			
cg06800849	16	63633414	89180587	89180637	N/A	AAAACAAAGTCACGCCGTAGCGCAGACTGCAGCGTTGGTCCCGGGTGTCG	R	Body;Body;Body	ACSF3	0.8699457	0.9506414	-0.080695714			
cg06807837	8	73768455	1877952	1878002	N/A	AGGGCACAGCACCGGGGCAAAGAGGGCTGGCCCAGGTACAGGAGGCCCCG	F	Body	ARHGEF10	0.8033443	0.8383043	-0.03496	0.8175988	0.8383043	-0.020706
cg06811732	1	47728383	219749669	219749719	N/A	GGCCACATGAAGGCATATTAGTTCTGCAGGCCGTGCTGAGCTACAGCACG	R	N/A	N/A	0.8192614	0.8705129	-0.051251429	0.8325688	0.8705129	-0.037944
cg06815308	1	41743306	3088524	3088574	N/A	TGGGCCCAGGGATGCTCCTTCAGCACCGGGGACCCCGTTCTACTGGATCG	F	Body;Body	PRDM16	0.8822386	0.9153029	-0.033064286			
cg06816239	1	53706463	169679199	169679249	N/A	TTTATTCATAGTTCAGTGTACATTAATGTCATTTCTACAATTACAATACG	F	Body;TSS1500	SELL	0.7777186	0.86534	-0.087621429	0.8285875	0.86534	-0.036752
cg06816350	5	28613456	2278885	2278935	N/A	TGAGATCAAAGTCTTCCTCCATAGAGTCCTGAAGCGTCAGGGGGTAGACG	F	N/A	N/A	0.6166	0.72702	-0.11042			
cg06825317	1	48702486	247501316	247501366	N/A	CATTTATGACTGGGGGAACGCAACAACCAAGGCATCCTTGCCTCCTGACG	F	N/A	N/A	0.7942871	0.8474143	-0.053127143	0.8168563	0.8474143	-0.030558
cg06829791	1	11645323	208257939	208257989	N/A	AAGATCTCCTCTGTGGGCACCAGCTGGGGACAGTCCTGGGGGAACAAACG	R	Body	PLXNA2	0.8576271	0.8876786	-0.030051429	0.8675588	0.8876786	-0.02012
cg06834313	12	17770372	108851556	108851606	N/A	ACAGCAGCCTAATGGCTTGGAATTAGCCCCAGCTATTTCTGAGGTTTCCG	R	N/A	N/A	0.5870886	0.4762314	0.110857143			
cg06835221	5	44797432	72794567	72794617	Island	CGCCCCCAGGGCAGCCGCCCCTGGCTCGACCTCGCCCCCGAGAGTCAGCC	R	5'UTR;1stExon	BTF3	0.12829	0.1091733	0.019116714			
cg06836849	12	61680409	100751051	100751101	N/A	TGTGAGAACCACCTTGTTTCCCTTGGTGAACACCTGGAAGTCAGTTCTCG	F	1stExon:5'UTR:1stExon:5'UTR	SLC17A8	0.41059	0.5240929	-0.113502857			
cg06839417	3	40679445	149106151	149106201	N/A	CGGTGTTGCCTCCAACCTGGAGGAACTGGTCTGAAGAGAACAAGTATTAC	F	N/A	N/A	0.9095329	0.9431357	-0.033602857			
cg06847021	16	70691510	89165406	89165456	N_Shore	CTTCCTGGGGGAAGCACCCTCTGGGCTCTGCTGCCACTGGGCACTCAGCG	F	Body;5'UTR;5'UTR	ACSF3	0.8685843	0.9115457	-0.042961429			
cg06859084	2	30624392	137523042	137523092	Island	AGGCAGCCAATGGCTGCGCAGAGGTGTACAGCAGATGGCGTCTGACTGCG	R	N/A	N/A	0.1062416	0.0751406	0.031101			
cg06861736	22	40607450	20918809	20918859	N/A	CGGCGCTACAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGTTCCAGGCT	F	Body;Body	MED15	0.3663914	0.4183429	-0.051951429			
cg06873343	7	53721355	2667608	2667658	N_Shelf	CGGAGTTTCTCTTCAACACCCGGATCCCAAGCAGCATTGCACGGGGGTGA	F	N/A	N/A	0.75024	0.8166243	-0.066384286			
cg06875832	5	31604389	178980927	178980977	S_Shelf	ATTTGGGGAACTGCTGGGTAGAGCCATGAGGCTGGTCCCAAAGGTCACCG	R	Body	RUFY1	0.8277229	0.8728	-0.045077143			
cg06879394	6	32793312	13274151	13274201	N/A	TCCCGGCAAACTCACACTGCGGTTGCATGTGATTTACTGGGCACGGGGCG	F	Body	PHACTR1	0.63472	0.7310314	-0.096311429	0.6765838	0.7310314	-0.054448
cg06886738	14	61790357	102515026	102515076	N/A	GCGCACGCTGATCAACGAGCTAGTGAAAGGTGCGTGAGAGGCCGAACTCG	R	Body	DYNC1H1	0.8858214	0.9154414	-0.02962			
cg06887580	6	22644499	31550699	31550749	S_Shore	CGGGAGGAGGTCAGCCCAGTATGGGAATCAGTTCTTCTCAGGGAACCCAG	R	TSS1500;TSS1500	LTB	0.8233271	0.8829729	-0.059645714	0.8558225	0.8829729	-0.02715
cg06888626	1	33788380	47137631	47137681	S_Shelf	CGCAGGTCCTCCTGTTGGGAATCCATACAGCTGAGCTTTGGTACCTGGCC	R	1stExon	C1orf223	0.8839614	0.91028	-0.026318571			
cg06889756	19	16617391	47184939	47184989	S_Shelf	ACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACG	F	Body;Body;Body;Body	PRKD2	0.7853329	0.8415414	-0.056208571			
cg06902025	7	12705443	1545815	1545865	S_Shore	CCAGGGCCCTGCACCCTGCGCTGTGTGGGCAGCGAGTCCGGAAGGAGACG	R	N/A	N/A	0.6516786	0.7106557	-0.058977143	0.6562075	0.7106557	-0.054448
cg06902368	1	13779504	36989731	36989781	N/A	CGCTCTGTTGAGGTACGTAGTTATTCATCATACAATGGTGTAATATTAAA	R	N/A	N/A	0.8722514	0.91619	-0.043938571			
cg06903075	11	17743447	71709751	71709801	N/A	ATCAGAATATGAATCTTGTCACTGATGGGACAAATGGCGCTGGGGCTGCG	F	TSS1500:TSS1500:TSS1500:	IL18BP	0.8798457	0.9093071	-0.029461429			
cg06907210	17	17792440	48500456	48500506	N_Shelf	TGATCCAGCAATTCTACTTCTGGGTATATACCCAAAATAATTGAAAGTCG	F	N/A	N/A	0.5610529	0.6573214	-0.096268571			
cg06909503	1	21653383	164725227	164725277	N/A	CGGGTTTTACAATGAATGTTAACTTGCACCAGGAGGCTACCTTGGGCCCC	R	Body	PBX1	0.8695543	0.9177757	-0.048221429			
cg06923967	16	71691348	25108522	25108572	N/A	GAGCTGACCACGGACATTTGATAGCATTTGGGGCACAAACTGCTTACACG	F	N/A	N/A	0.7243557	0.8178471	-0.093491429			
cg06924873	2	61704480	172943770	172943820	N_Shore	CGGGGCTACTGGGCCTGAGTCTTTGCATTATCTGTGCTCTGGGTCAAGAC	R	Body	MAP1D	0.6998086	0.7978957	-0.098087143			
cg06931418	19	38788463	1402419	1402469	S_Shore	CGGGGGTGGAATTAGGCCTCCCCCAGCCCAGGGTAGCCCCTTAGGGTCAA	F	TSS1500;TSS1500	GAMT	0.7226357	0.7993357	-0.0767	0.7520163	0.7993357	-0.047319
cg06934654	16	35628319	89180742	89180792	N/A	CGCGGCACAACCAAAGGCAGGTTTAGCCCCTTGGGACGTGGCTCTCGCGT	R	Body;Body;Body	ACSF3	0.8541557	0.9053486	-0.051192857	0.8845263	0.9053486	-0.020822
cg06936290	7	23804420	13889871	13889921	N/A	CGCCTTCTCGTGGTTAGAGGTGTGAGTCATGCTTCCTGTTAAGCCCAGAG	F	N/A	N/A	0.6057771	0.7206329	-0.114855714	0.6780075	0.7206329	-0.042625
cg06939307	1	40770505	32408132	32408182	N_Shelf	AGAGAGTAAAACCATGTTACAGCCTTCTGTGGGAAGCCATTTGGATGTCG	F	N/A	N/A	0.6729	0.7868557	-0.113955714			
cg06941869	1	49721466	168254154	168254204	N/A	CGATGATTCACCAGTGCTTGATGATTAAGGGGTATTGGTGCAGTGCCACT	F	Body	TBX19	0.9242457	0.95772	-0.033474286			
cg06943197	1	48713393	9414341	9414391	N_Shore	CGCTTGTTACTAGGGTGCCCGAGTAAAGGAGACAAAGAGAACCCAAAGGA	R	5'UTR	SPSB1	0.88536	0.9179029	-0.032542857	0.90274	0.9179029	-0.015163
cg06943912	19	14667459	10715612	10715662	S_Shelf	AGGGTGGGCTGGCTGGGAAGGATGGCAATGCCCATTGCTGACATCCGCCG	F	Body	SLC44A2	0.6218	0.6902143	-0.068414286			
cg06954520	18	48713391	68095624	68095674	N_Shelf	CTGGCCACAAGCACTTATGTGAATTGGAACTCAGGAAATGGTCAAAATCG	F	N/A	N/A	0.7795957	0.8676986	-0.088102857	0.8087275	0.8676986	-0.058971
cg06961237	14	57752373	38217808	38217858	N/A	CGTGAGAAAAAAATGCCATGCAAGAGATTAAAGAGGACATGAACTTGAGG	R	N/A	N/A	0.63813	0.7487229	-0.110592857			
cg06966462	2	19784422	9612807	9612857	N_Shore	CGGGTCTCAAACTAAAAAAAAGAACAATCATCTGTGTGTGCAGAGGTCAT	R	Body	CPSF3	0.91198	0.9418671	-0.029887143			
cg06969979	1	53742480	3557200	3557250	Island	CGGGCGCTCCACCCCGCCCTGCTGACGCTCAGAGCCTGGGGCGTTCCACC	R	Body	WDR8	0.7199714	0.7573571	-0.037385714			
cg06971353	18	59686395	77867044	77867094	N/A	TGAGAGCAGAGTGTGCTTGGGGGCCCCTGGCACTTCCCACAGGCCCCCCG	F	1stExon;5'UTR	ADNP2	0.1867757	0.27565	-0.088874286	0.1894138	0.27565	-0.086236
cg06977014	7	51682432	87288184	87288234	N/A	CGAATGTTCTTTAACCATTATTTGAGGGTAAGTCTGCCGGCAACACATTT	R	Body;5'UTR;Body;Body	RUNDC3B	0.7116443	0.7761457	-0.064501429			
cg06983322	16	17661500	728084	728134	N_Shore	CGGGCATGTGGTGGCCGCCCACCAGGGGCCTTCACGTCTGCCCTTTGTGA	F	3'UTR	RHBDL1	0.8312286	0.8762671	-0.045038571	0.8401488	0.8762671	-0.036118
cg06985153	15	61674347	90438687	90438737	S_Shore	TGTACAGGACCCTGGAACCACACTGCCCTGATTCAAAGCATGGTTCTGCG	R	TSS1500;TSS1500	AP3S2	0.92948	0.9583314	-0.028851429			
cg06996029	11	60702342	67017617	67017667	Island	CGCAGGGGCCGCAGGACTTTGGCTTGCACAGCTTCTTCGTCACTCTCTTC	R	Body;Body	KDM2A	0.8949657	0.9205286	-0.025562857			
cg07005506	16	29608506	85089777	85089827	N/A	CGGCACGACGGTCTGCAGTGGGGATCCAGGATCCCAGACATGGATCCTAA	F	5'UTR	KIAA0513	0.5224171	0.64838	-0.125962857			
cg07011029	8	65629357	1848040	1848090	N/A	CCTGGTGACACTCTCCCAGCTGTGGCTGAATAACTAATGTCTAACAGGCG	F	Body	ARHGEF10	0.7388857	0.8378857	-0.099			
cg07012231	7	55696464	47384322	47384372	N/A	CGCGCCTGTGACCCGCGGGTAGATTTCTTACCACGTCCTCCTTTGTGCTG	F	Body	TNS3	0.8925314	0.9207429	-0.028211429			
cg07012823	6	60743496	155777070	155777120	N/A	AATTATTTTGTCTTTGTGTCATAGGAAGCACCTGCAGGGAGCAGCTCTCG	R	TSS200	NOX3	0.6695129	0.7506857	-0.081172857			
cg07023208	6	16611366	32797253	32797303	N/A	AAGGGAAGCCAGCTGGCTGCGGGACAGAAACAACGTCTGGCCATTGCCCG	F	Body;Body	TAP2	0.8565829	0.8873671	-0.030784286			
cg07028598	2	11646456	33832460	33832510	N/A	CGCCCACTGCTCCTGTGGCCCCACCCAGAAGGGTTTCAGCATGCAGAAGG	R	N/A	N/A	0.7015714	0.7817214	-0.08015			
cg07034103	13	51658396	39885248	39885298	N/A	CGGCCTAACTGACTGACACAGCCAAAGGCTTCAGAACCGGGTGAGTCTGG	R	N/A	N/A				0.8390575	0.8740314	-0.034974
cg07035454	8	26722410	107552054	107552104	N/A	GTCAGATGGGACAGTGGTCCCTAGCGCTGAGCCAAAGGGCCTGAGTTTCG	R	Body	OXR1	0.7496843	0.8499086	-0.100224286			
cg07039404	13	72711453	20715713	20715763	N_Shore	TCCTGGGCAATTGGGTTTGCTATTCCTAAGCTCTCCAGAGCCTCTGGGCG	F	3'UTR	GJA3	0.7543471	0.8221543	-0.067807143			
cg07042170	8	25733391	8831422	8831472	N/A	AGTTCCCAAGTGCAGAGGTAGCGATGCCTGCATCAGCAACCACTATCTCG	F	N/A	N/A	0.75047	0.8372614	-0.086791429	0.78534	0.8372614	-0.051921
cg07046436	16	39728414	30663252	30663302	Island	GGTTCAGGGGGCTCACCATGTGAACAGCCATGACATCTTCTAGCACCACG	F	Body	PRR14						
cg07050917	18	28749445	3221492	3221542	N/A	CGGGGTAATGAAGCTGTACCTTGCAAGGTATGATAAGTCAGTGGGATCAT	R	TSS1500;TSS1500	MYOM1	0.8862943	0.9239814	-0.037687143			
cg07052004	15	59725506	93132129	93132179	N/A	TCCCAGACATCACCTCACCAGCTGCTGTGGTCAGGATCTCTGTCCTTCCG	R	N/A	N/A	0.83868	0.8734971	-0.034817143	0.8443888	0.8734971	-0.029108
cg07057579	15	41764311	95870112	95870162	Island	CCGTTCTGGCCTTGGAGAACGCAGTGGCTCACAAGGGCACCGCTAGCACG	R	N/A	N/A	0.3098271	0.2559614	0.053865714	0.2995613	0.2559614	0.0435998
cg07057744	17	63702398	4545074	4545124	S_Shore	GGAGGTCGCTTGGGGTCGGAATGTGGGTGGCAGGTCTCCAATCAACTCCG	R	TSS200	ALOX15	0.4614371	0.5257243	-0.064287143			
cg07059469	6	27604307	152421432	152421482	N/A	GCATACGTAATCTGACCAGGCCCCAGTCAGCCTGAGTAGTGACAGCAACG	F	3'UTR;3'UTR;3'UTR;3'UTR	ESR1	0.6257443	0.7137757	-0.088031429	0.6769	0.7137757	-0.036876
cg07078108	5	52795330	560367	560417	N_Shore	GTGTTAATAAGCAAAACAAGCAGCTTAAGAAGCTGGACAGGCCAGGTGCG	F	N/A	N/A	0.8088786	0.8646243	-0.055745714	0.8271488	0.8646243	-0.037476
cg07079828	3	56640399	16925048	16925098	N_Shore	CGCTGCAAGTGAGATCCTGTCCCAAAAGATGAGCCTGACTTAGGCTGGGC	F	TSS1500	PLCL2	0.7644157	0.8413857	-0.07697			
cg07084746	3	32682482	128294647	128294697	N/A	GTGGTAGGGGCTTCAAGAATACGCATCAAATGAACCCGAACCCAAGGACG	R	5'UTR	C3orf27	0.8228714	0.8668557	-0.043984286			
cg07087293	16	55706465	23313392	23313442	Island	CGCCACGAATATGTCCACAGACCCCTCATCCGAGTGTACCCCACGTCCCC	R	TSS200	SCNN1B	0.098186	0.060605	0.037581	0.1025479	0.060605	0.0419429
cg07088771	6	19775327	32057846	32057896	S_Shelf	TTTGTGGAACTTTGAGCAGGTGGTTCTTGTTTTGAGGAGCCTACAACCCG	F	Body	TNXB	0.8176957	0.88047	-0.062774286	0.8460688	0.88047	-0.034401
cg07092896	2	47620350	152006936	152006986	N/A	ATTATTTTCTCTCTCCCACCAGCTAAATATAGTACTGAAATGTTGATCCG	R	N/A	N/A	0.5701143	0.7287671	-0.158652857	0.6789788	0.7287671	-0.049788
cg07093570	1	59739305	70953380	70953430	N/A	CGCCTTCCACATTGACTCAGACAGGTATGCATCTCTCAGCATGTGCCTGC	R	N/A	N/A	0.89653	0.94034	-0.04381	0.9228813	0.94034	-0.017459
cg07094487	1	65687306	46751642	46751692	N/A	TGCTTGGCTTCACTCTTACGCCGGCTGGCCATCAGGGCTGCAGCACATCG	R	Body	LRRC41	0.8507843	0.8799243	-0.02914			
cg07100000	5	66733445	170877840	170877890	Island	AAAGCAGGTTGGGCCTGGGAGGCGGCCCAGGCGGGCAGGAGAACAAAGCG	F	Body	FGF18	0.5478286	0.6254671	-0.077638571			
cg07111834	1	63791472	114402309	114402359	N/A	GAAGATATTTGGTTCTTAAAATATTCACAAGTTTCACTTTTAAGTTCACG	F	Body;Body	PTPN22	0.5669757	0.7166414	-0.149665714			
cg07115462	3	55619302	12584270	12584320	N/A	CGTCCCTAGAATGTGGGGACCCAGTGGTAGTCGGCTGAGCATAGGATTGG	F	N/A	N/A	0.4822857	0.57154	-0.089254286			
cg07119076	2	17799462	33596547	33596597	N/A	CGAGCCATTGTATCCATTTCATAAATGAAGACAGAGTGGTCATTGTTTGA	F	Body;Body;Body;Body;Body	LTBP1	0.83178	0.8651643	-0.033384286	0.8413113	0.8651643	-0.023853
cg07119404	11	74796456	117187223	117187273	S_Shore	TTAACTGTCCCGTGTAGAATCACCGTTTATTTCTCTCTGTATCTCCAGCG	F	TSS1500;TSS1500;TSS1500:	BACE1	0.0804026	0.0548806	0.025522			
cg07125469	6	41676462	125623573	125623623	S_Shore	GGTGACCTCATCCAGTTTCATGGTTTTACACTGTCAACTGAAGAATAACG	F	TSS1500	HDDC2	0.8556229	0.8915643	-0.035941429			
cg07125981	10	38695416	35330496	35330546	N/A	TTTCCTGAAATGAGCTTTTCTTTTTCTTTCTTTTGTCAGACAGGATCTCG	R	Body	CUL2	0.8499514	0.9366571	-0.086705714	0.8932338	0.9366571	-0.043423
cg07146984	6	32624431	109706151	109706201	S_Shelf	CGCAGAAGCACTCTGTCTTGCTGCTTTCAAGAAAATAAATGGTTAAGAAG	R	N/A	N/A	0.9079271	0.9421886	-0.034261429	0.9145725	0.9421886	-0.027616
cg07148452	15	14627362	90176987	90177037	N/A	CGCCTCTGCAGCTGTCCCTGCTGCTGCCGCATGAGCTGCACGTTCCGCTC	F	Body	KIF7	0.6765857	0.7124886	-0.035902857	0.68464	0.7124886	-0.027849
cg07150777	2	51666482	239996253	239996303	N/A	AAATGAGTGTGTGGGCACGTGCATCCGACTGTGCCCCACGCAGCCTCACG	F	Body	HDAC4	0.9117757	0.9359143	-0.024138571	0.9171438	0.9359143	-0.018771
cg07152828	16	67640457	30586481	30586531	S_Shelf	GGTTGATTCCATATCTTTGCTATTGTAAACACGGCTCTACAGTAAACACG	R	N/A	N/A	0.5842143	0.70574	-0.121525714			
cg07154904	12	14797471	133143645	133143695	N_Shelf	CGCCAGGGCGCCTGTGCTGGGCAGTGGTTGGGAGCAGGAGGTGTGTCCCG	R	Body	FBRSL1	0.8798643	0.9091014	-0.029237143			
cg07157107	8	44798353	42623730	42623780	N/A	CGGTTATTACCAGGATCAGAGACTGAGGCAGACATGAAGGGCGAATAAAA	F	TSS200	CHRNA6	0.6450914	0.7155186	-0.070427143			
cg07157396	6	29666364	170760710	170760760	N_Shelf	AGCAGCCGGTGCACAGCAGAGCCCATGGGAAAGGCCCCGTCTCAGCTTCG	F	N/A	N/A	0.7966857	0.8389643	-0.042278571			
cg07161146	7	40748444	151526959	151527009	N/A	CGGTGGCCCCGTGTACAGCCTGCGCAGCTGCCAGAGTTCCTGAGGAGACC	F	Body	PRKAG2	0.8172871	0.8537429	-0.036455714			
cg07166450	3	38719467	156834067	156834117	N_Shelf	CTCATGTGCCTCTGATAGCTCTGGACAGAGCCCATACTGTGTGGCGGACG	F	N/A	N/A	0.8659243	0.9007586	-0.034834286	0.8840325	0.9007586	-0.016726
cg07166546	14	47657313	35805898	35805948	N/A	CGGGGGCAGCCCTCCCCCATGCAGTCAGGGCCAGAGGAGCATAATATTGC	F	N/A	N/A	0.2794629	0.1930414	0.086421429	0.2441388	0.1930414	0.0510973
cg07167114	12	41779441	52828203	52828253	N/A	CGCCCCCACAGGATGCTCATAAAAGCCACGAGACCAGGGCTCTCCAGCCA	R	TSS200	KRT75	0.8407643	0.8948314	-0.054067143	0.8678675	0.8948314	-0.026964
cg07167688	1	29614497	36989783	36989833	N/A	TGCCTGAGGCCGCCCGCTGTTCAGCGGAAGAGCCAACATCTGTGCTATCG	F	N/A	N/A	0.8172329	0.8489343	-0.031701429	0.822485	0.8489343	-0.026449
cg07169439	1	40715477	10874315	10874365	N/A	CGCAGGGGCTGCACTGAGCCCCAGTACTGGGGCCAGTTTCTGGGGCCCTT	F	N/A	N/A	0.9130786	0.9464386	-0.03336			
cg07176410	8	65759312	68424742	68424792	N/A	AACACTAATGACTCTGCCTGGAGCTGGTTCCACAAAGCCTGGAATCCCCG	F	Body;5'UTR	CPA6	0.8004186	0.8684486	-0.06803	0.8487525	0.8684486	-0.019696
cg07180125	10	62659409	114039492	114039542	N/A	TGCTCTGATAAAAGTCAGGAGGCTTCTATTTTTCCTGGTAAGTACCCCCG	F	N/A	N/A	0.5147043	0.60586	-0.091155714			
cg07180988	12	66780348	59325286	59325336	N/A	TTCTTCACAAAGCAACCCATGTCTCCTGGTTAAGCATGGACCAGATTCCG	R	N/A	N/A	0.7943171	0.84469	-0.050372857	0.8114375	0.84469	-0.033252
cg07192594	16	57779499	71221950	71222000	N/A	CGCAGTCTGGGCCTTGTGTTGTTTGAACTTTCCACTGGAACCAAAGGAAG	R	5'UTR;5'UTR	HYDIN	0.6849357	0.7518571	-0.066921429			
cg07193667	4	42721425	48501509	48501559	N/A	CGCATGGTGCAATCATACCAACTTCTAGCACAGGCCAAACCAATGGGAAA	R	Body	FRYL	0.8949614	0.9477986	-0.052837143	0.9255213	0.9477986	-0.022277
cg07201215	21	10631429	36419478	36419528	N/A	AAAAAAAGATCTTCCTGGCTTTACTCTGCTTTCAGTACCCCCTCAGAACG	F	Body	RUNX1	0.1010909	0.1951657	-0.094074857	0.1503275	0.1951657	-0.044838
cg07205154	1	37716438	176147105	176147155	N/A	TGGCAAATCACAGGGACCTAAAGACTGAAGTAAATGCCAGGCACATAACG	R	Body;Body	RFWD2	0.7588086	0.8187614	-0.059952857			
cg07215695	2	72726451	85637834	85637884	N_Shelf	TGAGACCAGCAAGGAAAGCCATGTTCTCCATTCAGGGCCTGGGGCAGGCG	R	TSS200	CAPG	0.7691729	0.8322686	-0.063095714			
cg07217293	11	22714340	121000200	121000250	S_Shore	CGGTTGGTATCTTTGTGGGTTCCATCAGCTTCTTGACCTCTCTCAAAAGG	F	Body	TECTA	0.6603214	0.7199429	-0.059621429			
cg07218487	12	27671356	49418559	49418609	N_Shore	CGGGCACTGAGAACTTTGGCCTAACCCCAAAAAAACTCAGGCTAAGGTGA	R	Body	MLL2	0.8625329	0.8998386	-0.037305714			
cg07223240	6	65634351	170468271	170468321	N/A	CGCCCGCCAGGCTGCGGCTGCCCTGCAGGAGCTGGGACTGACTCTAATTG	F	N/A	N/A	0.7148714	0.7831871	-0.068315714	0.7123938	0.7831871	-0.070793
cg07229212	8	62794419	11056726	11056776	N_Shore	GTTCAGCCTAGAAAGGCTAGTAAACAACTCTGGGTGGTGCAGGGCCTACG	R	Body	XKR6	0.6744229	0.7766129	-0.10219	0.71811	0.7766129	-0.058503
cg07231911	1	65769307	94141047	94141097	N/A	AAAGACCCAGTGTTTATAAATAAATCAATGCACTCTAATTAGTGAACACG	R	5'UTR	BCAR3	0.46295	0.52866	-0.06571			
cg07233230	1	31761398	241912768	241912818	N/A	CGGATGAATTTTCTCTGAGCGAAAAGCCAAGCTTTCTCTAAGTCATTTTT	F	Body	WDR64	0.6765043	0.7802486	-0.103744286			
cg07236939	6	63781454	110722253	110722303	S_Shore	ATCCATATCTTCCCTGAAGACAGTTGTCCTTGGCCACTCCTTGGGCTCCG	F	Body;Body	DDO	0.8877771	0.9132314	-0.025454286	0.8904713	0.9132314	-0.02276
cg07238926	10	20748418	118350475	118350525	N/A	CGGTGGGAGGGAACATCTGGAACATTAGACAGGGTAAGCCACCTTTGCAA	F	TSS200	PNLIPRP1	0.6215757	0.6907671	-0.069191429	0.6212188	0.6907671	-0.069548
cg07239452	8	37663335	1864422	1864472	N/A	CGGGGTCCTATCTCTGTGGGAATCACACACGTGTGTCCTACTACACATGG	F	Body	ARHGEF10	0.90586	0.93035	-0.02449	0.917265	0.93035	-0.013085
cg07254055	6	14642485	35011768	35011818	N/A	ATGGAACCAGTGTAAAAGAACCTTTCTGTGACAACCAAGTAAGTACTTCG	F	Body	ANKS1A	0.7972386	0.8580071	-0.060768571			
cg07257628	3	44667458	69027233	69027283	N/A	CGGGATCAACAAGCAACAGCCCTGTGGGCAAATCCAGCCCATGACATGTT	R	Body	C3orf64	0.8814343	0.9281514	-0.046717143	0.9117438	0.9281514	-0.016408
cg07259733	12	40712510	25103643	25103693	S_Shore	CGGGGGCCAGGAGGTTTCACAAGGACTCAATGGCTGATTAAATGCTTACA	R	TSS1500	BCAT1	0.7026686	0.7593557	-0.056687143			
cg07264682	10	62764327	60082823	60082873	N/A	CGGTGGTTGGGCTCACCCTAGGGATACAATATGTGTTCCTAATTCCTTCC	R	N/A	N/A	0.6634557	0.7326371	-0.069181429			
cg07265976	4	47702324	2696715	2696765	N/A	TTGCAGTGACCCTGACTGCGAAGGGCACCGCTGCGAGAATGGTGTCTACG	R	Body	FAM193A	0.88374	0.9275614	-0.043821429	0.9039625	0.9275614	-0.023599
cg07266046	2	54665509	202804175	202804225	N/A	CTGTAGTTTTCCCAAGGTCATATCACTAATAAGGACACAGCCAGATTTCG	R	N/A	N/A	0.6978914	0.7784157	-0.080524286	0.7420363	0.7784157	-0.036379
cg07271580	4	44796425	159095085	159095135	N/A	CGTGGAGGCTACACTATCTACTCTGAACTATGATATTCAGAGAATGGGCT	F	TSS1500;TSS1500;TSS1500	FAM198B	0.73122	0.8297843	-0.098564286	0.7863788	0.8297843	-0.043406
cg07283896	6	30761438	11855283	11855333	N/A	CGGGGAACTCCCTGGCTTAAAAGCACAATGACTCATGAGTTCTCCGTGAT	F	N/A	N/A				0.1613175	0.2163986	-0.055081
cg07284407	20	21742410	57429858	57429908	Island	TCTGAGATGGATCTTGCGTCTGGCCCCGGAGGCAGGGGCTGCAGAGGCCG	F	1stExon;1stExon;3'UTR	GNAS	0.5315614	0.5918386	-0.060277143	0.5518175	0.5918386	-0.040021
cg07287107	15	35618464	40224001	40224051	N_Shelf	CTCTCTTCTTTTTCCTGAATCATTTGGGAGCTAACTGCATATTTAATACG	R	N/A	N/A	0.8586043	0.9168357	-0.058231429			
cg07287698	12	13681340	97957454	97957504	N/A	CGTGATGTCACAATTCAAGTGTGCTTCCTGTCACTTATGTGTAGTTTAAA	F	TSS200	MIR135A2	0.82029	0.88642	-0.06613	0.8475388	0.88642	-0.038881
cg07292237	12	71704488	132269687	132269737	N/A	CGGAGTCAAATCTGGTGGTGGTCGAGGCTGCCTGATAACTTCCTGGCTCG	F	Body	SFRS8	0.9012814	0.9384371	-0.037155714			
cg07293406	5	54707452	103013792	103013842	N/A	CGTGGTTTGGGATAAACTTGATGGTGCCATTGGTTTTTAGTATATCCTTT	R	N/A	N/A	0.8905243	0.9236514	-0.033127143			
cg07296661	2	71624472	167163732	167163782	N/A	AAGAAACACTGCCATCAGACTCCAGCAATGTGGTTCCAATGTCATCAACG	R	Body	SCN9A	0.9166457	0.9395043	-0.022858571			
cg07296841	12	46678308	13307263	13307313	N/A	GACATCTGCCCCAAATATTAGGCAACTGGCACTCATTACTGTAAGAAACG	F	N/A	N/A	0.57108	0.6884029	-0.117322857			
cg07313162	5	56644315	34587700	34587750	N/A	CGTCTCTCAGCTTAGAGGCCCCCTCTGTGTGTCTTGAGCTGTGTGTGACT	R	N/A	N/A	0.5221329	0.5987343	-0.076601429			
cg07321730	5	43752421	179302907	179302957	N_Shelf	CGGGGACACTCACCCACCACCCTGGTGTTGTAGTAGTCGGGCAGCATGCG	F	Body;Body	TBC1D9B	0.8597829	0.9046057	-0.044822857	0.8786925	0.9046057	-0.025913
cg07342322	1	35681378	192508724	192508774	N/A	CGTAGTTTTCAGGATATAGATTGTAATGTTGATGTTACAAAGAGAACTGC	R	N/A	N/A	0.4490543	0.5456357	-0.096581429			
cg07347431	4	46779339	159134926	159134976	S_Shelf	TATTTATCACCTGACAGCAGTTGTGTTATTTCCCCAATTCTTTGTCTTCG	R	Body	TMEM144	0.8781314	0.9216957	-0.043564286			
cg07349899	11	73725368	11443325	11443375	N/A	TTCTCTGCAGAGTCTCTGCAGAGTCTCTGCAGAGGTCAGGACTGGCCACG	R	Body	GALNTL4	0.8607114	0.9034371	-0.042725714			
cg07359183	1	26664505	208358018	208358068	N/A	AATGAGAGATGTTAAAGCCAGATATTGGGCACACCCAGCAAAGCCTCCCG	R	Body	PLXNA2	0.7950357	0.8455329	-0.050497143			
cg07360028	12	60768463	13364332	13364382	N/A	CGTGTGGGCTATCTGCTAACATGAGGAAGAGCTGCACTAAAAACCATCAC	R	5'UTR	EMP1	0.5269829	0.6346243	-0.107641429			
cg07360250	5	37622429	176830358	176830408	Island	CGCGCAGCTGCCGTCCGCATCCTCCTGAAGGCGCAACAGAGCTAACCCGG	F	Body	F12	0.4365271	0.5068486	-0.070321429			
cg07362003	2	72605436	157682747	157682797	N/A	CGAAGTTTTAAGTAAATTATGTGTTCCAGCTACATGATTTCTATTTGGTA	F	N/A	N/A	0.7260443	0.8119729	-0.085928571			
cg07368857	3	27733507	71276336	71276386	N/A	ATCCGAGGAGACATGAGGATCATAAAAGCTGCCCGATGTCACCATGGTCG	F	5'UTR;5'UTR	FOXP1	0.5817729	0.6726071	-0.090834286			
cg07371452	16	13679406	139780	139830	N/A	CGTCCCCTTCACTGCCCGGGTCGGCGGTCGCAGCCTCAGCACGCCCAACG	R	Body;Body	C16orf35	0.7676957	0.8081729	-0.040477143			
cg07380504	10	70649414	84228439	84228489	N/A	TCTAAAGTGCCTGCTGATATTCAGTGAGGCATTTCCCTGTAGCTGCAGCG	F	Body;Body;Body	NRG3	0.8886286	0.9160986	-0.02747			
cg07382156	1	22799386	2085526	2085576	S_Shelf	TGGGTGCTGAGTGATATGTGGGTCATGATGCCAACGCCGACGTCCCTGCG	R	Body;Body;Body	PRKCZ	0.87297	0.90674	-0.03377	0.8923538	0.90674	-0.014386
cg07385388	17	45719408	110138	110188	N_Shelf	TGTGGTCCCACTGGTACAGCACGCCACACCTGGGCTGGAGCTCAGACTCG	R	Body	RPH3AL	0.7787671	0.8318957	-0.053128571	0.7927938	0.8318957	-0.039102
cg07397891	1	54621409	246582071	246582121	N/A	CGGCCTCCCAGCGTGCTGGCATCTGTTGCTGTGCTCTTCTGCCTGCGTGC	F	Body;TSS1500	SMYD3	0.6926414	0.7696429	-0.077001429	0.7381888	0.7696429	-0.031454
cg07408232	6	10764503	30113978	30114028	N/A	TTCTGGACATCTGTCTGTCCCTGGAACAGCCTGATGTGGGCAGATGGTCG	R	Body	TRIM40	0.7475286	0.8215814	-0.074052857			
cg07412186	6	62753380	16719376	16719426	N/A	CGTGAAAGGCCAGATTTCTCTTAATTGCGTTGATATTGTGGAGATGAATC	R	5'UTR;5'UTR	ATXN1	0.78359	0.8523557	-0.068765714			
cg07416916	2	22667400	36825888	36825938	S_Shore	TATGTTATAACTAATACATGGGTGCCCCATACACAGGGCTTACAATGTCG	R	TSS1500;TSS1500	FEZ2	0.8577857	0.91322	-0.055434286			
cg07428907	17	43695420	78165917	78165967	S_Shore	CGCAGGCTGTGCTCATTCTGGGTGTGAGATGACGGGTGGATTTTATTTTC	F	Body;Body	CARD14	0.6680429	0.7352429	-0.0672	0.7110688	0.7352429	-0.024174
cg07433769	18	44792462	13620827	13620877	N/A	CGGTGACATTGGAGAAATAGCTTCAGTTTGTGGAGACGTTCTCAGCTCCC	F	TSS200:Body:Body:Body:TSS	C18orf1	0.8128257	0.8637	-0.050874286			
cg07435445	14	32754442	103396379	103396429	Island	CGGAGATCCAGGTGGTGCTGGTGGAGAATGGGCCCGAGACAGGCGGAGCG	R	Body	AMN	0.4916043	0.5800457	-0.088441429	0.5520138	0.5800457	-0.028032
cg07437263	17	65667300	30817129	30817179	S_Shore	CGGCCGGAGAACATCTGCCTTGCTGCACCTGAGGCCCAGCAGAGCCGTTC	F	3'UTR	CDK5R1	0.7712914	0.8329929	-0.061701429			
cg07438099	6	55614435	31834178	31834228	S_Shelf	CGTCTACCAAAACCCTTTCCGGCAAATTGAACAGGCTGGGTATTTGATGA	F	Body	SLC44A4	0.74818	0.8168043	-0.068624286			
cg07443710	10	37736340	71206848	71206898	N/A	TTCCCCCTAAATCTCACTGTCAAGTTATCAAGAAAACAGATCTCAGGACG	R	N/A	N/A	0.8121	0.86639	-0.05429	0.8413263	0.86639	-0.025064
cg07447769	13	67603376	24723265	24723315	N/A	TGTGGAAAACGACCCAGTGTGATGGCAACAGGCAGGGGGCAGACAGGACG	F	N/A	N/A	0.7225986	0.7824243	-0.059825714	0.76415	0.7824243	-0.018274
cg07451659	13	31767477	114290741	114290791	N_Shore	TACTTCAGAGTTTATAAATTCTGTGAGGAGACACTGATGACTGGGAACCG	R	Body;Body	TFDP1	0.8919971	0.92005	-0.028052857			
cg07457626	6	16702431	155347581	155347631	N/A	TGAGTTTCTCAATTTTTTTTCCCTCCTGGTGGGGGTAGACTGTTTCAACG	R	N/A	N/A	0.8164671	0.9020743	-0.085607143	0.8419238	0.9020743	-0.060151
cg07464578	22	59676382	42828946	42828996	N/A	AGAGAGGAGGCGTCTCCTGGGCCTCTGCAGGGGACCCACAGAGGTTCTCG	F	TSS1500	NFAM1	0.8736729	0.9082157	-0.034542857			
cg07464621	6	62784380	74063014	74063064	N_Shore	CTAGGCCCTTGGATGAAGTGAACCAGTTTCCAGCCAATGCAATGAAGCCG	F	3'UTR	DPPA5	0.7255914	0.8160071	-0.090415714	0.7817713	0.8160071	-0.034236
cg07469700	4	20803442	115785488	115785538	N/A	TCAGAGGCCATTGGTTTGCTTTTCATTTCCCTTTTGGTATTCCCCTGACG	R	Body	NDST4	0.7457614	0.8285214	-0.08276			
cg07471190	20	30635361	1097586	1097636	N_Shore	CGCAAAGGCCCAAACAGAACACATGAAACAGGGAAACTGGCTGGGAAGCT	F	5'UTR	PSMF1	0.9112143	0.9376143	-0.0264	0.9138638	0.9376143	-0.023751
cg07473223	14	46685478	105819210	105819260	N_Shore	CGCCTCATCACTGTCCCCTGGGGTGACGGGCCCCCTCATCACTGTCCCCT	F	Body;Body	PACS2	0.6131686	0.6920271	-0.078858571			
cg07480608	3	25680356	15352493	15352543	N/A	CAGGTTGAACATGAAGCACACAGGATGAGTCAGTGTTTTCTGGCCAATCG	R	Body;5'UTR	SH3BP5	0.8485829	0.9258271	-0.077244286	0.87375	0.9258271	-0.052077
cg07481097	3	18684381	112959879	112959929	N/A	TGCTGGGATGAAACCACTTTAGAAATAAACCCCTACAGGGGCAGAGGACG	F	5'UTR	BOC	0.6593014	0.7400314	-0.08073	0.6953475	0.7400314	-0.044684
cg07490283	14	24791374	75938492	75938542	N/A	AAGGTTGTGGCAGCGGGTTGCCTTCTGTCTCGGGGGTCTTGAGGCTGTCG	R	3'UTR;3'UTR;3'UTR;3'UTR	JDP2	0.8877086	0.9195743	-0.031865714			
cg07494499	17	37721459	837017	837067	N/A	CGTGGTCAACTTTAGAAATGTGCCTTCGTGTAAGCTGGTTTTTATAAAAT	F	Body	NXN	0.52976	0.6812829	-0.151522857			
cg07496457	4	40808321	184929183	184929233	N/A	CAGTGACACCAGCTAACAATGACAGGGCAGGGTTTCAATCCAGCAGCCCG	R	Body	STOX2	0.8873957	0.9156443	-0.028248571	0.9031375	0.9156443	-0.012507
cg07496621	7	54778387	46390325	46390375	N/A	ATATGGGCTGTTTCCAGTTTTGGGTGGAGTCCTTTTTGCAACTGTCCTCG	F	N/A	N/A	0.7270829	0.7944257	-0.067342857			
cg07501462	6	50731432	31673880	31673930	S_Shelf	CGGGGTATGCCAGACAACCACAGGGAAAGTCATTCCAAATCATTTACGGG	F	TSS1500	LY6G6F	0.9266086	0.9579129	-0.031304286			
cg07505363	8	57764390	146046335	146046385	N/A	CAGCCATAAGCACAGGGACACAGGCAGATACCACCAGCCCGGGAAGGACG	R	N/A	N/A	0.7539414	0.7982657	-0.044324286			
cg07509935	14	35669497	24780167	24780217	Island	CGTGTGCGCGCTCAGCATGTACGCCAGCGTGCTGCTCACCGGCCTGCTCA	F	1stExon:1stExon:Body:TSS15	LTB4R2				0.3597475	0.26678	0.0929675
cg07513789	5	52677473	127981594	127981644	N/A	CGGTAAGTACACTTCTGGAATGTTTCAGTTTGGATTAAGCATCCTGAAAC	R	N/A	N/A	0.7170414	0.8048771	-0.087835714			
cg07527729	10	61738425	134472187	134472237	S_Shelf	TGGAGCCCAGAGGGCCTAGAGCATCCGTGCCCAGAGACCACCCAGCTGCG	F	Body	INPP5A	0.8594986	0.8872586	-0.02776			
cg07534892	12	60751310	123930117	123930167	N/A	CGACCCACGGATTCAGAAACTTTGAGGGAGGGCTCCAGCATCTGTGTTTT	F	N/A	N/A	0.7582057	0.8483443	-0.090138571			
cg07538339	8	38727360	93107298	93107348	N/A	CGCTATCTCCCATCACCTCTGCTATCCAGACAGGACTCACCGAGGTGAGA	R	5'UTR;1stExon	RUNX1T1	0.0966367	0.0607149	0.035921857	0.0776969	0.0607149	0.016982
cg07539709	17	14743453	80545454	80545504	Island	TGTAGATTTCCTGGGTGTGGCCTGGAAGCGGCCTGAAACGGCGGGAGCCG	R	Body	FOXK2	0.7335043	0.8087443	-0.07524			
cg07539983	5	15685471	151067341	151067391	N/A	CTGTTGCACTGAGCAGTTCATATATAACAGGAGTGACCCAAGTTGAAACG	F	TSS1500	SPARC	0.7585957	0.84898	-0.090384286			
cg07541020	10	54689482	44068714	44068764	N_Shore	CATCCCAGTGCTAAGTGGTCTCAGCAAAACAGATAGAATGATAAACCACG	F	5'UTR;5'UTR;5'UTR	ZNF239	0.7949429	0.8466571	-0.051714286			
cg07562742	4	20723439	153455963	153456013	N_Shore	CTCCAGTAGTGTTGGGAGTCTATCAATGAGGGAGTCTAGCTTTATTCACG	F	5'UTR	FBXW7	0.0533959	0.0880497	-0.034653857			
cg07572028	1	73743467	3695198	3695248	N/A	TTCCTGATGCAGCTTGTGATGCGTGAGATGCTGGAAATGTATTTAACTCG	F	N/A	N/A	0.8920529	0.9261614	-0.034108571			
cg07575896	5	72640404	157001092	157001142	N_Shore	CGCAAGACACGAAACTGTACTTATGGGTATGGTTCCAATTTTATCAATAT	F	Body	ADAM19	0.8551257	0.9278114	-0.072685714	0.8898	0.9278114	-0.038011
cg07583296	19	67672407	6002914	6002964	Island	CACTGACGACGCCCACCTGTAAGCCAGGGCTCGTGGTGAGCAGGGGTTCG	R	Body;Body	RFX2	0.8369614	0.8882686	-0.051307143	0.8676325	0.8882686	-0.020636

cg07584582	22	35708444	19723500	19723550	N_Shore	ACAACAGCCCAGTGGAGTGGACTGGAGGTTCCTGCCTGAGAGGTATCCCG	F	N/A	N/A	0.88679	0.9195086	-0.032718571			
cg07587588	8	47661317	81083356	81083406	Island	CGCATCACGGCCGCCAGCCCCTGACGCTAGCCCCTTCGCCACCTCCCAGA	F	Body;Body	TPD52	0.1873986	0.1282314	0.059167143			
cg07587653	11	59751316	70338480	70338530	N/A	GCTGCTGAGAACATGGCTGTGGAACCGAGGGTGGCGACCATCAAGCAGCG	F	Body;Body	SHANK2	0.8851714	0.9152357	-0.030064286			
cg07589202	2	50703373	10081532	10081582	N/A	CGCCCCTGGCATTCCTGTGGCCATATCAAATATTTATATAGTGCTTAGAG	F	N/A	N/A	0.7468657	0.8225371	-0.075671429	0.787275	0.8225371	-0.035262
cg07590004	7	49614402	139522635	139522685	N/A	GGCAGATTGGATGCTTTCTACCTGACATGAGGACCAGCCAGGAGGCTGCG	F	5'UTR;5'UTR	TBXAS1	0.8135671	0.8534243	-0.039857143	0.8305363	0.8534243	-0.022888
cg07592809	11	53737507	17591873	17591923	N/A	CGCTGGTCCACTTGCAGGTACAGTCGGAGCCCTTCACGGTCGTAGAGCAC	R	N/A	N/A	0.8731557	0.9265386	-0.053382857	0.9016413	0.9265386	-0.024897
cg07600499	5	35676426	115141054	115141104	N/A	CGTGGTAGGTAGCCTTTTTGTCCAAGGCAAACATACAGCGAACCTTAAAG	F	3'UTR	CDO1	0.7506086	0.8065986	-0.05599			
cg07602210	3	32651360	155585263	155585313	N_Shelf	CGGCCCTGTTTCATATATTTTGTCTGAGTTTTTTTGTTTGTTTCAGGCAG	R	N/A	N/A	0.8230714	0.8905271	-0.067455714	0.849245	0.8905271	-0.041282
cg07610468	7	68683507	1949632	1949682	N_Shore	GGGTGAGCTCTGTGCAGCTTTCAAACAGGGCACCTCTTGTGTGATTAACG	R	Body;Body;Body	MAD1L1	0.85396	0.8929	-0.03894			
cg07615875	7	61719395	101882758	101882808	Island	CGAGCGTATCAGCAAAAGCCATACCCGTCACCAAAAACCATCGAAGACCT	F	Body;Body;Body	CUX1	0.9068543	0.95788	-0.051025714			
cg07624650	19	24684319	37064219	37064269	Island	CGTTGTTGGACTACGTTTCCCACAGGCCTCAGGGCCGCGGATGAACTTCG	F	5'UTR;TSS200;5'UTR	ZNF529	0.1290791	0.0687189	0.060360286			
cg07629149	10	24660355	334731	334781	N/A	CGGTGCTTGAGGACCAGGCAACACAGTCGTGGGTGACCCGCAGCTCTTTC	R	Body	DIP2C	0.8692357	0.9019286	-0.032692857			
cg07632615	3	56746500	150819587	150819637	N/A	ATCTCACTAGCTCATGCCTAATAAATCCAGTGTGGGAGACAGTGGAGTCG	R	Body	MED12L	0.8133129	0.8784071	-0.065094286	0.8409075	0.8784071	-0.0375
cg07637516	10	18767352	111974273	111974323	S_Shelf	TGGGGCTGTTGCTATGGTACTGGGGCCAACAGCAGGTTCATCAAAAGCCG	R	Body;5'UTR	MXI1	0.6413329	0.7144129	-0.07308			
cg07638044	19	21715419	54137365	54137415	N/A	CTGTGCCCGGCCGTGACTGAGGTTCTTAGATATGGAGACACTGCTGGCCG	F	Body	DPRX	0.8990214	0.9176671	-0.018645714	0.887325	0.9176671	-0.030342
cg07638320	13	29721303	20986392	20986442	N_Shelf	CGCCCCCACAAAACATACAGACCGAGAGACATACGAGAGACTCTGGTCAC	F	Body	CRYL1	0.7644443	0.8524557	-0.088011429	0.7968713	0.8524557	-0.055584
cg07643000	3	66788383	11666825	11666875	N/A	CGTCTTCTAGAGTTTTGTTGTCATAGAGGCAAATGAGATGCCAAATGCTA	R	Body;Body	VGLL4	0.8036914	0.8669457	-0.063254286			
cg07664999	8	71810443	105264286	105264336	N/A	TGACTGATTCTTTGAGATTAATCCATGGCTTCAGATTGGACCAGAACTCG	F	3'UTR;3'UTR	RIMS2	0.7898914	0.8523543	-0.062462857			
cg07665487	8	50709323	132915715	132915765	N_Shore	CGCAGAGGTTTAACACAGCCTTCCTCAAAGTGGGTCAAAGTGGTCCAGGA	R	TSS1500	EFR3A	0.8624886	0.9107286	-0.04824			
cg07669002	14	69650473	92979305	92979355	N_Shore	TAGCTGGCCCCAATAACAAAGCATTAGCCCCAATAACAAAGCATTAGCCG	R	TSS1500	RIN3	0.7519271	0.81643	-0.064502857			
cg07670188	12	73779442	124066860	124066910	N_Shelf	TGAAACCTGAAGCGGGAAACTGGATCCTGGGACACTACTGCCCCCTATCG	R	N/A	N/A	0.1903629	0.2930214	-0.102658571			
cg07673376	2	36639325	220429911	220429961	S_Shore	CGGCCCCACAATCAGCCTTGGCTGGAGGAGCCCAGGCTGGCATGCTTCCT	F	Body	OBSL1	0.8874771	0.9260871	-0.03861			
cg07673538	2	70809483	36824338	36824388	N_Shore	AAAGTCTAACGTTCTAGGTGGAGTATATTGCCTGTGCATAAGTACCAACG	F	Body;Body	FEZ2	0.4639971	0.5610671	-0.09707			
cg07674459	15	21658498	100892205	100892255	S_Shore	CGGAAGGCCTGACTGAGGGTAGAGGATCTGCTTCCAAAATGACTCACTCA	R	TSS1500	FLJ42289	0.8485914	0.89499	-0.046398571			
cg07676849	11	70699422	71845665	71845715	N/A	CGTGACTCTGTCATTAAAAAAGAAAAGAATATCTGTGTTTGCAGGTGAAA	R	TSS1500	FOLR3	0.6836714	0.7484314	-0.06476			
cg07683142	11	13781403	2704514	2704564	N/A	CGCCATTGCCCATACTCAGGCTGACAGGTTCTGGAGGTGCCATGGACTCC	R	Body;Body;Body	KCNQ1	0.7566543	0.8181186	-0.061464286			
cg07683276	6	30658434	144184358	144184408	N/A	CGTGGCTGAGTTGATACTTTAGGAAGATCACTGCCATTAATCATCTGTAT	R	TSS1500;Body	C6orf94	0.5773229	0.7093786	-0.132055714	0.6712363	0.7093786	-0.038142
cg07691897	11	73774347	112000518	112000568	N/A	CGGCTTACAAGGCCCAGCAACCTCTGGTCCCCATTGACTGCCTGGTCCCC	R	N/A	N/A	0.8309414	0.8929943	-0.062052857	0.8316088	0.8929943	-0.061386
cg07699767	5	35693350	138212370	138212420	N/A	CGTTGGCCTTTTTGGTTCTGAGGGATTCATCCCACTGGGCAGATCTAAGA	F	Body;TSS1500	CTNNA1	0.7356286	0.7942571	-0.058628571	0.7613863	0.7942571	-0.032871
cg07699978	12	68721402	63194001	63194051	N_Shore	CGGCATCAGGTAGTGTGCTAAGAAGGAAAGTAAATAATGACTATACATAT	R	Body	PPM1H	0.89221	0.9350214	-0.042811429	0.9071488	0.9350214	-0.027873
cg07702526	16	28781474	967972	968022	S_Shore	GCCATGTCCCCAGCTCTGCACCTGTATGTCTTGCGGGCAGCAGAAGGGCG	F	Body	LMF1	0.8836229	0.90298	-0.019357143			
cg07713135	13	35606424	99093756	99093806	N/A	TGCTCAGAAAGGCCCAGAAAACCCGGAGGGGCCCTGCGGGGCTCCTTTCG	F	Body	FARP1	0.8493957	0.88354	-0.034144286			
cg07726222	16	14698399	2125875	2125925	Island	GGGAGGCACAGGGCCTGGGGCGACCACTCACTTGGAGGGGTTGGTGTACG	F	Body;Body;Body	TSC2	0.9146186	0.93176	-0.017141429			
cg07732336	10	35612386	17038941	17038991	N/A	CGAAGCCAAAAGCCAAGGCACAGTGAAAGAGAATTAAATTTTAAAAGTAA	F	Body	CUBN	0.4820557	0.6308871	-0.148831429			
cg07735851	16	37679334	3707175	3707225	N/A	CGCTGCCTGTGGCCCTGGGACATGCGGAGGCCGCTGGTGCCCACTGCCCC	R	Body	DNASE1	0.7648929	0.82624	-0.061347143	0.7986488	0.82624	-0.027591
cg07736012	3	43765334	151129001	151129051	N/A	CAGTGAATTTCAGGGGAGTCCTCATGGGTTTGTTTTTGCCCCATATATCG	R	Body	MED12L	0.8725671	0.9244071	-0.05184	0.8991875	0.9244071	-0.02522
cg07737503	19	30706374	1132895	1132945	N/A	CATTGACACTTGGTTTTCTACCAAAGCGAGAACGTTCTTTTCCCAGGACG	F	Body;TSS1500	SBNO2	0.4627843	0.59681	-0.134025714			
cg07743730	13	30700407	108817948	108817998	N/A	CAATGATAATCTCATGTTGAAATACTCAGCTTTGAAGCTCATAACAAACG	R	N/A	N/A	0.5699186	0.6382271	-0.068308571			
cg07745886	8	43680369	42150794	42150844	N/A	CGGCCAATCCCTGCTAGTTCTGCAGCCCTGGCTTCCTCAAAAGCAGGTCC	F	Body	IKBKB	0.59571	0.6609143	-0.065204286			
cg07760622	10	33671441	117754806	117754856	N/A	CGGATGGAAGATTTGAGCCTGAAAAGTGGAAAGGACTCAAAACTCAAGAA	F	N/A	N/A	0.8499086	0.8872786	-0.03737			
cg07764386	15	65781498	41444182	41444232	N/A	GCCGTTCGCCCCCCACTCCTCAGGCCTTGGGTGGTTGATGGGACTGGGCG	F	N/A	N/A	0.6365186	0.6841629	-0.047644286	0.641575	0.6841629	-0.042588
cg07766779	6	59692452	149887504	149887554	Island	CGCCCTCACCTCCCGGCCGCGGCTGCCCTCTGCCCGGGTTGTCCAAGATG	F	TSS200	C6orf72	0.1529757	0.1341971	0.018778571			
cg07766875	10	32783326	124089760	124089810	N/A	CGGCCCCCTGGCTGCAATCCTGCCTGGGAAAGGAGGTTTGAGATCAGGTA	R	Body	BTBD16	0.7538457	0.8168271	-0.062981429			
cg07771287	10	65737412	14996663	14996713	S_Shore	AATCATCTCTGCGTGATCTTGGGGCAAATAAGATCCCAATAATGCCTTCG	R	TSS1500;TSS1500;TSS1500;	DCLRE1C	0.2202421	0.3808086	-0.160566429			
cg07773582	16	32807409	4845285	4845335	N/A	CGCTCCCTGGCTCCCCACTGCTGGAGGCCCAGGGAGGAAGACGCCGGCCT	R	TSS200;Body;Body	LOC440335	0.7509957	0.7993614	-0.048365714	0.76317	0.7993614	-0.036191
cg07777352	7	12639304	75958866	75958916	Island	CGCGTGCGCTGCCAGTTCCCCTGGGGCCTTAATTGTTGCCTTCGCCGCCA	F	3'UTR	YWHAG	0.8343586	0.8838229	-0.049464286			
cg07779313	2	38694401	192731534	192731584	N/A	CACAAACACCAGCTTTGAAATCGGCTGGTATTGTCTCAGAACTTGAAACG	F	N/A	N/A	0.5542214	0.6911671	-0.136945714			
cg07783291	19	63728307	33178679	33178729	N_Shelf	CGGCCTTGCAAAGTGCTGGAATTACAGACATGAGCTAACGCAGCAACATG	R	N/A	N/A	0.4774	0.5503071	-0.072907143			
cg07784054	22	70625436	50785141	50785191	S_Shelf	GACTGACGGTGGGGGAGCACTGACCAACAGTGGAGGCACTGACCAGTGCG	F	5'UTR	SAPS2	0.8565586	0.91245	-0.055891429			
cg07784872	16	46736314	85687041	85687091	S_Shelf	TGGACCCTGCGTGTGTGCGGGGCAGCCTCTGCGTGGCTAGGGGTGGCACG	R	Body;Body	KIAA0182	0.8347086	0.9329357	-0.098227143			
cg07795346	16	42623327	84800637	84800687	N/A	CGCTCATGAGAGCTGGTGGAGAATCAAGAAGCCCTCTTGATTCAGTGGTC	R	Body	USP10	0.9032214	0.9314743	-0.028252857			
cg07798137	1	15808397	17332259	17332309	S_Shore	CGTGGGCAGCACGCCCACCGGTTATGGGACCCTGACGATAGGGACATCAA	R	Body;Body;Body	ATP13A2	0.9180371	0.9431414	-0.025104286			
cg07801448	4	44763495	40356774	40356824	N/A	CAAAGAGGTAAATAATTATATAAACTAGAGGCCAGTCACCCACCACTACG	F	3'UTR	CHRNA9	0.6623957	0.7701114	-0.107715714			
cg07807481	10	25766453	135082125	135082175	Island	GAGCCAGGAAGGCCCTTCAAACTCAGCCCAAGCCGGGGGGCGTCATGACG	R	Body;Body;Body	ADAM8				0.8829975	0.8355814	0.0474161
cg07825414	22	65756335	19712640	19712690	Island	GGGGCAGTGAGGACGCTGTGGACACTGCGGACGCTGTGGGGACAATGACG	R	N/A	N/A	0.7919186	0.8488771	-0.056958571			
cg07827008	12	72725380	133338719	133338769	Island	CAATGTGCTGGCGGGGGCCGGGGCTGGGGCCCGGGGAGGCCACCAGGGCG	R	TSS1500	ANKLE2	0.20752	0.2516786	-0.044158571	0.225095	0.2516786	-0.026584
cg07828140	6	24773365	168630047	168630097	Island	CGCCTGCGCCTGAGACTCACCGGTTCCCAAACCGCCTGCACTTGAGACTC	F	N/A	N/A	0.7370729	0.7800914	-0.043018571			
cg07829804	12	26635500	10325287	10325337	N/A	CGTAGCAGCAGAGAGCACTTTGAATGCAGAAAGAGCTAGTTTCAGTACTT	F	TSS1500	OLR1	0.7568629	0.8527286	-0.095865714	0.7959475	0.8527286	-0.056781
cg07830156	1	16645342	101174567	101174617	N/A	AAACTTAACCTCTAGTCCTAGTTTTCTTATTACCTAGCTGTGTGGCTTCG	R	N/A	N/A	0.6300171	0.7513129	-0.121295714			
cg07839742	6	16727424	84761960	84762010	N/A	CGGCAGCTCCACGGGCAGCTGCTCTCTGTATGGCTGCCACTCCTGAGAAC	R	5'UTR	MRAP2	0.5293614	0.6643486	-0.134987143			
cg07844072	19	54658360	1372272	1372322	S_Shore	CGCCTAGGACAGCCCCACCTCAGAGAACAGTCTGGCCCCGACGTCCACAG	F	Body;Body	MUM1	0.6798314	0.7242371	-0.044405714	0.6995463	0.7242371	-0.024691
cg07857278	19	28627337	45883112	45883162	N_Shelf	CGGGCCTGGGATGGGCCACCACACCACTGGATATTCCTGGGAGTCACTGC	R	3'UTR;3'UTR	PPP1R13L	0.8540557	0.9054286	-0.051372857			
cg07861456	16	46803400	75654252	75654302	N_Shelf	CGTGTGAGTTCTGAGAAACGGAATGTTCCCCGGTGTTCAGGTGTGATCAG	F	Body	ADAT1	0.6898214	0.7747929	-0.084971429	0.7225863	0.7747929	-0.052207
cg07871153	10	23638436	79602008	79602058	N/A	CGCTTGACTGTCCAGCACAGTAGAGCTGGCGGGAGGCAGCAGCGCAGCCG	F	Body	DLG5	0.7565557	0.8094714	-0.052915714	0.7702838	0.8094714	-0.039188
cg07877517	5	31724479	55488249	55488299	N/A	CGGCCAGGAGCCACTTCTGCGGGTGCCCAGAGAAGCAAAAGTCGCCGGTC	F	Body	ANKRD55	0.8512629	0.8833957	-0.032132857			
cg07877900	16	24648392	57576862	57576912	N/A	AAGAAACCTCTCTTCACTTGTCCCAGACCTCGCGGGGAAGCTAAGATTCG	F	1stExon;5'UTR	GPR114	0.6456686	0.7061643	-0.060495714			
cg07886142	5	74665485	126793022	126793072	N/A	CGGTCCTTTGGTGTCATTCACTGCTGCTGCTGCTGTTGCTGCTGCTACCA	R	3'UTR	MEGF10	0.5866129	0.6465757	-0.059962857	0.6188338	0.6465757	-0.027742
cg07887753	8	21600488	57817338	57817388	N/A	CGCTAGGCTTAGATAAAATACCAAGAAATACTACTGCTAGAGGCAAACGG	F	N/A	N/A	0.9062329	0.9303457	-0.024112857			
cg07887891	3	49687407	33429950	33430000	N/A	CGTGAGTTTGTCCCAGTGAAACAGGCTAAATAAATTTTGGCACCAGCAAA	R	3'UTR;3'UTR;3'UTR	UBP1	0.8899743	0.9401857	-0.050211429	0.9134375	0.9401857	-0.026748
cg07891862	8	58717452	141774605	141774655	N/A	CGGAGAGCAAACAGGGCTAACACAGAAAGCCCTTGTAAAAAACAGAACGA	F	Body;Body	PTK2	0.7705714	0.8972371	-0.126665714			
cg07898120	6	36702496	31854882	31854932	N_Shelf	GCTTGCTCTGCTGGTCGCTCTGGAAGTTGGGGTCCAGGTTGTCCACTGCG	R	Body;Body	EHMT2	0.88902	0.9157086	-0.026688571			
cg07903144	6	22602394	33358872	33358922	N_Shore	CTTACCTGGGTGCTGTTACTGGTACTGGGCTCAGGGCCTTTGGAGTCTCG	F	TSS1500	KIFC1	0.7541886	0.8502014	-0.096012857			
cg07909418	2	65703419	158481014	158481064	N_Shelf	CGCTGTATTTTGGAAGTGGTTATTTTCAGATGTGATTTTGGAGTAGTTTC	R	Body;Body;Body	ACVR1C	0.8856586	0.9130471	-0.027388571	0.881765	0.9130471	-0.031282
cg07915896	15	26618485	65129816	65129866	S_Shore	CGGTGCACAGAAGGGGAATTGACTTCAGGCTATGGTAAGGACTGTGGGTT	R	N/A	N/A	0.69421	0.7807757	-0.086565714			
cg07927310	10	10635466	50729975	50730025	N/A	TGACTTCTGGATATCTCATCCTCTTTATTCTCTCAGCTTGAGAGCCATCG	F	Body;5'UTR	ERCC6	0.88973	0.9223557	-0.032625714			
cg07929629	2	44631434	241523174	241523224	N_Shelf	CGCATCTGACCACTTCTCAGGTTCATGGGTGTTGAGGAGGAGCCCTGTGG	R	N/A	N/A	0.8950229	0.92752	-0.032497143			
cg07929642	16	40808374	89390685	89390735	N/A	CGGGGCTCCTGTATGTTCCACAGCCCAGTGACCAAGCATGTGTCTGAGGG	R	5'UTR	ANKRD11	0.7928586	0.8659129	-0.073054286			
cg07929956	16	40693318	70437897	70437947	N/A	CGAGTTGTGGTATCACTCTGTCACCCATCCTGGAGTGCCATGGCATGATC	R	5'UTR	ST3GAL2	0.82006	0.8889871	-0.068927143			
cg07935012	18	39718441	49866407	49866457	N_Shore	TGCGCATTGATACGCAGACCAGGCAAATGCAGCTCCTGGAAGCCTCCTCG	R	TSS200	DCC	0.1744429	0.1407243	0.033718571	0.1685063	0.1407243	0.027782
cg07944936	6	61808391	107950685	107950735	N/A	CGTGCCCATGTGGGTAACCTCATGGCATACTTTGGCCTTGACTTTGACGT	F	Body	SOBP	0.8366814	0.8940743	-0.057392857			
cg07945582	7	31740434	26206579	26206629	N/A	CGAGGCTGTTCACAAAGGGTATTTTCAGGGGCAAACCCTCTACCACATGA	F	Body	NFE2L3	0.7900157	0.8606914	-0.070675714			
cg07948480	2	66765452	120996546	120996596	N/A	CGGGCAGGGGACCTTGGACCAGGACCTCTGACTAAGCCTGAGTCAGGGCT	R	N/A	N/A	0.7518471	0.79968	-0.047832857			
cg07950786	1	49667353	110307572	110307622	N/A	CGCTGCCCTGGATGGCCTGGAGTCCATGCGTCAGATCCTAGGGAGGTGCC	F	TSS1500;TSS1500;TSS1500	EPS8L3	0.83366	0.8942543	-0.060594286	0.8553638	0.8942543	-0.038891
cg07950964	14	44788301	23813089	23813139	N_Shelf	GCATCCATCCCAACCATGAAGAATTTTCTGGCTGGGCCTGGTGGCTCACG	R	N/A	N/A	0.7133786	0.8054257	-0.092047143	0.7592525	0.8054257	-0.046173
cg07960624	8	62713349	119208486	119208536	N/A	CGCAAGCAAGCTTGGTGTTTTAGGGTGTCTCCAGATACATAAGCATTGTC	R	3'UTR	SAMD12	0.6828186	0.7695	-0.086681429			
cg07963147	3	52601443	141086820	141086870	N/A	GTGGTCAGTGTCTATTCTCCTCTGCCTCTGTGCTGTGGCCCTGGGCTTCG	F	5'UTR	ZBTB38	0.8923486	0.9230214	-0.030672857	0.9072725	0.9230214	-0.015749
cg07981328	1	10773404	21724633	21724683	N/A	CGCATGCGCCGCCGCTCATCAAAATGCTGCTCTATTTATGAAAAATCCCG	F	N/A	N/A	0.5232086	0.6055371	-0.082328571			
cg07992385	2	17684374	169058521	169058571	N/A	CGAGCCAGAGCTGGGGCTTCCTGAGAAGTTTGGGCCCCCCGCCCCCCGCTA	F	Body	STK39	0.6234329	0.6959886	-0.072555714	0.6282563	0.6959886	-0.067732
cg07998677	3	17657309	184302124	184302174	Island	CGACCTGGGGCGCACAGTCCAAGAGTTCCCCTGATCGTGTGGTTTCCAGG	R	N/A	N/A	0.5787471	0.6550871	-0.07634			
cg08000413	2	72691313	166930049	166930099	N/A	GACAGCTTCAACTTCTTCACCAGAGAATCTCTTGCGGCTATTGAAAGACG	F	1stExon;1stExon;1stExon	SCN1A	0.8848257	0.9257429	-0.040917143			
cg08003102	4	37702453	88451496	88451546	N/A	CGTGGCAGGGGTGTTCTATGCAGTTTATCATGTTAACTAACTTAAAACTC	R	TSS1500;TSS1500	SPARCL1	0.6920843	0.8159286	-0.123844286	0.7458088	0.8159286	-0.07012
cg08014499	11	30773478	2162545	2162595	S_Shore	CGCTAAGCCCGCAAGGCAGAAAGAACTCTGCCTTGCGTTCCCCAAAATTT	R	Body;Body;5'UTR;TSS1500;B	IGF2AS	0.6771114	0.7537257	-0.076614286	0.7078538	0.7537257	-0.045872
cg08019044	2	51615408	45355494	45355544	N/A	CGCTCTTCTGTTATATTTCTTGGTGGCTTCAGTAGTCATGATGACACTGC	F	N/A	N/A	0.8113057	0.8671714	-0.055865714	0.8358575	0.8671714	-0.031314
cg08034916	1	37721485	3184620	3184670	Island	CGGCCCTCAAACCATGACCCCCGAATCTAACAGGGTGCCCGTTTGCACAC	F	Body;Body	PRDM16	0.8711057	0.9033914	-0.032285714			
cg08034986	1	55699400	26860677	26860727	S_Shelf	GACTTTGGGTTATGGTCACATGTCTGCCACCTGCCTGCTGAGGGACCTCG	R	Body	RPS6KA1	0.7381243	0.8176614	-0.079537143	0.7673988	0.8176614	-0.050263
cg08035281	12	39681348	53900003	53900053	N/A	GTGCACCCTTTGCTCCCTGCTCTTTCTGCCTCTGGGCTCATGTATCTGCG	R	3'UTR;3'UTR;3'UTR	TARBP2	0.85553	0.8866214	-0.031091429	0.8694075	0.8866214	-0.017214
cg08035351	7	43606408	130005993	130006043	N/A	CGGGTGGAGGGATGGTCTACAGGTTACTCATTACACAGCCATTCAATTA	R	Body;Body;Body	CPA5	0.6995957	0.8015943	-0.101998571			
cg08039560	21	12679491	45575832	45575882	Island	CGAGCCGCCTTGGCTCTGGGCCAGCACTGACCCCGACTGCTGACGAATCG	R	N/A	N/A	0.7057286	0.7740071	-0.068278571	0.710945	0.7740071	-0.063062
cg08044713	16	27725461	87447756	87447806	Island	CGTGTGCCGGGCAGGTGGGTTACTCGTACACAGAGAGGGCCCGTGTGCCG	F	Body	ZCCHC14	0.8404943	0.8897086	-0.049214286			
cg08046044	14	72739303	54419614	54419664	N_Shore	GGCGCGTTCCCACTCTCTTGTCAAAACTCACAGAGGTCTCTCCGGAATCG	F	5'UTR;5'UTR;5'UTR	BMP4	0.1532714	0.0940126	0.059258857	0.13122	0.0940126	0.0372074
cg08060987	3	45795306	42744889	42744939	N/A	GGGTCACTTGGCAAGGCTTGTGGGTACTTGGAATGGCTGGTATCCTCTCG	R	TSS1500	HHATL	0.8541386	0.8999386	-0.0458			
cg08083427	16	33694365	88908622	88908672	Island	TGTGGACCTGCACGCCCAGTGGGTGTCCCAGGAGCCTGCGAAAGGAGGCG	F	Body	GALNS	0.8182471	0.8402157	-0.021968571			
cg08090385	1	72676406	1099583	1099633	Island	CGGGGGGTTAATTAAAGCATCGGCTCTTCACGCCCTAAGAATTTTGTTCA	R	N/A	N/A	0.8460629	0.7484	0.097662857			
cg08096367	15	46789473	95384471	95384521	N_Shelf	CTGCTGCTGAGCCCCAGCTTGCTTGTGTTATATCTTGTACCTGTGTTTCG	F	N/A	N/A	0.92631	0.9527671	-0.026457143			
cg08099115	3	67726460	55649447	55649497	N/A	ATTAGTAGATTCTTAGATATTTGATAGAGAAACTCCAAGCTCTCCAAACG	R	3'UTR	ERC2	0.5549957	0.6151586	-0.060162857	0.5800375	0.6151586	-0.035121
cg08099570	16	14623314	57937637	57937687	Island	CACAGCCAAGACAGGCCCCAGTACTCGGGACCTCAGAGACACAGAGGACG	R	Body	CNGB1	0.6421414	0.7345386	-0.092397143	0.6937988	0.7345386	-0.04074
cg08106319	6	56651494	37849427	37849477	N/A	TGGGCTGCAGGAGCTTTGCTGTTTTCAGATCTCCTTAGCCAAAAGTACG	R	Body	ZFAND3	0.7016443	0.7960614	-0.094417143			
cg08108641	9	49654470	135042030	135042080	S_Shelf	CGGAAAATTCAGAGCCAGCGTTTCTCAGACTGCTGATGGACAGATCAGAA	R	5'UTR	NTNG2				0.6493513	0.7565	-0.107149
cg08113187	16	10729498	87469329	87469379	N/A	CGGATGCGGGAGTCCACTCGCTTTAGAGTTCTTTAAGCTTAAAATAGCAC	F	Body	ZCCHC14	0.6460071	0.7486743	-0.102667143			
cg08113526	15	11665481	101845481	101845531	N/A	TGCCTGCCCTCTGTGGGCAGCTAGGCACCCTTACCCGGCCAGGAGGCACG	R	Body;Body	PCSK6	0.7860086	0.8383886	-0.05238	0.8143475	0.8383886	-0.024041
cg08117126	2	57740321	3691651	3691701	Island	CGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAGGAGA	F	Body;Body	COLEC11	0.88506	0.9189929	-0.033932857			
cg08120035	2	35725460	30872901	30872951	N/A	CGCACAGCCAGGCTGGAGAAAGTGGATTTCGAGGAATGATGCTCCCTTGC	F	N/A	N/A	0.8831657	0.9121429	-0.028977143	0.8994638	0.9121429	-0.012679
cg08125436	16	58712311	7855305	7855355	N/A	CGCAGCCTCCCTGGGCCTGCCAGACACCCGATTATTTAATTACGGTTTTC	F	N/A	N/A	0.3747129	0.3159786	0.058734286			
cg08128361	16	20744404	67336052	67336102	N/A	CGGGAGGCCACACCCACGGCCTCAGACACAGGAAAACAAAGTAATGTGGG	R	Body	KCTD19	0.8420443	0.9132786	-0.071234286			
cg08130275	3	66628359	171773170	171773220	N/A	CGGGTGTCAATAAGATGTAATTAAAGATACAGGACAATAATCACATAGCA	R	5'UTR;5'UTR	FNDC3B	0.4427471	0.6132371	-0.17049			
cg08131499	12	44785464	109090588	109090638	N/A	CGTGTGCTAATCTAAATCAACCCACCTCAGGACTGAGGACTTTCTATATT	F	Body	CORO1C	0.7291857	0.8253386	-0.096152857			
cg08135368	13	67656346	113614263	113614313	N/A	ATCATGGGAGATGCACAGTGGACACGCTGTGGCCTGTGCTGTCTGTGACG	R	N/A	N/A	0.7906871	0.8675571	-0.07687			
cg08137948	1	10808499	236686804	236686854	N_Shore	CAGACGAGGAAGCTGAGAAAACCCTGGCGTTGACCCCGTGGACCTGGGCG	R	5'UTR;1stExon;5'UTR;5'UTR;T	LGALS8	0.1566771	0.0937819	0.062895286			
cg08140558	6	38697430	29968797	29968847	N/A	CGACACATTTATTTATTGTTTGCCTCAGGGCTATTGTAACACCTGTGCCC	F	Body	NCRNA00171	0.8564086	0.8928271	-0.036418571			
cg08153408	10	54708386	12874786	12874836	N/A	CGGGGCCCTGGACACTACACAAAGAGCTAGCTGGAGAGTGAGACTCTCTC	R	TSS1500	LOC283070	0.8915129	0.9293757	-0.037862857			
cg08156531	17	27791427	42993050	42993100	S_Shelf	CGCCAACTCCTGCATGAGGCAGGTGGTACCTGGAGCCAGACCATGGGTCT	F	TSS200;TSS200	GFAP	0.8863014	0.90994	-0.023638571			
cg08162124	13	48618502	113428094	113428144	N_Shore	CGCGGGGCGTTGGCAGGTGCCACACAGAGGGCACCACGACTAAAAACACC	R	Body;Body	ATP11A	0.8887629	0.9348286	-0.046065714			
cg08163163	1	58713465	16415115	16415165	N/A	CGGCTGGGCCTGGCTCAGCCTCCAGGGCCTGCCGGTCACGTAGCCAAACT	R	N/A	N/A	0.5878229	0.6366486	-0.048825714			
cg08165487	1	36705434	59211967	59212017	N/A	CGAGGTACACTTAGGAAGTAGCAATCATAGCTGAATGAATGGAAAAAGAG	R	N/A	N/A	0.8509786	0.9074686	-0.05649			
cg08165969	1	17780495	2751152	2751202	N/A	CGTCCGGGTGACCTCAGGGCACTGGGAGTATGTATTTGGAGACCACCCAT	R	N/A	N/A	0.5761343	0.6306614	-0.054527143			
cg08170427	8	65681495	144410815	144410865	N/A	TTCCTGTTTTAGGCCTTTGCATGTGTAAAGCTGCCATGAACATTCCCACG	F	Body	TOP1MT	0.7014414	0.7719771	-0.070535714	0.7321275	0.7719771	-0.03985
cg08171142	6	59783420	53013942	53013992	N/A	CGTCTGCCTGGGGCCCAACCTGTAACATCACAAGAAGAAAAACATCTGTA	R	TSS1500	GCM1	0.8372443	0.8798786	-0.042634286			
cg08176812	4	31649323	187204810	187204860	N/A	GCCTGCGGGCAAGGTGCTTGCCTTTTCTTTCTAAGAGCAGTTCTCAAACG	R	Body	F11	0.8217786	0.8633414	-0.041562857			
cg08186671	17	17609327	1494960	1495010	S_Shelf	CCGCGGTGCCTGTCAGCTCATCTATGATGCTGGTGTCTCCTTCATCGTCG	F	Body	SLC43A2	0.8294971	0.9005671	-0.07107	0.8784488	0.9005671	-0.022118
cg08192143	17	41748310	728927	728977	N/A	CGGCCCTCCAAGCGGAGCTTCTTACGGCAGAGTCCATCTCTTTTGGCCCA	F	Body	NXN	0.9196971	0.9474586	-0.027761429			
cg08194384	6	25743381	30633353	30633403	N/A	CGCCGCTTATATTTGAGCTCCTGCCGCTCGTGCCGGCTCAGCTCCACGTC	F	Body;Body	DHX16	0.8639757	0.9103271	-0.046351429	0.8769313	0.9103271	-0.033396
cg08196090	15	20743364	41836511	41836561	Island	CACTGAACAAGCAAAGCCCAGAATGCTCCGAGATAAGACCGGGAGAGGCG	F	TSS200	RPAP1	0.1270857	0.0948873	0.032198429			
cg08203192	2	63804454	45880618	45880668	S_Shore	CTTTTTGTGTAGACCAAAGAACCCTGAAAACATATACCTCCAGAGGAACG	F	Body	PRKCE	0.8613643	0.9075386	-0.046174286	0.8789625	0.9075386	-0.028576
cg08211091	4	59647315	2061923	2061973	Island	TGTCCCCTCCCGGGCATCCTGGGTGGGGGCGGGTGCCAGGGCAGGTAGCG	R	Body	NAT8L	0.2045243	0.2851329	-0.080608571			
cg08212266	7	18615341	101513100	101513150	N/A	CGGGGAAAGCTGAAACCGGGGTTTACATTCCTGGGAAATGCCAGAGCCTG	R	Body;Body;Body	CUX1	0.8425757	0.8839986	-0.041422857			
cg08222943	8	25618326	100795832	100795882	N/A	TTCAGCTAAGTCATCAGTCAGCTAAAATCCTTCATTAGTCAGCTAAAGCG	F	Body;Body	VPS13B	0.8446257	0.90497	-0.060344286			
cg08229522	1	23715502	155741408	155741458	N/A	CGTCTGTGGTCACAGATACTTGGGAGGATGAAGTACGGGAATCGCTTGAG	R	Body;Body	GON4L	0.7707414	0.8260357	-0.055294286	0.7999525	0.8260357	-0.026083
cg08233864	13	48753305	113631110	113631160	N_Shelf	ACACCATGGCGGGAAGACGACAGAGCCGTGAGGAGACACACACCAAACCG	R	Body	MCF2L	0.74479	0.7834357	-0.038645714	0.7629075	0.7834357	-0.020528
cg08234178	7	17692431	150035390	150035440	N_Shelf	CGTGCAACACAAGGAGCTGAGAGGCAGCTGGGAGAGCAGCTTTATTATCA	F	N/A	N/A	0.6507586	0.6706814	-0.019922857			
cg08235551	22	48739334	49798682	49798732	Island	CGGCCCCTTTCAACACCCTGAAGGTTCTGCATGTGTCTTTGAAGAGCAGA	R	N/A	N/A	0.6420857	0.7235757	-0.08149			
cg08241330	16	65681509	8806663	8806713	N/A	CGCCGTTGCCGAGGCAACCAATGGGATCAAATCGCAGAGGAAATCTATAA	R	5'UTR;TSS200	ABAT	0.7031029	0.80426	-0.101157143			
cg08242636	16	16623470	67062389	67062439	N_Shore	AAATTTATTGGGCTCCCACTGTGTGCTAGACCCACATAAAGGTTCTCACG	R	TSS1500;TSS1500	CBFB	0.6907914	0.7643957	-0.073604286	0.71947	0.7643957	-0.044926
cg08246318	6	39710431	42894099	42894149	S_Shore	CGTGTGCGTCCCCTGCTTGCCCAGCGCTGGCAGGAAATCCAGACTTTCCC	F	N/A	N/A	0.6567129	0.7408129	-0.0841			
cg08250825	6	12673336	7540834	7540884	N_Shore	TGGTGTGACTGGGTCTGTATCCAAACCCGGTTCGGTTCCTGGAGCCAACG	R	TSS1500;TSS1500	DSP	0.64755	0.7444243	-0.096874286			
cg08268075	11	72714303	15132656	15132706	N_Shelf	CGGGCAACACGTGCTCTGCTCTACCCAATGCTTGGGCTCCTGTGCCAGGC	F	TSS1500	INSC	0.8243243	0.8739871	-0.049662857	0.8477825	0.8739871	-0.026205
cg08271443	16	71808428	4845348	4845398	N/A	TGGGCCCTCTCCCCTGGGCTGGGCGGCCTCTGCTGGCCCTGGGGAGGGCG	R	TSS200;Body;Body	LOC440335	0.8027486	0.8459371	-0.043188571	0.8227338	0.8459371	-0.023203
cg08276171	14	20741398	104850405	104850455	N/A	CAGGCTGGAGGGGTGGTTCGAGCAGCTGGTCCCAGCCGAAGCTGAAGCCG	F	N/A	N/A	0.4310357	0.5244657	-0.09343			
cg08282385	19	20684419	52800115	52800165	N_Shore	CGGCTTAAGATTAACTTTAATAGCAGGAATTTTCCTGGATCTAATCATTA	F	TSS1500	ZNF480	0.0881416	0.1250129	-0.036871286	0.0949151	0.1250129	-0.030098
cg08287344	11	16725506	134091648	134091698	N_Shelf	CGGCAAATGAAAATGAAAGGCCTTACACTCAACTAGTTCCATCCTTAGAA	F	Body	NCAPD3	0.8752886	0.9314829	-0.056194286	0.8992663	0.9314829	-0.032217
cg08288330	19	28760354	50315909	50315959	N_Shore	CGGTCCTCGCAGAGCTCAGCTGCACCTCCAGATTCTGCCCAAACATGTGG	F	Body	FUZ	0.8479643	0.9047143	-0.05675	0.8681225	0.9047143	-0.036592
cg08297393	2	39645383	100937505	100937555	N_Shore	CGCCTGTAGTGTGTCAGCTATGTGCATTTTCCTTCAGGATGAGCAAAAT	F	Body	LONRF2	0.67724	0.8085657	-0.131325714	0.739595	0.8085657	-0.068971
cg08298644	9	12746454	140359477	140359527	N_Shore	CGAGTCCTGCCTGCCTCACTGAGGAAGGATGGGCCCCAGGCCCACCCAGA	R	Body;Body	PNPLA7	0.7578229	0.8410357	-0.083212857			
cg08299521	5	72800510	179344619	179344669	N/A	TATGCTGGGGGAAATCCCTGCTAAGTCGGGACCCTGGCAGGAAGTGGCCG	F	N/A	N/A	0.6421943	0.7338229	-0.091628571			
cg08301299	16	14764334	2317849	2317899	Island	CGGCCCCGACCACTTCCGGGCCACGGCCTCGACACCTCCCACTCCGCCCG	F	5'UTR;TSS200	RNPS1	0.1715171	0.1091743	0.062342857			
cg08317133	11	18787489	63871228	63871278	N/A	CGGGCATGCCCTGTGGCCTGGCACCCAGCCCTGAGCAGGGTGGCCTCTGC	R	Body;TSS200	MACROD1	0.7947586	0.8236857	-0.028927143			
cg08322234	17	39602400	55663284	55663334	N/A	ACTGGCTCAGATCAGGACCCCAGCAGAAGGTGCCAGGACTGCAGCTCGCG	F	Body;Body	MSI2	0.8450229	0.8869914	-0.041968571			
cg08322244	17	43669347	8066669	8066719	S_Shore	CGCGCCCAGGTCCCAGCACCTAGCGACCCGCCTTCAGCACTTGGAATGGG	F	TSS1500	VAMP2	0.2890071	0.1837929	0.105214286	0.2588888	0.1837929	0.0750959
cg08328750	17	59809375	39675355	39675405	N/A	CGGTTTTAACACTTGGATTACAGGTTCATCTCTCCATGCCAGAAGAGAGC	F	TSS200	KRT15	0.7444014	0.8224857	-0.078084286	0.7772775	0.8224857	-0.045208
cg08331313	5	10787489	151066460	151066510	N/A	CGCGCTCTGCCTGCCGCCTGCCTGCCTGCCACTGAGGTATGTGTGACCCC	R	1stExon;5'UTR	SPARC	0.3065314	0.4031571	-0.096625714			
cg08339172	17	23739506	63692987	63693037	N/A	CGAGGCTTGAATTTACTATCCTACTTTGGAGAAAACAGATGATTCATTTG	F	Body;Body	CCDC46	0.6970843	0.8074843	-0.1104	0.7537113	0.8074843	-0.053773
cg08345575	16	23803486	4524283	4524333	Island	CGGGCCCAGCCGCCCCCTTCGACACATACTCGATGCATAGACAATGGGGG	R	5'UTR;TSS1500	NMRAL1	0.27534	0.1928986	0.082441429	0.3169825	0.1928986	0.1240839
cg08346210	4	69733417	130012176	130012226	N_Shelf	TGAGAAGTACCAAAACAAATGGTCTTGACCTGGGCTCCCAAATCCAAACG	R	Body	SCLT1	0.83837	0.8635657	-0.025195714	0.8228363	0.8635657	-0.040729
cg08346735	4	23681323	184829966	184830016	S_Shore	TCTTCAGGTTTCTCAGCAGTAACCTAACATTGAATCTGAACAGAAAACCG	F	Body	STOX2	0.88823	0.9261257	-0.037895714	0.903375	0.9261257	-0.022751
cg08352115	17	28709379	66356057	66356107	N/A	GGGGCACAGGGGCCCGAAACCATCCCAAAGTTCCAGGGAGCTGGGAGACG	F	Body	ARSG	0.7573114	0.8139157	-0.056604286	0.7791525	0.8139157	-0.034763
cg08352439	7	67636461	55637123	55637173	N_Shelf	TGCCGTCTGCGCACACAGGAACATGTTAGGAATTTGCATGCTCTACATCG	F	Body	VOPP1	0.67086	0.7430686	-0.072208571			
cg08355537	1	24666393	245026452	245026502	Island	CGCCGAGCCCCTGCGCTCCTTGCACAATACAGCGGCGAGGAGCCCGCCAAA	F	Body;Body	HNRNPU	0.0905109	0.059323	0.031187857			
cg08357012	13	15704458	99090919	99090969	N/A	CGCAGTCCGTTCTTGGGGTCTGCACGCTCGCAGTCAGCCCTCAGGGGCTA	F	Body	FARP1	0.8404743	0.8707857	-0.030311429			
cg08358233	10	70647479	48634114	48634164	N/A	CGAGCCAGCCTGGAAGTAGACCCTCCAACCCAACGTATGCCACATAAGGC	R	N/A	N/A	0.5984829	0.6587129	-0.06023	0.6183425	0.6587129	-0.04037
cg08365301	10	58771375	5523060	5523110	N/A	CGGCTGGAGGGGCTCTCAGAACATCTGGTGCACGGCTCCCAACTCTCTTC	F	N/A	N/A	0.8382986	0.8864914	-0.048192857	0.8625275	0.8864914	-0.023964
cg08368055	16	60648429	72129315	72129365	S_Shore	CGGTAGCCTTCTGCCCCATCTCTGTGCTGCTGTACCTGTTGTTTAAAGAG	F	5'UTR;TSS1500	DHX38	0.6148129	0.6709871	-0.056174286			
cg08373769	7	27797401	158064946	158064996	S_Shelf	GGTCCAAATGGAAAAACAGCCCCCCGGGACGTCTTGTCTTCGGAGAGCCG	R	Body;Body;Body	PTPRN2	0.9031957	0.9286971	-0.025501429			
cg08373904	11	40715366	1543275	1543325	N/A	CGGGGCCGTTTGCACGTCCTTCTTCATGAGGCATCTGTTCAAGCCTCTGC	F	Body	HCCA2	0.8000929	0.8455129	-0.04542	0.8155013	0.8455129	-0.030012
cg08386537	2	54651395	171569381	171569431	N_Shore	ATCAGTGGGCCAACAGGGTCAAAGTTAGTGGCTTGGTGGTTGAAAGCTCG	F	Body	LOC440925	0.6518071	0.7539986	-0.102191429	0.7181963	0.7539986	-0.035802
cg08396863	2	44632322	220117599	220117649	N_Shore	CGCCCCAGTACCCTCAAACCTTATTGCTGGCCCCTGCTGTCTGAGCTTAC	R	TSS1500;Body	TUBA4B	0.5813314	0.6863643	-0.105032857			
cg08401916	7	34680362	156296983	156297033	N/A	TGGGAAGGCACTGGAGGCGAGGGCTCCGGTCTGCAGCTGTGAAAAACACG	R	N/A	N/A	0.8732943	0.9115371	-0.038242857	0.8834613	0.9115371	-0.028076
cg08408971	5	49801382	145298422	145298472	N/A	TACCTTGGCATCCCTGTGATACAATGGCCTCCATTAAAACACTACCTTCG	R	N/A	N/A	0.8251714	0.8749429	-0.049771429	0.8490825	0.8749429	-0.02586
cg08409983	11	65727506	64112480	64112530	Island	CGGCCCGCTGCTGCCAGCGCCTCCACCAGCGCCTCCCGTTCCTGGGACGC	R	Body	CCDC88B	0.8913714	0.9253986	-0.034027143	0.9060675	0.9253986	-0.019331
cg08416522	21	16654433	30451568	30451618	N/A	CGTGTTCCAGGTGGATCACAAGGCATTTGGCCAAGACTCAGGCCACAGGA	F	TSS1500	C21orf7	0.52803	0.6038157	-0.075785714			
cg08419450	10	65690351	90013989	90014039	N/A	AGTCATAGGTAGAGGCAGGGTCACAGTTACACCATGGCCCTGGGGGCTCG	F	N/A	N/A	0.7955886	0.8821643	-0.086575714	0.8382088	0.8821643	-0.043956
cg08421934	6	22673355	33942413	33942463	N_Shore	TCTTGGACAAAAGGCAGTCTTCATGGGCAGAGTCTCCAGCCCACCTGCCG	R	N/A	N/A	0.5892314	0.67838	-0.089148571			
cg08428985	6	56726301	169566620	169566670	N_Shore	CGGTAAAATCCTGTGGTGTGTGCAATGCAGGGATCTTCTCAAAGTCACTG	R	N/A	N/A				0.8638538	0.8922429	-0.028389
cg08429815	2	70621406	102163204	102163254	N/A	CGGCTCTAGTCAAGCACTTAGGGATGAATTAGTTATACCAAGATAGTTAT	R	N/A	N/A	0.9004186	0.9431271	-0.042708571	0.9207538	0.9431271	-0.022373
cg08429871	13	15686414	107078237	107078287	N/A	GGGCAACGGACTTGCAGACAACTCGAATCTTAGAGAGCTTGGAGGCCTCG	F	N/A	N/A	0.8657229	0.9013357	-0.035612857	0.8670863	0.9013357	-0.034249
cg08437403	11	12744467	1669832	1669882	N/A	CGGGGAGAAAGAGGTGGTCCCTCCTGCCTGCTGCTGATGCCCACGGCCTC	F	Body	HCCA2	0.7491186	0.7752857	-0.026167143			
cg08442823	11	52726384	45951803	45951853	N/A	AGGTGGTTACACACAGCTGTTTCCGTGAGGGTGACCGTGTCTGCAGCACG	F	3'UTR;3'UTR	PHF21A	0.6994414	0.7890243	-0.089582857			
cg08445323	16	17719317	4015030	4015080	Island	CGGGGGTCTCAGAGCCGCCTCTCACCCCCGACCCTCCACCCAGGGGTCTC	R	3'UTR	ADCY9	0.8251314	0.8730229	-0.047891429			
cg08446121	2	53635345	95522487	95522537	N_Shore	CGCTTTTAAAACATGGTTTATATACATTATAGGAGGTGCCTAATGAGAGA	R	Body	ANKRD20B	0.5159871	0.6899529	-0.173965714			
cg08450017	3	19666408	45984838	45984888	N/A	CGCGTGGGTCAGAGATGGATGGGTGACTGATACCCCACACTCCCTTCATT	R	TSS200;Body	CXCR6	0.6974929	0.7891871	-0.091694286	0.7243375	0.7891871	-0.06485
cg08455184	19	53610334	12998927	12998977	S_Shore	CCTGCCTCAGTCTTCCAATGAGTGACTATGAGTTATGTGTCTGTAATACG	F	TSS1500	KLF1	0.8934057	0.93433	-0.040924286			
cg08456051	4	71669340	190225902	190225952	N_Shelf	CGAGGCATGCTGGTCTCTAACTTGCTCAGAAATTAAATACTGTAAGTTAT	R	N/A	N/A	0.6362686	0.7142514	-0.077982857			
cg08461352	8	39640312	58910391	58910441	S_Shelf	CGAGGATTTTGCTGGTCCCAGAGCCAGCCCTTAGAGATAACTGTTATTAT	R	5'UTR	FAM110B	0.4441157	0.5532657	-0.10915			
cg08463231	15	59627373	78103228	78103278	N/A	GCAGAGGGCACTCATTCTGCCACAGCCTCCCAGGGAGGAGTCCAGGCTCG	R	N/A	N/A	0.7505914	0.8064214	-0.05583			
cg08466517	4	15694349	122138632	122138682	N/A	CGGCTTGTGACAGCTGTTTGAAAATCATCTGTTACCACCATGGTAGCCAG	F	TSS1500	TNIP3	0.8557229	0.9032129	-0.04749	0.869855	0.9032129	-0.033358
cg08468011	6	51622441	103553855	103553905	N/A	CGCCCCCATATTGAGAGGTCTTTATTCTGCATGGAAAGCTTAGTTTGTCA	R	N/A	N/A	0.6606714	0.7432	-0.082528571			
cg08470053	19	66741386	53605221	53605271	N_Shore	TCAAATTGTCATATCCAATCTCAACTCACCTCTCACCTGGCCCCAGGGCG	R	5'UTR;5'UTR;5'UTR	ZNF160	0.7816129	0.8339314	-0.052318571			
cg08480068	16	17773373	29674959	29675009	N_Shore	TGGGCAGCCGGAGAAGCAGAACACGCGGGAGTTGCCGGAGGACCTGGCCG	F	5'UTR;5'UTR	SPN	0.6945757	0.7918114	-0.097235714	0.7392388	0.7918114	-0.052573
cg08482359	7	74801381	622834	622884	N/A	GTGTGTAGACTCAACGGCCCTGAAATGCGCTTCCGGGAAAGGTCAAAACG	R	Body;Body;Body;Body;Body;B	PRKAR1B	0.8657514	0.90625	-0.040498571			

cg08488569	4	36631431	1749241	1749291	N/A		GTTTCCTTGAGCCCCCCAAAGGCGACTGCGTGGATGTGCAGGGGGTCCG	F	N/A	N/A					0.73666	0.8360057	-0.099396
cg08500171	6	57676314	31590674	31590724	S_Shore		CGGGTTTCTGGATCTCTAAGGACTTGCCCTTATACGTATCAAACAGGTTG	R	Body;TSS200	BAT2		0.8448229	0.9012029	-0.05638			
cg08503285	4	10759359	846652	846702	S_Shelf		CATCCCCCAGGGAGGGCGTCTCTCATAACCTCAGAAGAGCACTGAGCCCG	R	Body	GAK		0.83217	0.8624286	-0.030258571			
cg08504310	19	57706471	36214022	36214072	N_Shore		GGAGAACCAGAGCCCGAGGTCTGGAGGGAGCCTGGGCCACACACCCCG	R	Body	MLL4		0.8650057	0.9006786	-0.035672857			
cg08506127	2	58769448	87018958	87019008	S_Shore		CGGTCCCTCGGCCTGGAATGCTGGTCTGTTTAAGCCCCTGGAGGCAGCTCC	F	TSS200:5'UTR:TSS200:TSS3	CD8A		0.7302971	0.7857957	-0.055498571	0.76057	0.7857957	-0.025226
cg08508763	3	34614318	42201380	42201430	N/A		CATCTGGGGGTGTTGGGCAGTGCTTCAGCAGGACAATTCCTCCGCCAGCG	R	TSS1500;Body	TRAK1		0.5136143	0.6290271	-0.115412857			
cg08515811	17	3664367	7792149	7792139	N_Shore		CACCAGTTGTTTCTCCATGTCCTCGTCCCGGGGTGAGCTGACGAAGATCG	R	Body	TBC1D16		0.8964814	0.93129	-0.033480571			
cg08534055	16	72702451	9190392	9190442	S_Shore		CGAGTCCAAAATGGCCACACTGAAGTGAGAGATATAAAGAGGGCTTGGCA	R	Body	C16orf72		0.8104286	0.8645771	-0.054148571			
cg08535411	7	40620337	151826219	151826269	Island		CAGGTTTACTGCCTTGACCTGGGCCCCAACCAGGCCTGGAACACTTGCCG	F	N/A	N/A		0.81574	0.8702329	-0.054492857	0.8425075	0.8702329	-0.027725
cg08537804	11	23690509	117652230	117652280	S_Shore		GTCTCAAAACCATGCTCTGAGATGAATGGCTACAGGAGCTGGGATGCTGG	R	Body	DSCAML1		0.8544786	0.8934371	-0.038958571			
cg08542396	1	74779355	145001340	145001390	N/A		CGCTGGGTCTTCATGGTTCAAGAGCTATTGCTCTTTTTCACAGTTCCCAGCGCTA	R	Body	PDE4DIP		0.7415914	0.8219643	-0.080372857	0.7654025	0.8219643	-0.056562
cg08560465	6	58746446	151055012	151055062	N/A		CGCTGCTGGAAAACGGCCTGGCAGGAATCAGCTCCAGTTTATGGCCCCT	R	Body	PLEKHG1		0.88512	0.9265829	-0.041462857			
cg08568767	10	25618308	133606037	133606087	N/A		CGTGAGGTTTTTGTTTAGCCATGAAGAATGTCTGCTTCTGCAGATGCCCA	F	N/A	N/A		0.5069543	0.6279786	-0.121024286	0.5616713	0.6279786	-0.066307
cg08571905	16	35697474	66669578	66669628	N/A		TGCAAGACTCAAAGGGAGTCAGTCAGGGAGATCTCACGCATGAAGCACAGTCG	F	Body;Body	CMTM4		0.8767729	0.9252957	-0.048522857			
cg08572757	12	23621465	125582465	125582515	S_Shelf		CGGTTCCTGCTGCTGCCTCCTGGGCCATCTAGGCACGTCCCCGCCGCCGC	F	Body	AACS		0.6987414	0.7663643	-0.067622857	0.7368275	0.7663643	-0.029537
cg08577341	5	47705451	167001123	167001173	N/A		CGGCTTCTGCTGCGGATGCCTTTCTCAATTACAAAACGGTGAAAACAGAG	R	Body	ODZ2		0.45612	0.4888129	-0.032692857			
cg08583240	2	51774312	102460597	102460647	N/A		GCTTTTTCCAACAGTTCCATTGTGAACGTGCCTGGTGAGTCTACTCTTCG	R	Body;Body;Body	MAP4K4		0.9317043	0.9537286	-0.022024286			
cg08586541	19	62621315	51198938	51198938	Island		GAGGCAGGCACAACATCACACAATGATGCCTCCGCGCGCGCGTGCACGGACG	R	Body	SHANK1		0.0700243	0.0423124	0.027711857			
cg08597802	1	10786463	19657280	19657330	N/A		CCTGGGGCACACCCAGCAGCAGCCCAGCAGCAGGTGATGGGGTTTGGTCG	R	N/A	N/A		0.8854443	0.9201957	-0.034751429			
cg08611402	4	70724304	80933006	80933056	N/A		AGATGCAGATGACACAGTCCCTGAATACACTAATCCCAGACATCAGTCG	F	Body;Body	ANTXR2		0.6647043	0.7505157	-0.085811429			
cg08612871	1	50696481	35220334	35220384	N/A		CGTGGATTAACCCAGCCTTAGGGGTGAAGTGCTTAGAACAGTGCCTGACA	R	TSS1500	GJB6		0.83896	0.8899657	-0.051005714	0.868265	0.8899657	-0.021701
cg08619893	12	12791379	104319429	104319479	S_Shelf		TGTGATTGTAAATATAGACCCACTTCATTAGGCTCAAGTAGGGCGTCTCG	R	Body	LOC253724		0.6242986	0.6801471	-0.055848571	0.643805	0.6801471	-0.036342
cg08620470	10	53726398	70288376	70288426	S_Shore		GAGGGCGGATCCGATGAGGTCAGCAGTTCGGACCAGCCTTGACCAATACG	F	TSS1500	SLC25A16		0.8747757	0.9195186	-0.044742857			
cg08621957	2	31758403	219181531	219181581	N/A		CGGAACTGCCAAGCACTGGTATCAGGGACTTGGGATGGCCTGAACCATCG	R	Body	PNKD		0.71335	0.7942343	-0.080884286			
cg08622666	6	73685346	13695743	13695793	N/A		CGCGGCGGCAGATGTGATCCTCTCTCTCTTCATTAGATTGGGGGTAT	F	Body	RANBP9		0.7325471	0.8271029	-0.094555714			
cg08627397	16	70621374	89984028	89984078	N_Shore		CGGTTGTAACAAGTATTTACTGTACCAGTAAATATAAAAATATTAATGT	F	TSS1500	MC1R		0.3517157	0.5150729	-0.163357143			
cg08629379	10	61684328	118350470	118350520	N/A		AAGGTGGCTTACCCTGTCTAATGTTCCAGTATGTTCCCTCCCACCGGATCG	F	TSS200	PNLIPRP1		0.6033886	0.6565386	-0.05315	0.591605	0.6565386	-0.064934
cg08637514	7	44786372	150212707	150212757	N/A		CGCGTGGCTTGGCCACATTTAGAATCTGTTCACCTCTGTGTTGAAATGCTT	F	5'UTR	GMAP7		0.6668129	0.74921	-0.082397143			
cg08638960	6	67714361	168641710	168641760	N/A		CTCACATTCATTCCCCTGCTTTAGCTGACCTTGTTTCCATTCTTTGGACG	F	N/A	N/A		0.7954871	0.8630971	-0.06761	0.826825	0.8630971	-0.036272
cg08644106	19	27634385	4102601	4102651	Island		CCACCTTGTGGGTGGGTGTTCAGACCCAAAGGCAGAACTGTCAGAAGACG	F	Body	MAP2K2		0.8032586	0.8433886	-0.04013	0.8124363	0.8433886	-0.030952
cg08652722	6	55647457	30542193	30542243	S_Shelf		CATCTTCTCTTTCCTTTAAATCTCTTTTGTGGCCAGGCACACTGGCTCACG	F	Body;Body	ATXN7		0.7629186	0.8031571	-0.040238571			
cg08657449	8	26761452	105351661	105351711	N/A		CGTAGGAAGGCTGTGGGTCCTGTTCACCCCAGAACNGGTCAATTTGGT	R	TSS1500	NTSF4		0.8671243	0.91071	-0.043585714			
cg08657587	13	53787423	112572321	112572371	N_Shelf		CATGTGCTGGGGGGACCAGGGGGCTGCACTACTCCCACGCGGAGGTAGCG	R	N/A	N/A		0.8854457	0.92521	-0.039764286	0.892765	0.92521	-0.032445
cg08675117	19	65772402	5993794	5993844	N_Shore		CGGGACAAACAAATCCTTGGGCTTGTCGAAGCCCTGAACTTGAGACACCA	R	3'UTR;3'UTR	RFX2		0.69545	0.7822086	-0.086758571			
cg08675521	11	29691309	18716666	18716716	N_Shelf		GAGCAACAGAGAGCCCTGGTCTGGAAATATGTGGTGGTTTCTTCTTCTTG	F	N/A	N/A		0.75172	0.8343914	-0.082671429			
cg08678851	5	52806359	91710051	91711001	N/A		CGGGGCTGCAAGTGGGCACTTTCCAGGCCAGCTAGAATTCTGGGTGGGCTCC	R	N/A	N/A		0.8575814	0.8873186	-0.029737143	0.8456813	0.8873186	-0.041637
cg08683071	11	71698391	2690561	2690611	N/A		CAAAACTATAAAGGATACCCATTCTCCCATGCCCATCTAGAGGCTGCTGCG	F	Body;Body;Body	KCNQ1		0.8807129	0.91008	-0.029367143			
cg08691235	2	68606343	179395935	179395985	N/A		ACCAGAAAGATCAAGACGACTTTGGCAGCAAGAATTCTAACAAAGCCAGG	F	Body;Body;Body;Body;Body	TTN		0.8947514	0.9240029	-0.029251429			
cg08691332	2	35732424	72142653	72142703	N/A		CGGGCCTTTTAAATATACACACTTCATTAGGCTCAAAGTAGGGCTTCTTGA	F	Body	CCDC27		0.8301886	0.8853686	-0.05518			
cg08692210	3	61755326	52188851	52188901	Island		CCCAACATGAGATTGACCAATTGCATTCCAGCCTGGGCAACAAGAGGGCG	R	TSS200;TSS200;TSS200	WDR51A		0.1615857	0.21301	-0.051424286	0.1751863	0.21301	-0.037824
cg08693997	15	73673366	95713013	95713063	N/A		CGCTGACTGGGTGTGTGCGCTGTCCATGAATGAAACTTCTAGTCATCGAGAG	R	N/A	N/A		0.8166529	0.8779	-0.061247143	0.83906	0.8779	-0.03884
cg08695703	17	70647370	73762337	73762387	N_Shore		CGGCCCCAAGTGCTGGCTTGATAACCTGTGCACACCTGCCTGCCCACCCTACATG	F	TSS1500	GALK1		0.9007357	0.9332086	-0.032472857	0.909075	0.9332086	-0.024134
cg08702740	7	56784486	157981275	157981325	Island		CGCTCGCCCCCTGATGGGGAAGCCCGCCACGCTCGCCCCCTGATGGGGAA	F	Body;Body;Body	PTPRN2		0.8562857	0.8932414	-0.036955714			
cg08703231	16	26722336	8738304	8738354	N/A		CGGGCTTTTACTGAGCGCCTGTCTCATGCTGAGTGTGTGAGTGCAATTCC	R	Body	C16orf68		0.7510314	0.8259	-0.074868571	0.7908588	0.8259	-0.035041
cg08725366	7	64717485	18329916	18329966	N/A		CGACTTTATAAAGACTGCATAACTTGGGGGCAAAGGACAGTTACTATAGCT	R	N/A	N/A					0.416355	0.3073157	0.1090393
cg08734623	11	55608471	65393258	65393348	N/A		GCTGATGGGAGCCAAGGGACCACAGAGCCTGGCACCACGCCGCCACGCCG	F	Body	PCNXL3		0.7046743	0.7485886	-0.043914286			
cg08751025	2	23748354	62591489	62591539	N/A		CCTGGAGAGCATGTTAGAAATGCAAACTCTGCCGGGCGTGGTGGCTCACG	F	N/A	N/A		0.5976529	0.6422514	-0.044598571			
cg08751876	5	66702311	34452378	34452428	N/A		CGGTGGTGGAGATGTTACAAACAGGGTCTCTGCTAAGCATATGCTGTATG	R	N/A	N/A		0.6204329	0.6891971	-0.068764286	0.651055	0.6891971	-0.038142
cg08754149	10	25678379	78204159	78204209	N/A		CGAGCGCTTTGGATTTCATGGTTCACGTGAGAATAATGTGCTGGTTCCGG	F	Body	C10orf11		0.7887857	0.87293	-0.084144286	0.84309	0.87293	-0.02984
cg08757100	6	49684493	33177744	33177794	S_Shore		CGGCCAGACCCCAACTTTGATGCCCTGATCTCTAAGATCTATCCTAGCCG	F	Body	RING1		0.9192943	0.9465757	-0.027281429			
cg08757624	7	19763353	132677298	132677348	N/A		CGGCTACTGAGCCCAGAAATGTGGCTATGCCAATCCAAGACTTGCTTAAT	F	Body	CHCHD3		0.7068571	0.79573	-0.088872857			
cg08761324	10	40771423	121357524	121357574	N/A		GGCTTGCTGCTGCTTTCTGTTCCAGTCAGATAATAATGGTGTTTCCCCG	R	TSS1500;TSS1500	TAL1		0.9298314	0.9572571	-0.027425714			
cg08762734	14	11658420	104584573	104584623	Island		GCTGGAGGTGGGGACAGATTCGACCCTTTGCTGAGTCCCTCCCAGGGCCG	F	N/A	N/A		0.7251471	0.76948	-0.044332857			
cg08767936	3	67690481	195600608	195600658	N_Shore		AGGAGGGTGCGACGCCTGGGCACCCAGACCCACAGCCTTGAAGGTGACG	R	Body;Body	TNK2		0.8820514	0.9064143	-0.024362857			
cg08771171	5	64710327	138211084	138211134	N/A		CGTGTCTTTTGTTTGGGTTTTCCAGAAGCTTTACTGTTATAAAGCACCAT	F	Body;TSS200	CTNNA1		0.66446	0.7502429	-0.085782857	0.72628	0.7502429	-0.023963
cg08772222	5	15697350	176828872	176828922	N_Shore		CGCTCCCAAGTGATCTAATTGTATGGTCTGAGACTACTTGCTCTGTAAA	F	TSS1500	PFN3		0.6740614	0.7674829	-0.093421429			
cg08772567	10	71605327	79033545	79033595	N/A		CTGTGCTGGGAATGGTGCCCAGCATATAGTAAGAATCAAACAAATACACG	F	Body;Body;Body;Body	KCNMA1		0.5951029	0.7138114	-0.118708571	0.6637238	0.7138114	-0.05608
cg08772752	3	19710377	48632672	48632722	Island		CGCCCCTCCAGCCCGAGTCCTGGTCTTGCCTGGCGTCCGCGCCGCTCCCG	F	TSS200	COL7A1		0.1400386	0.0991694	0.040869143			
cg08777211	7	54750305	130060960	130061010	N/A		TCACTGCAAGTGCACTATTGTATGGTTTGCACAACACTGTCTATAGTCG	F	Body	TSGA14		0.9026771	0.9402714	-0.037594286			
cg08781549	2	51674431	239970152	239970202	N/A		GGATTAAATTACAGAGGTGAATGGTGGCCACGGCCAGTGCGCAGCTCACG	R	3'UTR	HDAC4		0.9202529	0.9422057	-0.021952857			
cg08782420	5	15665500	141508150	141508200	N/A		CGGGGAGAGGCAATCACCTTCAAAAAGAGTAAGCACTTAGTGCCTGCCAT	R	Body	NDFIP1		0.8626043	0.9019643	-0.03936			
cg08784238	15	34737482	28511044	28511094	N/A		CGGGAGCACTTACAGTGCGGCCATCACTGCCCGAGGGGAGCTGTACACCT	R	Body	HERC2		0.8912714	0.9173186	-0.026047143			
cg08788712	17	54613446	55604163	55604213	N/A		CGCTTTTCTTCCTCTCTCAGCTCCTTCTTCTTAATGTGTTGCTGTAACCG	R	Body;Body	ATP5G2		0.8512443	0.9305371	-0.079292857	0.89588	0.9305371	-0.034657
cg08798307	7	15765495	141190187	141190237	N/A		CGTGCACATGGGAGAATGCTAGATGAACATAAAGGCAAAGGCCAGGTGA	F	N/A	N/A		0.7482371	0.8063943	-0.058157143	0.7738888	0.8063943	-0.032506
cg08799967	13	46626409	99383002	99383052	N/A		TGGATCTGAGCACTGTGCTCTGTGACTGATAAACGGGGCCTTAGGAAACG	F	Body	SLC15A1		0.8302543	0.9045929	-0.074338571			
cg08800670	6	66644473	436784	436734	N/A		CAGTTTCATCTCTGGTCTGATCAACTCACCTTGGGTCGGAAAACCG	N/A	Body	TAS1R1		0.6594957	0.7342214	-0.074725714			
cg08805208	12	39737436	131589169	131589219	N/A		CGGTGCCCCGAGGTGCCCTACAGAACACTGAGGCTCCCTCAGCCACAGTC	R	Body	GPR133		0.7750086	0.8136671	-0.038658571			
cg08806779	16	39757315	86965605	86965655	S_Shore		CGGCTTCATTTCAGAGGTGTGCCAAATGCGCTCAGAGAGGCTCGGTGACC	R	N/A	N/A		0.57553	0.6975243	-0.121994286	0.6420638	0.6975243	-0.055461
cg08808367	1	55653426	178063320	178063370	Island		GGGCTCAGGTGTGTGTGGGTCCCTCCCGGGAGAGGACGCAGAAGAACCCG	F	5'UTR;TSS200;1stExon	RASAL2		0.1917014	0.2547629	-0.063061429	0.2023063	0.2547629	-0.052457
cg08809251	11	40716502	129722544	129722504	N/A		CCGGTGCTCTCCATCACACAGCCCAATGATCCCCTGTCTCCTTGTTCTG	R	Body	TMEM45B		0.8605843	0.9301529	-0.063568571	0.89257	0.9301529	-0.037583
cg08816228	19	17620347	1379219	1379269	S_Shore		GGTGCTTCCCTCAGTAATGGGGGGTCGTTGGTGGTGCTCTGGGTTGTCAGCCG	R	N/A	N/A		0.7705871	0.8392857	-0.068698571			
cg08822136	3	15807423	127345113	127345163	N_Shelf		ATAACACGTTGGTCTCTCTTTTAATTCTAGCCACCCACCTTAGTGAGACG	R	N/A	N/A		0.8153914	0.8729943	-0.057602857			
cg08835403	17	42729442	4436630	4436680	N_Shelf		CCCCCAAAGCTGGCCTAAAGCAGGTGATGTGCCCCAAGGTGAGGCCTTGG	R	Body	SPNS2		0.8956514	0.92546	-0.029808571			
cg08850729	1	59734422	60036715	60036765	N/A		CGGCTGTCATGACAAGTGCTTTTTGAATGTATATGGATTAAAATTACTT	R	Body;Body	FGGY		0.9147443	0.9491714	-0.034427143			
cg08861091	19	25657397	51891339	51891389	N/A		TACACAATGGTCCCACTACCCAGCAGCTTCCAGCAGGCAGAAATGCAGCG	R	TSS200;TSS200	LIM2		0.7362571	0.7881886	-0.051931429	0.7519775	0.7881886	-0.036211
cg08866695	12	30707379	109596237	109596287	S_Shelf		CCCGCCTTAACCTGGCCAGGGCAGTGGTGGCTGTGTGCAGTCATCCTCC	F	Body	ACACB		0.4895614	0.6216857	-0.132094286			
cg08885409	17	67727390	55969571	55969621	N/A		CTGGGCTGCCTTGGCCTCAGACCCCTTGTCTGTGAAGTGAGATAATAACG	F	5'UTR	CUEDC1		0.7632471	0.8292657	-0.066018571			
cg08887327	2	39719421	238582364	238582414	N/A		GAGCAGGCCTCAGCATGCTCTCCTCAGAATGATCTGAATTGTCCCCAAACG	F	Body	LRRFIP1		0.4606171	0.5561114	-0.095494286			
cg08899094	15	49794312	101860935	101860985	N/A		CGGCGGCTCGGCTGCTCTCTTGCTGCTTTAACATGACTGCAGTGATTAGA	F	Body;Body;Body;Body	PCSK6		0.5788629	0.6385214	-0.059658571	0.5994013	0.6385214	-0.03912
cg08894891	19	57635490	19040964	19040914	Island		CACCAGCTCGGCGCGAGCCTGGCGGATCGCCGCGCGCGCGCGCGCGCGCG	F	Body;Body;Body;Body;Body	SLMAR3		0.7429557	0.7959829	-0.053037143			
cg08898866	17	31694463	13941263	13941313	N/A		TCAGTGAATCCTCATGTACTGATCAACCAGCTTCAATAATGATCAACTCG	R	N/A	N/A		0.8261114	0.8975543	-0.071442857			
cg08901662	2	44640348	131595321	131595371	S_Shore		CGGAGCTCAGCACCACCAGCGTCGCAACCGCCCTCCCGGTCGCTCACCT	R	N/A	N/A		0.1532941	0.0970041	0.05629			
cg08905415	17	58605368	78831519	78831568	Island		TCCTGTTTTCCATATGTTCTGAAGATATCCCCCTGCCAGCTCGGTCCCG	R	Body;Body	RPTOR		0.9093957	0.9376429	-0.028247143			
cg08906309	17	45651328	8263420	8263470	N/A		CGCCAAAGTTCCAGGTGTGGAAAAGTTATTCTGAGCAAGGAGCTAGTCAA	F	Body	LOC100128288		0.8229186	0.8657871	-0.042868571			
cg08907118	16	43639412	27482516	27482566	N/A		CGGAGCAGTTAGGAATGTTCTCAGGGACTCTCTGCGTGTGGTCAGGAGGCT	F	Body	GTF3C1		0.6849886	0.7153671	-0.030378571			
cg08908843	15	17658492	49283846	49283896	N/A		CGGCTAGCAGTGGAGCCACCATCTTAGATTATAGCTAGCTAGCCTCATTT	R	3'UTR	SECISBP2L		0.9030957	0.9408543	-0.03775857			
cg08908606	22	67690479	43548696	43548746	S_Shore		CCGCGAACTGGCCTTGCCAAAGAAGCCTTTCCGAGTCACGCCAGCAGCT	F	5'UTR;5'UTR	TSPO		0.2080283	0.4059957	-0.197787429	0.3068063	0.4059957	-0.099189
cg08891246	3	71676306	142608228	142608278	Island		CTGGGAAAAACATTCCCCAAAGCAAAACCAGAAGCCCTCCCTGAGAATCG	F	TSS1500	PCOLCE2		0.0919267	0.1305329	-0.038606143	0.1044895	0.1305329	-0.026043
cg08891922	5	14719420	132161548	132161598	Island		GGCCTGCCTGTTCAGTGGTCCCGGGGTCCCGGGGACCTCTGTTGGCTGCG	R	1stExon	SHROOM1		0.5762543	0.6862471	-0.109992857	0.6295825	0.6862471	-0.056665
cg08917117	10	12787487	115059021	115059071	N/A		CTGTGGACTTGGGGAGCAGGATGAGTCACCTTGGTGCGCAAGGAGTGCG	N/A	N/A	N/A		0.8678888	0.9070586	-0.03917			
cg08929713	8	43719460	143436137	143436187	N/A		CGTGTTTCCTCCAGCTCAGTGTGGAGGCTGCTGGCCCTGCCATCTGTAAG	R	5'UTR	TSNARE1		0.78506	0.8345986	-0.049538571	0.8161763	0.8345986	-0.018422
cg08933276	7	18752453	2770410	2770460	N/A		CGCTCTGTCTTTAATGACAGAAACACAAAAACCAGCTGGCCTTGCAGACG	F	3'UTR	GNA12		0.8573286	0.8998071	-0.042478571			
cg08936501	1	15614473	117722652	117722702	N/A		GTCCTTCCATCAGTTACAACTGTACAACACAAGCTCAGCCTAGCCTGATTCG	F	Body	VTCN1		0.78742	0.8633429	-0.075922857	0.8105613	0.8633429	-0.052782
cg08937107	16	14769380	3136857	3136907	S_Shelf		AATCTCTGCCCTCCTCCTGGGCCCATCCTCCGGCCCATCCCGCCGCCAAG	R	N/A	N/A		0.6480371	0.7122357	-0.064195571			
cg08938727	3	26756373	134074767	134074817	N/A		CGGCAGCAATCCTGGTACAGGGTGGCATAACAAAACAGCCATGTTTACAT	F	3'UTR	AMOTL2		0.87307	0.9202386	-0.047168571	0.8851938	0.9202386	-0.035045
cg08940490	2	50753369	237514003	237514053	N/A		CGTGATGTGGCCATCATGAGCAAAAAGCAAGGGCTGTTTCCACAGAGGA	R	N/A	N/A		0.6942114	0.7652414	-0.07103	0.7278688	0.7652414	-0.037373
cg08941515	16	1263128	3585441	3585491	N/A		CGACCACCATCCTGGTTTACATGGGCGACGAACTGTCGGTCGTTAAAGC	R	Body;Body	ZLIAP1		0.8903257	0.9223557	-0.03203			
cg08948225	8	12668353	27288300	27288350	N/A		GTCATAGATCACAGCTGCTTTTGGGGCAAAGGCCCTGGGGATCATTTTCG	R	Body;Body;Body;Body	PTK2B		0.9174657	0.9506657	-0.0332			
cg08948841	4	28706431	1244042	1244092	Island		AGAACGTGGCACGGGCAGGCAGGTTCTGGCTGAGGGCCCAGCATTGTCAGCG	F	TSS1500;TSS1500;TSS200	CTBP1		0.5981857	0.6998929	-0.101707143	0.5846788	0.6998929	-0.115124
cg08949143	13	14660453	30947713	30947763	N/A		CGGCAAATAAATGGCCCAGAATGGCTTCCTGTTAGAAGAAAAAAGGGACA	F	Body	LOC100188949		0.8528486	0.9061186	-0.05327	0.8626663	0.9061186	-0.043452
cg08949924	20	1368714	60952381	60952431	N_Shore		CGCCCAACCTGTCCTCCTCAACGACGAAGTGTGCTGGTCGTCAAAGTTAAA	N/A	Body	BAT2		0.8318471	0.8637557	-0.031930857			
cg08952407	5	37607371	42756860	42756910	N/A		AGTTGGTAAGAACTGCTGGTGGTAGGAGCTCCAGCATAGCGCACAGGGTG	R	TSS200	CCDC152		0.6983529	0.7851643	-0.086811429			
cg08957733	12	28601465	130618630	130618630	N/A		CGGCTTGTGGAAGCATGATTCCACTGCAGCTCTCGCCTGTGCCTCCGTGT	R	N/A	N/A					0.7177538	0.7782314	-0.060478
cg08961072	6	10652441	31591771	31591821	S_Shelf		CGTGGCTCTAAACCAAGCCGCCAATGCTCCCTGGTCTCAAAGTTAAAAA	R	Body	BAT2		0.9002229	0.94514	-0.044917143	0.9249363	0.94514	-0.020204
cg08963616	8	37667502	17249585	17249635	N/A		CGGACAAAGTCACGGAATCTTGGGTGTCTGGTCAAGAGGTTTAATTTCAA	F	Body	MTMR7		0.8410171	0.9057986	-0.064781429			
cg08966413	16	26621507	23154937	23154987	N/A		CGCGAGAGATAACAAGGTAACCATTTAAAGGCTGGGGAAGTAAAAGGAA	F	Body	USP31		0.8624986	0.8968029	-0.034304286			
cg08973191	8	72775383	144894328	144894378	N_Shore		ACGGGCATCGCTGTGGTCTGCTGCTGCTGGGGGGTGCTGGTGGGACGCTGACG	R	Body;Body	SCRIB		0.9123429	0.9443114	-0.031968571	0.9279875	0.9443114	-0.016324
cg08973672	3	13733351	87210807	87210857	N/A		CGTGGTTTCAGAGTCCTGAGGATGCTGAGGCCATTCACTTTGTATGACA	R	N/A	N/A					0.4114438	0.5188886	-0.107445
cg08975529	11	52651356	70309722	70309772	Island		CGCCCTCCTCGTGGCCCGCAGCCCCCGGCTCCCAGGCCAGGGATCTGGGT	R	N/A	N/A		0.7269243	0.7706557	-0.043731429	0.7371825	0.7706557	-0.033473
cg08980711	10	43629500	98945025	98945075	N_Shore		GGAGTGCAGGTGCAGGGTGCAGGTGTGAGGACGGAAGCTGACAAACCCG	R	Body	SLIT1		0.20518	0.2605286	-0.055348571			
cg08982017	10	18689318	43252305	43252355	S_Shore		CCTTTGGCAAATCTGAGACGGGAACCCCTCTGGTCAAGCCCCTCCTCTG	N/A	Body	TACR2		0.7660314	0.8132	-0.047168571	0.766785	0.8132	-0.046415
cg08983011	11	33669419	118774009	118774059	N/A		TGGTGAAGACATATACGAACTGCGAGGGAGGCTTTCCGGGGAGCGCCCCCG	R	Body	BCL9L		0.7151243	0.7838243	-0.0687			
cg09000302	3	69664454	43414570	43414620	N/A		CGGGTTTCAGGGTTCCAGCAGCTACCTGCCCTGGTGAACAATGCAGATTT	F	Body	ANO10		0.83098	0.8639571	-0.032977143			
cg09002049	6	10753314	30434602	30434652	S_Shore		TCCTGGATTTCTCCCAGTAGGACTAGGTTTCTTTTATCCTCCCAAGCCTC	N/A	N/A	N/A					0.1749038	0.1117533	0.0631505
cg09002231	13	46608412	46036179	46036229	N/A		CGGCGGTAAGGATCCAAAGACCTCCTTATAGTGAGGGCTTCATAGCCTCG	F	N/A	N/A		0.8741671	0.9202186	-0.046051429			
cg09002358	5	53688502	57541568	57541618	N/A		CGCACAAAAGAGAATAGGCACAGCCTTGGTTGCAGGTGTTCTTCAGTGA	R	N/A	N/A		0.7119686	0.7741329	-0.062164286			
cg09003509	12	56691326	130502003	130502053	N/A		CGGATGCTGGTTTCTGCACAGACACCCTCCGTCTGCGTATTAAACACGCA	F	N/A	N/A		0.87785	0.9041157	-0.026265714			
cg09006159	2	52694461	98329811	98329861	N/A		CGGTTCCCTGTCGGAGTCGCTCCTTCCTGAAACATGGGCTTTGCCTTCG	F	TSS1500	ZAP70		0.6152414	0.6933929	-0.078151429			
cg09012538	3	36738485	52185079	52185129	N_Shelf		CCCAGCTGCTTTGTGTTGATACTGAAGTCCACACAGGTAACTGCATCTCG	R	Body;Body;5'UTR	WDR51A		0.8796786	0.9214543	-0.041775714			
cg09016242	16	66740444	51185110	51185160	Island		CGGATTGGAAATGTTGAGGCTTCGCTTGCTTCCTCCGGACATGCTGGCT	F	TSS1500;1stExon	SALL1		0.0984499	0.074851	0.023598857	0.0940503	0.074851	0.0191993
cg09016735	2	12717332	11883947	11883997	N_Shelf		CCATGAATTTCTTTGGTCTTGTGGCCTGTTGTAGGTTCTGGATCTGGA	N/A	N/A	N/A		0.87088	0.88998	-0.01911			
cg09019347	17	56632405	3493618	3493668	N/A

cg09377531	8	65665378	141046469	141046519	N/A	CGGTCAGGCTCCGCACATGCTGCCATTGAAGACATCAGAGCTGACCGA	F	Body;Body	TRAPPC9	0.9389829	0.9657557	-0.026772857	0.9505	0.9657557	-0.015256
cg09379340	6	68734313	155507793	155507843	N/A	TCTGTGGCATGTTCAGCCCAGCGTTTCACTTGGCAGGAATTCTGAAAACG	R	Body	TIAM2	0.1833043	0.2896429	-0.106338571	0.23789	0.2896429	-0.051753
cg09380555	13	62641376	53277872	53277922	N/A	TAATAGCCCCCGGGGGTTCACAGATCTTCTGGCAGTGGGTGTAGCTCCG	R	Body;Body	LECT1	0.9076171	0.9370871	-0.02947			
cg09385815	16	60656344	57416169	57416219	Island	CGGCTCCAGGCTACTGCTTTCGCCTGTGTGCTTCGGGCTCCAGGACCACAG	R	Body	CX3CL1	0.8448471	0.8750857	-0.030218571			
cg09389280	3	25691343	170141005	170141055	S_Shelf	CGGCCATTTTACTGCTGCTGACTGTTCTTCCCTGCATCCGGATGGGCCAG	F	Body	CLDN11	0.8381171	0.8916229	-0.053505714	0.86105	0.8916229	-0.030573
cg09394509	3	19742320	50486444	50486494	N/A	AAAGATAATTTTTTCTCGCCCACCATCAGCAGGAAGATCAGTCGTTTTCG	F	Body;Body	CACNA2D2	0.9140586	0.95269	-0.038631429			
cg09394608	13	33668467	4747249	4747249	N/A	TTCCTTGGTTTTGGATCCTAGCTCTATCACTCATAAACAGTAGAACCTCG	R	TSS1500;TSS1500	HTR2A	0.82934	0.8798471	-0.050507143			
cg09413529	12	57706321	115112225	115112275	Island	GTGCAGGAAGAGCGGGTGCCCGTTGAAGAACTGTTGGCCCGCCAGGCCCG	R	Body;Body	TBX3	0.6707643	0.7424057	-0.071641429			
cg09414426	6	34720496	112558319	112558369	N/A	CGGTCATTAACCTGGGAGTACTGAGGACAACAACAAAGGAGCTTCGGAGA	R	Body;Body;Body	LAMA4	0.8474543	0.87915	-0.031695714			
cg09415386	1	64663306	29445461	29445511	N_Shelf	CGTTCCACAGGTCTGGAAGCCTGGTAGCTCTTCCTACAGGCCATCTGGC	R	3'UTR;3'UTR;3'UTR;3'U	EP841	0.9021814	0.93444	-0.032258571			
cg09415720	13	28718483	76244804	76244854	N/A	CTTTACCATTTGTCACCACCACCTGTGATTGACTTCGGTGAGAAACTTCCG	F	Body	LMO7	0.6220043	0.6885729	-0.066568571			
cg09421083	10	22687502	134358535	134358585	N_Shore	CGTGCAGACATTCTCCCAACACTGCCCGACAGGTCGATCTGGGTGCTTAC	R	Body	INPP5A	0.6601614	0.7484729	-0.088311429			
cg09422291	19	17674400	7586940	7586990	N_Shore	GGACTTGCCTGTCATTACAGAGCAATGGGAAGCCGAGGGCAGGTTCTCG	R	TSS1500	MCOLN1	0.3329157	0.4747071	-0.141791429			
cg09424896	19	73775321	16284351	16284401	N/A	CGGGTTGCCAGGCTGTTGTGTACCAGTGTCTGGCACCAATCTCCCTGCCCT	F	TSS200	CIB3	0.7019986	0.7726129	-0.070614286	0.7264413	0.7726129	-0.046172
cg09428251	8	49623370	68658408	68658458	N/A	CCTCCTCCTGTCTCAGTGCAAGAAGTGCTGCATGGTGCACCCCAGCGCTG	F	1stExon;1stExon;5'UTR;5'UTR	CPA6	0.1802329	0.3218114	-0.141578571			
cg09435227	3	38623476	55505073	55505123	S_Shore	CGGGCTTGGAGTCCAGCTGCCTGGGTTCAAATCCTGGCACCTTTACTCCC	R	Body	WNT5A	0.7295157	0.7600086	-0.030492857			
cg09438522	3	30688372	15000765	15000815	N/A	ACCCTGATGTTACCTTTTTTGTCTGGGTGCATTTTGGTTAAATGTCCACG	R	5'UTR	NR2C2	0.7352714	0.82959	-0.088318571			
cg09450200	7	30632347	148903195	148903245	N/A	AACACACTGTCATCAGTGCAAAGAAGTACTGACACCAGCGACGCACTCG	R	Body	ZNF282	0.74877	0.8124686	-0.063698571	0.7720925	0.8124686	-0.040376
cg09459581	2	31686383	173685275	173685325	N/A	CGTGTCATGGAGAGCCGTTGCTTGGATATAATGATTGGCACATTAGATTC	F	Body;TSS1500	RAPGEF4	0.8069343	0.8649529	-0.058018571			
cg09470012	1	11780402	44509516	44509566	N/A	ATCACCCACATAAATCCCTCTGTCTAGGTCACAAAGCCCTGAGTGGCCTCG	F	N/A	N/A	0.8516386	0.8913529	-0.039714286	0.8761763	0.8913529	-0.015177
cg09472600	1	11603488	183537770	183537820	N/A	ATCTAGAATGACGTCCTTTTTCCTGTGTGGATGTTTTCCACTCCCTATCG	F	Body;Body	NCF2	0.6680057	0.72437	-0.056364286			
cg09474105	3	29640464	73160429	73160479	S_Shore	CTTCCTCCTCCACTGCATTGTTTACTGGGCTCATCCTAACTCTGAAAACG	N	N/A	N/A	0.9208943	0.9433886	-0.022494286			
cg09479818	19	11665330	33880790	33880840	S_Shore	CGCCCCTGTTCTCAGCAGGCCCCCGGGCAGGCCCCTAGAGCCAACACCCT	R	Body;Body;Body	PEPD	0.8315614	0.8676929	-0.036131429			
cg09501047	1	15643436	164615911	164615961	N/A	CGAGCAGGGACATATCCTAACAAATGTACACAGGTATGTGTGACTTTCTA	R	Body	PBX1	0.8741943	0.9213071	-0.047112857			
cg09501687	5	31735424	150169781	150169831	N/A	CCGGGCATTTGCAATCGCAGAATCCTGGAGCACACTGAATGAGT	R	Body	C5orf62	0.6650886	0.7684843	-0.103395714			
cg09504873	16	37631362	66774626	66774676	N/A	CGGATGTGAAGGCTAGAGCTCTCAGTCAGGAGGAAGAGAACCACACCCTA	F	Body	DYNC1LI2	0.6322657	0.7443871	-0.112121429			
cg09505918	1	35650331	212797670	212797720	N/A	TTCTCATTTGAAAAATTTTTATTTTGGCACCCACTTGAGTACCTGGCACG	R	TSS200	FAM71A	0.8107914	0.8653143	-0.054522857	0.8407575	0.8653143	-0.024557
cg09506319	1	58664372	2122601	2122651	S_Shore	CGCGTTCAGATCTAGGACCTTCTGGCACCCTTAGGAGAAAGCTTTCGGAGG	R	Body;Body;Body	C1orf86	0.6945643	0.7425214	-0.047957143	0.6914213	0.7425214	-0.0511
cg09508934	13	43697353	113717379	113717429	S_Shelf	CGCCTGTTGCATGTCCTTGGCCATCACAGGCCGCACTCGTGTGGAGTTTT	F	Body;Body	MCF2L	0.8856257	0.9241014	-0.038475714			
cg09511896	1	11751427	228246937	228246987	Island	CGCCCAACTTCTGCGAGCCCAACCCTGAGACGGGCTCCCTTCGGCACGCGC	F	Body	WNT3A	0.2834114	0.2171943	0.066217143	0.2810075	0.2171943	0.0638132
cg09518151	2	42689454	99918664	99918714	N/A	CGTGGAATCAATGGCTTGCTTATCGGCTGACTGGTACAGTTGTTTCT	F	TSS1500	LYG1	0.8882757	0.9172743	-0.028998571			
cg09518447	19	16631427	2216725	2216775	Island	TGTGCCCCGCCAACTTGTCATGACTGAGGCGGCACCTGAGCTGAGCACCACG	R	Body	DOT1L	0.7823714	0.8227657	-0.040394286	0.804975	0.8227657	-0.017791
cg09520904	11	54789374	69462943	69462993	S_Shore	GATCAAGTGTGACCCGGTAAGTGAGGGTGATGTCCCAGGCAGCCTTGCCG	R	Body	CCND1	0.57607	0.6351886	-0.059118571			
cg09520976	8	15620491	124603599	124603649	N/A	TTTTTGTTTTTGAGACACAGTTTGGCACTGTTGCAAGTGGCACGATCTCG	R	N/A	N/A	0.72825	0.8037586	-0.075508571			
cg09521872	7	59631529	50800547	50800597	N/A	CAGAACATTGGTTGAAGCAGTCTCCAGGTGGCAGGAACAGTGATCG	R	5'UTR;TSS1500;TSS1500	GRB10	0.9026971	0.9279829	-0.025285714			
cg09527731	5	22655387	132097228	132097278	N/A	CGGCTGTGGGTCTGCTCGCGGAGGTCTTTCCATGTTCACCCGGATCAACAT	F	Body;Body;Body;Body	08-sep	0.8281457	0.8638943	-0.035748571	0.8425188	0.8638943	-0.021376
cg09531492	22	67804394	50632560	50632610	N_Shore	CGAGAAGCCAGGGCCTCAGGAGTCCTGTGCCCCATACACCCCATGAGGGC	R	Body	TRABD	0.8774643	0.9013686	-0.023904286			
cg09536516	7	14714432	30934475	30934525	N/A	CGCTCTTCTGACAGGTGCTCCCTCTATGTAGAACTAACAGGGAAGAGTGCT	R	N/A	N/A	0.8785243	0.9046429	-0.026118571	0.8894338	0.9046429	-0.015209
cg09548495	1	33644366	41960295	41960345	N_Shore	CGCCCAACTTCTGCTCACAGCAAGCCAGGGTCTTCAGCTCCAGCTCCAC	F	N/A	N/A	0.8389086	0.8692414	-0.031142857			
cg09556286	6	43616383	47010177	47010227	N/A	TTGAGCTCTGTGCTCCTTCCTCTTACCAGACCTGATAGTGACTTTAAGCG	F	TSS200;TSS200	GPR110	0.6465043	0.7577114	-0.111207143	0.6704188	0.7577114	-0.087293
cg09558000	2	20807432	121991892	121991942	N/A	CGTGGAGTGCCTGTCATGGGGTGGTGGATGACCCTCCCAGGTCCCGCAGC	F	Body	TFCP2L1	0.69285	0.7679657	-0.075115714	0.7232013	0.7679657	-0.044764
cg09562331	3	20774469	50596116	50596166	N/A	TTCCTCCTCTCCACTGCATTGTTTACTGGGCTCATCCTAACTCTGAAAACG	F	3'UTR	C3orf18	0.7111843	0.7690043	-0.05782	0.6984513	0.7690043	-0.070553
cg09570250	4	15607417	110676767	110676817	N/A	CGGAACAAGAGGAGTCGAACTCACTTTTGTATATAACAAGCCCACTCTC	R	Body	CFI	0.88544	0.9360757	-0.050635714			
cg09584702	1	66754418	229047840	229047890	N/A	CGAGTGTCCCCCAGATTTTATAAGCATCAGGCTCTTCAAAACCTGGATTT	R	N/A	N/A	0.8196343	0.8665129	-0.046878571			
cg09591867	17	10753325	79098558	79098608	S_Shore	GCGCTGGATCGCGCCAGAGCTGGTGGACGAGGTGCATAGCAACCTGCTCG	F	Body	AATK	0.8937457	0.9373471	-0.043601429	0.9153575	0.9373471	-0.02199
cg09594635	16	14717301	89126866	89126916	S_Shore	CCCCTCCTGAAGACAGCAGACGTATGAGCACTCCACCAAGGGAACAATCG	N	N/A	N/A	0.7965586	0.8499186	-0.05336			
cg09599062	3	52775318	141995701	141995751	N/A	CGAGCTGTGACTAATATCTGCTGTTCTCTAGCAAGGGCCTCTGTGCTAAT	F	N/A	N/A	0.7072486	0.80875	-0.101501429	0.7693788	0.80875	-0.039371
cg09609051	11	18714421	65102941	65102991	S_Shore	CGTAGTGAGGTTCTTGGTGTTGGAAGATTTTGCACCTGCAGAGAAATAGGGTTG	F	Body	DPF2	0.7733314	0.86098	-0.087648571	0.8192563	0.86098	-0.041724
cg09610987	3	49736342	49028238	49028288	Island	CTGAGCCCCGGTCCTGGGTGCATGGTCTGCTCGGGTGCATGTTCTCCGCT	R	Body;Body	P4HTM	0.26162	0.37418	-0.11256			
cg09614389	20	16659427	25450839	25450889	N/A	CGGGGAGATGGGGACGCACAGTTCTCAAGGACTCCCCGCTGCAGAGCCAGC	R	Body	NINL	0.6669371	0.7528957	-0.085958571	0.6716613	0.7528957	-0.081234
cg09614810	6	71609947	74227212	74227262	N_Shelf	TTTCCAGATCGTAAAACCAGAATTAGATGTCTTTCACCTAAATGTCTTCG	R	3'UTR	EEF1A1	0.8768857	0.92403	-0.047144286			
cg09615826	16	35751343	21415657	21415707	Island	CGGCAGCAAGTTTGGCATATTATTACCTGAGTGGTGAAGTCTATGATAT	F	Body	HPR-3	0.7464671	0.8029443	-0.055477143	0.7569163	0.8029443	-0.046028
cg09618893	6	35758375	31856773	31856823	N_Shore	CGCTGGGCAGCTCCAGGGACCCCAGAGGGACCTCCATGTACTCACTGGGG	F	Body;Body	EHMT2	0.46763	0.5326471	-0.065017143			
cg09623279	10	25628412	45395734	45395784	N/A	ATGTTTCCAGCAAGACTCAGACAAGCACTTCAGTGGCTGTGGGTGGCAGG	R	N/A	N/A	0.8004971	0.8533014	-0.052804286	0.8188975	0.8533014	-0.034404
cg09625781	10	69756353	45488298	45488348	N/A	CGGGGTCAGGACTGACTGCAGAATGGAAGATTCCCTTCTGACTTTGGTCTC	R	Body	RASSF4	0.8938071	0.9313771	-0.03757	0.9144025	0.9313771	-0.016975
cg09626521	3	50671445	113933104	113933154	N/A	CCCAGGGAATTGGTCAAGCCCTGCCATTAAATATGGACAGTTCTAATCTA	N	N/A	N/A	0.45139	0.6132643	-0.161874286	0.565695	0.6132643	-0.047569
cg09638638	3	49754483	77335810	77335860	N/A	CGCTCTCAGACTGACAAAAGTGGTTATAAGGAATATTCTACATGGATGAT	R	Body;Body	ROBO2	0.8760429	0.9139057	-0.037862857	0.89238	0.9139057	-0.021526
cg09644974	2	56709435	177358138	177358188	S_Shelf	TGCTCTGATGCTGCAGACATTCTGTTTGATGCGGAGAAGGCCAGCCAATTCG	R	N/A	N/A	0.7949414	0.8760857	-0.081144286			
cg09649473	3	35717386	149071414	149071464	N/A	CCAAGGTCGTTGATAACTCTGGGTTCTGGTTTTCTTTAC	R	N/A	N/A	0.85634	0.9004671	-0.044127143			
cg09654116	7	32736356	158816213	158816263	Island	GCAGCCAGCGGCGGGCATTGTGAGGTGGGTCAGCAGCAGTGTCTGCATCG	F	Body	LOC154822	0.8385229	0.8797614	-0.041238571			
cg09655191	17	24725478	73915849	73915899	S_Shore	CGGCCTCCTGGCACTGCGACAGATACCGAGCTGACAGCTCTTCGTTCTCT	F	Body	FBF1	0.9161829	0.9427714	-0.026588571			
cg09658183	17	25686311	18139506	18139556	N/A	CGTGGCTGCCTTGGGCCCCATGCAGCTCCTCCCCGGGATGCCCCATGCT	F	Body	LLGL1	0.64782	0.7193871	-0.071567143	0.6902275	0.7193871	-0.02916
cg09663494	16	55652367	67223733	67223783	N/A	CCGAGGGCTACCTGGGAGGCTTTGCCTCCTGAGTCTCGAGGTCTGGACGT	F	5'UTR	CYP3C3L	0.7756971	0.8195286	-0.043831429			
cg09670128	12	25629482	52627047	52627097	Island	CGCCCGCCGCTAGGTCCATCCCGGGCCCAGCCACCATGTCCATCCACTTCA	F	5'UTR;1stExon	KRT7	0.1059896	0.0637149	0.042274714	0.0817146	0.0637149	0.0179998
cg09671122	3	46774453	28291744	28291794	N/A	CGAGTGCAGGCAAATCTTGGGGTTAGAGGAAGGAGAAATCACTTTTTAG	F	Body	CMC1	0.9015457	0.9302914	-0.028745714			
cg09677896	18	40698452	48256237	48256287	Island	GCCAGCCTTTTCTTGGGGCTCCTCTGCCTGGTCTCGTCGACGCG	F	3'UTR	PAPPA4	0.8998044	0.9352929	-0.037291429	0.9162713	0.9352929	-0.019022
cg09687025	13	52777412	77459109	77459159	N_Shore	CGTCTTCTTTGGACCTCCTGAACCGAGAGAACCCAGAGGAACCCCACCC	R	3'UTR;1stExon	KCTD12	0.1511	0.22133	-0.07023	0.1755888	0.22133	-0.045741
cg09694527	12	44612488	123918498	123918548	N_Shelf	CGGCAAGTTAAGAGGTGAAGTCAGGATCTTAATTCAGAGATGCTAGTCCT	R	Body	RILPL2	0.8964071	0.9404643	-0.044057143			
cg09695187	16	20646422	81970170	81970220	N/A	TCTGTCACTTTACCTTACAATCACGAAGCCTGCGTAAGCCAAGCAGCCTTCG	F	Body	PLCG2	0.8832957	0.9159929	-0.032697143	0.8935375	0.9159929	-0.022455
cg09699193	5	70618502	9457024	9457074	N/A	CAAGTGAACAAGAGAGATCAAGAACTCCAGTCCTTGCCCTGCTCCTCTCG	F	5'UTR	SEMA5A	0.8294871	0.0709	-0.044112857			
cg09702315	10	54796380	133677197	133677247	N/A	CGGGACTCCTGCTTACCCTGCTGTCCTGGAGACCTTGGGCAGCCTGATA	F	N/A	N/A	0.6807143	0.7343443	-0.05663			
cg09706929	15	49635457	52118098	52118148	N_Shelf	CGGGGCAGCACTGGAAGTCACATAGTAGTGGGCAAGCCTGTGCTATTCCTC	F	N/A	N/A	0.7533514	0.86263	-0.109278571			
cg09710580	7	69799334	148767490	148767540	N_Shore	CCGGGTGCTCTTGCTGTGGATTCCTGGGGATACCAATCCATCCTGGTCC	R	3'UTR	ZNF786	0.8288571	0.89213	-0.063272857			
cg09718739	11	46667350	85644435	85644535	N_Shore	CGAGCTAATTTTAAAAATTTATTCATGTAGAGAAGGGGTGCTCCCTATG	N	N/A	N/A	0.8599271	0.9172714	-0.057344286			
cg09720207	12	71663331	54400125	54400175	Island	AATTCGCGAGTGGCAGCGGGAGATGGGCCCTCGATCTGGCAGCGGGCTCG	R	N/A	N/A				0.0635663	0.077735	-0.014169
cg09726623	2	36722494	121317623	121317673	N/A	CCCCCTCCTCCTCCTCCAGCCCCAGGAGCCCGGTTTCGCTGACAGAAAATA	N	N/A	N/A	0.8023014	0.8577729	-0.055471429			
cg09730170	20	31716412	23586680	23586730	N/A	CACCTGCCTGGGTGCTGTTCCCTCTCCCCTAAACAGGAGATGATTTAAACG	F	TSS200	CST9	0.7631857	0.8170429	-0.053857143	0.78056	0.8170429	-0.036483
cg09734123	6	14706353	158966047	158966097	N/A	CGGTTTAGGAAGCTGGCACCTTAGAGCCGCACAGGGAGAGGATGCTGCCC	F	Body	TMEM181	0.8568471	0.9053471	-0.0485	0.8858963	0.9053471	-0.019451
cg09743596	16	16632345	89180843	89180893	N/A	CGGTCATGCCATACCGCTCCAGCAGGGTGTGGCCCTGGTATGTTTCCAC	R	Body;Body;Body	ACSF3	0.78206	0.8316943	-0.049634286			
cg09755397	4	62677495	102341105	102341155	N/A	TGTTTGGTCTTTTTGACTTTGTTGCTTTCTTTAAGGTTGCCTCG	R	N/A	N/A	0.8426071	0.9018	-0.059192857			
cg09758896	10	10641308	131694575	131694625	N_Shore	CGGGCTTGTTTTTGCATGGTGGCTGCTATGACCACTGAGGCCACCTGACA	R	Body	EBF3	0.8410743	0.8779829	-0.036908571			
cg09760618	2	13679457	23324204	23324254	N_Shore	CGGGAGGCACCCACACTCACCCAAATGGCATCTGTACTCAATACCGCAC	F	TSS200	ALPP	0.8132314	0.8776814	-0.06445	0.8331025	0.8776814	-0.044579
cg09762752	2	16699451	15871869	15871919	N/A	CACTAAGCTGGTTTCCTCCTCCATGTAATTCTCCTTGGCACCG	R	N/A	N/A	0.8519171	0.8879614	-0.036044286			
cg09767076	12	65786485	124199914	124199964	S_Shelf	CGACCTCCAGAAATGAATGAGAAGGTGACAAACAGAAGTGAAATGAGAAT	F	Body	ATP6V0A2	0.5009286	0.6622086	-0.16128			
cg09781936	22	47766424	19749961	19750011	N_Shore	CGGCCACTACTGCTGTGCCATCATGTGGGGGTAGCCCATGGCCTCACACCC	F	Body;Body;Body	TBX1	0.8904643	0.9226229	-0.032158571			
cg09793619	10	54751398	131650331	131650381	N/A	AGCTAGAATAGCCGGGAATCACATTCCATGCCAAATGAGGCAAGCAGTCG	R	Body	EBF3	0.8746857	0.9112429	-0.036557143			
cg09795027	17	27739494	74006440	74006490	S_Shore	CATGAGCTGGAGGGCGAGAGGAAGCCAACTGCTCAGCGAGGACCCCGCG	R	Body	EVPL	0.7169314	0.7728814	-0.05595			
cg09799039	2	60665326	24021385	24021925	N/A	AGGCAGGCAAGGGGACGGCCAGGATGGTAGGTGGGGCCCCAAGTGTTCCG	R	Body	HDAC4	0.8838571	0.9253414	-0.041484286	0.9126125	0.9253414	-0.012729
cg09812406	12	12786311	131303993	131304043	S_Shore	CGGCTGGAGGCTGCTGCCTACATTTTGGTTCACACTCTGTCACAAACAA	R	Body;Body	STX2	0.5717757	0.67237	-0.100594286			
cg09814480	7	45619442	134916235	134916235	N_Shelf	CCGCCTTATTATCAGAAATGAGGACACTAACAAGGAGTGAAATAAATCC	F	TSS1500	STRA8	0.8989257	0.9358086	-0.036882857	0.92442	0.9358086	-0.011389
cg09816756	4	43766409	69047758	69047808	N_Shore	CACTTAACGCCTGGAGACTGTGTGGTTCATAAAACAGGGCCTTAGGCTCG	R	TSS1500	LOC100130017	0.6760343	0.7410371	-0.065002857	0.701865	0.7410371	-0.039172
cg09847250	16	62637382	65397909	65397959	N/A	TCAACTCTCGCCCCTGCAGGGATTCTCTCATGTTGTGGGTCTCAAGATCG	F	Body	LOC283867	0.8452971	0.7864043	-0.058892857			
cg09848074	7	58753481	139172610	139172660	S_Shelf	CGTGGAGCCCAGTGAGACTTGGGTTTTCGGCCACTTGCAATCAGTTCCTC	R	N/A	N/A	0.5606429	0.6495943	-0.089951429	0.6049925	0.6495943	-0.044602
cg09850101	14	61761349	60195307	60195357	N_Shore	CGAGACCTTATCCACCTGTTTGCTCCTGTCGATCTCGTCTCATCTATT	R	Body;TSS1500	RTN1	0.5633414	0.6611457	-0.097804286	0.582955	0.6611457	-0.078191
cg09853648	11	47613493	69492642	69492692	S_Shelf	CGGGGAAAAAAAAAGGACTTGAAACATTATTCACAGAAAGAGCAACAGCTG	F	N/A	N/A	0.7543843	0.8467957	-0.092411429			
cg09853702	12	53639421	47665230	47665280	N/A	CGAGGCTGTAAATCTTGTGGGTTTCCAGTGCCACCACAGACAGACTAA	R	N/A	N/A	0.7418857	0.8049343	-0.063048571			
cg09866695	1	26675465	221274496	221274546	N/A	CGGGCAAGTTGTTATTTTTCTTCACCCCAGATCTTCTCCAAAGAGAA	F	N/A	N/A	0.80722	0.8646914	-0.057471429			
cg09869357	1	26722330	12613315	12613365	N/A	GTAGGTCAGGCAGTGGGGATGTGGCCGTGAACTTGGGCAGGGGCTCGTCG	F	N/A	N/A	0.77078	0.8711114	-0.100331429			
cg09869858	12	71658424	48120416	48120466	N/A	CGCCAGGTTGAACAGTTGGTGGGTTAAAGAGAATCCCCCAGCCTGTT	F	TSS1500	P11	0.9254	0.9559229	-0.030522857			
cg09871837	1	41752384	46640020	46640070	N/A	CGGTGCTGGGCTCCTCAGGTTATGGGATGGGGGTTGCTGAACATCAGTCA	R	TSS1500	TSPAN1	0.7157957	0.7742057	-0.05841			
cg09874605	15	22658335	68123157	68123207	S_Shore	CTTTCTCCTGCAAATGAGTTCCTGTGACATCCCAGAGCCCTTCCTCTG	R	Body	12XCOR1	0.8682643	0.9040627	-0.035822857			
cg09874873	6	72738301	160555573	160555623	S_Shore	CGGGCTCTGCTCATCCCTATGCATCATGCATGTGGGAAGCCCCAGGCTCC	R	Body;Body	SLC22A1	0.8619943	0.9009343	-0.03894	0.8863425	0.9009343	-0.014592
cg09874992	1	30743382	31314608	31314658	N/A	ATCTCATGGATCTCTGCAGCATATAAAATGGTGCCCCATTCATTCTTTCG	R	N/A	N/A	0.7876043	0.8755557	-0.087951429			
cg09883851	15	33775382	50344782	50344832	N/A	CCGGTGATATGACTTACTCTCACATGTGGCAGATATCTCAAGTGTTGCCGA	F	Body	ATP8B4	0.8743429	0.9044443	-0.030101429			
cg09884851	12	31711353	79809356	79809406	N/A	CGAGGGAATCGTAGGCAGCTATTTATGTGCTATCATACAAAAATGTTTAA	R	Body;Body	SYT1	0.7670071	0.83594	-0.068932857	0.796725	0.83594	-0.039215
cg09885657	13	40675351	113791997	113792047	N/A	GGTTCCTTCTGGAGGCTCTGGGAGAGTCTCTGTCCCAGGCTCTCTGCTCG	R	Body	F10	0.9158857	0.9431543	-0.027268571			
cg09886931	7	62753449	97834674	97834724	Island	GACAGGATGGCCGCTGGGCATGTGCGCTGCACACACAGGAACGGACGCG	F	Body	IAH1K2	0.8740788	0.8946986	-0.02062	0.9157463	0.8946986	0.0210477
cg09891807	6	45676449	107881776	107881826	N/A	CCTGACCCCTAACAGGTAGCATCCTCTTCATACACCTATGGATACTCACG	R	Body	SOBP	0.8861671	0.9177757	-0.031608571			
cg09892454	5	61793388	149433536	149433586	N/A	CGGTCATTTCACTCAACAGCTCGGCCCAGCTCTGAAACTTGGGAAGGTGA	R	3'UTR	CSF1R	0.9337786	0.9614671	-0.027688571	0.9433688	0.9614671	-0.018098
cg09892671	1	37679500	82951578	82951628	N/A	CGGTTTATGAGTCCACCACCATTTGCATCATAATAGGTTTGGTAAAGTCT	F	N/A	N/A	0.80809	0.8922143	-0.084124286			
cg09895909	1	47698321	26829607	26829657	N_Shelf	GCAGTTTGTTGCTCATATAAGGATTCTGGGGGCTATGGGGGCTCACG	F	N/A	N/A	0.7473843	0.81926	-0.071875714	0.7746013	0.81926	-0.044659
cg09913449	8	72645496	42400586	42400636	S_Shelf	CGGGGTGAGAGAGCCATGTTCTGGCTGTCACATCCTTGCTAGGCTGCTGT	F	5'UTR;5'UTR;5'UTR;5'UTR	C8orf40	0.8869443	0.9241086	-0.037164286	0.9085225	0.9241086	-0.015586
cg09915729	10	31641337	121513707	121513757	N/A	CGTGACCCTGGGCCAGGAGTCCCCTGGCCCAAGATGGGCAAATAAGTCTCT	R	Body;Body	INPP5F	0.8375243	0.8905429	-0.053018571			
cg09916030	21	29691468	37949247	37949247	N/A	TCAGTGCTGTTTATCTTCTGAATTGAACACCATGGAGCTGTTGCAGCTCG	F	TSS1500	CDN14	0.8738557	0.9070057	-0.03315			
cg09919570	16	65663332	49311782	49311832	Island	CGCTCCGGCTCCCGACCTCCCCGCTGCCGAAGCAACTGGGTCAGCCTTTC	N	N/A	N/A	0.2786029	0.2252571	0.053345714			
cg09946832	8	47620329	143690524	143690574	N_Shelf	CAGGAAATGTCGTCACCCATGGCGCAGGGCGCTGAGCAGGGCTCTTCACG	F	N/A	N/A	0.0996839	0.0681781	0.031505714			
cg09950208	10	31760452	130841235	130841285	N/A	TGAGAACATAAACTGTGGGAGTAGAACAAGACCACACCTCTGTGTGTGCG	R	N/A	N/A	0.5491657	0.6643143	-0.115148571			
cg09966309	6	43729341	166954799	166954849	N/A	AGAGCGGCGACCACTGCCACCACAGAAGTAAATTCCCCCTCCCCCCTCG	R	Body;Body	PPS6KA2	0.71267	0.7884429	-0.075772857			
cg09967633	16	18647392	84918794	84918844	N/A	TTAAGCTCATTGTTCTTTCCGGCAGGCGGAAGCCTTGGTGCTTGGATACG	F	Body	CRISPLD2	0.6075057	0.7125286	-0.110022857			
cg09983301	2	38679392	69404831	69404881	N/A	TTCAGTAAAATTTGCTGCGCAGTTGGATTTGTGCCAGAGCTGCTAGATCG	F	Body	ANTXR1	0.4588129	0.62267	-0.163857143			
cg09989546	15	62628404	62808066	62808116	N/A	ACCCTTCTGGGCAGCAATCGCAGAACAATATCCCCTCTGGATTCTCAACG	F	N/A	N/A	0.8457189	0.8926057	-0.046887143	0.8748063	0.8926057	-0.017799
cg09991769	14	36602455	103242929	103242979	N/A	CCTTTGGGGCAGAAGGCAGAGGCCTCGGGAGAAATGCGCAGGCCCAGCG	R	TSS1500;TSS1500;TSS1500	TRAF3	0.8279414	0.8655329	-0.037591429	0.84414	0.8655329	-0.021393
cg09995854	2	59773443	113810244	113810294	S_Shore	TTTCTTGTCAGCAAATTTAAAACCTCACAGCATATTCTGCACTCATTACG	R	5'UTR;5'UTR	IL1F8	0.9283729	0.95925	-0.030877143	0.94025	0.95925	-0.019
cg09997119	14	47757497	77890

cg10317638	1	35635505	43738602	43738652	Island	CGGGCACTGTGCTCTGTTTGGTCGCTCTGCTGGTTCTGGTGAAACAGCTG	F	Body	TMEM125	0.7791114	0.83592	-0.056808571			
cg10320997	4	63618455	119808935	119808985	N/A	CTGTTTCAGCACTAAGAAGCACTATATACAGTAAGTCCTCACTTAAAACG	F	TSS1500;TSS1500;TSS1500	SYNPO2	0.6500429	0.7509686	-0.100925714	0.7083	0.7509686	-0.042669
cg10325659	14	39704455	94423950	94424000	N/A	CGGCCCTCGAGCACAGGCTGTTTTCATGCCACCTTGCAGGACGGGGGACT	R	TSS200	ASB2	0.8355957	0.8760271	-0.040431429	0.8589075	0.8760271	-0.01712
cg10328844	15	42807337	98417731	98417781	N/A	GACTTTTGCAGGGCTGTGCCTCCTTTCCCCCAGACAAATCCATCACG	F	TSS200;TSS200	LOC91948	0.7403671	0.8240643	-0.083697143	0.76029	0.8240643	-0.063774
cg10335482	8	23713502	706845	706895	N/A	CGCATGCAGAGAAGTGACATGATAAAAATGGCTCCAGAAAGATTATCCCG	F	N/A	N/A	0.7422743	0.8253014	-0.083027143			
cg10338112	16	58770459	30820353	30820403	S_Shelf	CGCCCAGCCTGGAAAGTCTTAAAATAATTTTGTAAACCTGACAGATTTAT	R	N/A	N/A	0.8687614	0.9356214	-0.06686	0.8955338	0.9356214	-0.040088
cg10351808	19	65690472	35632493	35632543	Island	CGGGGAGGGGCGTCTTACCTCTGCTGCTGGTTGAACTTGCACCGGCATCT	R	Body;Body	FXYD1	0.3750129	0.4273	-0.052287143			
cg10352418	16	23752355	66876938	66876988	N_Shore	CGAGCCCTGGTCGTTGTTTGTGCCTCCACCTGGTGCGTCCTTCTGTCTTCC	R	TSS1500	CA7	0.8338857	0.8748714	-0.040985714			
cg10354655	12	12690337	23146960	23147010	N/A	CGGGTTATATTTGAGAGACAATATGCTCAGCATTGTTCATTAGGTCTAAT	R	N/A	N/A	0.8530429	0.9041629	-0.05112			
cg10355814	10	24656369	134460330	134460380	Island	CGCTCGCTGCCACGCTCTGTGGGTTGACGCTGCTGCCATGCTCTGTGGGTC	F	Body	INPP5A	0.8078457	0.8471471	-0.039301429	0.8182538	0.8471471	-0.028893
cg10359932	14	64753440	32835247	32835297	N/A	TCCTCTTCTCATTTATGGAGCTGTCCAGCCGTTATGAGTAAACGTCTGTCA	R	5'UTR	AKAP6	0.7536788	0.8264014	-0.072722857	0.79708	0.8264014	-0.029321
cg10365563	7	11707401	21469772	21469822	S_Shore	CGTCTTTGACAAGCAGTGACACATTAGTGAGCTCAGCAGATACTGGCCAG	F	Body	SP4	0.6905914	0.7935386	-0.102947143			
cg10365769	4	69675468	7589937	7589987	N_Shelf	AGCCCGAAGCCGGCTCCAAAGTGACACTTGAGAAATGGGCTCTCAATGCG	F	Body	SORCS2	0.7656957	0.8201186	-0.054422857			
cg10367137	10	57683344	30283289	30283339	N/A	CGCAGCTTGTGGATGTAATCCAGACACCCTGGGGTGAAGAAAAGCTACC	F	N/A	N/A	0.9257414	0.9534	-0.027738571	0.940335	0.95348	-0.013145
cg10369319	6	31618337	111369619	111369719	N/A	CAAGGCTATGGTGCCTGAGTCATGTGTGCTGACTATACACACACCACCTCTA	R	TSS1500	LOC442245	0.7234743	0.79821	-0.074735714	0.7255088	0.79821	-0.072701
cg10369363	12	33638438	52404422	52404472	N_Shelf	AAGCTGGGATGGGGGCTAAAAAACTCAGCCGGCTCATCCTTCAGGGACCG	R	Body	GRASP	0.6149143	0.7085557	-0.093641429			
cg10369509	13	48736395	23949135	23949185	Island	AACGGAAAAGGCAAGTGATGAAAAGCCACAACTCAGGACAAGCACAGGCG	R	Body	SACS	0.1730329	0.2141757	-0.041142857			
cg10370850	11	32693474	70027143	70027193	S_Shelf	CGGGCCCCTGCCCTTCCCCCATCCTGGGCTGTCTGCCCTGTGGCCTG	F	Body;Body	ANO1	0.7473	0.8069414	-0.059641429	0.7650363	0.8069414	-0.041905
cg10373147	14	61747413	45133024	45133074	N/A	CGGGAACAACAATCAAAACATGTCAACTGAACTGAAGTGGGGCCCACTTGT	R	N/A	N/A	0.7733929	0.8379843	-0.064591429	0.8053725	0.8379843	-0.032612
cg10383428	12	65777324	6604190	6604240	S_Shore	CGAAGACAGGTTCTGAATATAGACCCTGACTTTTTCACTGTTTGGTTTCT	F	5'UTR	NCAPD2	0.8353943	0.8849	-0.053095714	0.8631013	0.8849	-0.025389
cg10387511	14	29726472	38049805	38049855	N_Shelf	TTATGATTTGGCATCCTAGACTCAAAACCAGACTCTGGGCTCCCAATGCG	F	N/A	N/A	0.8756214	0.9166257	-0.041004286			
cg10399402	8	32729354	26496601	26496671	N/A	TCCTGTGGCTTATGGAGTGTGCTCAGCTCGTTATGAGTAAATGGCTATGCTCG	R	Body	OPYSL2	0.8933914	0.9157914	-0.0224	0.9300775	0.9157914	0.0142861
cg10406676	16	29634411	3494094	3494144	S_Shore	CGCTTAGGCTGCAGCTGCGGGTACAATACGTAATGCCTCTATAAACATTT	R	5'UTR;TSS1500	NAT15	0.40788	0.4810557	-0.073175714			
cg10415570	16	48647473	73053379	73053829	N/A	CGGGCTGGCATTCCTGGCTGGGCATAAACACGTTTTAAAAAATGTCTGT	F	5'UTR;5'UTR	ZFHX3	0.77463	0.8379257	-0.063295714			
cg10423842	6	61754407	56200769	56200819	N/A	CCCTCTTCTTGTTGCAATTCTTCTAATGTGCTCATCAACCG	R	N/A	N/A	0.6784171	0.7720143	-0.093597143	0.7065938	0.7720143	-0.065421
cg10431950	17	67785358	73754560	73754610	N/A	GCGCCCAGAGGGCCTCAACCTGAGTGAGCGGTGGCTCTCCCACATGAGGCG	R	Body	GALK1	0.9249063	0.9080714	0.0168348			
cg10444255	2	73796412	189718141	189718191	N/A	GTGGATACCATATGTTTGGCATCAGTCCTTAAAGTTCTGCCACATGTTCG	F	N/A	N/A	0.7302286	0.7968114	-0.066582857	0.7465563	0.7968114	-0.050255
cg10448808	16	36650490	86599765	86599815	Island	CCAGGGAAGTTAGCAACGTGCTGACTGACAACTTAATCCTCCGAATTCGCG	F	TSS1500	FOXC2	0.1953157	0.1201751	0.075140571			
cg10449489	5	17684413	148046220	148046270	N/A	AAATTCTTCAAGCTCATTAAAAGACAAATACACCCTGCTATCACTAATACG	R	N/A	N/A	0.7418443	0.8075571	-0.065712857	0.7561	0.8075571	-0.051457
cg10453977	2	41613465	73053331	73053381	S_Shore	CGACAGTGCGTAAACAGTGATGATCAAGTCAGGCAGTGGCACTAAACCTA	F	TSS200	EXOC6B	0.1343913	0.0907583	0.043633			
cg10472064	3	19620446	50452888	50452938	N/A	CGGTCCTGTCACCTATGAGAGCCGCTGAAGATCGGATATCAAAGGCTGAC	F	Body;Body	CACNA2D2	0.7626329	0.8188771	-0.056244286			
cg10476003	6	10660315	31540219	31540269	N/A	CGCTCTCCTCCTCCACCTCCTCGTGATTCCCGCGCTTGGTCTGGG	F	1stExon;5'UTR;5'UTR	LTA	0.7470471	0.7976829	-0.050635714	0.7637388	0.7976829	-0.033944
cg10477073	12	44803311	123477123	123477173	N/A	GGGTAGCGTTGGTAGCGGGGGACGTGAAAGGCGGCAGGGCGTGAAAGCG	R	Body	PITPNM2	0.8899371	0.9248871	-0.03495			
cg10477603	10	55644370	126849704	126849754	Island	GGGGTCTCTTTTTGCAAACCAATGACACAACCCCACATGGGCCGGCCTCG	R	TSS200;TSS1500	CTBP2	0.1010589	0.1360586	-0.034999714			
cg10484693	10	48864356	29214692	29214742	S_Shore	GAATCAACAGTTGTACAGTAAAGATTATTATGACAGACTCACACG	F	N/A	N/A	0.8399457	0.8783043	-0.038358571			
cg10495931	16	32746441	72232102	72232152	N/A	TGTAATAGAAATCATCAGTTGCCATGGCGACGTGTTCCAAGAGCAGATCG	R	N/A	N/A	0.6485	0.76926	-0.12076			
cg10499832	17	68799374	41450195	41450245	S_Shelf	TCCTCTATCACATCCTGATAAAGGCCGCTTGAGGACACCTTGGTCTAGCG	F	Body	LOC100130581	0.6709914	0.7691586	-0.098167143	0.6892938	0.7691586	-0.079865
cg10501065	11	32733424	2164976	2165026	N_Shore	CGGGTCCAAATAATTTTCTTGGACGTTAATTTCCGGGGACGTCAAAACAC	R	Body;Body;5'UTR;Body	IGF2AS	0.5117529	0.6412486	-0.129495714			
cg10507762	3	72715318	101284875	101284925	S_Shelf	CGTGGCTTTGATGAAGACATTGCTAATGAGAGCTTGTTAAAGTGAAATG	F	3'UTR	RGMMTD1	0.92328	0.9530086	-0.029728571			
cg10508347	1	45645456	8384659	8384709	Island	CGGCTGCATTCTCTTTGGCATCGAGTTCAGCTACGCCATGGAGACGGCGT	F	1stExon	SLC45A1	0.8526529	0.88839	-0.035737143			
cg10513862	1	7464343	17906056	17906106	N/A	CGTTGGCAATGCAAGAATGTCTACTGTTACTAATATTGCCATTAACCTGC	F	TSS1500;5'UTR	ARHGEF10L	0.9011057	0.9414629	-0.040357143			
cg10513866	5	15646406	139070639	139070689	N/A	CCCCAGGACAGTTCAAGAGGTGCTGGCTGATGAAGCAGGTCCAGAGCATCG	F	N/A	N/A	0.8564829	0.9006114	-0.044128571			
cg10516089	7	10683326	50800620	50800670	N/A	CGGTACTAGGTGCCGTGGCCCACAGGGGAGAGTATGTAATGAGTTTGTCA	R	5'UTR;TSS1500;TSS1500	GRB10	0.8693886	0.89678	-0.027391429			
cg10519465	11	62668402	124765397	124765447	N/A	CGAGCCCCGGCCAGAGGATGGTCTCACTTTGAACTCGTAGTCTTGGCCCCA	F	Body	ROBO4	0.7113971	0.7692129	-0.057815714			
cg10520780	16	53654362	49655451	49655501	N/A	CGGGTCCCAGGGGCCTGCCTCAGACCCCCAAGTGCCCTGAGTTTATG	F	Body	ZNF423	0.7313357	0.78717	-0.05648	0.7564338	0.7878157	-0.031382
cg10522770	7	64643457	158646303	158646353	N_Shelf	CGGCTGCTACAGACAGATGATTTATGCTATCTTATGAGTGAGAGCTGCAC	R	N/A	N/A	0.7283729	0.8031957	-0.074822857	0.7582075	0.8031957	-0.044988
cg10523000	1	19802351	118198739	118198789	N/A	AATTTAATACTTATAGTAGCTCTTGGCTGGGAATGGTTACCCTCCTCACG	R	N/A	N/A	0.7258929	0.8085014	-0.082608571			
cg10523645	2	57633337	241717162	241717312	Island	CGCGCGGGTCCTTCAAAGTCTCTGTCACTGTCCCTGCAGGGTCCCTCG	F	Body	KIF1A	0.8215971	0.8797786	-0.058181429	0.8305813	0.8797786	-0.049197
cg10528989	14	43706323	96722306	96722356	N_Shelf	ATCTGCAGGTCTGCAAGTCTGCCCGATGTATTGTTGGCGAAACACG	F	TSS1500	BDNFRB1	0.6491343	0.7506529	-0.101518571	0.6937063	0.7506529	-0.056947
cg10535478	6	36735418	132859643	132859693	N/A	GAAGGGCATCACAGTGACTCCCCACCAAGAAGTCAGCACAGGCCAGCGACG	F	1stExon	TAAR9	0.8271371	0.8636157	-0.036478571	0.8434563	0.8636157	-0.020159
cg10536101	1	5362394	16400330	16400380	S_Shore	GTTAAATTCATGTTTGGTTTACTTTGTGCCCCAAATGCCAGGAGTCTCCCCG	F	TSS1500	FAM131C				0.2710663	0.1966757	0.0743905
cg10547761	20	21642389	5829461	5829511	N/A	CGGAGGATAATAGATGAATGGTCAGAAAAAAACAAACCCAGAAAAAGCG	R	Body	C20orf196	0.7826457	0.8475286	-0.064882857			
cg10552698	3	15773439	58418944	58418994	N_Shore	CCATTTCCAGAACTTTTTAATCATCCCAAGCAGAAACTGTCCATTACTCG	F	Body	PDHB	0.1153404	0.1618057	-0.046465286			
cg10557351	2	16621300	197508083	197508133	S_Shelf	CGGGTGGCACTGGTGTGGATGCAAACCAAATTCCTACCGCGACATGTTG	F	Body	CCDC150	0.8973557	0.9254414	-0.028085714			
cg10566699	11	19687499	60551807	60551857	N/A	TTTCATAGAGCAGTGGTCCCCAACCGTTCTGGCACTTGGGGACCAGTTTCG	F	TSS1500	MS4A10	0.5108329	0.5900386	-0.079205714			
cg10572858	15	15615421	72742016	72742066	N/A	CGCTGCCAGGCAAATATTAAAATTTTGATAACAGCAGGTCCAGAGCATCG	F	N/A	AKAP6	0.8456657	0.9089557	-0.0633			
cg10573553	21	28704508	47918580	47918630	Island	CGAGCCCTGGCTCGCCGGGTCATTCAGGGCTCGTCCACCTCATCCTCTG	F	Body;Body;Body;Body;Body;B	DIP2A	0.9071157	0.9345814	-0.027465714	0.917735	0.9345814	-0.016846
cg10574283	6	25749442	157110510	157110560	N/A	CGTGTCATCACAGCAATAATGTGGGCAGAAGGCACATGTTTGTGAAGAGC	F	Body;Body;Body	ARID1B	0.7797429	0.8275529	-0.04781			
cg10574897	1	61725466	85157233	85157283	S_Shore	CCGGAGAAGGTGTCACCTCCCAGTTTGCAGTGACGTATCCAATCCTGG	F	TSS1500;TSS1500;TSS1500	SSX2IP	0.8172343	0.8669071	-0.049627857			
cg10577216	6	12657387	143265045	143265095	N_Shore	AAACCTATTATCAAGAGATTCCTTCTGGTCTCCTCGAAGTCATCCCCAGCG	R	5'UTR	HIVEP2	0.6569029	0.7834029	-0.1265			
cg10579668	6	39808410	169238387	169238437	N/A	GTGTTCGGTTCGGGTGCCGTGGGCGGGCTCTGGGATTGCCTGTGTCACCG	F	N/A	N/A	0.78867	0.86065	-0.07198	0.8044888	0.86065	-0.056161
cg10582808	1	10656483	99774415	99774465	N/A	CGCTCATACTGGCTTTGCTGTTTGTAGAGGAAAGGTGGGCTGGTTTT	F	3'UTR;3'UTR	LPPR4	0.8121414	0.8639014	-0.05176			
cg10582858	11	37725465	121069561	121069611	N/A	CGGGGGCCTCTTGGTGTTTCTTAGTATCCTGTTGAGGTTTTGGGCGTC	R	N/A	N/A	0.8849643	0.92515	-0.040185714	0.8949075	0.92515	-0.030243
cg10585586	1	61711335	85362120	85362170	S_Shelf	CGTGTGAGCTTGGCTAGTGTGATACTGTAGGCAAATATTGTAATTCTCAA	F	5'UTR	N/A	0.7999571	0.8610957	-0.061138571	0.8209275	0.8610957	-0.040168
cg10599543	5	30665328	33649717	33649767	N/A	CGATCCCACTCCGCTGACATGGTCCAAGTGCAGCGAGGAGTACATCACCC	R	Body	ADAMTS12	0.9001643	0.9301143	-0.02995			
cg10599737	5	40716428	56107106	56107156	N_Shelf	CGATGGCTCTCAAAGAATCAGTGAAGTGAG	F	N/A	N/A	0.85626	0.89838	-0.04212			
cg10597661	8	30690326	8256332	8256382	N/A	AGCTTACAAAGCCTGCTTGTTAATCAGCCCCATCACATGTCTTTTGACCG	F	N/A	N/A	0.8884243	0.9123986	-0.023974286			
cg10613815	8	39674358	11283299	11283349	N/A	CGCTATACCAGAGGCAGGAATTTGCTACTTACTGCCAAAAGATCTGT	R	Body;Body	C8orf12	0.5689914	0.6629157	-0.093924286			
cg10614045	11	10612413	20182122	20182172	Island	TTTGAAAAGTGACAGCTCTGACAATGAAGTTCAACAAAGTTCTCCACTCG	R	TSS1500	DBX1				0.1416075	0.0993147	0.0422928
cg10614223	19	53779306	18111389	18111439	N_Shore	CCTTGTTTCTTTCTTTCTCTCTCTCTCTTTTTTAAGAAGATCTCG	F	TSS1500	ARHGC2	0.5687357	0.6229786	-0.054242857			
cg10616672	12	18751368	32112379	32112429	Island	CCCCTGGAGGCGGACCCCACTTGACTTAAACTCTGGGGCCCGGGAGCCG	R	5'UTR;1stExon	C12orf35	0.1788671	0.2179714	-0.039104286	0.191645	0.2179714	-0.026326
cg10616974	17	72639309	74511719	74511769	N/A	CGGTTCAGGTCACACGGGATGATAGTAGCAGTTGACTCAGTGGCAGCGT	R	N/A	N/A	0.4787914	0.6216557	-0.142864286	0.5450363	0.6216557	-0.076619
cg10621552	6	2861411	158464770	158464820	N/A	GCCGCCAGTGAGCTTGGCGGTAGCACTGCCTGGCGAACCACCTGAGTTTCG	R	Body	SYNJ2	0.9135714	0.94341	-0.029835571			
cg10621610	1	14724432	91175627	91175677	N_Shore	CGGCGCCCAATTTCCAGCCAAGCCCAGCTAGCTGAGTTTGTTCTCAGCTAA	F	N/A	N/A	0.69918	0.7680686	-0.068888571			
cg10625090	1	15644477	3731643	3731693	Island	GGAAGGTCCTGTTTGGAGAGAGCCAGAGAGCACCGCCGGGAGGCGCTCG	F	3'UTR	KIAA0562	0.8246271	0.8822943	-0.057667143	0.8404325	0.8822943	-0.041862
cg10625096	6	43611489	29518072	29518122	N_Shelf	GGGAAACTGGTTCTCCTATCATTAGTACTTTCCTGAAGGTGTCCCG	R	N/A	N/A	0.8360571	0.8865243	-0.050467143	0.8533838	0.8865243	-0.033141
cg10626792	11	27691306	1849375	1849425	S_Shore	ATCTGCGTTCGAGGCAGGCAGTGGGGGTTAGGCTGCTGAAGACCCTGACG	R	N/A	N/A	0.8817043	0.9156086	-0.033904286			
cg10634598	11	57673309	45740552	45740602	N/A	CGCCCACCTGCTCTCCTGCCACCGGCTGGGTTTCTCTGCCTGCCTGCCTT	F	N/A	N/A	0.8600143	0.8901414	-0.030127143	0.863255	0.8901414	-0.026886
cg10635645	12	65708506	12938397	12938447	N_Shore	CCTGCCAGACACACATCCCGTATTTAGGAAACGAACATTGTGTTCG	F	Body;TSS200	APOLD1	0.82437	0.8587057	-0.034335714			
cg10652915	10	44674381	130844960	130844910	N/A	CCAGGAATGTGAGCGCAAGCTCTCAGCCTCAAAGCTCTACCTCCTTCG	R	N/A	N/A	0.8961371	0.9274586	-0.031321429			
cg10664162	10	62645449	676761	676811	N_Shore	GAGAATGAAACTGGCAGCCATAGAATCCGGGCCTTGATGCCCAGGCCTCG	R	Body	DIP2C	0.8675543	0.91123	-0.043675714			
cg10669129	15	36688469	25444152	25444202	N/A	ATTGGTTCCCCTGGCCCTGTGCCCTGTGGTCCCGGAGTGGCTTCGGGATCG	R	TSS1500	SNORD115-16	0.7316643	0.8027371	-0.071072857			
cg10671380	15	71716423	80445874	80445924	N/A	GTGTGTTTCTCCTCCCAAGAGCGGCCAGGTCGAGGGCTTGTCCTCCTCG	R	Body	FAH				0.0389696	0.0603789	-0.021409
cg10684547	7	21617372	155580133	155580183	Island	CGGAGGTCCCTTGCGCTGGGCCGTGGTCGGGAGCTCCCGGCAGAGATGCG	F	N/A	N/A	0.072856	0.0436324	-0.029223571			
cg10687131	2	55799382	20871002	20871052	Island	CGAGCCCACCAACCATGCCATCATTCAGACCGCTGCTCAACTCCATGGCAC	F	Body	GDF7	0.5049086	0.6503371	-0.145428571	0.5664325	0.6503371	-0.083905
cg10687420	7	50700373	120935804	120935854	N/A	GGCAACATGGTTCAGGAGCCAAGCGCTGCACATCGCACACAATTTGGGATCG	R	3'UTR	C7orf58	0.9120643	0.9416157	-0.029551429	0.9284913	0.9416157	-0.013124
cg10687644	11	59777391	72527615	72527665	S_Shore	CTGTGCATTCTACAGACCTTCAGGCCTTCACAGCCTGCACCACCG	F	Body	ATG16L2	0.8077986	0.8456514	-0.037852857			
cg10692922	19	41616409	17594512	17594562	N_Shelf	ATGGCTTTCATTGTGAACCCCTCCTCGGGGCCCATGAGCCTCATGGAGCCG	R	Body	SLC27A1	0.8904471	0.9175071	-0.02706			
cg10703619	7	13789398	155014511	155014561	N/A	CGCCCTCTGCCTCAGGCAGGGCACTCCCCAACACATGGGCAGCTGCTCAC	R	N/A	N/A	0.8780971	0.9095043	-0.031407143			
cg10704263	17	40717502	76732905	76732955	N/A	AAGCAGCCTTGCAGCTGCCCTAGTGGCTGCAGCCTAAGTGATCCCCCG	R	Body;Body	CYTH1	0.6453357	0.7431643	-0.097828571	0.6925825	0.7431643	-0.050582
cg10706438	15	48688378	22930482	22930532	N/A	GATGTAGAGAGCTTCTGGAGAAGCTAGCCTCTGGAGAGGCTGGCAAGCTG	R	Body	CYP1P1	0.88617	0.9182071	-0.032037143			
cg10709461	20	48701317	22402729	22402779	N/A	CGGTGTCTACTGAAGCCCGCAGCACCTATCAGTGGATGCTACTTGCTTG	F	TSS1500;TSS1500	LOC284788	0.89694	0.9254629	-0.028522857	0.9134875	0.9254629	-0.011975
cg10712934	10	74657473	686201	686251	Island	CGCCCACCAAGGGCTTTGCTTTGTCCCCAGAGGTGCCCTTCGATGGGGTC	F	Body	DIP2C	0.8784543	0.9112357	-0.032781429			
cg10715092	20	16782479	26190034	26190084	S_Shore	GCCACCCCTGCTCCTCCACCCCCACCCCCCCCCCCCCTGAGGAGAAGG	F	TSS1500	ZSWIM6	0.28011	0.1747514	-0.105358571	0.2793025	0.1747514	0.1045511
cg10724054	17	2271377	3904396	3904446	N_Shelf	CGCCCTCACCTGCCTGAAAACCCAGGTGGAAGCAGGGCAGGAGAATGAGC	F	N/A	N/A	0.7378557	0.7886929	-0.050837143	0.7152563	0.7886929	-0.073437
cg10727820	12	11641314	131272183	131272233	N/A	CGCCTGAGCCACGCCCGCTCCTGCTCACCAGGCCTGCGTTGAGCATCT	R	N/A	N/A	0.7907214	0.8411857	-0.050464286	0.8171213	0.8411857	-0.024064
cg10728960	3	73806426	78079111	78079161	N/A	CCCTCTGGTGCGGGCGGGGTGTGGAGGCGCGAGGCCAAGACCGAACTCG	R	N/A	N/A	0.8437314	0.8831357	-0.039404286	0.8606063	0.8831357	-0.022529
cg10732797	3	32717469	10397182	10397232	N_Shelf	AAATGGGAGTCAGCCCAGGTGCCCCTTGGGTCCCTCCCAAGCTCTGACG	F	Body;Body	ATP2B2	0.7374829	0.7888157	-0.051332857			
cg10738119	7	37623493	75957040	75957090	N_Shore	CGCCTGTGAGAGGCACAAAAGCGGCAAAGCTTCTTCTACTAGTTCTTCTG	F	3'UTR	YWHAG	0.7418371	0.8125529	-0.070715714			
cg10762935	11	34618337	63441346	63441396	S_Shelf	TGATAGGCCATAATGCTGCATAAGACACATTCCTATCCTCCAGAGACTCG	R	N/A	N/A	0.7498671	0.8160329	-0.066165714			
cg10763564	2	7162798	242520882	242520932	S_Shore	CGGCCGGAGATAGTTTTTATACAACAGTTGATATCCACAGAATTGAGCGC	R	N/A	N/A	0.9240071	0.9550886	-0.031081429			
cg10764492	12	39758479	107039017	107039067	N/A	TCCTCGGTCACGAGGGTTAGTAAATCCCAACTCACGGGGATGGTGAGCG	R	Body;Body	RFX4				0.6655463	0.7576143	-0.092068
cg10767192	12	50751325	115135606	115135656	N_Shore	CGCACGCCAGTGTTTTGGGGAGCTGGAATTTACCCTGGGGCTTGTCTAA	R	Body;Body	INPP4B	0.7827543	0.8434071	-0.060652857			
cg10768318	20	26665421	25604462	25604512	Island	CCCCCCAGGGGTGGGGGACGTCCTGCAGTGGGGGACGTCCTGCTCC	R	Body	PKHD1	0.9082743	0.9349386	-0.026664286			
cg10769507	12	33745406	18797084	18797134	N/A	CCCATACTAAGGCTTTGATGCAGGGCCAAGCTTGTCTATTTGACACTTCG	R	Body	PDX1	0.1909143	0.3761829	-0.185268571			
cg10773526	4	74628302	143327279	143327329	N/A	CGGGGATAGAGAGGAAAGTCGATTCAGACTTGCTTTAAAAGGAATATTTTT	R	Body;Body	INPP4B	0.7827543	0.8434071	-0.060652857			
cg10775844	6	27623486	51548864	51548914	N/A	CCGGGCAGGTTGTGAGCATATGGGAGCACGAAGGACATTTGCAAGTGAAT	R	Body	PKHD1	0.9082743	0.9349386	-0.026664286			
cg10782668	13	69803428	28496082	28496132	Island	CCGGGCCAAAGGCCTTGAAGTCTCCGGAAATGCCGGGGTTCTTAGGAGGCG	R	Body	PDX1	0.1909143	0.3761829	-0.185268571			
cg10788466	6	19611326	28497605	28497655	N/A	CGGGGACGGCTGCATTCCAATAAAACTTTGTTAACAAAGCCAGGCTGACC	R	Body;Body	GPX5	0.7687157	0.8424086	-0.073692857	0.8000038	0.8424086	-0.042405
cg10795607	5	28685372	77250719	77250769	N_Shelf	GGGATTATAGGTGGGAGACACCATGCCCAGCCTGATTTTTATTTTAAACG	F	N/A	N/A	0.8447557	0.8928757	-0.04812	0.8731738	0.8928757	-0.019702
cg10803321	1	60648336	50823321	50629573	N/A	GTGACAGAGGTTCAGTCTGGTCCAAGGTGACAAGTGCTCAACATCAACCG	R	Body;Body;Body;Body;Body	ELAVL4	0.7711729	0.81416	-0.042987143			
cg10805819	17	63609394	6924109	6924159	N_Shore	AAAACACCCCCAAAATAAGAACACCCCAGAACTTTAGTCTCCTGTCCTCG	N	N/A	N/A	0.8887957	0.9227771	-0.033981429	0.9047263	0.9227771	-0.018051
cg10805880	19	65705421	50400850	50400900	N/A	CGGCCACAGCAGCTGGCATTTCCAAAGGAGCAGCTTCCAGTACTACCCCA	R	TSS1500;Body	IL4Il	0.6167929	0.7269443	-0.110151429			
cg10809556	1	66806387	156697624	156697674	N_Shore	TCTGAGAATTGCTCTTGTGTGTTTTCCTCTCTGCAGATCCG	F	1stExon;5'UTR;TSS1500;TSS	ISG20L2	0.1049584	0.1905286	-0.085570143	0.1251168	0.1905286	-0.065412
cg10819274	14	44761392	54182750	54182800	N/A	CGTAGGTATAACATAGACAATCTTTCAGGATTTGGCATTATGAAGTCATA	R	N/A	N/A	0.7521443	0.85188	-0.099735714	0.8097463	0.85188	-0.042134
cg10833066	12	50642484	111807467	111807517	S_Shore	AATCCAGGACATTTGCGTACAGCAGTTGTCCATACGACAGGGCGCCTCG	N	TSS1500	FAM109A	0.3626771	0.46466	-0.101982857			
cg10835584	18	63660445	55108852	55108902	Island	CACCAGGGCCCAGTGGCAACGGCCAAGCACAGGGATAGTTAGGAGCACTCG	F	Body	ONECUT2	0.3463329	0.4651343	-0.118801429			
cg10848367	11	49721344	62009065	62009115	N/A	CGAGGGCAAGCTTTCTGGTATGTGTAGCCACGTTGATGGGCTTGTCG	R	TSS1500	SCGB1D2				0.4768125	0.5478171	-0.071005
cg10850823	5	37659395	91988522	91988572	N/A	CGGACCATGGGTTGTGCATGGAGTGTGCTTGTTTTCCTGGACCTCAGTG	F	N/A	N/A	0.8106143	0.8693114	-0.058697143	0.830925	0.8693114	-0.038386
cg10855342	4	52766419	113276902	113276952	N/A	CGCCTGCTCTTTGGCCCTAGAGGTCTATGCAGCCCTTTGAGCGTTCTGT	R	5'UTR;5'UTR	ALPK1	0.8400029	0.8766486	-0.036645714	0.8556738	0.8766486	-0.020975
cg10859358	2	60695414	179672126	179672176	N/A	CCCTCCAGGGTTGGAGCGTCTGAAGAACTGAAAAGCACAGTCTTCTAC	F	1stExon;5'UTR;5'UTR;5'UTR;1	TTN	0.9050449	0.9301657	-0.025121429	0.9078845	0.9301657	-0.022321
cg10859442	11	23754337	73716367	73716417	N/A	CACCTAAGCTGGGCCTGGAAGACTGAACAGGCTCTAGGTGTGTGGAGACG	F	Body;Body	UCP3	0.8296914	0.8866857	-0.056994286	0.8496463	0.8866857	-0.037039
cg10860578	14	12732397	101689815	101689865	N/A	CGGGGCCCAGGACAAGTTTTTGTAAGTGTTG

cg11280756	17	18808350	48913424	48913474	N/A	CGCCGGCATCTGCAACGACATGAATCCCAACCTCTGGGTGGACGCAC	F	1stExon	WFIKKN2	0.78445	0.8324386	-0.0479885						
cg11290286	5	47675482	178043484	178043534	N/A	TCATACAAAGTTCAAGAAACTTTGGTGAGTAATTTACCCCCCAAAACACG	R	Body	CLK4	0.8945057	0.92475	-0.0302244286	0.9053838	0.92475	-0.019366			
cg11292878	6	68737404	31599211	31599261	N/Shore	GGAGTCGGGAGTGGAGGCCAGGGCCCCCCCACCACACGCAGAGAGGTCG	R	Body	BAT2	0.7407543	0.7760029	-0.0352485571						
cg11294011	5	62717414	132001686	132001736	N/A	CGCCCTGCGTTGCCTTCTCCACACACAGCCACGGTGACTTTGTTAAAAT	R	N/A	N/A	0.8193943	0.8747671	-0.0553820571	0.8488613	0.8747671	-0.025906			
cg11297586	4	54627352	3513846	3513896	Island	TCAGGTCCGGCTCCGAGAATGTTCCTGTGTCTGAGCCTGGAAGAGGCTCG	F	N/A	N/A	0.9017914	0.92837	-0.0265787571	0.911425	0.92837	-0.016945			
cg11303839	7	45780332	75405967	75406017	N/A	GTTGCTTTTTATATTCACCATGTGGGTTTCCTTCTCGTAAAGTGTTCACG	F	5'UTR	CCL26	0.7678029	0.8737143	-0.105911429						
cg11309462	2	11734355	25585661	25585711	N/A	GACAGGCGGCAGCCAGGATCCAGGCTGTGCACGGGGAACATTGAAGAACG	R	N/A	N/A	0.6228257	0.7301757	-0.10735	0.6669488	0.7301757	-0.063227			
cg11316517	5	65771413	72666838	72666888	N/A	CGTTTCCTTAAATAAGGTTGCTCACTTCAGGGCAATAGCAAGAAGGTTCA	R	N/A	N/A	0.5018886	0.6142871	-0.112398571	0.5438763	0.6142871	-0.070411			
cg11327039	11	19665382	65478175	65478225	N_Shore	AAACTCCAACAAATTCTGTAACTGGGCCCTTGAGCACCTATGCTCAGCCG	R	TSS1500;TSS1500;TSS1500	KAT5	0.84559	0.89047	-0.04488	0.8551625	0.89047	-0.035307			
cg11333968	11	46645400	7569641	7569691	N/A	CGGCTTCCACACTCAAGCATGGTGCAGCAGAGGAAACAGGTGGTTCTGAG	R	5'UTR	PPFIBP2	0.7963043	0.8604529	-0.0641485571						
cg11334822	6	55640418	30128266	30128736	N/A	CGCAAGCCTGTGGGTCACCTCACAACGCCACACATGGACCT	F	1stExon;5'UTR;5'UTR;1stExon	TRIM10	0.7060614	0.7924371	-0.086375714						
cg11336178	6	56685389	42931581	42931631	S_Shelf	CCTCTAGAGCAGACTACAGCTGGGGTGCAGGGATGTGGGTTCCACAGACG	R	3'UTR	GNMT	0.6203971	0.6696614	-0.0492646						
cg11344574	1	40752342	152196415	152196465	N/A	CGCTTCCCTTATAACATGGATATCATGGGGTTCTAATTATTCCACAGGCAG	R	5'UTR	HRNR	0.7466957	0.8275657	-0.08087	0.7938325	0.8275657	-0.033733			
cg11345955	15	38700386	86086674	86086724	N/A	CGCCTTTATATGCCTGCCTGTGAAATTGGTTGAACAAACACTGTGTATTA	F	Body;Body	AKAP13	0.8729786	0.9202829	-0.0473042086	0.8889763	0.9202829	-0.031307			
cg11350520	7	21756367	151074519	151074569	N_Shelf	GCCCTCCTGGTGCCTTTCTCCACACACAGCCACGGTGACCATGAAG	R	3'UTR	NUB1	0.8857286	0.9187929	-0.0330642086						
cg11358405	15	12739457	91382972	91383022	N/A	GATGGTCAGCGGGCCCTTTCCTGAACGCCAGGCCTCTTGCAGGGCCTACG	F	N/A	N/A	0.6495857	0.7406157	-0.09103	0.6881975	0.7406157	-0.052418			
cg11362622	12	14611476	107836508	107836558	N/A	ATAATTGTGCTTCTGGAGGCCCAGGGGGACTCTTAAGTAAGGAGCTTCG	R	Body	BTBD11	0.60476	0.7108957	-0.106135714						
cg11365710	12	29683412	115256061	115256061	N/A	AATAACAGTTAACGATGACGTGACGTTCCGCAGGGCCAGGAGCTCAGGAGCG	F	N/A	N/A	0.8838586	0.92511	-0.0412514 29						
cg11367539	7	62760466	150741096	150741146	Island	CGCCTGGCCATCGCCCGAGCCCTTATCAAGCAGCCCACGGTGCTGATACT	F	Body	ABCB8	0.91986	0.9444043	-0.0245442 86						
cg11374596	2	68647315	29744454	29744504	N/A	TTGGCCTGTTTCTAAGTTTGCCTTTTCCTTCTTTGTTTTTAGGGAACG	F	Body	ALK	0.8149314	0.8804957	-0.0655642 86						
cg11377054	13	13680395	112189885	112189935	N/A	CGCCTGGAGATGCTGTGCACAAAGATGCAACGCTCAGGGCAGTGATGTGG	R	N/A	N/A	0.84917	0.8963271	-0.0471571 43						
cg11377088	13	29658449	73301103	73301153	S_Shore	ATGAACTCTTCTGCCTTGTTTATTATCCCCCAATTATCTCCTTGAAGGT	R	Body;TSS1500	C13orf37	0.1068619	0.14247	-0.0356081 43						
cg11378052	14	40745472	74027108	74027108	N/A	GCGTGAGCCACAGCGCCTGGCTCAGTCTTTACTTTTCATAACAAGAAACG	F	TSS1500	HEATR4	0.80914	0.8787943	-0.0696542 86						
cg11379605	1	73775425	117109623	117109673	N_Shelf	CTCCCACCTCAGTTTCCAAATAGCTGGGACTACAGGGATCGCCTTCACG	F	Body;Body;Body	CD58	0.71863	0.7687114	-0.0500814 29	0.724385	0.7687114	-0.044326			
cg11381404	3	36642458	104813499	104813549	N/A	TTTCTTTGCAGCCTTTCTTCTGGATCTCTCTCCATCATAATGACAACG	F	N/A	N/A	0.7865757	0.8667271	-0.0801514 29	0.8232138	0.8667271	-0.043513			
cg11384661	1	40715407	238025414	238025464	N/A	AAATGAAGATTCCCTTGGCTGCAAGTGAAACCTAGCTCAGACTCCCTTCG	R	TSS200	LOC100130331	0.6913443	0.7888871	-0.0975428 57	0.754765	0.7888871	-0.034122			
cg11398136	2	20613414	112942805	112942855	N_Shelf	CTGGAAGCTTCCACCGGTGTTGATGCATGTGGTCCCCTGGGGGCACACCG	F	Body;Body	FBLN7	0.9018557	0.9275	-0.025644286						
cg11406274	6	31810404	29856564	29856614	Island	CCGGGCCTGGCCTCCACAAGAAGGGAGACATCAATGGGACCAACACTAA	F	Body	HLA-H	0.5558871	0.6894529	-0.133565714	0.584	0.6894529	-0.105453			
cg11407540	4	72642494	110833100	110833110	N/A	CGTACATTTTTGACCAGCACTTGGAACACTACCTCAGGGTAACTTAAATG	F	TSS1500	EGF	0.9060429	0.93701	-0.0309674 13						
cg11411220	10	29691443	35630062	35630112	S_Shelf	CGCTGGGGCCCCTTGGGATCTGCCTGCCATCAGCTCACTCAGTCGCTTGC	F	Body;5'UTR	CCNY	0.6348114	0.7307914	-0.09598						
cg11417360	2	56713461	218955163	218955213	N/A	CGAGAAGTGAAGCGTGCACTATCTTGGACTCTCCAGCAGCTTCCTGTCTG	F	3'UTR	RUFY4	0.6861743	0.7493886	-0.0632142 86						
cg11422156	10	51687471	45477807	45477857	N/A	GCATGAGCACCTCCCTCCACAAGGCTCTCCCTCCACAGGGCTGGCACACG	R	Body	RASSF4	0.6724143	0.7376443	-0.06523	0.69692	0.7376443	-0.040724			
cg11429044	19	17789461	13947473	13947523	S_Shelf	CGGCCGGCTGGGGTTCCTGGGGATGGGATTTGCTTCCTGTCACAAATCAC	R	TSS200;TSS200;TSS1500	MIR23A	0.4647229	0.5896014	-0.124878571						
cg11435225	22	59804443	32014422	32014472	N/A	CGCAGGTGCTGGGCTGTCGGGGAGGCCTCAGGCCACCTCCAGGAACAGAA	F	3'UTR;3'UTR	SFI1	0.7188157	0.78629	-0.0674748 86						
cg11436027	7	21794331	134468027	134468077	N/A	GAGAAATCCCTTGGCTCGAGGATTAAGTCTTAGGCCAGCTCAGACTCCCTTCG	R	5'UTR;5'UTR;5'UTR	CALD1	0.8542757	0.8974729	-0.0431974 13						
cg11440240	10	61738505	134542379	134542429	S_Shelf	CGGCCCGGCCACCGGGCTCAGCAGCTGGCTCCCTTCACCAGGGAGGCTCC	R	Body	INPP5A	0.8929429	0.91845	-0.0255071 43						
cg11450715	2	14637438	17627404	17627454	Island	GGTGGAGCGGGCCCAGGCCGTAGGGCGGTGGAGGGCGCGGGACGGAGCG	F	N/A	N/A	0.5814943	0.6500771	-0.023582857	0.5644513	0.6050771	-0.040626			
cg11462099	13	51627371	113540512	113540562	Island	CGGCCAGCGTCTCCAACAGGGTGACCATCCGCTCGGCTTGCTGAGCGTTT	F	3'UTR;3'UTR	ATP11A	0.3050514	0.2101414	0.09491	0.2997288	0.2101414	0.0895873			
cg11463113	2	68621334	208989831	208989881	S_Shore	GGTGAACTTTTGTTGCAGTTGGGTGTTTTGTTGCCTGCTGGAAGCTT	F	TSS1500	CRYGD	0.7258071	0.81898	-0.0911728 57						
cg11465943	11	49693442	60833378	60833428	N/A	CTCCGACAGGCACTGCACCTTCCAGCTGCGTGCACTGAGGCTGGTCTACG	F	N/A	N/A	0.7352686	0.7966314	-0.0613628 57	0.74018	0.7966314	-0.056451			
cg11466837	11	59747439	120009682	120009732	S_Shore	CGCAGGTAGCAATAATCTAAGGTCTATATGTATCTTGTTGGGGCCATTGG	R	TSS1500	TRIM29	0.8576871	0.9096514	-0.0515964 286						
cg11471262	4	70691347	3318911	3318961	Island	TGCCTTGGTGGACCTTGTGAATTAAACAAGTCTGAGTCCATGATGAACAG	F	Body;Body	RGS12	0.7823257	0.8479086	-0.0655928 57						
cg11480762	10	18657490	73103395	73103445	N/A	GCATGAGGCACCGCTCGCTTGGGTTTTCTTGTGACCCAACCACATTCTCG	F	Body	SLC29A3	0.8076543	0.8565743	-0.04892	0.82875	0.8565743	-0.027824			
cg11484872	6	23783474	31543169	31543219	N/A	TGTGAGGGGTATCCTTGATGCTTGTGTGTCCCCAACTTTCCAAATCCCCG	R	TSS200	TNF	0.7215743	0.7901657	-0.0685914 29						
cg11485655	17	48611393	36032204	36032254	N/A	AAAGATAATTGGACACCATTCCCACTCTCAGGGGCTTATGCTGGAGTCG	R	N/A	N/A	0.8621014	0.9006871	-0.0385854 14						
cg11486637	11	63661397	77599072	77590022	N/A	GCTTCCAGCTTGGCCATCTTCTGCACCTAAGAAGGCTTAAGTCCAGGCG	R	3'UTR	RPTOR	0.8261314	0.87994	-0.0538085 71						
cg11497526	17	41621318	35902366	35902416	N/A	TTTATAGTCTCTGTTTTCATATTCCCTTTTGCTCACTGGTCTGAGGAATCG	R	Body;Body;Body;Body;Body;B	SYNRG	0.7112386	0.8349429	-0.123704286						
cg11499091	17	57748339	78735302	78735352	N/A	CGCGGCAGGAAACCCATGCATCTTCCGTCTCCTGCGGGCAATGCAGGAGC	R	Body;Body	RPTOR	0.6546114	0.7502	-0.120408571						
cg11520439	9	50621494	107536568	107536618	N/A	TCATAAGAATCAGTTGCACATAATAGCCCCCTCCTCCTCCTCCTCCTCC	F	TSS200	LOC286367	0.5751157	0.6546729	-0.079557143						
cg11520719	6	57642393	157391679	157391729	N/A	CGATGCTGAGCTCCTAAACTGATGCTGACATATGTTATAAACTGAGCAAA	R	Body;Body;Body	ARID1B	0.6793171	0.7707486	-0.0914314 29	0.72708	0.7707486	-0.043669			
cg11531239	6	67605448	161348903	161348953	N_Shelf	ACTGCATTTGATCTCTCTGAATATCCTTTCTACCCACCAGGCTGCAATCG	R	N/A	N/A	0.8532014	0.89622	-0.043018571						
cg11534593	11	26750381	120044544	120044594	N/A	TGAAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	R	N/A	N/A	0.7551971	0.8104086	-0.055211429						
cg11538516	4	72683447	170949479	170949529	S_Shore	TGCCTGCCCATCCTCCTCCTCCTTAGACAGAAAACAGCGAATTCCATTCG	F	N/A	N/A	0.8137143	0.8577843	-0.04407						
cg11539052	2	67714346	179347266	179347316	S_Shore	CGCTCTGTTAGCCAGGCTGAAGTGTGTGGGTGACATAGCTCACTGAT	R	Body;Body	MIR548N	0.5453714	0.6354771	-0.090105714						
cg11543592	12	40733358	115124067	115124117	N_Shore	CGAGGTGTGGTGGCCCGAGAGTGTTGGCTCATAACACCCCCTCCCGCATC	F	N/A	N/A	0.4560557	0.5419257	-0.08587	0.4801638	0.5419257	-0.061762			
cg11554153	7	32658462	209615	209215	S_Shore	CGCAAGCAAGGATCTTGTGATTAAACAAGTCTGAGTCCATGATGAACAG	R	Body	FAM20C	0.8124357	0.8500757	-0.03764	0.8325063	0.8500757	-0.017569			
cg11555640	21	42702429	40754783	40754833	S_Shore	ATTTTTTTGAAAAACCACATACTGTTTTCCATAGCAGCCACACCATTCG	R	Body	WRB	0.7314414	0.7962571	-0.0648157 14	0.7656288	0.7962571	-0.030628			
cg11557823	12	32689331	88429167	88429217	Island	TTGTAGTGCAGAAGCTGAGGGCGCTGGTGGGTTCCACGTGCGTCCTCCG	F	TSS200	C12orf29	0.1607014	0.2093014	-0.0486	0.18025	0.2093014	-0.029051			
cg11558107	15	27718412	60700174	60700174	N/A	CGCATCGTGGAGATAAAACCTTTGTTTCAGGCTGGGTGGCTCACG	R	N/A	N/A	0.7696043	0.8578271	-0.088222857						
cg11572675	2	53632239	86155952	86156002	N/A	AGCAGGCTATTTGTGCCAGCAGCTGCAACCTGCTAGGGTCCCCTTTCACG	F	N/A	N/A	0.7743343	0.8112986	-0.0369642 86	0.7853638	0.8112986	-0.025935			
cg11572844	5	26714443	129239273	129239323	N_Shore	CGGCTCTCCTGATGATATCTGTTCAAGAAATGAGAACTATGGTCTATTTT	R	TSS1500	CHSY3	0.83716	0.8884314	-0.0512714 29						
cg11576486	5	15764413	1511473	1511523	N/A	CGCCTCGCTCACCCTACGTGGGGACATCACCTGCTCACCTCGCTCACCCT	F	Body	LPCAT1	0.8442014	0.9030729	-0.0588714 29	0.8672625	0.9030729	-0.03581			
cg11584246	13	66635483	113676726	113676776	N_Shore	GCCTGCTGTGGGTGGAGGACCCCTGCCTGTCCCTGTGGCCCTGGCACG	F	Body;Body	BCF2L	0.8274443	0.8836686	-0.0562242 86						
cg11586034	1	17611360	150117110	150117160	N/A	GGGTTCTGTGCTGGTTGTTAGAACTCATCTCCAGGTAGCCCACGGATACG	R	3'UTR	VPS45	0.7102971	0.7595	-0.049202857						
cg11586857	6	12639487	31540136	31540186	N/A	CGCCCAGCAGTGTCCTGCCCTCTGCCTGGGCCTCGGTCCCTCCTGCACCT	F	1stExon;5'UTR;5'UTR	LTA	0.7775814	0.82729	-0.049708571						
cg11587635	19	50806492	35782698	35782688	N_Shelf	CTTCTGGCCTGGGTGGAAGGTCCATGTTCCTGTTTGGTGAACACCAG	R	TSS1500;TSS1500	MAG	0.8099071	0.8620614	-0.0521542 86						
cg11590974	5	42618459	41142881	41142931	N/A	CGGGATGGTAAATCTGTTCATTGTGCTGGGCCTAGCAGTAATTGTGCTAG	F	3'UTR;3'UTR	C6	0.8591843	0.91303	-0.0538454 14	0.893225	0.91303	-0.019805			
cg11594821	6	25664508	30458601	30458651	S_Shore	GCAGTTCTCTTTGACTCCCAGTATTAGGAAATCACGGGGGAGTTTCTCTCG	R	Body	HLA-E	0.6364171	0.7196986	-0.083281429						
cg11595454	7	40727434	99995398	99995448	N/A	AGTCCCAGGCCCTTCCTGATGGGTTTGGGTGGAGCAGCTCTGCTGCTCCG	R	Body;Body;Body	PILRA	0.8839029	0.9181	-0.0341971 43						
cg11607742	19	40660192	38869946	38869996	S_Shelf	TTGAGTGCCTCAGTGCATGTCACGTGAATGAACAACCTCTC	R	Body	PSMD8	0.9437029	0.9649143	-0.0212114 29						
cg11614536	10	26678433	30348709	30348759	S_Shore	CGTGGCCCAAACCCAAGTGACAAGAAAGAAGGGAATGGTGGTCAGCTCAC	R	TSS1500	KIAA1462	0.1531029	0.1809443	-0.027841429						
cg11622516	3	20682461	120165600	120165650	N_Shore	CGGCATTGTACACTAGGGGTATATTTGGGAGCTCCTCTATGTTCTTTAG	R	Body	FSTL1	0.8994714	0.9312257	-0.031754286						
cg11642199	7	37781359	780967	780417	Island	CGGACGCTGTCGAGCGACGGGCCATCGCGGGCGCCCTCACCCAC	F	Body	HEATR2	0.8819614	0.9034057	-0.0214424 86	0.8707563	0.9034057	-0.032649			
cg11650763	5	24600419	92930530	92930580	Island	CCTTGGTTTTGAAATGCGGAGGGCAGGCTCTACATGGGCTGGGGTCCG	R	N/A	N/A	0.7496443	0.8153043	-0.06566						
cg11650948	12	52600355	31798865	31798915	N/A	CGCTGCCTTGTCCCCCTGCTCAGAGGCAGATGTGACTTAATAGGAAGAAT	F	TSS1500	C12orf72	0.60318	0.6757157	-0.072535714	0.6319475	0.6757157	-0.043768			
cg11653516	6	60626420	116860017	116860017	N_Shelf	CTAACTATGTGCTGGTGGGAGCCAAACCTGGTCACCGCGAGCG	F	N/A	N/A	0.9019943	0.93846	-0.0344657 14						
cg11654904	1	65645348	40945066	40945116	S_Shore	CCTCCACGGCCTTCTTTGGATGTTGCAGCTTCACCCAGGTGCTGGCCTCG	F	Body	ZNF642	0.7460929	0.7857029	-0.03961						
cg11666098	5	27706493	29151828	29151878	N/A	TAAGAACAAAGCCTCATTCTATTCTAAGTGGTCTCATTCCATCTATTTCG	F	N/A	N/A	0.8305871	0.8867814	-0.0561942 86						
cg11669998	19	60753415	18879431	18879481	N/A	CAACAGGGGGCCACCAGGGGGCAGGCCGGGCGGCCGTCTGGGGGTGGCG	F	Body;Body	CRTC1	0.8499571	0.88526	-0.0353028 57						
cg11680826	19	49683374	37710094	37710144	S_Shore	GACTGTTTTTGCTGTCCAGCTTCCCTGTGATGCCCACGTCATCCTCCG	R	N/A	N/A	0.68296	0.8262157	-0.1422557 14						
cg11685489	7	67796312	121755577	121755627	N/A	CGGTGGACCTAAAATTATATTTCCAGCTCTAATATCAGTAGGGTATGACC	F	Body	AASS	0.9001486	0.93444	-0.0342914 29						
cg11691164	5	25798505	102982781	102982831	N/A	CGGAAAGTGTCCTCAGAGGTTAACAAGGATCATATGCCAGGTTCTGGGC	F	N/A	N/A	0.9231643	0.9410829	-0.0179185 71						
cg11697111	7	46737438	1126903	1126953	Island	CGCTGCAAAAGCCGTCGAAGTTTGGCCGGAATTGGACCCCTTCTTTCG	F	5'UTR;Body;Body;Body;5'UTR	GPER	0.1678814	0.1180299	0.049651571	0.149965	0.1180299	0.0319351			
cg11697618	7	74800328	137866502	137866552	N/A	CGGGCTCGGCTAGGTTGCTCTTGCTGTGCAATTCTGGAACTCATGCAAC	R	N/A	N/A	0.8428557	0.8880229	-0.045167143						
cg11699208	8	60635471	1813963	1814013	N/A	CGGTCTTGGCCTTCCCAGCAGTGTCTCTGCGCGTGCCCACCGGGCTCATCCT	F	Body	ARHGEF10	0.8091457	0.8485671	-0.0394214 29	0.8216275	0.8485671	-0.02694			
cg11699517	17	18725430	79419796	79419846	N_Shore	CCCCCGTGGGACGTGGGGCAGGCAGCGAGCTTGAGTGTTTGCGCTTCCTCG	F	Body	BAHCC1	0.9314557	0.9581143	-0.026658571						
cg11704201	12	32694329	132303491	132303541	N/A	CGCTGAACTCCAGATCCGGGCTTCTGTCTGTCTGTCACAGAACCTGA	N	N/A	N/A	0.8698814	0.91501	-0.0451285 71	0.8875988	0.91501	-0.027411			
cg11706849	2	34802445	135047381	135047431	N/A	CGAGCTGTGACGACAAATGTGGCTCACCAAGGAAGGTCTTTAGAGACTCT	F	Body	MGAT5	0.9182457	0.9516029	-0.0333571 43	0.930825	0.9516029	-0.020778			
cg11712286	21	30719477	46349088	46349138	N/Shelf	CGGCCCACGCATTTCCCATCCTGAAGGGTCCAGCTCATAGGCCGGCCCAT	F	TSS1500	ITGB2	0.88107	0.9194171	-0.0383474 13	0.9063088	0.9194171	-0.013108			
cg11714430	2	44676360	191517695	191517645	S_Shelf	CGTTGGCCGGTCTCAACGCCCTCGGCCTCACGACGCACAGGCCTCG	F	5'UTR	NAB1	0.7783	0.8395943	-0.061294286	0.8053188	0.8395943	-0.034276			
cg11716160	12	10794403	7342787	7342837	Island	CAGTGCTTTGCTGCGACCCCCACCTCTGCCCAGGAGTTCGAGGGAGGTCG	F	5'UTR;TSS200;5'UTR;1stExon	PEX5				0.6617154	0.096128	-0.034413			
cg11718780	1	67777408	200728684	200728734	N/A	AACCAAAACTGGTACTTCGAAAAATCTGCAGCTGGGCGCGGTGGCTCACG	F	Body	CAMSAP1L1	0.5297414	0.5752114	-0.04547	0.5490438	0.5752114	-0.026168			
cg11719283	19	30641437	42574717	42574767	N/A	TCCTTGTGGGGTTTGTGGGCCTCAGCCCACTTCTTGGACAGTCTTGACG	F	N/A	N/A	0.7352429	0.7776229	-0.04238						
cg11731300	1	47747404	161008542	161008592	Island	CCCCCCGCCGCCGCCGCTGCCGACGAAGACCCCCTCCGTCCTTCG	F	Body;Body;Body	TYD1				0.1122689	0.1646186	-0.05235			
cg11732134	1	43804325	10732912	10732962	N/A	CGGCGGCTCCGTTCCACGTCCGCCTCCTTTGGCCTTAATATTTAATTTTG	F	Body;Body	CASZ1	0.8780686	0.9072943	-0.029225714						
cg11738782	7	17687425	121727301	121727351	N/A	CGTGCCTTGATGAGAAGAAAATGGAAACTATTTATCTGGATGTAA	F	Body	AASS	0.8479329	0.9059443	-0.0580114 29	0.8746525	0.9059443	-0.031292			
cg11746813	12	73692302	54448490	54448140	Island	TAACGTGAATTTTTTCATCCATGGGTACTACTATGGGTTCTGCTGGCG	F	1stExon;Body	VKX2-4	0.2784714	0.35957	-0.081098571						
cg11748354	6	43676496	53200697	53200747	N/A	CGGAAGACTGAGGCCACACTAAGCCTGACAGACGTATGATGAGCAAGGAA	F	5'UTR	ELOVL5	0.72115	0.7940957	-0.0729454 71						
cg11759288	21	48647434	46696759	46696809	Island	CGGCCGCTCCCGAGAGCAGGTCATTACTGTGACTCACATTCCAGAGAGGC	F	Body;Body;Body	POFUT2	0.9123086	0.9399586	-0.02765						
cg11761483	17	63711354	70723386	70723436	N/A	CGTCACTTCAAAGAACATGTTCTCTGGAGAGGAGACATGCCCTCAGCTGC	R	Body;Body	SLC39A11	0.6389829	0.7204943	-0.0815114 29						
cg11763066	6	62696377	158640499	158640549	N/A	TTGCTGGCAGCAAGGACTTCCTGGTTACAGTTCTATCCATCAGCGGTGA	R	N/A	N/A	0.4168729	0.5194857	-0.102592857						
cg11771602	2	27662407	134976155	134976205	N/A	CGGCAGACCATGGAAGGGAGCCCCGTGGTGAACCCATCCTAGACCAGATC	R	N/A	N/A	0.8751557	0.9129757	-0.03782	0.9000988	0.9129757	-0.012877			
cg11780053	19	12642462	7268027	7268077	S_Shore	GCAGAGCCGGCTTCATGGACAGGAAACCTGGGCCCTGTGTTTTCATCCCG	R	Body;Body	INSR	0.9061043	0.9311386	-0.025034286						
cg11781135	10	57627450	30818581	30818631	N/A	CGTGAAGTTTGTGCTGGTCCGAGTCGAGCTATCTTCACGCGGTGAACG	R	N/A	N/A	0.5173971	0.6037271	-0.08633	0.5391163	0.6037271	-0.064611			
cg11790673	1	17654304	212845129	212845179	N/A	CGGGCTTTTCCTACCAGTATTTGTGTTTTCTTTAGGTGTGAGAGACACA	R	N/A	N/A	0.61833	0.6848571	-0.0665274 43	0.64922	0.6848571	-0.035637			
cg11801374	20	60727326	30597694	30597744	N/A	AGTGCCAAAGCCAAGGATTCGAATTCAAGCAGCCTATCTTCAAAGCCCAG	R	TSS1500	C20orf160	0.6971714	0.7536543	-0.0564828 57	0.7210738	0.7536543	-0.032581			
cg11802797	1	44621315	10437649	10437699	N/A	CCGGAGATTCCTGGTGGATAAACTTGATGGTTATTGATGATT	3'UTR	KIF1B	0.3702143	0.46591	-0.095696714							
cg11804789	20	19662318	24929716	24929766	N/A	CGGTTGCTTTGTGGCTGATAGATCTGAAGGTGAAGAGCTTCTGGCCAAAA	F	TSS200	CST7	0.7328186	0.82347	-0.0906514 29	0.7632475	0.82347	-0.060223			
cg11804940	12	45639380	122402696	122402746	N/A	CGTGGGAGACTGAAGCAGGAAATCTCATGAACCCGGGAAGGTGGAAGTTGC	F	Body	WDR66	0.7169157	0.7846571	-0.0677414 29	0.7528013	0.7846571	-0.031856			
cg11812100	5	63766431	40685989	40686039	S_Shelf	CGTCAGGGCTGAGAAAAAAAACTTGTTAGGAGATATTCAATACAAACAA	R	Body	PTGER4	0.6838286	0.7753286	-0.0915						
cg11823736	8	41775364	39792275	39792325	N/A	AACAAGGCCTGTCTGCAGACATCGCCTTGGCCTTGATGGAACACCG	R	TSS200	IDO2	0.7319157	0.7978814	-0.0659757 14						
cg11824179	19	25792392	18826937	18826987	N_Shelf	CAACAAGGGTGGGCTGTGGCTGCTGCACTCACTACAGGGTCCCCAGGGCG	F	Body;Body	CRTC1	0.8810043	0.9096586	-0.028654286	0.8895013	0.9096586	-0.020157			
cg11824764	17	65809456	78812487	78812537	N/A	ATCTGTGCAGAATGCAAGGGAGCAATCGGCAAGAGGGCGCGGCAGACAG	R	Body;Body	RPTOR	0.8091614	0.8496586	-0.0404971 43	0.826785	0.8496586	-0.022874			
cg11828741	11	47804326	10715167	10715187	N/A	TAAACCACCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	R	TSS1500;TSS1500;TSS1500	NR1I3	0.6857443	0.7653671	-0.079822857						
cg11830605	8	14794434	58926487	58926537	N/A	CGTGCTGGCATGCCTGTCACTGTGCTGTGAAAGTGACTGGGACATGGGCC	F	5'UTR	FAM110B	0.8381343	0.8889986	-0.0508642 86	0.8650013	0.8889986	-0.023997			
cg11832000	10	64620508	61153075	61153125	N/A	CGGCATGGTGCTTCTCAGCTATGCCTGATATTGTTATGTAGAAATGTAGG	F	N/A	N/A	0.7928414	0.8361671	-0.043325714						
cg11834730	12	44675460	124942248	124942298	S_Shore	CGGGAGGGCCCCGGGGCAGCCCAGAAATAATCACATGATTGTGAAACACA	R	Body;Body	NCOR2	0.5851771	0.7273914	-0.142124286	0.6631763	0.7273914	-0.064215			
cg11835695	19	50731350	1555445	1555445	N_Shore	GGCAGGCGGGTGGTGTTTACAGATGGTTTACAGATGTGCTTCTCTGCAG	3'UTR	MEX3D	0.90825	0.9344286	-0.026178571							
cg11838542	7	14757360	2128505	2128555	N/A	CGGTGGCAGAGGGTGAGCACCAGCCCTGTGTGAACCTTCAACCTCCTCT	R	Body;Body;Body	MAD1L1	0.8283	0.8670586	-0.03875871						
cg11844769	2	59604466	27505593	27505643	N/A

cg12159577	4	57744346	57186067	57186117	S_Shelf	AATGATAATCCCCATGCTTGTACTATAAACACTTTCAGGCCAGGCACG	R	Body	KIAA1211	0.8565014	0.9084186	-0.0519171143	0.8655938	0.9084186	-0.042825
cg12163800	17	30747492	74475355	74475405	Island	CGCCCCTGCGGAAGCAGACAAGGGACAGGTGGGCATACGCTTGTCTACGC	F	Body;Body	RHBDF2	0.86182	0.8977657	-0.035945714			
cg12164472	8	62681306	54794628	54794678	Island	CGGGAAAGCCACCCCGGTCCCGGAGCGCCCGCTTCCCTAGAGGCCCTGGC	R	Body;Body	RGS20	0.0976853	0.0665111	0.031174143	0.0780563	0.0665111	0.0115451
cg12171980	19	14782483	8395847	8395897	N_Shelf	ACATGTTGGCCAGGCTCAAACTGCGTTACCAACTCATCTGCCTGCCTCG	F	Body	KAIN3	0.8495371	0.8916571	-0.04212	0.8779063	0.8916571	0.013751
cg12175883	10	46616503	119449252	119449302	N/A	CTATTTCTTCTTTCCTTTGGGTTCTCTTGGTGATAGGCAGTTTGCCATCG	R	N/A	N/A	0.5433743	0.6487971	-0.105422857	0.5812325	0.6487971	-0.067565
cg12175922	12	60684445	116077537	116077587	N/A	CGCCCTGCGGAATCCCTCCAGGAATTACTCCCTGGTCCTCTCGACTGGC	R	N/A	N/A	0.6721	0.7573443	-0.085244286			
cg12191488	3	60639488	123607235	123607285	S_Shelf	AAGTCCAGCCACCATATATATTTTTGACACTACTCAGAAACAACAAACG	F	N/A	N/A	0.8291971	0.8779857	-0.048788571	0.8545813	0.8779857	-0.023404
cg12196389	10	26702445	35504007	35504057	Island	CGAGTTCTCACTGCGTGTGTCTTTCTTTGAACCCTAAAAGTTTCATCTGG	F	N/A	N/A	0.46156	0.7208357	-0.259275714			
cg12196692	5	49781470	41071405	41071455	N/A	GAGCATGCTCAGTTCATATGACTGATTTTCACTAAGTGTAAACAATCAACG	F	1stExon;5'UTR	HEATR7B2	0.8700971	0.91719	-0.047092857			
cg12196847	14	32632340	81426577	81426627	N/A	CGTGAGATTATTTTAGGTGGAGTGCCCACCTGGCATTAAATAACCGTGAA	R	Body;Body;Body	TSHR	0.8473557	0.9009243	-0.053568571			
cg12205555	12	66764493	28837108	28837158	N/A	ATTATGCCTCCAGGATCTGGTTCTCCTTACAGAGGTTGCCACTGAGGTTTTCG	R	N/A	N/A	0.9182314	0.9503229	-0.032091429			
cg12216419	13	17720317	114220724	114220774	S_Shelf	CCAGAGGGAACCCGAATTCCCTGTTGAGTGCGACTTTCTTTCTTTTTGCG	F	N/A	N/A	0.8948529	0.9276071	-0.032754286			
cg12216688	2	66611326	121197381	121197431	N_Shelf	CGGGCTGCCCTCTTGAGTCACCTATGTAGGGCCCTGGTCTACGTGGTGAA	F	N/A	N/A	0.7387814	0.7876843	-0.048902857			
cg12223279	10	23613323	132004186	132004236	N/A	CGGAGCTAAGCGACGTTCCCCGTCTCTCATGACTGTGGCCCCGAGCATCT	R	N/A	N/A	0.8216271	0.8782329	-0.056605714	0.8437263	0.8782329	-0.034507
cg12229555	17	12757390	80260379	80260429	N/A	CCCGCGCCTCCCAAGCCACCTCACACTCGGGAGAGCCGCGACGAGCCC	R	N/A	N/A	0.7276029	0.8033271	-0.075724286			
cg12247500	11	33748474	111796862	111796912	N_Shore	CGCATACTCTGTAGCGTTTTCTAAATGCACGTGTTTCACTTCCCGGGCAT	R	Body	C11orf52	0.9419629	0.9685886	-0.026625714			
cg12249537	3	69619360	100990781	100990831	N/A	CGCCTGTGGAGCATAAGGAACTATGTGAAGATCACACCGACACTGGAACT	F	Body	IMPG2	0.8035329	0.85576	-0.052227143			
cg12252868	2	41662497	112383396	112383446	N/A	ACTGACAAGCCAGCACTCCTAAGTGGAAACACGTGGGCACAGACAAAAATCG	R	N/A	N/A	0.7925	0.8442471	-0.051747143			
cg12256688	12	73764327	131200855	131200905	S_Shore	CGGAGACAACTGCAGTGTACTGTGTGCAGATTACAAACTGGGGGCGAGACG	R	N/A	N/A	0.0580314	0.0906643	-0.032632857	0.0683213	0.0906643	-0.022343
cg12257170	19	41755415	2222026	2222076	S_Shelf	GGAGGACTCATCCAAGGTGGCCGGCTCGGCTCCAGGTGTGAGAGGCCG	F	Body	DOT1L	0.8868671	0.9203029	-0.033435714	0.9004425	0.9203029	-0.01986
cg12262781	6	14741406	116866784	116866834	N/A	CGCTTTGAGACAGGAGTGCTGCTTCTGCACTTCTGCTGCTTTTGCTCTTTG	F	5'UTR;TSS200	FAM26D	0.7102843	0.7715657	-0.061281429			
cg12279397	10	17648332	47882836	47882886	N/A	CCGGGCCCTGCTCTTCCGCGGGAGGAATCATGCACATTCTGCCAGGGTT	R	N/A	N/A	0.5562443	0.6441571	-0.087912857			
cg12281647	17	41802347	2598799	2598849	Island	TGGGGGCCTGAGCTGCTGCGACCCCGCAGGTGAAGGACTGCATGGAGCACG	F	Body;Body	KIAA0664	0.9042	0.9310457	-0.026525714			
cg12303627	1	30788443	75549256	75549306	N/A	AAGGATTGAGAATCACAAATGGTTTTTCTCTATAATCTCTTCTCACTTCG	F	N/A	N/A	0.2326071	0.3553014	-0.122694286	0.2615538	0.3553014	-0.093748
cg12305798	2	43735381	24396650	24396600	N_Shore	CGATGGAGGTATAGCTGTTCTTGGCTGCTGGCTGCTGAAGGTATTTGCG	F	TSS1500	C2orf84	0.8408971	0.8950029	-0.054105714	0.84968	0.8950029	-0.045323
cg12314424	5	28600414	1806843	1806893	N/A	CGGCTGTGCCATTTTACATTCCCAGCAGCAAGGCACAAAGTTCAGTTGC	R	Body	NDUFS6	0.86406	0.8988643	-0.034804286			
cg12342520	7	20616359	1393991	1394041	N/A	CGCTGCCCTGTCCATAGGCGCCAGCGCGACCCCAAATCATTTGCACCCAG	F	N/A	N/A	0.9207971	0.9429914	-0.022194286			
cg12344249	5	53602509	16479970	16479920	N/A	CCTGAGAGATTCCTGGTAAGGTATATTTTAGATTTAGATGCTGAAA	R	Body;Body	FAM134B	0.8012486	0.8634071	-0.062158571			
cg12354382	3	38769407	133118839	133118889	N/A	GTCCAGTGGCTTTTGGTTTACAGCCCCAGCATCCCTGTGGCCTGGTCACG	F	1stExon;5'UTR	BFSP2	0.8213586	0.8613257	-0.039967143			
cg12366968	7	39774478	1883876	1883926	N_Shore	TTGGCAGGGGGGCCTGTGGGACCACCACACTTCTCCCCAAGGGCACACCG	F	Body;Body;Body	MAD1L1	0.71833	0.7753657	-0.057035714			
cg12400790	7	25799407	2635181	2635231	S_Shelf	CGCTGAGGAGTGGAGAGGCAGGAGAGCATCCATCTAGGTCCTCGTCTA	R	Body;Body	IQCE	0.8869014	0.9305571	-0.043755714			
cg12405246	1	35704380	24655061	24656011	N_Shelf	CCACAAACCATTTTCTGCTTGTGATAAAGCCTGAGCCCCTGCATCAACG	R	Body;5'UTR;Body	GRHL3	0.8377343	0.87949	-0.041755714			
cg12419482	11	72697497	72933282	72933332	S_Shelf	CGACCTGGCTTCCTGGTGAGTGCCCAGCCAACCCAGCCCTGGCTTGTAGGA	F	5'UTR;5'UTR;5'UTR	P2RY2	0.8388343	0.8834343	-0.0446	0.8582538	0.8834343	-0.025181
cg12420683	7	32739351	26578547	26578597	N/A	CGGCTTGACACAAAGGATGTGCATGCTTTATGTTGTCAGATGATATAAAC	R	TSS200	KIAA0087	0.6538286	0.7510643	-0.097235714	0.6769013	0.7510643	-0.074163
cg12421814	4	46709340	3449570	3449620	N_Shore	CTGGCCTGGAGCACAGCAGCCCTGCCTTGCTGCCAGTTTTGCCCGCACCG	F	Body	HGFAC	0.8011043	0.8353029	-0.034198571			
cg12423493	11	36744342	64007813	64007863	N_Shore	TGTCTTCCTTTTACAATTGAGGAAATAGGCTCAGAAAGGCTAACTGGCCG	R	TSS1500;TSS1500	FKBP2	0.57173	0.6837671	-0.112037143	0.62746	0.6837671	-0.056307
cg12423623	2	56808425	45469414	45469464	N/A	CGGAGCTGGACTTGTTTCCAACACAAAAAATAGTTGCCAGAGACATATTT	R	N/A	N/A	0.5584386	0.7089443	-0.150505714	0.6386563	0.7089443	-0.070288
cg12434085	6	35732301	138576877	138576927	N/A	CGGGTGGAAGCCATCAAAATAATGAAAGAGGTGAGGAGGGCACTGGAGATC	F	Body	KIAA1244	0.8631857	0.9041471	-0.040961429			
cg12435134	4	70732498	76860890	76860940	S_Shore	ACAGGTGTGAGCCAACGCGCCGCCCTTTGAGCATAATTTTAAAAGTACG	R	Body;Body	HAAS	0.6661543	0.7547471	-0.088592857	0.7245875	0.7547471	-0.03016
cg12449055	2	54711380	24009752	24009702	N_Shelf	CGGGCTGAATGCCCCTTGCTTTGATGTTAATATTGAATCCTGCAGCCCTG	F	Body	HDAC4	0.8718171	0.9231814	-0.051364286	0.8948325	0.9231814	-0.028349
cg12450872	15	42665329	63386759	63386809	N/A	CGGGAGCCAGGCCTCTTAGCTTTGCTATTTGTGTCAGTTCCCAAGGGAAC	R	N/A	N/A	0.8113143	0.8701529	-0.058838571	0.832215	0.8701529	-0.037938
cg12472290	5	12804374	52841682	52841732	N/A	CGTGACAGATTTCCTGTCAGAAAACTGAGGTATTGTTTGGATTCC	R	N/A	N/A	0.6940686	0.7808614	-0.086792857			
cg12473849	3	51783304	136882749	136882799	N/A	CCGAAGCACATAACAAAAGCCAAGTTAAGAAGGTTAGCGATTTAGTTGTC	F	N/A	N/A	0.6267243	0.7300929	-0.103368571			
cg12477903	5	54612392	176829557	176829607	Island	TGACGGCCTCGGGGAAGGGCGCCAACCGGGCTAAGAGCTCACCTGGCACG	R	Body	F12	0.4995029	0.5600043	-0.060501429			
cg12481426	20	41684308	32950490	32950540	N_Shore	GGTGCTCAACTGCTGTCCCAGCTACTCAGGAAGCCCAGGTGGGAGGCTCG	R	TSS1500	ITCH	0.6325457	0.7158129	-0.083267143			
cg12484153	6	49726362	31634875	31634925	S_Shore	CGGTGGCAACTCCAGACCTTTGGCGCCCCAGTTTTGCCGCCCCAGGTT	R	Body	CSNK2B	0.8287757	0.88169	-0.052914286	0.8631625	0.88169	-0.018527
cg12510035	12	11679332	53228633	53228683	N/A	CGCCCTGTCACCTGTGCACACACCCTGGACCTGGGGAGGAGTGGTGGGCC	R	TSS1500	KRT79	0.8564857	0.8911057	-0.03462			
cg12510087	12	21683486	132887175	132887225	S_Shore	AGCTGGGAGCTTGAAAGCCCACTTCCTTCCAAGTTGAAAAATCACAGCCG	F	Body	GALNT9	0.4930357	0.5680443	-0.075008571			
cg12513352	10	45671384	11204956	11205006	S_Shelf	TATGTGGGCTCCTGCCATTATTTATCCCCCTCCCCCTCCCCCCCCCCCC	F	Body;Body	CUGBP2	0.7227471	0.7852371	-0.06249	0.7255575	0.7852371	-0.05968
cg12517061	20	34791477	35520777	35520827	N/A	CGGGGGCAGGATTTGATGTTTTGTTTTTAGCCATGTTTGTCAATGACAAT	F	3'UTR;3'UTR	SAMHD1	0.93096	0.9642257	-0.033265714	0.9382788	0.9642257	-0.025947
cg12519676	4	53611306	174912210	174912260	N/A	GGCCCTGTTAGTGTAGCGTGACCCCTGGCGCATTCGCACAGATAATACCG	R	N/A	N/A	0.24818	0.1671343	0.081045714			
cg12522144	2	14756450	97526855	97526905	N_Shore	GCCCTCCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	F	Body	SEMA4C	0.8968571	0.9216243	-0.024767143			
cg12530994	10	58663360	5136782	5136832	N/A	AGTGAGTCATCCAGAGTAAGGTAGGAAACACGAACCTTACAACCCAATACG	F	Body	AKR1C3	0.1510571	0.1037597	0.047297429			
cg12533565	7	15612387	6694373	6694423	Island	GGGAGGCTGAGGGTCCCAGTCCTGGGTGCGGTGCCTTCCCTCAGCCCTCG	R	N/A	N/A	0.8957914	0.9252671	-0.029457714			
cg12547531	7	2267302	30960786	30960836	N/A	TGCTGATGTGGTCCATCTCCCCTGTGTGAGTGCACTTAGCCCCTGGGAGC	R	Body	AQP1	0.7412571	0.8169086	-0.075651429			
cg12556586	15	71741368	59733552	59733602	S_Shelf	GCCACACTTGTGGCAGTGTCTCAAGAGCCACATGTGGCAGTGACTACCATACG	F	5'UTR	FAM81A	0.7609429	0.8233271	-0.062394286			
cg12561776	17	27775410	30844705	30844755	N_Shore	CTAGGCCAGTTCCCAGGCAGCTAATTGGAGCATTTATCTGAAGCAAAGCG	F	Body	MYO1D	0.8245943	0.8801029	-0.055508571			
cg12564698	11	17706308	68458524	68458574	N/A	TCTGTGTGCTGTAACCTGAAGTCAAACCTTAAGATAATGGATAATCTTCG	R	3'UTR	GAL	0.5779271	0.7117714	-0.133844286	0.6285113	0.7117714	-0.08326
cg12569119	10	50794348	105541150	105541200	N/A	CCTTCATTTCTCCTTTTGCCTGCTGGCTAGATCTGAAAACTTCCACG	R	Body	SH3PXD2A	0.7498671	0.8032214	-0.053542857			
cg12606682	11	37640443	62190604	62190654	N/A	CGGCAGAGGCTGGAGCAGTTGGGGATCTTCAGCTTCTAAATGCTAATTAC	R	3'UTR	SCGB1A1	0.82957	0.8737029	-0.044132857	0.8356688	0.8737029	-0.038034
cg12614113	10	67604494	79133935	79133985	N/A	TTGTTTGCAGCTCTCCCCTTCTAAGAGTTCAGGACTCTGGTAGTCAGAGCG	F	Body;Body;Body;Body	KCNMA1	0.8935829	0.92594	-0.032357143			
cg12617684	11	52687505	2364835	2364885	N/A	CGGTTCATAGCTGCTTCTGGGAGGCCTCAGGAAGTTTCAGTCATGGTTG	F	N/A	N/A	0.7898986	0.8412671	-0.051368571	0.8036438	0.8412671	-0.037623
cg12629909	6	60685336	32126616	32126666	N/A	CGTGCTTCAGGAGCCTCTGCAGGTGCCAGACGCTTCTTCTTCTTCTCCG	F	Body;Body	PPT2	0.7497229	0.8239071	-0.074184286			
cg12635463	6	66607428	163607896	163607946	N/A	CGGGAGGCCGACTAAATACCTCCTGACTGTGCCCCTCAGCGGGTAGGAAC	R	Body;Body;Body	PACRG	0.8887614	0.9206114	-0.03185			
cg12641739	1	67665358	235062535	235062585	N/A	CGCACCTGAGTGGAGATTTCTCATGCAGCACCAAGGGATTTCTGCCATCGT	R	N/A	N/A	0.8172829	0.8747643	-0.057481429	0.8418275	0.8747643	-0.032937
cg12648523	17	20702318	37884634	37884684	N_Shelf	CAGAGTGGGTCTGGATCGTTGGACGCCAGTGTGTGAGCAGTGCCCTGCG	R	3'UTR;3'UTR	ERBB2	0.8809529	0.9074414	-0.026488571			
cg12648616	1	18676467	109944060	109944110	S_Shelf	GTTAACAGCACTGTAAATCCATTTCGGCCCTATAATTTCTGGAGCAAACG	F	N/A	N/A	0.7927357	0.8720629	-0.079327143			
cg12654519	4	11694380	148715234	148715284	N/A	CGGGAGCTGAAGTGTAGGGGAGGGAGCAGGCTCGAACACAAATAATTATG	F	Body	ARHGAP10	0.5116757	0.5922814	-0.080605714			
cg12655250	4	23774508	2860776	2860826	N/A	CGTAGGGCGTTGCTGGTACAAAGTCAAAACCTGCATCATTGGGCCCTGCG	R	5'UTR;5'UTR;5'UTR;5'UTR	ADD1	0.8743757	0.9344771	-0.060101429			
cg12658400	1	64770382	1974826	1974876	Island	CCCCTCCCCCACTCCTCACTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCG	N	N/A	N/A	0.9200826	0.9422514	-0.022168571	0.9173713	0.9422514	-0.02488
cg12660813	1	22724472	3192343	3192393	N_Shelf	CGCCCCCCTGGCTCTCACTGGTGGTTCTCACGTCACCCTCAGCAAAAGGT	R	Body;Body	PRDM16	0.60454	0.6873071	-0.082767143	0.6217738	0.6873071	-0.065533
cg12666899	15	22733402	68711872	68711922	N/A	GAAGTGACAACAGGGACTCTATTTCCAAACAATGGGTACACTCAGTACG	F	Body;Body	ITGA11	0.86765	0.8981243	-0.030474286			
cg12678507	7	40764393	1934407	1934417	N_Shelf	CCGGACTGTTGGCTGGTTCAGCTCCCAGCCCTGGTCACCCCGTGCTT	R	Body;Body;Body	MAD1L1	0.8456629	0.8879686	-0.042305714			
cg12678686	3	70764488	127327369	127327419	S_Shelf	GCAGATCTGGTGGAGCAGCTGGAAGCCAGGACGAGAGATAGTAAGTGGCCG	R	Body	MCM2	0.8093386	0.85506	-0.045721429			
cg12681784	17	63686433	79428750	79428800	Island	CAGGAGGGTGGGCACGGGGTGGGTGAGGCAGGTCTGCAGCAGCAGACCG	F	Body	BAHCC1	0.84189	0.8829629	-0.040972857			
cg12684958	4	25719432	7492145	7492175	N/A	ATAAATGGTGCCTATTCAGTGTTCATCAGGTTTCACCAATTAAGTCTCG	R	TSS1500	PPP6R2	0.8145	0.8684043	-0.053962286			
cg12693436	10	40620324	47130971	47131021	N/A	CGTCTCCCCAGCTTGGCCTTGGTGCTCTGGGACCTCCCCAACTGCACAAC	R	N/A	N/A	0.69872	0.7666157	-0.067895714	0.7312838	0.7666157	-0.035332
cg12695586	3	51664362	8810077	8810127	Island	GTGCCCTGTTGTTTCAGATGAGTTGGGTTCCTGGGAATGGGACAAGCACG	F	5'UTR	OXTR	0.1029351	0.1408686	-0.037933429			
cg12701674	13	72650407	114908876	114908926	N_Shelf	TGGTTGTCCTGGCTGGCACCTTCGGACACATGCTCTCACACG	F	N/A	N/A	0.5927114	0.64814	-0.055428571			
cg12704854	6	15705363	30942969	30942919	Island	CGGCTGCCATGGTCCCGCCGGCTTCCCCGCCGGCTTCCCCGCCGGCTCC	F	Body;Body	RNF39	0.26697	0.2343543	0.032615714	0.2558025	0.2343543	0.0214482
cg12708799	10	63602355	438227	438277	N/A	AAGGCGGCTCTGCTGAGCCAGGAAGTGCCGGGCCGAGGCAGGAGAACACG	R	Body	DIP2C	0.7957629	0.8229786	-0.027215714			
cg12711832	8	54697402	68258899	68258949	S_Shelf	CAGGATGCTGGTGCAGGTCCAGGGCCACCAAGCAAGGTTGTGGAGATCG	R	N/A	N/A	0.6525971	0.7231414	-0.070544286			
cg12713012	4	55681374	3471866	3471866	N_Shelf	CTGAGTGGTGGTTAGAGCTCTGCACGCTGCTGTGAGGTCACAGCG	R	Body;Body	DOK7	0.8312257	0.8744757	-0.04325			
cg12718579	8	29713460	53322451	53322501	N/A	CGGGACATGAGCCCGCTTGTTCGCTCACTCTCAGTGAAAAGAGTTTTGAA	R	TSS200	ST18	0.7731143	0.81271	-0.039595714	0.785365	0.81271	-0.027345
cg12730853	1	47642422	64935328	64935378	N_Shore	CGCGGAGATTAAAGGATAATGTGCACACCCCCGAGCCCAGTGCCGGGCAC	F	TSS1500	CACHD1	0.1860643	0.1365486	0.049515714	0.1736875	0.1365486	0.0371389
cg12734023	2	43719375	64863580	64863630	N/A	CAGGAGGGTGGGCACGGGGTGGGTGAGGCAGGTCTGCAGCAGCAGACCG	F	Body;Body;Body;Body	SERTAD2	0.68006	0.7826571	-0.102597143			
cg12734688	1	62760361	48308440	48308490	N/A	ATAAATGGTGCCTATTCAGTGTTCATCAATTAGCTATTTGAGAGCATTGCAG	R	TSS1500	PPP6R2	0.8145	0.8684043	-0.053962286			
cg12748491	4	24709441	169801641	169801691	S_Shelf	TATGTGGTTACCGTTTTGTCCTCAAGGAATTTTCCTGTTGCTAAATCACG	R	Body;Body;Body;Body	PALLD	0.77365	0.89119	-0.11754			
cg12758082	13	41646354	113407769	113407819	N_Shelf	CGCTGCCCGGCTTGCCAGCTTCTGGGCCTGCCTACCGCTGCTGGATGAGA	F	Body;Body	ATP11A	0.7333457	0.7917214	-0.058375714			
cg12769506	4	70726327	187647740	187647790	Island	CCGCGGGCTTCCGAGCCAGGGCAAACTTAAGCACCAAACGGCCGAAAGA	N	N/A	N/A	0.1275929	0.0878531	0.039739714	0.1155638	0.0878531	0.0277106
cg12777730	10	72732366	63657985	63658035	N/A	CGAGATTAACTTAGAGAGTTGGATTTTTGGCTAGTAAAGCAGCAAGAATA	F	N/A	N/A	0.6137471	0.7267086	-0.112961429			
cg12782654	11	67740303	66085299	66085349	S_Shore	CGCTGGCCCAGCTGGAACCAGAAAGCTTGAGTATAGGGGGAGAGGCTGAC	R	TSS1500	CD248	0.4697329	0.5737886	-0.104055714			
cg12784386	17	43792403	79031712	79031762	N/A	CTTTTCTTCTCTCTCAGGTGTGACGTATGCAGCCAAAGGCTACTTTGACG	R	Body;Body	BAIAP2	0.8398514	0.9027571	-0.062905714			
cg12784990	14	53640309	44408473	44408523	N/A	ACTGGCAAATGCTTACCTGAAGTTTACTTCCTCTGCTCACTTCCG	R	Body	OSMR	0.8019071	0.8600914	-0.058194286			
cg12788878	3	50766420	124860616	124860666	Island	GCCAGCCTCTCCCATTGTCCATTCGCAGGAAAGGGCTGTCTGGCTGGTCG	F	Body	SLC12A8	0.2266497	0.4025629	-0.175913143			
cg12789488	10	28791370	133760222	133760272	N/A	CGGCTTAGCATCTGAAGTGATGGGTTGAAGCCAGCTGTGCCGACCGAAGCA	R	Body;Body	PPP2R2D	0.7701286	0.8649043	-0.094775714			
cg12797879	20	50772475	13283868	13283908	S_Shelf	TTGAAGCAGCAGCGTCTGATCTTCAACAGCCTACCTACCTGCAGCAGCG	N	N/A	N/A	0.8968729	0.9298514	-0.033297857			
cg12804647	1	33732448	48470601	48470651	N/A	CACTGAAGTAGACACACATGAGTTCATGCCACTGCTTTGCTTCAAACCCG	F	N/A	N/A	0.8780543	0.9064871	-0.028432857	0.8867725	0.9064871	-0.019715
cg12805865	11	38759443	27061999	27061949	N/A	CGGGCAAGAAGCAACAAGTTTCAGGCTGCTTCTACATCTGCCTAGGAAGA	F	TSS1500	BBOX1	0.7734214	0.8350029	-0.061581429	0.7945488	0.8350029	-0.040454
cg12806892	12	55795432	113340341	113340391	N/A	CGGTCTTCAACGAATGATTAGGAAACAACGGACATTTATGGGGTGTAAC	R	N/A	N/A	0.7211457	0.8072571	-0.086111429			
cg12810264	10	57690382	43329042	43329142	N_Shelf	CGTGGTCCTGGTCTGGTCTGCAGTCCTCATCTGTCGGCATTGTCTGCAG	F	3'UTR	BMS1	0.8759057	0.9074857	-0.03158	0.89492	0.9074857	-0.012566
cg12810800	2	49777420	159788345	159788395	N/A	TTGGAGGTCCACTCAGGGCCCCTTCCCATTTTCCTGTCCTGACTAAGGCAACG	F	N/A	N/A	0.6813243	0.7345871	-0.053262857	0.6888075	0.7345871	-0.04578
cg12819231	11	32748414	75946229	75946279	Island	AGCTCCACACATGGTTCAGAGAGAATTCTCCTGCCCAGGATCCCAGCCCG	R	N/A	N/A	0.1132339	0.1696	-0.056366143			
cg12827950	18	29779355	55968429	55968479	N_Shelf	CCTTCTTCAGAATTGAGACTTCTGGGCCATTTTAGCCAGAAGTATCTCCG	F	5'UTR;Body;5'UTR;5'UTR;5'U	ZNF804A	0.89076	0.9316471	-0.040887143			
cg12829666	3	55689479	153840379	153840429	Island	CGGGGGCTCTTTCCCTGGGCCCCAGAAAGGTTCTTCTTCGGAACAAAAACTCCCC	F	Body	SGEF	0.3433729	0.4068343	-0.063461429	0.3606063	0.4068343	-0.046228
cg12842791	5	68758409	86491450	86491500	N/A	CGCAACAAAAGTGCTATAGCATGTAGTCACTAATTATAAATTAGGAGATT	R	N/A	N/A	0.9138443	0.9428914	-0.029047143			
cg12848457	10	29688429	52566370	52566320	N/A	CGTTCTTCAGTTTGGTATAAGCCTATAAGTGTCCTCGGGCCATT	F	N/A	N/A	0.6387088	0.7386086	-0.0999	0.6742238	0.7386086	-0.064385
cg12859101	8	50714372	41464845	41464845	N/A	ACATCCCTTTGGCCTCCTGCTTTTAATTTCAGGAACATGACAAAACACG	F	Body	AGPAT6	0.7837171	0.8397757	-0.056058571			
cg12879425	4	25764458	68424495	68424545	N/A	GGCTTCTTAGCCATCATACCCCCTCTCTTTGGTGTGTGGTTTGGTTTCTCG	F	5'UTR;1stExon	STAP1	0.6654386	0.7328014	-0.067362857	0.7000238	0.7328014	-0.032778
cg12892471	12	70609360	50616779	50616829	N/A	CGGATAGTGGCAGCAAGGATTGAAACAATTTGTAGAACCCTGGAGAAGTC	F	Body;TSS1500;Body	LIMA1	0.5658914	0.7176471	-0.151755714			
cg12894629	3	30622444	195942717	195942767	N/A	ACACAACCTTTTGTCTTGTGTACGGTGCTGCTGCTGCTGCTGCTGCTGCT	F	TSS1500	OST4alpha	0.7160343	0.8182271	-0.102192857	0.74933	0.8182271	-0.068897
cg12903024	15	57653317	89765204	89765254	N/A	ATAGGCCTGGATTTGCCAGAGCTGCCACTGTAGATGTAGTCATATTTACG	F	TSS1500	RLBP1	0.8816543	0.9132829	-0.031628571			
cg12925682	5	62735434	38872169	38872219	N/A	AGAGAGCTGGACAGAACCAGGAGCCCTAGGTTCTGGTCTGATTGTGCG	R	Body;Body	OSMR	0.7100614	0.8071914	-0.09713			
cg12928081	14	45791498	102482233	102482283	Island	CTTTCTAGGATCAAGAATGCAGTTGCATGACATCGACGCTACTTTCACG	R	Body	PYHC1H1				0.9356138	0.9206871	0.0149266
cg12935786	15	21649334	89156942	89156992	N/A	CGAGCTGTGGTGACTTTGAGTCAGTTACATTACATCTCTGAGTCTCAGATT	F	N/A	N/A	0.6559243	0.7132143	-0.05729			
cg12944192	14	51800402	35683834	35683884	N/A	CGGCCCCAGCTTGTTTTTGGGGTGCCAGGAACCACACCCATGTAAGATGG	R	Body	KIAA0391	0.4952743	0.6186486	-0.123374286	0.5547175	0.6186486	-0.063931
cg12945054	7	21794502	12841881	12841931	N/A	CGCAGTGGTTCTCTAAAGGCTTACGCCTAATTAAAAGCCCAGAGGGTGCAGG	R	N/A	N/A	0.7586257	0.8440843	-0.085458571			
cg12958046	4	65735464	38019409	38019459	S_Shelf	TTATAGGAACTGCTGCTGTTGTGCAAATACCAGCTGCTGCTGCTGCTGCT	F	Body	TBC1D1	0.8845486	0.9136686	-0.02912	0.8888188	0.9136686	-0.02485
cg12963111	17	62626389	80893951	80894001	N/A	TTGTTGCTTTTGAGTGTTACCTCTGAGTCTGCCTGTGCTCCCTGGAAACG	F	Body	TBCD	0.8426086	0.8955114	-0.052902857			
cg12967319	14	57743308	101291997	101292047	N/A	CGGGCGACATAACTGGTTCCCAGATGTAAGCCAGAGGCTGTCACCCCCTC	R	TSS1500;TSS1500;TSS1500	MEG3	0.4877214	0.5502729	-0.062551429			
cg12969178	20	6273481	20152544	20152594	N/A	AGACCCCCTCCCAGAGTGGACTTTCTTCCTTCTGCTGGAGCTAGCTCCG	F	Body;3'UTR	C2orf26				0.8752313	0.9268343	-0.051603
cg12972064	3	36673443	171887343	171887443	N/A	TACTTAGCCAGTATCAAGTAATTAAAAACCACTCCATGGATGGGGCCACG	R	Body;Body	FNDC3B				0.5591863	0.4930043	0.066182
cg12973294	4	41621354	119869807	119869857	N/A	CTGGTTGTTTAAAAGAGTGTGACACCTCTTTCCCTCTCTCTTTTCCTTCG	F	Body;Body;Body	SYNPO2	0.7954543	0.83943	-0.043975714			
cg12974599	22

cg13389146	2	58633419	96808802	96808852	N_Shore	TGGGGCCAAGAGAGCAGCCTTTGTGGGGAGGGTCAGACCTGCCCCTTCCG	R	N/A	N/A	0.8371014	0.89653	-0.059428571	0.8693663	0.89653	-0.027164
cg13391235	16	45609448	85316611	85316661	N_Shore	AGTTGGACATCAGCTGGGGCTGGAGTCACCTGCAGGCTGGCCTGGGGTCG	R	N/A	N/A	0.8070943	0.8685457	-0.061451429			
cg13393036	8	20659308	95962371	95962421	Island	CTAAGTTCCGTGGGTCACATGAGAGCTAGGCTGCAGCGCCTGGGGAGCGCG	F	TSS1500;TSS1500	TP53INP1				0.313205	0.1639356	0.1492694
cg13395854	11	46795330	61308748	61308798	N/A	CGCCCAGGTCTTCCGTGGAGGACATTTTCACGGAGCAGGAGGCCCAGCACA	R	Body	SYT1	0.7832114	0.8314971	-0.048285714			
cg13396044	2	14655301	11748153	11748203	N_Shelf	TTCCTCTGTGCACTGAAAAACATTACCACTGCTTGATGCTGAGCCTCACG	R	Body	GREB1	0.9177657	0.9505871	-0.032821429	0.9296563	0.9505871	-0.020931
cg13404688	10	35779372	89876324	89876374	N/A	CGCAGCAGATTCAAAGGGTTTCTTATTTATGAAGAGCTGCTCTCCAATGGA	F	N/A	N/A	0.8512914	0.9040229	-0.052731429	0.87857	0.9040229	-0.025453
cg13422676	9	67690417	138399394	138399444	N/A	CGAGGAACGGTCGCTGCTCTGCCCCCAGGTGACGCTCTAGCTTTCTCTGTG	R	N/A	N/A	0.88844	0.9151529	-0.026712857			
cg13423371	9	48787309	138701748	138701798	N/A	CCTATAATTCCTTCTAGCCTTCTGTACCATGTTCCCTCCTTATGTACACG	R	3'UTR	CAMSAP1	0.9005957	0.9301243	-0.029628571	0.91695	0.9301243	-0.013174
cg13424284	1	52635352	26624129	26624179	N/A	GCCAGTTCCTGTGAGGTAGGGAGAGGTGCGGCCCACACCTGAGGACCCCC	F	Body;Body;Body	UBXN11	0.85115	0.8844	-0.03325			
cg13428066	11	59611432	2677768	2677818	N/A	CGCCTGACTAGCAATCAGGGAAATGTAAATAAACTCAGGAGCTCATGGCC	R	Body;Body;Body	KCNQ1	0.7347543	0.7958871	-0.061132857	0.7476738	0.7958871	-0.048213
cg13428921	9	20716343	138837056	138837106	N/A	GCCTGCAAAATGTCTGGTGCTCAGGCCATGGAGTGGCGCTTGAACACG	C	Body	UBAC1	0.9301214	0.9490943	-0.018972857			
cg13430450	9	40711508	107691064	107691114	S_Shore	CGCCTATCAAAAATCAAAGTCCAGGTTTGTGGGGGGAAAACAAAAGCAGC	R	TSS1500	ABCA1						
cg13441058	2	20666410	45028269	45028319	N_Shore	AGAACGCCCAGGGATTTTTCAGAGCAGAAAGCCGGTCCCCAGCGTGACG	R	N/A	N/A	0.6737657	0.75141	-0.077644286	0.7042013	0.75141	-0.047209
cg13443950	4	30633338	138584567	138584617	N/A	CGGGTGCCCACCCTAGAATTAACCCTAGGATGGTGAATCAGGATTCAG	R	N/A	N/A	0.40902	0.4931314	-0.084111429			
cg13446288	2	18640486	102313644	102313694	Island	CACTAACAAGGCTGGAGTCAACTGAGTTTGCCGCAGGGCAAGGGTTGTCCCG	F	TSS1500;TSS1500;TSS1500	MEP4K4	0.1167857	0.1392629	-0.022477143	0.1109004	0.1392629	-0.028362
cg13446918	1	49761440	8599482	8599532	N/A	TCAACCATCATAGTTTTCTTTCTTTTCCTTTTTTTTTTTCTTTTTTCTCG	R	Body;Body	RERE	0.8539886	0.8839486	-0.02996			
cg13446974	3	47681371	128293318	128293368	N/A	CGGCCTCATTTTGTCTTTTAATGAATAGTGACTAGCACAGCCTTAGAGA	R	5'UTR	C3orf27	0.8363757	0.8828629	-0.046487143			
cg13447566	9	64628452	133801594	133801594	S_Shelf	ACCACGTGACTTTAACTCAAGTGATGTTTGCCGCAGCGCCAGGGCCGTG	F	Body;Body	FBXO31	0.6032357	0.6802457	-0.07701	0.6257763	0.6802457	-0.054469
cg13456688	9	12725400	124965049	124965099	N/A	CGTTCCCAGGCTGCTCTTAACAGGGTAGTGGAGACATGTTTGAACTGTAA	F	3'UTR;3'UTR	LHX6	0.7851629	0.8317457	-0.046582857	0.8079563	0.8317457	-0.023789
cg13458803	3	17786494	119276917	119276967	N/A	AGGGCTGTGGTTGGTTCTTGGAACTGGTCCCCTCTACAGAATTTCCATTCG	F	5'UTR	CD80	0.8367986	0.9010343	-0.064235714			
cg13460850	3	61809481	184302398	184302448	S_Shore	CGCCCTAAGAGTCTCCCATGGCAGAACGGGTAGGGGGAAGGGATGCAGAGA	R	N/A	N/A	0.7834286	0.8373629	-0.053934286			
cg13461622	1	20757378	25291385	25291435	N/A	CCCTTCTTTGGCTGACCACAGTGCAACATTCTACAGTATACACCGGTGAATCC	R	TSS1500;5'UTR	PHNX3	0.7495757	0.8426629	-0.096087143	0.7835763	0.8426629	-0.059087
cg13462219	8	55784406	144649510	144649560	Island	CGCCCCCGCGCCCCGCCCGGCCCCCCACCAGTCTTCGCCGACAGCCCCTTCC	R	Body	C8orf73						
cg13462821	8	34777310	86214814	86214864	N/A	CGCTGGTCCTCTTGGAATCTTGAGAGCCATCCTTGAGGGGCTGCAATTTG	F	N/A	N/A	0.8237971	0.8873243	-0.063527143			
cg13465587	21	41686507	39040273	39040323	S_Shore	TTTCCTCCTCACGAGCTCCTCCGGGCCCACACTCCCTCTTAAAAGCG	R	Body	CFAP53	0.8845929	0.9251443	-0.040551429	0.9049075	0.9251443	-0.020237
cg13466546	17	31639438	77926436	77926486	S_Shelf	AAAGCCCAGGCTGCCAGGGAAAACACACAGGGCCAACTCCCAGGAGGCG	R	Body	TBC1D16	0.6554786	0.7134543	-0.058065714	0.6785513	0.7134543	-0.034993
cg13470969	1	41637327	152490870	152490920	S_Shelf	CGTGTGGTCTCTGTCTGGACCAGGCCTTCTAATGCCCTCTAAGAAGGCCA	R	N/A	N/A	0.6883929	0.7483957	-0.060002857			
cg13476200	9	19613404	124578224	124578274	N/A	CCTCTGGCCCACGTCCACCGCCCTGACAGCGGGGCTCCTGGAGGTCTGGT	R	N/A	N/A	0.7928557	0.8514157	-0.05856			
cg13480549	1	28770328	2058790	2058840	N/A	GGGGGGCAGTGGAGGTGCAGCCCCTCCATCTGAGGGACCTGCCCGGATCG	F	5'UTR;Body;5'UTR	PRKCZ	0.6938471	0.7739886	-0.080141429	0.71031	0.7739886	-0.063679
cg13486641	20	33731371	25479848	25479898	N/A	CAGTGACGTGGTGGGGACGGTGTGCTTGTGTGTAGGGACAGCTTTCCAGGCG	F	Body	NINL	0.8919457	0.9212743	-0.029328571			
cg13487445	9	51782338	134150226	134150276	N_Shore	CACAGGGTAGACACTGAGAGAGGCTCTGGGAGTGTCAGCGGCCATGCAG	R	Body	FAM78A	0.6028129	0.6786386	-0.075825714			
cg13487682	9	38660417	140151756	140151806	S_Shore	TGAGGGAGTTTCCACAGGTTTAAATGTTGTCCATATATCCTTTTACCG	F	Body	COBRA1	0.8869314	0.9160757	-0.029144286			
cg13491907	9	15793397	16144575	16144625	N/A	CGAATGTTTTGAGAGTATCTCTGATGAGTCAGAAGTGCGCTAGTGAAACA	F	N/A	N/A	0.7749414	0.8378143	-0.062872857	0.80099	0.8378143	-0.036824
cg13492600	19	69658503	6010231	6010281	S_Shelf	CGGGGACAGCGGCTCCCGCAACGGGCTGCACAGCACTCCGGAACAGACCA	R	Body;Body	RFX2	0.9208614	0.9502671	-0.029405714	0.9360288	0.9502671	-0.014238
cg13493652	7	55797398	6385721	6385771	S_Shelf	TACAGGCATAAGACAAATGATGAGCCACAAGTTTCTTTAAAATCCCG	R	5'UTR	C7orf70	0.7044386	0.7817214	-0.077282857			
cg13499717	3	22799466	157307519	157307569	N/A	ACCCAAGATTCAAATTTGTCCTGACCTGGAATAAATCAGAAAGTGGCTCG	F	Body;Body	C3orf55	0.6347086	0.72452	-0.089811429			
cg13500388	16	22691474	67062135	67062185	N_Shore	CGGGTATGAGCTACAGTGCCCGGCACCAGGACTAACTTTGAATTCAAACTC	F	TSS1500;TSS1500	CBFB	0.7384229	0.7964329	-0.05801	0.771455	0.7964329	-0.024978
cg13500819	5	12608463	138725400	138725450	N_Shelf	AGTGGTGAAGGACTCACCTGGTAAGCCACAGCTCTGCAGGCATCACAGGCG	R	1stExon	MGC29506	0.8005443	0.8606057	-0.060061429			
cg13501527	9	38748401	123640474	123640524	S_Shore	AACAAACATTTGCGTATAGACCTGTGCAGAGAATGGTACAATACACGCGG	R	TSS1500;TSS1500	PHF19	0.7970014	0.8520029	-0.055001429	0.8200813	0.8520029	-0.031922
cg13505693	7	17674504	155989496	155989546	N/A	ACGGTGTGGCCTCAGCCAGTGCGGGGGAACTGTGGCCTGCATCAGCAAACG	R	N/A	N/A	0.6491386	0.6977243	-0.048585714			
cg13518992	18	66804438	55109119	55109169	S_Shore	CGGGTCTAACAGGGAGAATCTTGTGTCCTACCTTGGCTGGGACAGGAAGT	F	Body	ONECUT2	0.4187843	0.5553457	-0.136561429	0.50791	0.5553457	-0.047436
cg13522279	2	32663312	144635077	144635127	N/A	TTATTAGATAAACTCAGGCCTCATGTTGCGAAATGTTGATCAAATACAG	R	N/A	N/A	0.7090357	0.7609343	-0.051898571	0.699465	0.7609343	-0.061469
cg13525013	10	40790389	98908962	98909012	N/A	CGGGCTGATGCGCCCAGCATGGATGAATGTCCTAGACACAGCCCTGGTGC	R	Body	SLIT1				0.9541838	0.9412671	0.0129166
cg13537801	17	54716453	79663039	79663089	Island	AGCTGCTGGAGCTGCTCAACCAGCTGGACGAGCGCAGGCGTAGGTGCCCG	R	Body	HGS	0.8318386	0.8559886	-0.02415			
cg13543683	9	23667462	101175220	101175270	N/A	CAGTCATCACGATTGGATCAGAGCCTTTTAGTCCAATCACATTCTACG	R	Body	GABBR2	0.7723529	0.8099071	-0.037554286			
cg13549444	12	6961341	7060524	7060574	N/A	CTTGCTTGCTCTAAAACGAGAAGTACAAGTTCCAAGTTGGAGCCCTCG	R	1stExon;5'UTR;5'UTR;Body;1	CTNNA1	0.7079086	0.78277	-0.074861429	0.7378088	0.78277	-0.044961
cg13554549	22	56655345	47191940	47191990	S_Shelf	CGCCCCGGGCTGGAGCCCCCAGCCCACTGCTTGGTGTGCGGCTGCTACAAA	F	Body	TBC1D22A	0.7609	0.7973886	-0.036488571			
cg13554818	19	49731440	43979316	43979366	N_Shore	TCCGTATTAATTCGGTATCACAGGAGCACCAATAAATAGTTTCTTCCCG	R	3'UTR	PHLDB3	0.4690243	0.62809	-0.159065714			
cg13557411	15	59764377	74703161	74703211	Island	CAGCAGGGGAGCCATACTCTTCCCCTCCCCTCCTCCTCCTCCTCCTCCTCG	F	Body;Body;Body	SEMA7A	0.8095871	0.8443771	-0.03479			
cg13558462	19	73616508	38572902	38572952	Island	TGTGGGCCAGGATCTGCCCGGAGGAGCTCGGTGAGGGCCTGGCACCCTCG	F	Body	SIPA1L3	0.8880257	0.9154457	-0.02742			
cg13559235	9	51803412	134714915	134714965	N_Shelf	TTTCCATGAGGCTTGCTAAATGTGCTCGGCCTTCCCAGGCCGGTGTTACG	F	N/A	N/A	0.8132443	0.8614614	-0.048217143			
cg13563669	6	56685359	53531701	53531751	N_Shelf	CGGGGGCCTCCCAACTTAAAGAAGAAGAGCCCTGAACACTGGGCCT	F	TSS1500	KLHL31	0.8985814	0.9450886	-0.046507143	0.9187588	0.9450886	-0.02633
cg13567386	1	62788432	93913447	93913497	N_Shore	TTGGAAACAGGGGTCCGACTGGCAGCGGAGTGGGGGCAGTCCAAGCTCCG	R	TSS1500;TSS1500;TSS1500	FNBP1L	0.1035934	0.0895091	0.014084286	0.1150011	0.0895091	0.025492
cg13568432	8	40664411	61789077	61789127	N/A	AGGATGGATGGGCTGCACGGTGGGCACGGAGCGCCTCTGCCGGAAACCG	R	N/A	N/A	0.8889371	0.9206471	-0.03171	0.90328	0.9206471	-0.017367
cg13568659	6	14643387	159438801	159438851	N/A	GAGCCCCTCAAAATCTGAGTCTGACCTGAAGGAGCCCAGCTTTCAAATCG	R	N/A	N/A	0.7439014	0.82634	-0.082438571			
cg13570075	12	67723993	123444414	123444464	Island	CCTTCCACAACAGGGCCCCAAAACCGTGCAGAGTGGGGCTTGCGGCA	F	Body;Body;Body	ABCB9	0.9143686	0.9490729	-0.034704286			
cg13579932	9	68710352	132112089	132112139	N_Shelf	CGCTGCCAGGTGAGGAGGCCTGGGCATCGAGTTTCTGTCTTTCATCCAAGC	R	N/A	N/A	0.8965957	0.9187386	-0.022142857			
cg13580226	1	14738310	3383460	3383510	N/A	CGCTGCTGCCTCCTGGGGACACTTCCCAGGGATTTCCGTAGAGGAGACCT	R	Body	ARHGEF16	0.8791714	0.9115257	-0.032354286			
cg13582500	11	38634605	57436966	57437016	S_Shore	ACTACACTGGTTTTCCCCTCCTCATTTTGAGACGGATGTCGGCTCTGTCG	R	5'UTR	ZDHHC5	0.5332786	0.5798771	-0.046598571			
cg13584258	9	26627318	92040726	92040776	N/A	AGCTGGAGGACACTGTGCCAGTCATGGTCCTGGGGTCACTGCAGGACCCG	F	5'UTR;5'UTR	SEMA4D	0.7736514	0.8311057	-0.057454286			
cg13586696	22	61635447	29458723	29458773	N/A	CGGTCCGCCTGCAGGCTCTGATTCACTCCAGGGACAACACTTAAAAACGC	R	TSS1500	C22orf31	0.8774443	0.9281129	-0.050668571			
cg13586765	9	45612416	139101392	139101342	N/A	CGGCCCAGATAACATCCTGCTTCTGCAGGCCCCTGCGCACGTGTTCCCCT	F	Body	QSOX2	0.9191057	0.9477943	-0.028688571			
cg13591497	9	73723329	126129566	126129616	Island	GGCACGGGCTGCCGCAGCATGCGCGAGGAGCTGAGAGGCGTGCGGCGCG	F	Body	CCR2	0.7611286	0.7881714	-0.027042857	0.7665175	0.7881714	-0.021654
cg13593566	14	10789470	95685640	95685690	N/A	CGGTGGAAGGAAGAGCAGCACGAATCTGAGGAGGCTGTTGAAGGCCCCA	F	Body	CLMN	0.7802243	0.8389	-0.058675714			
cg13595429	22	41667327	17564750	17564800	Island	CGCCTCTGCCTGGCCTTGACACGCACGGAGTCTACACTCAAGTGGCTTTT	R	TSS1500	IL17RA	0.8280771	0.8981829	-0.070105714			
cg13597723	7	21703474	78922577	78922577	S_Shore	TCGTCCATGGGCCTCCTCCCTGGGGCTTGAAGGGTCACACCTCCCCTCG	R	Body;Body	RPTOR	0.8765629	0.9273614	-0.050798571			
cg13597317	9	36706330	111033925	111033975	N/A	CGCATGAGGATTAGAAGCATCACAAAGAAAGCAGTCTCGGAAGTTTGTCA	R	N/A	N/A	0.8871414	0.9124214	-0.02528	0.8952025	0.9124214	-0.017219
cg13603599	11	10664400	67251939	67251989	S_Shore	CGCTCCTTAACTGCCGCCACATGCTGCATCTCTGAAGTCAGTTTCCACATC	R	Body	AIP	0.8494257	0.8914057	-0.04198			
cg13605542	3	51737454	58110814	58110864	S_Shore	CGGTTTGTATTATTAAAAGTCAGATCATACCTACATTACTGTGGGATTG	F	Body;Body;Body;Body	FLNB	0.8998229	0.9302771	-0.030454286			
cg13608034	9	11726448	134762167	134762217	N/A	CGGGTTCCAGGTTTACTTTCTAACGGCCGCAGTTTAAGTTTCCTTAACGA	F	Body	ARID2T	0.77443	0.86025	-0.08582	0.8229413	0.86025	-0.037309
cg13609385	8	58718509	41580932	41580982	N_Shelf	CGGCTCCGGGAGGCTGGTGGTGCATCCCTAACTAGGTCACCAAGGGCCCG	F	Body;Body;Body;Body	ANK1	0.7631529	0.8118129	-0.05496	0.782085	0.8118129	-0.036028
cg13613456	10	39713434	21434654	21434704	N/A	CGGTCAGTACTCTTTGGTGGCTGACATCCATTCTGCCTGCAACAAGGCTA	F	Body;Body	C10orf113	0.82442	0.8802514	-0.055831429			
cg13615027	8	25663473	100825070	100825120	N/A	CGTTTTCCAGTTCTCTGCTCTGGAGTATTCTTCAATATACCTATT	R	3'UTR	VPS13B	0.8023686	0.8577614	-0.055392857	0.8303675	0.8577614	-0.027394
cg13620366	9	11744460	138839624	138839674	N/A	CGGGCCCGCGTCCGAACCAAACGAGAGACGTGAGTGTCAGCCCAGAGGTT	F	Body	UBAC1	0.8948143	0.9255257	-0.030711429	0.9101963	0.9255257	-0.015329
cg13621612	5	53647483	1021202	1021252	N/A	CGCAGCAGAACTCTGGCTTGTGAGGACATCTGAGTATTTTAGGAGACCTT	F	Body	NKD2				0.9292825	0.9122829	0.0169996
cg13623052	10	29698508	135209313	135209363	S_Shore	CGAAGTCCGCCGCTCTCTCTCTCTGCACGGGATATCCTTTCACAGGGCCC	R	Body	MTG1	0.8996471	0.9350243	-0.035377143	0.9056363	0.9350243	-0.029398
cg13623749	6	60635479	15329886	15329936	N/A	GTTAAACCGCATGCGCTCTGTCTAGTCTGTGAAGGTCAGCCAGCCATTCG	R	Body	JARID2	0.5333257	0.6639643	-0.130638571	0.5944113	0.6639643	-0.069553
cg13624385	4	41784397	30722004	30722054	Island	CGCTGCAGATCCCACTGCTCCGACATGCGGGCCGAATGCAGGTGAGAAAA	F	TSS200;TSS200;TSS200	PCDH7	0.1246257	0.0973274	0.027298286	0.115456	0.0973274	0.0181286
cg13625816	8	60630032	37755160	37755210	N_Shore	AGTTGGTAGAGTTCTTCTCTCTGGTCCTAATCCTGGTGGATGTCTGCTCG	F	Body;Body	RAB11FIP1	0.8059714	0.8852129	-0.079241429			
cg13626582	15	62781427	57592083	57592133	N/A	ACGGCCGGGTCTGGGAGCCCCCCCCGCCCCCCCCCCCCCCCCCCCTGCG	R	TSS1500	LOC283663	0.7251586	0.8121814	-0.087022857	0.7556	0.8121814	-0.056581
cg13632935	9	50767337	130207507	130207557	N/A	CTTTAGCATTTCTCAGATCCTCACCCCACCTGTCCTGAGTCGGCATGTCCG	F	3'UTR	ZNF79	0.8960743	0.9221471	-0.026072857			
cg13633305	10	31611350	125648785	125648835	N_Shelf	CGAGTCCCCAGGACAATCAAGCTGACTTACTTGTCAAATCTCAAACATCA	F	Body	CPXM2	0.8683114	0.9085143	-0.040202857			
cg13637151	9	65750381	134375648	134375518	N_Shelf	GGAAATCCAGGGCTGGTGCTGCTGCAGCCCGGTGCTGCACATCCACCTCG	R	3'UTR	BATL1	0.7729486	0.8424571	-0.069508571			
cg13640959	17	55640352	26817574	26817624	N/A	GCAGGAGGAACTCACGGGGCAGGCCGCACCCCAACGATGAGGAGGACACG	F	Body;Body;Body;Body	SLC13A2	0.8321871	0.8613186	-0.029131429			
cg13643452	14	42786396	38725650	38725700	S_Shore	CGTGTTATGGGTTCTGCGGTCCTGATGAAACTCCCTGAACGGGAAAAAC	R	TSS200	CLEC14A	0.4660386	0.5953557	-0.129317143			
cg13645651	18	33679385	58040213	58040263	N/A	CGGCTTGCTTCTCGACTTCAGACTTCAGGAGCTTCTGCATCTGAATCTGT	R	TSS1500	MC4R	0.1606829	0.2394657	-0.078782857	0.1926963	0.2394657	-0.046769
cg13647831	13	15784482	111720063	111720113	Island	TTCTCATGGATCACGGTGGAGGAGGTCCTCCTCCTCCTCCTCCTCCTCG	N	N/A	N/A	0.3647943	0.4394843	-0.07469	0.3991863	0.4394843	-0.040298
cg13648045	17	62722493	32579022	32579072	N/A	CGGCCCTGGGAAAATGGGCTCTATTCTACCTGGAGCTAGCCTGGGAGGA	R	N/A	N/A	0.8225586	0.86141	-0.038851429			
cg13650484	2	59749350	95945517	95945567	N/A	ATCTGCATTTCTGAAGCCCCAGCCTTGGGGTTAGAGGCCACACCCGGTCG	R	Body;Body;Body	PROM2	0.8705743	0.9015186	-0.030944286			
cg13650687	3	46730335	71656024	71656024	N/A	CCGGGCGGGGCAGGAGCCATCTCAGCCTGGGGGCCGGACTGGGCTGGCG	R	Body;Body;Body;Body;Body;B	COL13A1	0.8440714	0.8993314	-0.05526			
cg13663170	4	15682404	1976361	1976411	N/A	CGGCGCTCACTAAGGCTCGGTCCTTCCCACGTGGTCCTGACCTGTCCTCT	F	Body;Body;Body;TSS200;Bod	WHSC1	0.89827	0.9312471	-0.032977143			
cg13663845	5	39704498	40692804	40692854	N/A	TTGGAATAGAGCCTTTCTAATATCTGGGCCTCTGCTGTGTGCCAAATACG	F	3'UTR	PTGER4	0.8874086	0.9335886	-0.04618	0.91009	0.9335886	-0.023499
cg13665184	16	52672409	68057162	68057112	Island	CGGTTGCTCTGGCGCCGCGACGGGGCCTCACGGTCCCGAGTCCCGACGA	N	TSS200;1stExon	DUS2L				0.2040413	0.1681529	0.0358884
cg13667095	11	19718333	134132696	134132746	N/A	CGGCTCCGCACGCCTCGCCGCAACAGCTCTCCGGAGAGTCCCTCCGCG	R	Body	ALG4B	0.81685	0.8456671	-0.028817143			
cg13667782	9	33614402	131789079	131789129	N_Shore	CGGCCCCAGTCCATCTGGGAGGGGGGAACCCACTCTGCTGTTGGTATGGC	R	Body	SH3GLB2	0.5451071	0.6444329	-0.099325714			
cg13668419	10	10730432	3197757	3197807	N/A	TACTAACTCACTAACAAGTCCACTAGGCCCGAGTGCAGGTTAGGGACTCG	R	Body	PITRM1	0.9215986	0.9448314	-0.023232857			
cg13672200	12	45645324	54387500	54387550	S_Shore	ACAAGGGCCTGATGCATCGGCTAAGGCGATGGTAATTTATTCCCTTCG	R	N/A	N/A	0.39053	0.5114	-0.12087			
cg13676816	9	25649326	91976972	91977022	N/A	CGGTCAGGCAGCAGGCTCTGAAGGCTGATCCTACACCGTCCCAGTGACTC	R	3'UTR	SEMA4D	0.9098529	0.9349943	-0.025141429			
cg13678479	19	35684501	59093222	59093322	Island	ACACCAGCCAGAGCTTATTCATGGTGAACACCAGGCCAGAGTGTGTAGCCG	F	Body	MGC2752	0.89392	0.9237143	-0.029794286			
cg13682669	6	31725424	17604379	17604429	S_Shelf	CGCCTGAGCCTAGAGTTTTGAAAGCAACCTGGGCAACACAGACCCCATCT	R	Body	FAM8A1	0.7772214	0.8243214	-0.0471			
cg13684541	17	44638374	44834262	44834312	N/A	CTGCTAGTCCACAGAACAATCATCTGTAAGACAATCACCTCTCTCTAACG	F	3'UTR	RSF1	0.8320571	0.88376	-0.051702857			
cg13685155	2	55701459	88473871	88473921	S_Shelf	GAAGACTTTATTTTTCATTTTTTATACTTCTTCATTGTTTGACTGTCTCG	F	Body	THNSL2	0.9263229	0.9533343	-0.027011429	0.9324138	0.9533343	-0.020921
cg13691441	3	33711323	124835190	124835240	N/A	CGGAGAGGACAAAGAGCCATTCCCTGGAAGAGACCATTGTAAAGCCTATA	R	Body	SLC12A8	0.9101743	0.9476243	-0.03745			
cg13691599	3	18796322	74863443	74863493	N/A	CGAAGGAACTTTCTCTCAACTCTGGTTGCACTATTTTTCTTCCTCTCTCG	R	3'UTR	GDA	0.8681286	0.9078057	-0.039677143	0.8740563	0.9078057	-0.033749
cg13691744	6	55696402	31842575	31842625	N/A	CGAGTTCTCACAGACTGTTGGGGAAGTCTTCTATACAAAAAACAGGAACT	R	Body	SLC44A4	0.4709057	0.5552143	-0.084308571			
cg13698883	9	18746396	38422614	38422664	N_Shore	GGCTGGGGTGCATCTGTGCTGCCGCTGGCTCCCTGAGTGGCCCTGGACG	F	Body	IGFBPL1	0.6443586	0.7093414	-0.064982857			
cg13700094	9	26715329	111518438	111518538	N/A	TTAACCCCCTCCAACCAGGGCTTGTTTTTTTCTTGGTTCTTTATCG	R	N/A	N/A	0.9056943	0.94406	-0.038365714	0.9240113	0.94406	-0.020049
cg13700250	4	14757311	77702233	77702283	N/A	ACTCAACGGGGCTCCCAGTTCCCAACACTCTTCGAGATGACCATTTTTCG	R	3'UTR	SHROOM3	0.83222	0.8932186	-0.060998571	0.8670888	0.8932186	-0.02613
cg13702185	4	41609415	3438579	3438629	N/A	GTGGGGCCTCCAGCAGGACCCCCTCCTGGGAAGGCTGGACAGCACAGTCG	R	Body;Body	RGS12	0.8766457	0.9149857	-0.03834			
cg13705888	6	74613433	32131722	32131772	N_Shelf	TAAGCTCAGGCTCCATGGGTTGGGTCTGAGCCTCAGCCTCATGGGTGGAATGCG	R	TSS1500	EGFL8	0.9225529	0.9479186	-0.025365714			
cg13708222	14	74698301	100613058	100613108	N_Shelf	TGGTCTGGGTCCCTGGGAGCCTCCTGGGGGCTCCTGGGGCCCATCCTCG	F	3'UTR	DEGS2	0.67743	0.7449671	-0.067537143	0.7278713	0.7449671	-0.017096
cg13714407	9	57719445	134604212	134604262	N/A	CGAGCACTTCTTATGTGTCCAGACTCTGATTAAATGCTTATGTACATCAT	F	Body	RAPGEF1	0.74531	0.8215043	-0.076194286			
cg13720278	3	26736409	180702012	180702062	N/A	CGGTGGAAAGGCTGTTCCAGGTACAGGCAACTGGCCTGGCAACTTGGATA	R	3'UTR	DNAJC19	0.8713043	0.9078571	-0.036552857			
cg13724170	3	58623248	12713226	12713276	N/A	CCTCAACATTCTGGTAGCCCAGTCTACAGCTGTGCT	R	N/A	N/A	0.8679457	0.9030086	-0.035062857			
cg13729931	11	52808439	115776731	115776781	N/A	CAGAAGTGCAAATTACGCAGGAATTGGTGCTAAACTTCTCCATTAACTACG	F	N/A	N/A	0.87233	0.91474	-0.04241	0.886565	0.91474	-0.028175
cg13731523	4	60600456	3047190	3047240	S_Shelf	GCGTATTCCATATGTATATTCAGCCCACCCTGAGGATCTGAGGGAAAAGCG	N	N/A	N/A	0.6744771	0.7244171	-0.04994			
cg13744910	9	50753429	138820110	138820160	N_Shelf	CCCAGCCGCAGAGTCTAAGAGAAATGATTTTACTCGGGCTGGGGGGTGGG	F	N/A	N/A	0.8908786	0.9199543	-0.029075714	0.9060213	0.9199543	-0.013933
cg13746919	10	14648355	81837573	81837623	N_Shelf	GAAAACTGGGCGATATCCTGTTGTTGTTGTTGTTGACACACAGCCCG	R	TSS1500;Body;Body;Body;Bo	C10orf57	0.7347657	0.8319814	-0.097215714			
cg13757263	3	14648396	53807593	53807643	N/A	CGTGGGAAATCTGCAAGGAGCCTGCCAGCAGAGATCTACAGCCACCTGGG	R	Body;Body;Body	CACNA1D	0.5766271	0.7726871	-0.19606			
cg13759931	9	22716312	30791170	30791220	N/A	TGCAGAAATCACGCGTTTTCTGCATAGCTCACATGGGGAGCTGTAGACCG	R	N/A	N/A	0.8266143	0.8596257	-0.033011429			
cg13763120	19	19655392	13809324	13809374	N_Shelf	GTGCAATGCGGGATCTCCAACTGCAATAACGTCCAATGTGGCGCAATCG	F	N/A	N/A	0.6949643	0.7621943	-0.06723			
cg13770982	9	44806409	102584806	102584856	Island	TCCTGAAATTGACAACTTTGAGTTGGGGTTCCCTCCCTGACCTTGCCG	R	5'UTR;5'UTR	NR4A3	0.0934994	0.13615	-0.042650571	0.111383	0.13615	-0.024767
cg13772849	17	48623329	29624227	29624277	N/A	CGACCTTTAAGTTTCCCAGAGAAAATGAGATGCTGATGTTGAAG

cg14111928	10	13774404	76602391	76602441	N/A	CGGGTGAAGAACATCTTTAACTTGGGAAATCAAGACCTTAAAGGATAAAAA	R	5'UTR	MYST4	0.77688	0.8600771	-0.083197143	0.8194163	0.8600771	-0.040661
cg14116388	14	54655495	69521670	69521720	N/A	GTTGTCTTCTGTCGGCGCCGCATGGCATTCCGCTGCCAGGTAGAGGCTCG	R	Body	DCAF5	0.9251729	0.95069	-0.025517143			
cg14117874	5	33742344	81684364	81684414	N/A	CGTCTCCCTGGAGACATCCTCGATGTCCCTGTTGTCTGTCACGCTGTGCA	F	N/A	N/A	0.7913014	0.8499357	-0.058634286			
cg14121665	9	29804393	19902147	19902297	N_Shelf	CGGCTCAGGGGTCGGTCAGTGGTGGCCCTGCTTGGTCCACTGTGAGTGCC	R	N/A	N/A	0.4802357	0.5408714	-0.060635714	0.4906413	0.5408714	-0.05023
cg14123750	13	40620382	114318492	114318542	N/A	AAATGCAGGTCCTGAAAGGCTACATAGTGTCTGACTCCATTCATGTGACG	R	N/A	N/A	0.8255971	0.88355	-0.057952857			
cg14124132	12	50660409	27619014	27619064	N/A	CGAGGTCACAGAGGTATAAAGTAAGAAGCATCCCTGGTTTGCAAGAAGATC	F	TSS1500	C12orf70	0.9034171	0.9363457	-0.032928571	0.9198638	0.9363457	-0.016482
cg14127859	9	20778392	96716928	96716978	Island	CACGAGAGTCGTAGCCTGGCAGTGCGCCTGCACTGGGGATGCTCACTCG	R	Body	BARX1	0.28252	0.2430714	0.039448571	0.27178	0.2430714	0.0287086
cg14128259	12	55649371	27848523	27848573	N/A	CGGAAAATGAAATAAGGGCAATAAAAATGAGGCAATTATCAATTGACTTT	R	TSS1500	REP15	0.7967829	0.8931086	-0.096325714			
cg14133064	9	63679375	5530115	5530165	N/A	CGTTGTGTGTTTCTGAATAAGTGACAGGTGCTGACTACCATTGATGCTT	F	Body	PDCD1LG2	0.4238414	0.5838686	-0.159527143	0.496225	0.5833686	-0.087144
cg14138312	9	39619464	6869699	6869749	N/A	CGGCCCACATGCAAGGGATGGTCCAGGCTTGAGTATAAAGGCTTTGGCCAT	R	Body;Body;Body;Body	KDM4C	0.8704943	0.9053743	-0.03488			
cg14143742	11	69752301	3915752	3915792	N/A	AGCCGAACAAGAGCCCAAAGTCTGACCTTGGGTAGATCTAAGAGATCAG	R	Body	STIM1	0.6387757	0.7437371	-0.104961429			
cg14145667	19	71740491	909533	909583	N_Shelf	GTCACTACACCTGGGCTTCAAGACCAGGGTGCCAGGCGTGGTGGTTCACG	R	Body	C19orf22	0.7297914	0.8195443	-0.089752857			
cg14146148	9	42743397	131302123	131302173	N/A	CGAGAGGGACTGGAGTAGGAAAGATGTCATACTTAGTACAGGTGTTTTTA	R	Body;3'UTR	GLE1	0.9058486	0.9451557	-0.039307143			
cg14147196	3	1163454	11078979	11079029	N/A	TAGATCATTTTATCCGCCACGGGAGTGTGATGCGAGAAGCACATGCG	R	3'UTR	SLC6A1	0.6150543	0.7023471	-0.087292857			
cg14150023	22	58635350	40720063	40720113	N/A	CATTCCCTGCTGCACCTCTTTCTTCACGTGATGAACCTTTCTGCTCCTGA	F	3'UTR;3'UTR;3'UTR	TNRC6B	0.8208814	0.8794786	-0.058597143	0.8423488	0.8794786	-0.03713
cg14152811	14	67764309	106153129	106153179	Island	CAGTGCTGCGGGCTGCAGCGAGTGTGTGTGCACACGCATGCCCATATACG	F	N/A	N/A	0.80297	0.8336357	-0.030665714			
cg14156446	9	15765375	127284971	127285021	N/A	GCTGCATTCTCTGCAAGACCAGTGTGGGCAAGGAATGACCTGTTCCAGGCG	F	3'UTR;3'UTR	NR6A1	0.8190714	0.8831471	-0.064075714	0.8488913	0.8831471	-0.034256
cg14157019	2	38738357	65541214	65541264	Island	ACGACGAGGAGATCGTCGCGCATCAACCCCCGGGAGAATCTGGATGACAG	F	Body;Body	SPRED2	0.8941729	0.9237114	-0.029538571			
cg14157930	2	1672747	132301321	132301371	N/A	CGGGGTGGCTCAGGCTCCAGCCTCCAGCATGCCTCGGTGCGCTCCCTTC	R	N/A	N/A	0.6218957	0.7385157	-0.11662	0.673105	0.7385157	-0.065411
cg14161241	6	24657439	144329909	144329959	S_Shore	CTGTGAGCACTGACCGTGAGCCAGGCACTGTCCTAAGCACTTTGCAGGTAA	F	TSS1500;TSS1500;5'UTR;TSS	PLAGL1	0.4228157	0.5188543	-0.096038571	0.4594225	0.5188543	-0.059432
cg14173033	17	11751349	80545310	80545360	N_Shelf	GTTTGCATTTCGAAGGTGCAGGAAATCTAGTCATGCTGGGGAAGTGGTCG	R	Body	FOXK2	0.8242329	0.9091671	-0.084934286			
cg14174005	2	59697360	97203640	97203690	Island	CGTGGCCTGAGTCCTTTGTTCAAGACTGGCTGTGGTGACCTAAGGAGTGCT	R	Body	ARID5A	0.4297771	0.5189929	-0.089215714			
cg14177140	1	29665388	220956859	220956909	N_Shelf	ATGTGTTCTCTGATCTGAGGGAGCCCAATGGCTGTGAGATACCATAACG	R	3'UTR	MOSC2	0.8404886	0.8826343	-0.042145714			
cg14182254	1	51721304	2949754	2949804	N/A	CGGAGTTGTCAATAACTCATTTTGTAACCTTGGGCCAGTCACCTTATCAC	F	Body	SFRS4	0.6230071	0.7326386	-0.109631429			
cg14188875	8	37641410	48691126	48691226	N/A	CACCAGCCTGCTGCTCCAGAGGGCCTGTATCTCATCCTGCTGCTGCCTAC	F	Body;Body	PRKCDC	0.9310171	0.9623857	-0.031378571			
cg14191466	14	27739473	103440432	103440482	N/A	CGCTCTTGGCGAAGCGCCACTGTGTCCTCAAGCTGTGCCTCGAGCCTGTT	F	Body	CDC42BPB	0.6730871	0.7517786	-0.078691429	0.697835	0.7517786	-0.053944
cg14197881	11	46630505	67044849	67044899	N/A	CGGTGGCTGGCAGAGCCACTGCCATACTCACCCAGCTTCTGGGAAAGAT	R	Body	ADRBK1	0.3984929	0.5433314	-0.144838571			
cg14202757	1	15680484	10056846	10056896	S_Shore	TGATTGCCTGGTGATTCGCACCTCTAGGAATCACAGTGATTCGCCACCTCG	R	TSS1500	RBP7	0.5156443	0.4529914	0.062652857			
cg14204124	9	40621343	37651160	37651710	S_Shore	CGCCCCCCACTAAAGCTCAGTCAAAGCTGCTGCAAGTTAGCGACGCGACCC	R	5'UTR	FRMPD1	0.1420944	0.2203143	-0.078219857	0.1795175	0.2203143	-0.040797
cg14204738	1	44783408	151799266	151799316	N/A	GGCCCACCATAAAGTATTTTGTGAGGATTAGATTATCCACATAAAACATCG	F	TSS1500;Body	RORC	0.8343357	0.9122529	-0.077917143			
cg14208070	17	46793397	4685804	4685854	Island	TGGGGAGATTGGGCCTTACCTCCCCTTCCACACCACATCCAGATGCTGCG	R	Body	TM4SF5	0.7164757	0.8128657	-0.09639			
cg14214834	3	20750404	123139305	123139355	N/A	CGCACTTTCCTACCTCCCACGGCCGGAGGAAAAAGAAGAGGAGCATAACA	R	Body	ADCY5	0.8926871	0.9221557	-0.029468571	0.9002138	0.9221557	-0.021942
cg14215105	1	50664392	153715578	153715628	N/A	CGTCACTAATTCTTCCATCATGCTCTGACCTGGCTCAAGGTCTCTGAATG	R	Body	INTS3	0.6155886	0.7521014	-0.136512857			
cg14220146	9	34618346	96068079	96068129	N/A	CGCTCCTCAGCGCTGTTCCCGGGAGACCTAAAAGGAGCGACCTCTGATCT	R	Body	WNK2	0.8645643	0.9106057	-0.046041429			
cg14220170	3	35697446	36966224	36966274	N/A	TTTCATTTATGCAGTTGAGGGCTCTGTTCTCCTCCTCCTCCTCCTCCTCC	F	Body	TRANK1	0.7297343	0.8194243	-0.08969	0.7623275	0.8194243	-0.057097
cg14228177	7	62614372	1606526	1606576	N_Shelf	CAGGGTTCACTGGGGTGTGGCTGAACATGACCTCCGTGTGGGGGTAGGCG	F	N/A	N/A	0.9001429	0.9410471	-0.040904286			
cg14229655	9	58798398	98052350	98052400	N_Shelf	AGAAAATTGGTCTTCATGTCATCCAACCTTGCAGTAAACTCTAAAAACG	R	5'UTR	FANCC	0.7387771	0.8073	-0.067952857			
cg14231845	4	62705431	75722231	75722281	S_Shelf	AAAATAAACTTGTAGTTACATATAGGGCAACAACATAAACAGACACACG	R	N/A	N/A	0.7269843	0.7978971	-0.070912857	0.7565125	0.7978971	-0.041385
cg14233847	17	24732453	70850382	70850432	N/A	CGACTTCCTGAGTCCTGTGCAGCTGGTGCCTGGGCAACCAGTTACT	R	Body;Body	SLC39A11	0.8030314	0.8603271	-0.057295714			
cg14234105	9	73719482	98550966	98551016	S_Shelf	CGCTCTGGCTGGCATGCCCACTTTGCCTCTGCTGTTGAACAAAAGGTCCC	R	N/A	N/A	0.7336214	0.8116786	-0.078057143	0.751075	0.8116786	-0.060604
cg14235676	17	7266311	66508939	66508989	Island	CGCTGCCCCCACCCCACGGCTCCTGGGGCCCTGGGCCCTCCGCGGCCCTC	F	5'UTR;5'UTR;5'UTR	PRKAR1A	0.1444243	0.1766914	-0.032267143			
cg14235701	9	52768300	139606200	139606250	N_Shore	CCCGAACCACGCCCAGCCCAGCGCCACCACCAGGAAATGGCTAAAAT	F	TSS1500	FAM69B	0.4118614	0.50122	-0.089358571			
cg14235846	17	29741509	800745	800795	N/A	CGGGCGGCCTCATTCACGTCCGGCATGTTCCGCTATTATTGAAAGGAAAT	F	1stExon;5'UTR	DNAH8	0.8894186	0.9236671	-0.034248571			
cg14236443	17	13807343	943270	943320	N/A	CGGGCCCCTGGCCCTGAGGGAGGCCTTGATTCAACTGGGAAGGAACACAG	R	Body;Body;Body	ABR	0.6807057	0.7529843	-0.072278571	0.6989075	0.7529843	-0.054077
cg14241074	4	50625493	103752952	103753002	S_Shelf	TGCTCCTAGAGCTATCACGATTGAGGACAAACGAATTTCTCTTTATCG	F	Body;5'UTR	UBE2D3	0.8805329	0.9094671	-0.028934286			
cg14242532	2	63747379	233879045	233879095	N/A	CGAGCTGCCCGCCCCGCCCATGGCAAGGAGCCTCATGCTGATGGCCCA	R	TSS1500	INCEF	0.6985057	0.7488029	-0.050297143	0.7208375	0.7488029	-0.027965
cg14244636	10	33638472	100055918	100055968	N/A	CGGTCAGCCTGTGTAACCTGATCCTGGGCAAAGTTATGGTTCCTTTCTGT	F	N/A	N/A	0.6291729	0.7100957	-0.080922857			
cg14245228	9	43756482	135619345	135619395	N/A	GGTTCACTGTCCTCTGCTGATCCTCACTGGAGATTTCAGGAAGGTCCG	F	Body	C9orf98	0.77449	0.8351071	-0.060617143			
cg14247862	17	69738313	80764631	80764681	Island	GATGCTTGCCCTCCTCCTGCAGCGGTGCCACAGGTCACACGTCACGG	F	Body	TBCD	0.9185814	0.9497686	-0.031187143			
cg14253096	9	3464935	138911192	138911242	N/A	CGAGGGGCCTCCTGCCACCCTGGAACCCAGCTCTGGCCCCGACTCACGGG	R	Body	NACC2	0.73289	0.78388	-0.05099	0.7393213	0.78388	-0.044559
cg14256028	13	32603333	110528090	110528140	N/A	TATGATTGCAAACCCAATTGTCTATTTTCATATGCAAATCCTGGCATACG	F	N/A	N/A	0.7086171	0.7931314	-0.084514286			
cg14261474	4	57741484	158555507	158555557	N_Shelf	GAGACCAGCATTGGGTGGCTGTCTCACAGTCATCACGTCACGCCGCCG	R	N/A	N/A	0.86832	0.9017871	-0.033467143	0.8736963	0.9017871	-0.028091
cg14264079	4	67647301	2944178	2944228	N/A	CGCACACCGATTTTTATGTTTCTGGGTTGTGCCGAGACACTGAGGGTTCA	F	Body;Body	C4orf10	0.8663043	0.9033086	-0.037004286			
cg14266927	14	30603413	75987682	75987732	N/A	CGGCTCCTAGAGGATTTTTGTATCCATGAGCTGAATTTCTAGACTAAGAC	R	TSS1500	BATF	0.9065357	0.9331457	-0.02661			
cg14270556	17	67659444	5373138	5373188	S_Shore	CGGATGTGGTCGCCTCCAGTAATACAAGCAGAGAAAGGAGGAGTTCAAT	F	TSS1500	DHX33	0.7293871	0.8080214	-0.078634286			
cg14276730	20	12772404	40040318	40040368	N/A	GACACTGGCAGGGTTCAAAGACTTCTGCAGAACTTGGCTAAAATCTGCA	R	Body	CHD6	0.5887386	0.6968829	-0.108154286			
cg14278073	6	15616384	38690735	38690785	N/A	CGCAGAAGATGCTGTTTCTTCTGTGGTGGATTATCGGGATCTCATTCCTT	F	1stExon;5'UTR	DNAH8	0.8894186	0.9236671	-0.034248571			
cg14286732	9	3871331 8	90208854	90208904	N/A	AGAATGGTGAAGTCAAAGTGATCAAACATGGAGCTGACCAGAACCACTCG	R	Body	DAPK1	0.6860814	0.7706029	-0.084521429			
cg14288464	20	34701353	43743301	43743351	N/A	CATTCCTAAAGTGTGTGTGCAGACAGGCTTTCGCACAACGACAGACG	F	Body	WFDC5	0.65466	0.7073714	-0.052714286	0.6790013	0.7073714	-0.02837
cg14289594	17	21643344	78882754	78882804	S_Shelf	CTGGAGTTCCTGGCATGCATACTCGTAACCGAGAACCAGCAGCTGGAGCG	F	Body;Body	RPTOR	0.8980129	0.92632	-0.028307143			
cg14290450	14	29807413	100614523	100614573	N_Shore	CGCCCAGGCACACATGCAAATGCCTGCGCACGTGGGCAGGCACCCACACA	F	Body	DEGS2	0.9078843	0.9443886	-0.036504286	0.928245	0.9443886	-0.016144
cg14299800	9	23617465	132564053	132564103	N_Shore	CGCCCTAGACTGAGCACTGGGGATGCAGCGGCCCCAAGACAGACCTGCCC	R	TSS1500	TOR1B	0.8594414	0.9029029	-0.043461429			
cg14302904	15	42698348	32964500	32964550	N/A	CCCCAATTGCCATTGCCATCCCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	F	Body;Body	SCC5	0.9002929	0.9321957	-0.031902857			
cg14306362	9	48760336	89364536	89364586	N/A	CGGAGAAGAAAAACTTTCTCACTGGGATGGTATGCAAACTCATTCTAAAA	R	N/A	N/A	0.67663	0.7581171	-0.081487143	0.69925	0.7581171	-0.058867
cg14321623	10	23620394	77566898	77566948	N/A	GCAGAATATGTTCTCACCTCTCAATTCATTGTGACCTTTAGCTGGAGGTCG	R	Body	C10orf11	0.9124814	0.94889	-0.036408571	0.931575	0.94889	-0.017315
cg14325153	3	62672290	138763994	138763944	Island	CGGCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGA	R	TSS200	PPP23C	0.4198314	0.25013	0.169701429			
cg14327505	14	24691377	90810928	90810978	N/A	CTTAAGCAGAAGACACAGATCTTTCCATGTTAGACTGAAAGGTGGCATCG	R	N/A	N/A	0.7002743	0.7718471	-0.071572857			
cg14328415	9	29702463	139847314	139847364	Island	CGCCGGCCCTGCCCACCACCGCCTCTGTAGTTCCAGGGGGAATGGTTCGT	F	Body	LCN12	0.8657943	0.9090229	-0.043228571	0.88378	0.9090229	-0.025243
cg14331163	9	28719448	77111663	77111713	N_Shore	CGGACGTTTTAAAGGAAGGGGACAGCTACTTCCATGGGACTGCATTTTA	F	TSS1500	RORB	0.1415527	0.24316	-0.101607286	0.1851175	0.24316	-0.058043
cg14339765	6	41647382	46048772	46048822	N/A	GCCTTTTGCTCTCACATTCAGCATTCTGTATATGATGGTTTAGTTG	F	TSS1500	ATL5	0.8330429	0.8908571	-0.057814286			
cg14339867	13	57655428	114107654	114107604	N/A	CGGCGGTTGCGATGTGCATGATGGTGTTGTCACTCACGGGCCATTCTCCT	F	1stExon	ADPRHL1	0.8779771	0.9029914	-0.025014286			
cg14340131	11	14644495	533457	533507	N/A	CGGCAGGTGAGGCAGCTCTCCACCCCACAGCTAGCCAGGGACCCGCCCCG	R	Body;Body;Body	HRAS	0.8284371	0.85967	-0.031232857	0.84142	0.85967	-0.01825
cg14343538	6	14771432	37108143	37108193	N/A	CCGTCCTGGTGGTCTTGATGGGGTTCAGGAATCTGCATTGTAAATAA	N	N/A	N/A	0.8993229	0.93202	-0.032697143			
cg14343652	7	71749369	130789013	130789063	N_Shore	CGTGAGTATCTGTGGTTCGGTGTGGAAATAGCTCTCTAGCCCATCTCCC	R	Body;Body	FLJ43663	0.5118314	0.64853	-0.136698571			
cg14365300	9	18622467	129252725	129252775	N/A	CGGAGCGACTTCCAGCCCCATGCGGAGCCGTTTCTATCAGCTGCCAACCT	F	Body	FAM125B	0.6917586	0.7572257	-0.065467143	0.705405	0.7572257	-0.051821
cg14367513	13	49758344	42231920	42231970	N/A	AAATCTGCTGGTGGGCCAGGGCCTCCAAGCTCATCTAAAGTATGGCCTG	F	Body	KIAA0564	0.9141943	0.9348286	-0.020643286			
cg14371649	9	53732407	32995965	32996015	N/A	CATCCAAACCTTCAGCAACTATGACCCTGATCAGTCAGCAGCACCAACAG	R	5'UTR;5'UTR;Body	APTX	0.4364343	0.4882729	-0.051838571			
cg14371731	10	44768357	81003175	81003225	Island	ATTAGCGGAGCCTCCGCCTATGATTGGCTTCGCCCGGGAAGCTGGAGACG	R	Body	ZMIZ1	0.5110514	0.5963243	-0.085272857	0.55694	0.5963243	-0.039384
cg14375890	6	51725503	13355672	13355722	N/A	CGCTTTCATTCATGGCTGAAGGAAGGAGTAAGGTGATTAGAATCTGTA	F	N/A	N/A	0.8284357	0.8999286	-0.071492857	0.868605	0.8999286	-0.031324
cg14376836	9	51800313	94606668	94606618	N/A	CGCTCCTCTGGTCTCCACGACCCACGCCGTTCCTCTGCCTGCCTGCCTG	F	Body	ROR2	0.7674986	0.8415043	-0.074005714	0.8092513	0.8415043	-0.032253
cg14378259	22	30758501	37765272	37765322	N_Shelf	AGTATCAGGCTGGCCGAGAGTCACCCATGTTCTCAACTGGAAGTTGGTCG	F	3'UTR	ELFN2	0.8991057	0.9315843	-0.032478571			
cg14378925	11	11759994	64635728	64635778	N/A	TGGGCTTCAGTATTTCTCGCCCTAGCTCTCCATCACACAGGTTTCCAACG	R	Body	EHD1	0.80467	0.8921086	-0.087438571			
cg14386061	8	20784426	21771446	21771496	S_Shore	GTTTGGTTCCTCCTCCTGGTGGTGCGCGCGCGCGCGCGCGCGCGCGCGC	F	TSS1500	DCK2	0.74569	0.8251114	-0.079441429			
cg14387182	6	46607430	126114653	126114703	S_Shelf	CGCAGTGCCTCTGGGATTGGTTGACTCACTTTTGGGTCCTACCTCCTGAT	F	5'UTR;5'UTR	NCOA7	0.8030557	0.8535243	-0.050468571			
cg14391855	11	25751415	66104174	66104224	S_Shore	CGGCCTCAGTCCCCCACAGGCCCCAGCCATGCTCTGGGGGCACCTTTGGCT	F	TSS200	RIN1	0.3024429	0.4288129	-0.12637			
cg14395060	22	2353363	32441170	32441220	S_Shore	ATCAGAGATTGTCTGGGAAACAGGCAGTACTGTATAGCCAGCAGATGACG	F	Body	SLC5A1	0.6587614	0.7732829	-0.114521429			
cg14403776	9	61692369	97050181	97050181	N/A	CGGCTAAAGGAATTTACGCCTGAAGAGTTTGAGATACCAATTCAAACC	R	Body	ZNF169	0.8994129	0.9325286	-0.033115714			
cg14405528	22	38651456	47372700	47372750	S_Shelf	CTCTGCAGCAACGGCGTGGACGGCTGCCACAGAGCCGATGAGTCCCAAG	F	Body	TBC1D22A	0.8131243	0.8536614	-0.040537143	0.8355	0.8536614	-0.018161
cg14405825	10	50766347	652597	652647	S_Shore	CGTGCTGTGATCTGAATTCTCATTAGGAAAGGGATCTCACTGCTTAAGCA	F	Body	DIP2C	0.8398229	0.9132229	-0.0734			
cg14406134	9	65663378	117014922	117014972	N/A	GCACCCTTTGGGTCCAGGCACATCGTGGGGGTCCATCATGCCACGATCAC	R	Body	CDA27A1	0.7612743	0.8234	-0.062125714	0.7739825	0.8234	-0.049418
cg14406859	17	33669434	16314182	16314232	S_Shelf	TGACCTTTCAGCTAAAATCAAGTGTAGTATCTGTTCTTATCAGTTTGACG	R	N/A	N/A	0.4650943	0.5898829	-0.124788571			
cg14409919	9	15767318	130312266	130312316	N/A	AGGGACTCCCCCGGGGAAGCAGACCAAGACCACAGAGGCTGTTGGCTGCG	F	Body;Body	FAM129B	0.8835843	0.9088429	-0.025258571			
cg14410476	2	41798436	95693023	95693073	S_Shore	TAGATGGTTCAAGGTTTCCCCACGCCCCTGTAATTTCTGCAGCATTGGCG	F	Body;Body;Body;Body	MAL	0.1949671	0.32819	-0.133222857			
cg14411823	9	40670392	139850608	139850658	N_Shelf	TGCTCTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	N/A	N/A	N/A	0.8551829	0.8834186	-0.028235714			
cg14420349	2	13638493	240100930	240100980	N_Shore	CGTGGGTGGCATCCCATGGGCGCCAGTCCTGCTGTGCCAGCGCAGCCACT	R	Body	HDAC4	0.8932786	0.9200343	-0.026755714	0.8933788	0.9200343	-0.026656
cg14420357	6	44799445	158464617	158464667	N/A	CCTTGACGACGAAACAACGAAAGTGGTGTCTGTTGTTTTCTACACACACG	F	Body	SYNJ2	0.8736886	0.9069843	-0.033295714	0.8912588	0.9069843	-0.015726
cg14426672	6	70804312	32093904	32093904	N/A	GATTCCAGGGATGAATAAACACGTCGCCCCCATGCTCTACTACAG	F	Body;Body	ATF6B	0.8211186	0.8758986	-0.05469			
cg14426785	9	56760344	101876671	101876721	N/A	CGAGAATTCATGAGGAGACTGCCACCTTCCTTAATAAAGTGGAGCCCCAA	F	Body;Body	TGFBR1	0.8409343	0.8990843	-0.05815	0.8713463	0.8990843	-0.027738
cg14443470	9	62692344	129252572	129252622	N/A	CGCCCTGGCATCCGTGGAAGACCTCACCATCCCGGTCAGGAGCAGCAGC	F	Body	FAM125B	0.7958443	0.8624014	-0.066557143	0.7974738	0.8624014	-0.064928
cg14451728	4	36715357	57092248	57092298	N/A	AACCCAACGTGACCCAATGGTATGTGGATAAGAAGGCCCCACTTCTTACG	F	5'UTR	KIAA1211	0.8579143	0.89494	-0.037025714			
cg14466942	6	26662447	17282700	17282750	S_Shore	CCGGGGCAGCTGTCCTCCGCGAATTTAGGCTTCCAACATTCCTCGG	F	TSS1500;5'UTR;Body	RBM24	0.63042	0.7461857	-0.115767143			
cg14471364	2	50606401	157177936	157177986	S_Shore	GAGAAATTCCGGGGTGCGGCCACTATGCAAGCATTCCTATTCTGACAGCG	R	N/A	N/A	0.8820529	0.9158443	-0.033791429			
cg14473485	6	72775387	37605107	37605157	N/A	CAGCTGCGCGGGGTCAGTCTTTGGTACAATGTGGACACTTTGGTGTGCG	R	3'UTR	MDGA1	0.8530943	0.9105871	-0.057492857			
cg14473597	10	10721329	135195243	135195293	S_Shore	TTCTCGCCGCTTGGACTTCTTAGTGACAATCTCGGCAAAGACAAACGCG	R	Body;Body;Body	PAOX	0.8937657	0.9329629	-0.039197143			
cg14474791	9	49726372	124499870	124499920	S_Shore	CTCTGTGGCCTTGGACTTCTTAGTGACAACTTCGGCAAGATCCTGATTCT	R	Body	DAB2IP	0.8820529	0.9158443	-0.033791429			
cg14476331	6	74765323	157322541	157322591	N/A	TGTGTAAAGTGAACCAGAACCTCACGTCATCTGCAGCTGGTCAGAGGACG	F	Body;Body;Body	ARID1B	0.8967214	0.9299329	-0.033211429			
cg14476630	11	41710410	72437781	72437831	Island	CCGCATTTGGTGATGGCGGTTCGACCCGTCGTCCCACCGGGACC	R	Body	ARAP1	0.9182871	0.9586343	-0.040374143	0.94742	0.9586343	-0.011214
cg14478815	15	33647443	62513374	62513824	N_Shelf	CGTTGTCCCTCCCACTGTGCCTGTGATTGTGCCACAGAGCCAAAAGGAAG	F	N/A	N/A	0.6203986	0.6891757	-0.068777143			
cg14480046	12	40778369	122444580	122444630	N/A	CGCGCTCCTGTTCAGCTTCTGCAACTTTCTAGCCACCTGTGCGCCCTTGG	F	N/A	N/A	0.75031	0.8203714	-0.070061429			
cg14480449	14	65680503	105933035	105933085	Island	CTTACCCCTACTGGGCATCAAGAGGCGCTTCTTCATGTTGCCTGCGCAGCG	F	Body	MTA1	0.88656	0.9149686	-0.032908571			
cg14480789	3	50738432	42642068	42642038	Island	GGGGAGCCCTTGCCTGGGGTAACGGCCTGGTTCTGGGCCCCTGGGCCG	F	Body	NKTR	0.2253857	0.2851386	-0.059752857	0.25231	0.2851386	-0.032829
cg14484434	8	41791401	141568128	141568178	N/A	CGGGAGGAGGTGATAGATTTGGCCCCTGTGCCCCAGTTAATGTCTCCCG	R	Body;Body	EIF2C2	0.8520443	0.8757057	-0.023661429	0.8910125	0.8757057	0.0153068
cg14485103	11	49795330	69017579	69017629	N/A	GCTTAGTGGACCAAGAGACTACCTAGGCCTCAGCGTCAGCTGTACGGC	N	N/A	N/A	0.8111243	0.8756	-0.061435714			
cg14486477	12	63686301	117256677	117256627	N_Shore	CGGCGTGCCTGCCCACATCGGCCTGCCCACATCGAGCCACACTCTA	R	Body;Body	PSMT2	0.6962371	0.7845314	-0.088294286	0.7403138	0.7845314	-0.044218
cg14487379	9	28771409	135481870	135481920	N/A	CGCGGAACCGAGAGTACGAAAAGTGAACTTCAACCTTTTAGCACCCTTGA	R	Body	DDX31	0.7983614	0.8549986	-0.056637143			
cg14491667	9	26791405	100267751	100267751	S_Shelf	CGGCCCTGGGGTCCACCACCCTTGAAGCCCCAGAGTGAGTGGGGCCTGAGG	N	5'UTR;5'UTR	TMOD1	0.82621	0.8826871	-0.056477143			
cg14502847	9	17674364	18490009	18490059	N/A	CGTGCTCAAAAGCCTTCACTGTCTCCAGCTGTCTGGAGTCTACTCAAGGA	F	Body;Body	ADAMTSL1	0.64319	0.7367229	-0.093532857	0.6904338	0.7367229	-0.046289
cg14503815	9	24710410	96674383	96674383	N/A	AAATAAATGTCAAGGTCAGCAAATCCACTTCTGGATGCTTGACCG	F	Body	ARID5A	0.8450671	0.89546	-0.050392857			
cg14508832	1	15618510	2404894	2404944	N/A	CGCCCATCTGGGTGCATCTCTGGTGGGAGGCTTCTCCAGGCCCAGGGCTGA	N	N/A	N/A	0.7990329	0.8556329	-0.0566			
cg14509631	5	25721491	52694172	52694222	N/A	GAGTTCTAAAGCAAAATCCCACAATCACTATGGTCTTCCTTCCCCAAGCG	R	N/A	N/A	0.5959229	0.6487357	-0.052812857			
cg14519736	3	15719736	15711699	15711749	N/A	CTTAACACTGCCACTGTGGATGCTTTCCTCTTAAGGTTATTTCTACCG	R	3'UTR	ARMRD28	0.89576	0.9457357	-0.049975714			
cg14519952	12	20603452	124491432	124491482	N/A	CGTCCTACTGGGGCTTTCAAGGGGACATCCCACATGACTGCAAGTCCCTC	R	5'UTR	ZNF664	0.6667343	0.76278	-0.096045714			
cg14520106	7	43602384	155366295	155366345	N_Shore	GGGTGACTCAGTGATTCCTCCTGCAGGAATTCACCCCACACATACACTCG	R	N/A	N/A	0.8513286	0.8963914	-0.045062857	0.8675575	0.8963914	-0.028834
cg14523639	6	71616508	33288839	33288889	Island	TCTATGACACGGCGGTCAGTGAAGAGAGCATCTTTGCGTTCTCCACTG	R	Body;Body;Body;Body	DAXX	0.7921629	0.8538514	-0.061688571			

cg14829516	17	23791443	38249430	38249480	Island	TTGTTCAGGGTCCGGCAGGTCCGGCAGCTTGAGCAGCAGCTTGGTGAAGCG	R	Body;Body	THRA	0.8186357	0.8998757	-0.08124			
cg14829814	12	53796451	108294894	108294944	N_Shelf	CGGCATCCTCACCAGTACCAAGTCCTTATCACGGGAGCTCAGGACTTACC	R	N/A	N/A	0.7782886	0.8563357	-0.078047143	0.7950663	0.8563357	-0.061269
cg14845909	5	32801396	851183	851233	S_Shelf	CGCCTGTGAGAAACTGAGGCAATTGCCTGAAGAGCTCGTGGAGCCGTTACTC	F	TSS200	ZDHHC11	0.8544129	0.8844614	-0.030048571			
cg14849655	1	30686382	67807980	67808010	N/A	CGCCATCACCTGCAAAGAAGGAATCTCATGGCTTGGCCCAAAGGAAGC	F	Body	IL12RB2						
cg14852107	1	50686366	20827563	20827613	N/A	GCAGCCGCCCAAACAAGGCATGCAGTACTATCTAAGCAGCCAGGACTTCG	F	Body	MUL1				0.9302238	0.9127429	0.0174809
cg14863186	5	16651478	2103163	2103213	N/A	CTGGAAAACTTGCTGCTGCCCTGATTTCCTGGGGAAGTTCTCCCTGAACCG	F	N/A	N/A	0.6703529	0.73347	-0.063117143			
cg14867639	12	56735415	100590495	100590545	N_Shelf	CGAGCCACTGTGCCTGGCCGCTATCCATCTTGTTGTAGGTTCAGGTATT	R	N/A	N/A	0.6345843	0.7120971	-0.077512857	0.6760475	0.7120971	-0.03605
cg14871771	7	39712301	637222	637272	N/A	AGGAATCAGAAGAGGCCGTCCTTCCACGGAGCCAGAGAGTACCCACCCG	R	Body;Body;Body;Body;Body;B	PRKAR1B	0.8884929	0.9133229	-0.02483			
cg14878471	14	37680353	61188077	61188127	N_Shelf	GGGGATGTCGGATCCTCTGCTGGGCCAAGTCCTGCTGCGCTTCCAAAACG	F	Body	SIX4	0.36303	0.4282629	-0.065232857			
cg14879418	5	7262370	72571312	72571362	N/A	CGGCCTGGTGATGGGGAATCTCCCCTGTGTTTGCTCAGAGCTGAAATTCCA	F	N/A	N/A	0.67653	0.7585957	-0.082065714	0.7085725	0.7585957	-0.050023
cg14882082	14	66761401	100845427	100845477	S_Shelf	CTCCATCATCATGAAGCGCAGGTCTGAAAACTGCTGAAAACTCAAAACACG	F	1stUTR;5'UTR	BOAR25	0.79596	0.8443586	-0.048398571			
cg14887752	1	13752489	35370638	35370688	N/A	CGGGGGGCACCCTTGCCCTGTGGTGGCCCACACAGTCTTCACAGGTGTC	F	1stExon	DLGAP3	0.5286686	0.6037114	-0.074842857	0.5673925	0.6037114	-0.036319
cg14892359	11	16703464	11860337	11860387	N_Shelf	AATCAAACCCATCTGTCTTGCTCCAGTCATCTGCCACTCTTCCTCTTACG	F	N/A	N/A	0.80623	0.84547	-0.03924			
cg14912034	10	23712443	30918851	30918901	N/A	CGAGAAGTATTAAGGCCAGAAGAGAGTTAGCACCTGCTCTCAGAACACAA	R	TSS1500	LYZL2	0.6885614	0.7322914	-0.04373			
cg14917044	12	27717494	122579820	122579870	N_Shelf	CACGGCCAGCAACTGGTGGGCAGGGCTCGCGGCCGTGCGAAGCCCGG	F	Body	SETD1B	0.8087043	0.8446543	-0.03595			
cg14919082	2	18685310	54901055	54901105	N/A	CGCCCAGCGCCCAGACTCCAGAACACAGGATGCCCCACCCTGTGGAGAAA	R	N/A	N/A	0.5407114	0.6741357	-0.133424286	0.6235913	0.6741357	-0.050544
cg14927519	7	62688452	28450696	28450746	S_Shelf	AAGCTTCTGGGGTCTGAGGGGACCACTGTACCTGATACGCGCGCAATCCG	R	TSS1500;5'UTR	CREB5	0.3002257	0.3981614	-0.097935714			
cg14936008	14	56774321	107260064	107260114	N/A	CGGAGGGGAACAAGGGGGTTGAAGACATTTATCCTTTGCCT	R	N/A	N/A	0.9119129	0.9349814	-0.023068571			
cg14939641	19	19714470	11043850	11043900	S_Shelf	GAGCAAGCCCCGTCTCAAAAAATTAATAAGGCTGGATGCGGTGGCTCACG	R	N/A	N/A	0.5598686	0.6428286	-0.08296			
cg14945578	20	43618365	3776324	3776374	Island	GTTGGGGTAACATCTAACCTGGGGTCCCGCGAAAGAGCCCATCAGTTCG	R	TSS200;TSS200;TSS200	CDC25B	0.0375981	0.0534697	-0.015871571			
cg14948822	2	14652498	27545006	27545056	N/A	CGGTAAAATGTTTTCCAAGTTGAGGCCTCCTGGGGCAATGCCTTTATCCT	F	Body	MPV17	0.9105843	0.9374814	-0.026907143			
cg14952949	12	74745477	81109806	81109856	S_Shelf	CTGCCTAGCTGTCCTATAGGCCACAGTGTGCCAACAGAAATTCGACAG	F	TSS1500	MYF5	0.4149114	0.4882857	-0.071374286			
cg14957089	11	35646442	331092	331142	Island	CTAATAAATGTGAGCCCTGGACTCTGAGGCCGGGCAGCGAATGTTCTGCG	R	N/A	N/A	0.8420743	0.9132557	-0.071181429	0.8861713	0.9132557	-0.027084
cg14957943	3	33631490	48632783	48632833	Island	CGGCAGGCGGGAACCCAGGCACCCGCCCTCACCCATATCCCTGAGAGGTC	F	TSS200	COL7A1	0.2503014	0.1960914	0.05421			
cg14975547	2	10661330	75827618	75827668	N/A	CCGGGGCAGCAACACTTCTGGCTCCACGCCGCCACCTCACGGAATT	R	N/A	N/A	0.8698357	0.9228814	-0.053045714	0.88989	0.9228814	-0.032991
cg14988869	5	43784499	177615731	177615781	S_Shelf	CGGGGTTCCCAACAAGTAGCTTCCAGATGGCCTGGTGAGGCTGGAGGCA	R	TSS1500	GMCL1L	0.8384757	0.8874757	-0.049	0.8661025	0.8874757	-0.021373
cg14996807	19	35763366	17759239	17759289	Island	CGCTGCAGGCAGTCGGCGTTGAGCAGGTCCTGGCACTTCTCGTGGCACTT	F	Body	UNC13A				0.8111988	0.87151	-0.060311
cg15007123	12	10807315	111798634	111798684	N_Shelf	CGTTGGCCTTGGTCTGGGGGAGAGGGGTGAGGGATGTCCCCTACCAA	R	3'UTR	FAM109A	0.63294	0.6817386	-0.048798571			
cg15008984	7	40603429	142568715	142568765	N/A	GGGTTTGGTGTGGGGCATCTCTCACAGAGGCTGTTGGAGCCCGGCTCACG	F	3'UTR	EPHB6	0.81773	0.8599971	-0.042267143			
cg15010616	5	21677470	149093472	149093522	N/A	CGAGAGTGGCTTCAGTGGAACTGGAAGATCCAAGATGAGTTCATTCAGGT	F	N/A	N/A	0.8291229	0.8866986	-0.057575714	0.856035	0.8866986	-0.030664
cg15012161	6	35632507	113955683	113955733	N/A	CGTCTGGCACAATCAGTGAAAGAAATATGGGCCTGGGTCCGGGTGTTAAA	F	N/A	N/A	0.5808214	0.7367714	-0.15595	0.65633	0.7367714	-0.080441
cg15012692	10	67723363	134209903	134209953	Island	CCGGGCCCACCGGGGACGCGCGCCCTCCGAGCAGTTTACACAGAACACGCCT	R	TSS1500;TSS1500	PWWP2B	0.13115	0.1776386	-0.046488571			
cg15014679	11	31755502	27695210	27695260	N/A	CGGTGCTCCTGAAATTTTCCATAGACAGTGTATTCTTGTGGTAATTAGT	F	Body;5'UTR;Body;5'UTR;5'UTI	BDNF	0.8518957	0.9180471	-0.066151429			
cg15015996	1	25631447	3382565	3382615	N/A	CGGCCGTGAGGCCTGTGGAGCTGACATCTATTGGGCACAGCTTCGCATG	F	Body	ARHGEF16	0.6886157	0.7623143	-0.073698571	0.7242	0.7623143	-0.038114
cg15029037	4	28694507	146729164	146729214	N/A	CGGTATCAGGTAACCTGGAGCAATTGGGAAAATTTTGCAAAGATTCCGA	R	Body	ZNF827	0.83327	0.9086214	-0.075354429			
cg15033269	13	63740315	42631489	42631539	N_Shore	GGTTAAGTAACTTGCCCAAGGTTCCTTAGCAAAGCCAGTCTCTGAATACG	F	TSS1500	SS18L2	0.86472	0.89529	-0.03057	0.8561575	0.89529	-0.039133
cg15049778	4	36703506	15000756	15000806	N_Shelf	TCCCTCCTTTAGCTACTGCCTTCTTTTTCTGCTTTTACATTGCTGAACG	F	N/A	N/A	0.8035486	0.8726586	-0.06911	0.846425	0.8726586	-0.026234
cg15063715	11	65763300	10857436	10857486	S_Shore	CCAAGGCAATAGGCTAAAAAGTGTCTTGGGGGCCGGCATGGTGGTTTACG	R	TSS1500;TSS1500	CASZ1	0.87067	0.9323386	-0.061668571	0.8986013	0.9323386	-0.033737
cg15067032	19	31740479	31159573	31159623	N/A	CGGTGCAGGTGTTGGTCTATAGGCCAGGTCATATTTGCACACCCCTACTG	N/A	N/A	N/A	0.4934829	0.5740657	-0.080582857			
cg15076179	2	47759497	113804820	113804870	N_Shelf	CGGGCACAGAAAATACACAAGAGCAGCCTAAGCATGTTGTTGATAAAAA	R	5'UTR;5'UTR	IL1F8	0.80091	0.8790686	-0.078158571			
cg15076217	1	72727348	207975699	207975749	N/A	CGAGAAGTCCAGGGAAGAACTTGAAGAGCAAAATACACTCTTGAGTTTGT	R	TSS1500	MIR29C	0.8541271	0.8852386	-0.031111429			
cg15080351	6	57693503	3851517	3851567	S_Shore	CGCTTAGCTCTTATAAATGTTTCTGTTGTTATTATTATTGGATTTGGTTA	F	3'UTR	FAM60B	0.8791114	0.9187557	-0.039644286			
cg15089481	1	52616463	40251192	40251242	N_Shelf	CTGCTCTGCACGGAGACCTGAGCCATGGTGGGAGGCCTATGAGAGCCCCG	R	Body	BMP8B	0.8127514	0.8488257	-0.036074286	0.8287913	0.8488257	-0.020034
cg15092825	12	55787322	93131197	93131247	N/A	CGGGAGTTTGTGATGTGTTTCCAAGACTTCATCCCAGGTCTTATCCTGTA	R	5'UTR	PLEKHG7	0.8136786	0.8946143	-0.080935714	0.8587925	0.8946143	-0.035822
cg15106452	9	25747373	140115474	140115524	N_Shore	CCCCCACAGCGTTGGTCAATGATCTCTGTGTTGGGGCCAGGCACG	R	1stExon	RNF208	0.8996471	0.9274214	-0.027774286			
cg15110243	11	70777429	78501744	78501794	N/A	CGAAGCCTTGAGACAGCAAGGACACTGAGCCTGGGTGGGTTTCC	F	Body	CUX2	0.7478329	0.8073714	-0.069538571	0.7792825	0.8073714	-0.028089
cg15110800	1	66609386	34352660	34352710	N/A	CGGACTTTGGAGTCAAAGAGATGGGTTTGAATTCTGATTCCTCCACTGAA	R	Body	CSMD2	0.5612857	0.67788	-0.116594286	0.59781	0.67788	-0.08007
cg15115171	10	41626495	17604829	17604879	N/A	CGTCTTACGGCTTCCCAGAAAACGTTTGGCAAGGGACATGACCAGACAT	F	N/A	N/A	0.5541314	0.6578043	-0.103672857	0.5784363	0.6578043	-0.079368
cg15126021	5	18708479	1672851	1672901	N/A	CGGGCCCACCTCGAGATCCTCTGAGGATCTCTGAGCAGCCAACAACAC	R	N/A	N/A	0.37297	0.4602229	-0.087252857	0.3768025	0.4602229	-0.08342
cg15126273	13	32799459	28578045	28578095	N/A	CGCAGACAGCTTCTAGAGAAAAGTCTGGTGAAGCAGCAGTTGATAATAGA	F	3'UTR	FLT3	0.7378086	0.8045886	-0.06678			
cg15126897	1	31784360	192155550	192155600	N/A	CGCACAAATTGAAACTAGACTTGAAAGCCTCAGTGTGCGAGCCCCCTAAC	R	N/A	N/A	0.6486129	0.74128	-0.092667143	0.70051	0.74128	-0.04077
cg15128638	3	70719300	124493484	124493534	N/A	TGCTATGGCCAATGCTCTGAACGGCAGATTTAAGCAACACAGG	F	Body	ZNF511	0.5873814	0.6687529	-0.081371429			
cg15129876	11	45666361	82865069	82865119	N_Shelf	TAATCCCAGCTACTCCTTTAAAATTTATAGACTGGGCGCTGTGGCTCACG	F	N/A	N/A	0.7918886	0.8512186	-0.05933	0.8221513	0.8512186	-0.029067
cg15137213	17	41778448	585596	585646	N/A	CGGAAACTGAAAACACAACAAGCAGCAGCTAAGCATGTTGTTGATAAAA	R	Body;Body	VPS53	0.8369571	0.91645	-0.079492857	0.8698338	0.91645	-0.046616
cg15139063	2	64656451	106959868	106959918	S_Shore	CGTGGGCATGTGATCTGTGAGCCCGTGGTCCCCACGGAAGCGGTGAGAACG	R	N/A	N/A	0.8864071	0.9221214	-0.035714286			
cg15151778	8	63626332	145502134	145502184	N_Shelf	GGGTCTCCAGCACACCCGACAGTGTGCTGCTGGACTGAGGAGGGGTCTG	R	Body	BOP1	0.8486943	0.8968671	-0.048172857			
cg15157403	1	42672460	234880737	234880787	N/A	GGAGGAACATTGATAAGAGTGCCACATGCAGGCCAGGCGTGGTGGCTCACG	F	N/A	N/A	0.4504457	0.4915129	-0.041067143			
cg15171791	15	54705472	40272006	40272056	S_Shelf	CGGGACCAAAATTTAGTGTTCTGTACCATGTTGGTTTCACATCACGGCTT	F	Body	EIF2AK4	0.76518	0.8532429	-0.088062857			
cg15173586	8	36800466	124784802	124784852	S_Shelf	TTTCTTTGCCATTTAGCTTAGTTTATCACAGGCTAACTGCAGAACCCACG	F	Body	FAM91A1	0.687777	0.7719486	-0.084178571	0.7285263	0.7719486	-0.043422
cg15222091	6	36627454	167536069	167536119	N/A	CGGGCATGGCTATTTCTCGGAACCCTCTGAGGTTAGAGCTGTCATGGTCT	F	5'UTR;TSS200	CCR6	0.7422929	0.80428	-0.061987143			
cg15224459	17	58692479	81042023	81042073	N_Shore	CGCTTTTGTGGTGAGTCTTGCTGTAATGATAGCTTATATTTACAAATACC	F	Body	METRNL	0.6576614	0.74163	-0.083968571			
cg15229496	18	50713372	45939850	45939900	S_Shelf	AAGAATGCACTACCCTTAATGTCTCTCTTGTAGTAATTTTCCATCTATCG	N	N/A	N/A	0.7884871	0.8292614	-0.040774286			
cg15236196	17	55768314	62969344	62969394	N_Shelf	CCGGCTATTGGTCTGATTCAGATGGGCCATTTTACCATTGTTGTATAT	R	Body	FLJ32065	0.8621786	0.9217314	-0.059552857			
cg15240476	6	64614464	26094913	26094963	N/A	CGGGTCCAGAAAATGCATAGATACATGTGTAAAAATCTGGTAAGGTTATG	R	3'UTR;3'UTR;3'UTR;3'UTR;3'L	HFE	0.90649	0.9352514	-0.028761429	0.9052188	0.9352514	-0.030033
cg15241519	11	50673503	121440892	121440942	N/A	CCTGCCGCACTTCACCTTAATGTCTCCTTCTGCAACCAGTGTATCTG	R	Body	SORL1	0.79816	0.8335914	-0.035431429			
cg15260951	18	40726457	77165200	77165200	N_Shelf	CGGCTGCCCATCCTCTGTTGTTGTTGTTGTTGTTGGCAGTTTGGCGGT	F	Body;5'UTR;Body;Body;Body	NFATC1	0.8134157	0.8790043	-0.065588571			
cg15262954	20	21797476	62198872	62198922	Island	CGGACCCAGTCACGCTGCAGTACTGTTGCCTGACCGACGACCGCCAGGCT	R	Body;1stExon	PRIC285	0.5270657	0.6590629	-0.131997143			
cg15268191	3	58799460	171704056	171704106	N/A	CGATGTGATCATTCATTAAAAAAGTATGCACTATGCACAACTGTGTGGC	N	N/A	N/A	0.7396671	0.8414314	-0.101764286			
cg15272974	15	47619381	64130186	64130236	S_Shelf	CGTGAGGTGGAATGAATTCTTTTTCTGGTGTTTAAACACAAGCTGTAAGA	N	N/A	N/A	0.82212	0.8944529	-0.072332857			
cg15277108	12	17622504	113843048	113843098	N/A	AGCTCCCAGGTCCGCAGTGTCTCTATTTTGTCCTATTTTGTCCCCCTGG	F	TSS1500	SDS	0.9312029	0.96089	-0.029687143			
cg15284635	3	56682475	10858504	10858554	S_Shore	CCAGCATGAGATGCAGACCGAGGCCAGGGAGCCCTTGCTTTGGGTAGGCG	R	Body	SLC6A11	0.5373771	0.6149371	-0.07756			
cg15290957	2	26618377	23918891	23918941	N/A	CGGCCACCAGCAGCGCTGGGTCATCCCCACCATCTGACGGCCCCCAACC	R	Body	KLHL29	0.87722	0.92281	-0.04559			
cg15296129	4	66713367	10954244	10954294	N/A	CCGGTGCCTCTCCAAGCGTGTTCTGCGTTCCAAGGATGTGTGCAAGAAG	F	5'UTR;5'UTR;TSS1500	RPL34	0.1450529	0.120204	0.024848857			
cg15309004	6	44725368	39040812	39040862	N/A	CCAGTGGGATGGGCTCCTCTCCTACCAGGTGTGTGGTGCATCCAGGGA	R	Body	GLP1R	0.8674929	0.8995671	-0.032074286			
cg15322185	22	56779496	38516895	38516945	Island	TCCCCGCCTCTGACCCCTTTGTTCCTAGGTAAGTCCATGGCCTACATGCG	F	Body;Body	PLA2G6	0.8655929	0.8965586	-0.030965714			
cg15329133	5	66605427	135468951	135468001	N_Shore	GAGTGCCCTTGGAGTTCCAGAGTCTGGAGATCTCTGGGTCACTCGAATCG	F	TSS1500;TSS1500;Body;TSS	SMAD5	0.5783886	0.6575	-0.079111429			
cg15339435	11	50752433	128169430	128169430	N/A	CGTGTAAGTGAAAGCAATGACTCTCTGGTGTCCTCTACAAATTTCCCACA	F	N/A	N/A	0.6406386	0.7154086	-0.07477			
cg15347097	12	50700367	110909654	110909604	S_Shelf	CATGGGCCAGGCGCCAAGTTTAATAAAGTTTTTGTTATGAACTTTTCACCG	F	Body	C12orf24	0.9025814	0.9314	-0.028818571	0.915035	0.9314	-0.016365
cg15347627	4	62635466	2941570	2941620	N/A	CGGCTGTGCCAGGTGCTGGACAGCCACAGCCTTGGCTTACCCCCCCGCC	R	Body;Body	C4orf10	0.80251	0.8610771	-0.058567143			
cg15355387	3	38646406	85007817	85007867	N_Shore	TTCATTAATAACGAAGGGTTGCACTCAGAGAAGCGTTCACAATCCCACCG	F	TSS1500;TSS1500	CADM2				0.1683863	0.1212227	0.0471635
cg15360771	12	52716450	109983073	109983123	N/A	CGGGGCCCGGCTCATCTGGCACCATCTGCAATGTGACAAAGCCACCCAGC	R	N/A	N/A	0.7697257	0.8256857	-0.05596	0.7927163	0.8256857	-0.032969
cg15370309	17	69664452	9141550	9141600	N_Shore	AGGCAAGCTCTGTGGCTTCAGCAGCCACAAGGACACCTCCCAGGGAACG	F	Body	NTN1	0.7177829	0.7578414	-0.040058571			
cg15370992	10	34651411	11342792	11342792	N/A	CGCGGGCGCGCTCTCCTGAGTGAGTATGTTTGGATGCGGCGATTTTCTC	F	Body;Body;Body;Body	CUGBP2	0.8176114	0.8630471	-0.045428714			
cg15374234	17	17794381	72709026	72709076	N/A	CGGGGACCTTGTCTGAAGAGAAGATGCCCCTGCTGACACTCTACCTGCTCC	R	5'UTR;Body;1stExon	CD300LF	0.7090343	0.7841057	-0.075071429			
cg15382367	12	20685400	48348879	48348929	N/A	CGCTCAGAGGTGAGGCAGTCAGGGCCTCACCATGGCTACAACGCCATCAG	F	N/A	N/A	0.87897	0.9074257	-0.028455714	0.8851125	0.9074257	-0.022313
cg15388490	7	32727335	150501997	150502047	S_Shelf	GAATCTAGCCATGCCTCTCCTGATTATTAGTGCCTGGTGCTTTCTGCACCG	R	3'UTR	TMEM176A	0.7902486	0.85094	-0.060691429			
cg15397308	8	73620459	144900383	144900383	S_Shore	CGGGATCGAGGCCTTGGCTCCCTGCCCCTGATGTCCTGCTGCCCCCGCA	R	Body;Body;Body	PUF60	0.8121071	0.8501914	-0.038094286			
cg15401332	5	74657411	111319725	111319775	N/A	ATGACTGGTAACTGCAAAATCTGAGTGACCTTTTCCTCCAATGAAACG	R	N/A	N/A	0.5979886	0.7036343	-0.105645714	0.6552275	0.7036343	-0.048407
cg15406585	10	67766426	28525513	28525563	N/A	CGGGGGAAAGCGGCATGTTTTTATGTATTACTTGTATAATTAGTTTTTT	F	Body	MPP7	0.9012986	0.9303986	-0.0291			
cg15407257	20	12667307	23621186	23621186	S_Shelf	CCTGCAATGGCCCAGAGTTTTGGTGGTTTCTGGCAAAACGCTCCTCCG	N	N/A	N/A	0.6807543	0.7408443	-0.06009	0.7068675	0.7408443	-0.033977
cg15422033	8	43737437	143437575	143437575	N/A	CGGGCAGGCCCAGCAGGACAGCTGGACTCACACCTGCTGCTGGCGCAGGC	F	5'UTR	TSNARE1	0.8575971	0.89101	-0.033412857			
cg15428479	19	36642323	18698825	18698875	N/A	CGGCTGGGCCCCTGGAGGAGGAAGCTTTCCAAAGCTCTGTCTAGCCCATG	F	TSS1500;TSS1500	C19orf60	0.5703843	0.6629371	-0.092552857			
cg15428496	3	59632328	37940044	37940094	N/A	CGGGGCTCGTAGTAAGCACTCAATAGTGGCACTGAATATTATTATTATA	R	Body;Body	CTDSPL	0.8642643	0.9143386	-0.050074286			
cg15431934	15	41771369	40759208	40759258	N_Shelf	CGTGTGGCTTTCTGCAAGAGGTTTCCTTGGAACCTTTACAGCAATTCCG	R	3'UTR	BAHD1	0.5623414	0.6477457	-0.085404286	0.59904	0.6477457	-0.048706
cg15438548	10	27620384	123098791	123098841	N/A	CGTGGATTTTCTGCTTCTGGGCGGTATGTGTCTGTGAGTACATGCTCTGA	R	N/A	N/A	0.7439571	0.8078286	-0.063871429			
cg15439442	19	12720371	49654467	49654517	N_Shore	CGTGCTCCCGAAAGAAAAGAAGGCATAGACCACTACGAGGGTCTCAGGG	R	3'UTR	HRC	0.1227775	0.2093243	-0.086549286			
cg15442059	2	47671417	231598109	231598159	N/A	AATCAAACATCCTGGGCGGGACATGTGGGGGACATCGTGATACG	F	5'UTR;5'UTR;5'UTR	CAB39	0.8649489	0.92191	-0.056964429	0.8936238	0.92191	-0.028286
cg15444831	10	44761354	33371435	33371485	N/A	CGCTTAAAGCAGATTATTTAAGAGAAAGAAGGGAAGCAGACCAGCACTAG	R	N/A	N/A	0.8705843	0.9243171	-0.053732857			
cg15445281	13	68628352	51163726	51163776	N/A	CGAGGTACTATTACCTATGATGAGATTTCCTGAGACTATAAAATGAAGC	R	N/A	N/A	0.88599	0.9322286	-0.047238571	0.9069425	0.9322286	-0.026286
cg15447231	1	50779492	101537255	101537305	N/A	GTAACCCACTCTGCATCCACACTGACATATATAGCTGAATGAAGAATCG	N	N/A	N/A	0.67736	0.7472229	-0.069862857			
cg15448894	6	65713419	52840459	52840519	N/A	CGTGTTCTGGTGTTTCTTTAAATTTGTGCATCTTGTTGCTCAACACG	R	N/A	N/A	0.8082171	0.8681357	-0.059918571			
cg15451258	15	11740424	30117681	30117731	S_Shelf	AAACCACAACCTTAAAAGACAACTTCCTGTGGGATTTTTGGTGTCTGCG	R	N/A	N/A	0.5665429	0.6656857	-0.099142857			
cg15452590	11	28620354	607997	608047	N_Shelf	AGATGGTTCGTGTGATCTCAGAGGGCAGGAGGCCGGGCCAGACCTCTCG	F	Body	PHRF1	0.6554914	0.7029686	-0.047477143			
cg15453206	3	63650374	24729367	24729367	N/A	AGTCATTTGGCTGGACCTGGCCATGGGGCTGGCCATGCCACACG	R	N/A	N/A	0.8613329	0.89526	-0.033927143			
cg15465051	3	65769375	110627980	110628030	N/A	AATTCACCTGAAGGCATTGTTAAACCCAACTTTCCCAGGCTCCTCGTTCG	F	N/A	N/A	0.87545	0.9029914	-0.027841429			
cg15468243	14	60792468	105449615	105449665	N_Shore	CGGGAGTCATGGCTAATGTCCCCCACACCCAGGCTTTAATGGGAACCCAC	F	N/A	N/A	0.7633957	0.8046229	-0.041227143			
cg15470261	19	42657470	1698699	1698749	Island	CGGACCGCTTGGACTTCCAGATGGACGTGCCCCGGAAGATGCGCGCGCG	R	N/A	N/A	0.7403229	0.6166743	0.123646571	0.6715425	0.6166743	0.0548682
cg15470736	7	17774375	157056012	157056062	N/A	CGGGCATACAGAGAATCCGTGCCCTTTTGTGCCGTGCTCGCTTTGTGGGCT	F	Body	UBE3C	0.6805314	0.72782	-0.047288571			
cg15472885	3	36625381	71056608	71056658	N/A	CGAGAGCCACAAATGGGTTTGAAACAATTTATGATATCCGGCCTCCTTCG	R	Body	FOXP1	0.9101843	0.9438614	-0.033677143			
cg15474755	12	45699437	89263698	89263748	N/A	TTTGCGTATGTTCTTGTTAATTGATCCTTTAGCTAAAAGTCTTCTCTTCG	F	N/A	N/A	0.8685329	0.9329714	-0.064438571	0.9057863	0.9329714	-0.027185
cg15475502	3	65751473	122662340	122662390	N/A	ACGATGCTCTGTCCCCGGAGGGGTCCAAATCCCTGCGCTGGCGCAGGCC	R	Body	SEMA5B	0.6951086	0.757443	-0.062355714			
cg15475553	3	35717487	181101204	181101254	N/A	GCCATTCCCCAACCACACTGGGCACTTTCCAGGTATGTGCGCTTGGCTCG	R	N/A	N/A	0.8749371	0.9000914	-0.025154286			
cg15477363	2	55626313	68961987	68962037	N/A	CGAAAGAATCTCAGGCCTTACTGAGTTGAGGTCGTGATAAACAACTGCTG	R	5'UTR;1stExon;1stExon;5'UTR	ARHGAP25	0.5491186	0.6539943	-0.104875714			
cg15478443	6	61649473	111936579	111936629	N/A	CGCCCAGCTCTGCTGCCTGCTGAAGGCACCTGATGACGCCTTCCTCCTG	R	N/A	N/A	0.8310043	0.8763286	-0.045324286			
cg15484808	6	58711458	33242542	33242592	N_Shelf	CTCTCATGATTTGTCATTGGATCTAGAGCCCACCCTAATCAAATATAACG	R	Body	RPS18	0.7680514	0.8472971	-0.079245714	0.813965	0.8472971	-0.033332
cg15491567	2	48714319	71679675	71679725	N_Shore	CGTTGTGCTAAGAGGAAGAAAGAAGGCATAGACCACTACAGAAGGACC	F	TSS1500;TSS1500;TSS1500;	DYSF	0.6625157	0.7453757	-0.08286	0.7039338	0.7453757	-0.04142
cg15495091	13	19638304	113491819	113491869	N_Shore	CGCCGAGTGCTCCAAATCCTGTGCCGTTCAGAGCCCTCCACGCAGCGTC	F	Body;Body	ATP11A	0.9194771	0.94886	-0.029382857			
cg15497249	1	18750489	239485905	239485955	N/A	GAAATGTGTATTACTGCGGGCCCAGCTGCAAAATTGAACAAGCCCTCG	R	N/A	N/A	0.8271414	0.8744743	-0.047332857			
cg15497991	20	51797323	50142702	50142752	S_Shelf	CGCCTGCTAACAGCTCCCGTCGCCACCAGGTATCTGTTTAGGGAATCTAT	F	Body;Body;Body	NFATC2	0.74235	0.8250286	-0.082678571	0.77484	0.8250286	-0.050189
cg15505219	14	48650432	61858317	61858367	N/A	CGTCTTTTGGTTTTGTGCCATCTTTTAGTTTGCCTGTGAATGTCTATGAAA	F	Body	PRKCH	0.8011914	0.8563014	-0.05511			
cg15511625	3	33631342	10400548	10400598	Island	TGCGGAGCCCCGCGAAGCCATGGGCCAATCACCTTCTTTACCATCTCCG	F	Body;Body	ATP2B2				0.86361	0.8933014	-0.029691
cg15516558	1	53702460	161091980	161092030	S_Shelf	ATAGGTCAGGGCAATGCTTGCAGCATCAAGTTCCTCAGGAGTTTCTGTCG	R	Body;Body;Body	DEDD	0.7413743	0.7973029	-0.055928571			
cg15518883	9	33728453	35650561	35650611	S_Shelf	GGGGACTTGTGGGTCCTCTTAGGGGCTGTGACGCTGCTATTTTCTCATCTCG	F	Body	SIT1	0.8066771	0.8697543	-0.063077143	0.8349875	0.8697543	-0.034767
cg15519092	17	70787491	77752671	77752721	Island	GGGAGGGTGTTTCCCTCCCGGAAGGGGCTCTCTGCACAGCTGCTCCCG	R	Body;Body	CBX2	0.17258	0.2242743	-0.051694286	0.19719	0.2242743	-0.027084
cg15526941	1	56647

cg15834202	5	25629477	58865918	58865968	N/A	GGCGCCACTGAGCTGTGTCATCACGAGGGCCCTGATACATGAATATTCG	F	Body	Body;Body	PDE4D	0.7638014	0.83157	-0.067768571		
cg15836722	2	41707353	113593785	113593835	N/A	CCTTTTTACACAGGTGTCTGAAGCAGCCATGGCAGAAGTACCTGAGCTCG	F	Body		IL1B	0.8344057	0.8892129	-0.054807143		
cg15841378	1	12661422	26535593	26535643	N/A	TACTGGGAGACTCCCTAAAAATAATATCAGGTCGTGCACAGTGGCTCACG	F	N/A	N/A		0.7420743	0.8309271	-0.088852857		
cg15845673	12	18764500	25099560	25099610	N_Shelf	CGCTGCCCGGAGTATTATTTAAAGACTTTTTCCTCGACTAACTGC	R	Body		BCAT1	0.6926971	0.8070429	-0.114345714		
cg15848095	4	69749382	38426028	38426078	N/A	CATTCTTGACCTTGTTGTTTCAGGTGCCTGATAATTCTGGGCTAATGACG	F	N/A	N/A					0.6916563	0.77134 -0.079684
cg15852490	6	49730310	37544545	37544595	N/A	CGTTTCTCGTATCACTGCTGTGCTGGCTGTTGCGCAGGTTGCTTCTCA	F	N/A	N/A		0.6903514	0.7539086	-0.063557143	0.7129188	0.7539086 -0.04099
cg15862380	10	65746452	457264	457314	N_Shelf	CATAATCTTAATAAAAATAAGTCACGCTGTGCTGTTAATTTCCCTTCACG	F	Body	DIP2C		0.9325414	0.9585214	-0.02598		
cg15866367	13	72789416	49796387	49796437	S_Shore	CAACCTCATTTCAAAGAAGTACAGAGCGGCGGCCTTTAAACTGCTGCTCG	R	Body	MLNR		0.8989529	0.9360143	-0.037061429		
cg15878101	18	69623457	8605965	8606015	N_Shelf	CGGGGGAGAAGTTTCAAGTATAAACAAAGGCCAGAACCAGAAGAGTATGTA	R	N/A	N/A		0.84905	0.94218	-0.09313	0.9107825	0.94218 -0.031398
cg15890332	12	16647453	107067104	107067154	N/A	CGGGCTGTGAAAGCCTGTTGAGGTTGAGCTCTTGCCCTGCACTCTTGTCC	F	Body;Body	RFX4		0.4481371	0.5258657	-0.077728571		
cg15890469	14	62699367	75408846	75408896	N/A	GGGGGCAGCTTTGTTCTCTGTTCTCTGTTCTGCAACCAGTGCTTCGAG	F	3'UTR	PGF		0.6764014	0.7627671	-0.086365714		
cg15896259	8	56754311	23312661	23312711	N_Shelf	CGACGAAAACAATGCAAATCAACCACAAAGGGAAATGGTTCCTTGGTGG	F	5'UTR;5'UTR	ENTPD4		0.58024	0.6688857	-0.088645714		
cg15896579	11	65792373	47439533	47439583	N/A	CTGGATGGCAGACAGTGCGTGCAAGCATCACAGCCCACTGGAAGAGGCCG	R	N/A	N/A		0.8119257	0.8506829	-0.038757143		
cg15900058	2	55749348	206666368	206666418	N/A	CGCACACACACTTGTCCTATAGGGTTTTCTGACAAGGAAGGGTGAGGAAA	R	N/A	N/A		0.6088471	0.7045	-0.095602857	0.6595613	0.70445 -0.044889
cg15900221	1	40613339	3382243	3382243	N/A	CGGGCGGTGCTGCAAGACTCTTCTGAGCGCTCCTCACGAGAGTCCGCGC	F	Body	ARHGEF16		0.8277257	0.8911971	-0.063471429	0.8656688	0.8911971 -0.025528
cg15901647	1	13677320	18687127	18687177	N/A	CCTCACTTGGGAAAAGCTGTCAGTTCTGATTTACCCAGCCTTGGGACACG	F	Body	IGSF21		0.8265871	0.8725071	-0.04592		
cg15907795	5	19742460	137419777	137419827	N/A	CGCCCTGCTACCCCAGTGGACCAGGTCCAGCTCAGGGCCAAGTCCAGAG	R	1stExon;5'UTR	WNT8A		0.8876514	0.9235286	-0.035877143		
cg15909981	22	66728342	37465178	37465228	Island	CCCCAACCCTGATCCAGCAGTGCAGGGCCGGGCTCCAGAAGTGGGAGCG	R	Body	TMPRSS6		0.4627443	0.5208357	-0.058091429		
cg15921239	6	32604424	35765215	35765265	N/A	CGCCCCACAGCAGATTGGCCACAGCTGTGCCTCTGCCCACGGCCAGCCCT	R	TSS200	CLPS		0.83108	0.9104857	-0.079405714	0.8650038	0.9104857 -0.045482
cg15922693	12	39609436	51610688	51610738	N_Shore	CGCGGCGAATACCCCACTCAGCCCGACTGGAAGCCTAAAACCTTCACAG	R	Body	POU6F1		0.5686	0.6786743	-0.110074286	0.6310563	0.6786743 -0.047618
cg15925505	6	34690346	36854355	36854405	S_Shore	AAAGTGTGGCCTGCACGGTTAACAGTCTTAAAATACTACAAAACACGACG	F	Body	C6orf89		0.3252357	0.4661543	-0.140918571	0.3805638	0.4661543 -0.085591
cg15934958	3	20678503	37212104	37212154	N/A	GTCCACAACTCCTGGTCTCTCTCTTTGGGCTGCTACTATTTAACTGGGCCCT	R	5'UTR;5'UTR;5'UTR	LRRFIP2		0.74013	0.8083286	-0.068195571		
cg15935860	1	57640439	201282499	201282549	N/A	CGCTGGGCAGCAAGGGCCAGAAGACCACCAGAACCGCTACAGCTTTTAC	F	Body;Body	PKP1		0.83813	0.8947757	-0.056645714		
cg15940454	6	69607445	109038650	109038700	N/A	GAGGCTTCGGTGTGCTGAGGCCGGGGCAGCTGCTGGACTTCGGGTCTTCG	R	N/A	N/A		0.9208357	0.9480814	-0.027245714	0.9355225	0.9480814 -0.012559
cg15942562	12	30778322	6959471	6959521	S_Shore	CCCACCCTGCCCCCAGTGGACCAGGTCCAGCTCAGGGCCAAGTCCAGAG	F	Body	CDCA3		0.77269	0.8483614	-0.075671429		
cg15959363	4	59631374	113091339	113091389	N/A	CGTTGGAGCACATTCTGCTCATGTTAGAAGTTCATTGTTCTTTGTTTTTA	F	Body	C4orf32		0.81555	0.8976686	-0.082118571		
cg15965190	2	45687392	208370032	208370082	N/A	CGGGTACCCTTAAGAAAGTCAATGAAGTAACTAAGCTTGCTATTCAAACC	F	N/A	N/A		0.5528971	0.70362	-0.150722857		
cg15968932	11	70604448	19860035	19860085	N/A	CCGGGCAGGGGTCCACAAGGTATAAGGCAATGAATTCTGGGCTTTAGCCTAAG	R	Body;Body;Body	NAV2		0.8906088	0.9185814	-0.027972857		
cg15969756	5	50633400	34756596	34756646	N/A	GTGGTGTCCACAGCCGAAGGGGCCAGAAAGTGGGCTTAGCTCAGGGGCCG	R	Body;Body;Body;Body;Body;B	RAI14		0.89053	0.9235729	-0.033042857	0.8970463	0.9235729 -0.026527
cg15971496	17	67673377	695156	695206	N/A	CGGCCAGCTGCAGGGACTCCAGGCTCACGCCGTAGGTCTCCCCGCCAATC	R	Body	RNMTL1		0.8929443	0.9169414	-0.023997143		
cg15975539	18	36654445	24445318	24445368	S_Shore	CGCTCAGCTGTCCTGGAGTGGATGAAGCTGAGTGTTCAGCTAGTAAGAGTAA	R	Body;Body	C18orf16		0.8286971	0.8770014	-0.048304286		
cg15978561	2	73625449	240196956	240197006	Island	ATTTGCTGCCCCTCTCTCTGCGTCCTCAAACCAACATGTGAAGAGGCG	F	Body	HDAC4		0.6391614	0.7484143	-0.109252857		
cg15987431	1	29785485	231155746	231155796	N/A	CGGCTTCTTCGATGAAGAGGAGAATATTTCCAGGAGCAGAACTCCCTGC	R	TSS200;Body	MIR1182		0.9085286	0.9402714	-0.031742857		
cg15989608	6	17689412	31545321	31545371	N_Shelf	CGTCCTCCTCCAGGGCAATGATCCCAAAGTAGACCTGCCCAGACTCGGC	R	3'UTR	TNF		0.7778357	0.8429386	-0.065102857		
cg15994554	4	29944554	2944150	2944200	N/A	CCTCTGTGAGCGGGTGGTGAGCTCTGCTGGTGGAACCTGACTCCAGGGACAGG	F	Body;Body	C4orf10		0.8739914	0.9121814	-0.03819	0.8844713	0.9121814 -0.02771
cg15995125	1	34750333	17746597	17746647	S_Shore	CGCACTTCAGGGAACCGCACTTAGGGTCCGATGGGAAGGAGAATGGAGAC	F	Body;Body	RCC2		0.38867	0.4395714	-0.050901429		
cg16006738	1	15646379	47688728	47688778	N_Shelf	CGGGGCTGGGATCTGCACAACAGAAAAGACTTCAAAAGACCCAAGCAGCT	R	Body	TAL1		0.8163471	0.85283	-0.036482857	0.8241175	0.85283 -0.028713
cg16021223	1	38691405	20143217	20143267	N/A	CGTGGGGCCCCAAAATCACTAAGCCACAAGGGAAAGTCAAGCTGGAAACT	F	TSS1500	RNF186		0.6561171	0.7577986	-0.101681429	0.6979688	0.7577986 -0.05983
cg16023434	1	28664464	11395685	11395685	N/A	TCACACTCCTGGTCTCACTCTGTTGGGTGCAGTGGTGGTGCTGCCG	N/A	N/A	N/A		0.7843514	0.8563829	-0.072031429		
cg16039071	6	43806340	43968282	43968332	N_Shore	TCAGGTTGGCAATTAGCTACTTCCTCTCAGCTGCATGAGGCCACCAAACG	F	TSS200	C6orf223		0.2584543	0.298	-0.039545714		
cg16043635	1	50769331	3416414	3416464	N/A	CGTGGTCACAGGCTGCTCCATGCTGACACTGGCACCGCTGCTCACGCGG	F	Body	MEGF6		0.7649414	0.7997543	-0.034812857		
cg16046214	5	15672409	170289848	170289898	S_Shore	CCCCCTCATACGTTAACAGAGAATTGAGTAAGAGTGAAAATGTATGG	F	Body	RANBP17		0.2762986	0.3454229	-0.069124286		
cg16046505	1	72602470	246582116	246582166	N/A	GGGATATGATGGCTTACCTTGGGCTCAGAGGCCTGACAAAGGGGAGCACG	F	Body;TSS1500	SMYD3		0.5929929	0.6725057	-0.079512857		
cg16049864	8	50731357	95962084	95962134	Island	CAGCACCCTGGCTACACGTCTAACCCTAGGCTGACCAGGTGGGGGCTCTCG	F	TSS1500;TSS1500	TP53INP1					0.1679625	0.0557086 0.1122539
cg16055052	6	55658319	30657275	30657325	S_Shore	CAGGCTAGCCTGTGGTGGGGGCAGATCTGGGTCTGGGTCTCCAAGGTCG	F	Body	NRM		0.8809429	0.9260271	-0.045084286		
cg16055410	6	18667463	31146124	31146174	N_Shelf	CCTGCCTTCTACTCAAGCCAAGACTGGGTTGATCTGGGGCAACTCTGCAG	R	TSS1500	PSORS1C3		0.8571143	0.9061214	-0.049007143		
cg16061947	11	67621368	67032422	67032522	N_Shore	GCATGTCAGAGCTTGTGAGGTTCTCCTCTCAGTGGGTGGTGAGTCACTCG	F	TSS1500	ADRBK1		0.8679886	0.9017543	-0.033765714	0.878095	0.9017543 -0.023659
cg16067696	11	69624473	119522486	119522536	N/A	GCAGGTCGCGCCCGCAGAGCTCTTAGACAGCCCTGAGTCAGATGAATCACCG	F	Body	PVRL1		0.8652229	0.8873443	-0.022121429		
cg16068490	5	54732427	5139334	5139384	N_Shore	CGCACCTCACCGCGGTGGTGTACCCATCTCACCGCGGTGGTGCACGCCTTCA	F	TSS1500	ADAMTS16		0.8466957	0.8823814	-0.035695714	0.8496025	0.8823914 -0.032789
cg16079645	7	39682451	1039875	1039925	Island	CCTTCAGACTGTGGCTTCTGCTGTCAGGGCCCCAGTGTGCACAGGAGACG	F	Body;Body;Body	C7orf50		0.8078914	0.8608343	-0.052942857		
cg16084872	21	28761391	42879074	42879124	Island	CGAGCACGGGTCCAGCTGAAAAACTGCCCCATGTCCAAGAAGTTTGTGCG	F	Body;5'UTR	TMPRSS2		0.1211466	0.084335	0.036811571		
cg16089347	6	34731487	36431452	36431502	N/A	GGGAAATCCCCCATGAGCTGGCCTTCCATCCCCAGCAGCAGCG	R	5'UTR	HCD20		0.8685371	0.9036514	-0.035124286		
cg16090790	6	53704485	113674867	113674917	N/A	ATCTAATCCCATGAGCATTTCAAAGCCAGAGAAGTTTTCTCCAGCTGATCG	R	N/A	N/A		0.8542471	0.9006914	-0.046444286	0.87745	0.9006914 -0.023241
cg16114962	2	29808450	236445373	236445423	S_Shore	TCTCTCTGGTTCACCGCTGCACTTGGGGATGCCAAACAGACTCAAAGACG	F	Body;Body	AGAP1		0.8457614	0.8733486	-0.027587143		
cg16118212	2	66666494	56151071	56151121	Island	GCAAGCGGGGGCGGCAAAGAGGGGCCCTGGAGCAGGGGGCGCGGACCTCG	F	TSS1500;TSS200;TSS200	EFEMP1		0.1644014	0.1068396	0.057561857	0.1437425	0.1068396 0.0369029
cg16121907	8	47675479	99178504	99178554	N/A	CTCAGACCTGGAATAGAATCTGCATTGAACAACATCGCCAGTGGTTCTG	N/A	N/A	N/A		0.7806671	0.8336671	-0.053	0.8005125	0.8336671 -0.033155
cg16131972	20	38673439	45282877	45282927	S_Shelf	TAAAAAAATGGACCAAGGCCCTGGATAGACATTTCTCCAAACAAGATACG	F	5'UTR	SLC13A3		0.83223	0.8733629	-0.041132857		
cg16137250	1	37672369	91306963	91307013	N/A	GTATGCTCATAGATTGCAGTTGTCATGGTGATGATATCTAGCCATGTCTCG	R	N/A	N/A		0.6497114	0.7476771	-0.097965714		
cg16142906	22	26763227	32759777	32759827	N/A	CCCGGCCGCCAGCAGTACGGGCCTGGGGATGGCGCAACTTTTCCCACACC	F	TSS200	RFPL3		0.88905	0.94149	-0.05244		
cg16143569	6	33601471	28830152	28830202	N_Shore	GCTCTAAATATTTTCAATAATTTTTCACCCCTGCTCTAAGACTTGCCTCG	R	N/A	N/A		0.6873314	0.7556243	-0.068292857	0.7090513	0.7556243 -0.046573
cg16155588	13	35769419	113861933	113861983	N_Shore	TGAATGTATACTTTCATGTTTTAAGTTAAAAACATACATCATTTCTTCG	R	TSS1500;Body;Body;Body	CUL4A		0.6605729	0.7469243	-0.086351429		
cg16172864	7	72789463	1716623	1716673	N/A	CGCCAGTCCCTGGGGCTCATTTCCTCTCGTTGCCCTTGAAAACCCTTT	R	N/A	N/A		0.7658071	0.8342157	-0.068408571	0.8061138	0.8342157 -0.028102
cg16177445	3	58779335	65469946	65469996	N/A	CATTCCTTTTTGCAGATGACAAACATTAAAGGCCCTGGTTTTGGGAGCG	F	Body;Body;Body	MAGI1		0.5519286	0.6805943	-0.128665714	0.6081625	0.6805943 -0.07243 2
cg16178855	20	38639491	56269979	56270029	N/A	CGGGATACCAGGTCACAGTCATGGCAGCCTCACTTACCGGCTTTGTGGCT	R	5'UTR;5'UTR;Body;Body	PMEPA1		0.81748	0.8684829	-0.051002857	0.8309188	0.8684829 -0.037564
cg16179607	2	20764498	68476020	68476070	N_Shelf	TTTGTGTGTACTATTCATATGACACTCATCACATGCTAACTTACTTCACG	R	Body	PPP3R1		0.8751771	0.9188657	-0.043688571		
cg16183093	13	34638423	101830996	101830146	N/A	TGGGAGTTGGTTCCTGGTCCAAGTTGTAACCAGTTGTAACCTCACG	R	Body	MAUCN		0.5911429	0.67205	-0.080907143	0.628195	0.67205 -0.043855
cg16222629	8	54691423	143597394	143597444	N/A	AGTGTACCAGGTGCCACGGCTCCAGCTGTGCCTCCCTGGAACAAGAGTCG	F	Body	BAI1		0.8255486	0.8661171	-0.040568571	0.8481513	0.8661171 -0.017966
cg16225491	10	19605428	76854090	76854140	N/A	CAAGGTTCCAGATGGCTTGCCAACTCTGATTCAGTGGGATGGCAGCCTCG	F	N/A	N/A		0.8665186	0.9172414	-0.050722857	0.8936863	0.9172414 -0.023555
cg16229547	15	24796426	30011038	30011088	N/A	TATGAAGAACAGTGGTCATATTATGATGACAAACAGCCCTACCCATCTCG	F	Body;Body	TJP1		0.8378629	0.88416	-0.046297143	0.8514025	0.88416 -0.032757
cg16226627	15	75307574	75307526	75307576	N/A	CCCGGTGCTAAGTGAGACTTTAAGAGATATTTATGCCCTTAAATCCAGC	R	Body	SCAMP5		0.8027229	0.8590786	-0.056355714	0.8281475	0.8590786 -0.030931
cg16233920	3	51772480	47621797	47621847	S_Shore	AAGGCTCTCCAGACCACAGTTCTGGGATGGGTTGTGGGTGGTTGCCATTCG	F	TSS1500	CSPG5		0.8683914	0.9205757	-0.052184286	0.9000363	0.9205757 -0.020539
cg16239536	19	59745486	1079617	1079667	N_Shore	AGCCCGGGGTGCAGGACTCAGACAGAAACCTCAGGGAGGCGGGGCTGACG	F	Body	HMHA1		0.7446371	0.80056	-0.055922857		
cg16248435	6	49742472	15358299	15358349	N/A	ACTTTCCAATTTTAACATACATGCCCACAAAGAAAGCAGACACACTCG	F	Body	PARD2		0.6492771	0.7146629	-0.065375714	0.6713563	0.7146629 -0.043297
cg16248554	2	13664421	121637755	121637805	N/A	CTAAGCTGGCGACCACTCAGCACTACCTGTTTGCAGAGACAAACCTTTCG	F	Body	GL2						
cg16252691	12	58647496	94498235	94498335	S_Shelf	AGGAACAGAACTTCAAATGTACCAGTTTTGGCCAGGTGCGGTGGCTCACG	R	N/A	N/A		0.4627971	0.5474329	-0.084635714		
cg16257559	1	33796485	200864223	200864273	S_Shelf	AGGGGCCCTGTGTGCCTGTGTGTGTGTGTGTGTGTGAAAAACACCG	R	5'UTR;Body	C1orf106		0.8067471	0.8472171	-0.04047		
cg16268563	6	58782383	31513680	31513730	S_Shelf	TAATCATACTCCACATAGATGTTATACTTTACACAGACTGTGGCATTCCG	R	Body;TSS1500;TSS1500;Bod	ATP6V1G2		0.8195957	0.8561486	-0.036552857		
cg16271453	3	38605434	142027066	142027116	N/A	CGGTATAGTCCAAAAATGCAGTGACTGGGTATGTCTTATTTAACTGTTTT	F	3'UTR;3'UTR	XRN1		0.6362857	0.8045	-0.168214286		
cg16283572	10	37602392	32867640	32867640	N/A	GCGAGTGAGCAAACAAAGCTTCCTCTGTATTTACAGCCACTCTCCCATCG	F	5'UTR	C10orf68		0.8227814	0.8596529	-0.036871429	0.83777	0.8596529 -0.021883
cg16288421	4	10690460	54213525	54213575	N/A	GGCAGGCTCTCCTCCACCAATGTGTCTCATTCATCGCCG	F	Body	PTPD2		0.7555357	0.8476329	-0.092097143	0.79578	0.8476329 -0.051853
cg16289491	5	43605464	132383297	132383347	N_Shelf	AGGCAGGAGCCGGGGCTGCCCGCAGCACTAGTGGCCTGGTGTGGGATCCG	R	N/A	N/A		0.9183286	0.94355	-0.025221429		
cg16293853	11	50731506	281888	281938	S_Shore	GGAGGTGCGCCCCATGCCAGATGGACACTGAGGTCACAGGTTTGCACCG	F	Body	NLRP6		0.7408643	0.8203357	-0.079471429	0.7814088	0.8203357 -0.039287
cg16294668	12	29756428	32675257	32675307	N/A	CGTAGATCGGATCATTGCAAAAGACAGGAAATTTGGCAG	F	5'UTR	FGD4		0.6424243	0.7627329	-0.120308571		
cg16300838	10	58690349	135109211	135109261	N/A	CGTGGAGTGCTGGCAGCTGCCTCGTGCTCACAAGGTCCTGATGCTTTCCA	F	Body	TUBGCP2		0.79412	0.8359814	-0.041861429		
cg16306078	6	24761450	126000798	126000848	N/A	CGCCAGGATATAGTCAGATTTTCAGTTGGAAAAACTTGGCTTTATGAAGT	N/A	N/A	N/A		0.86966	0.9212329	-0.051572857	0.89037	0.9212329 -0.030863
cg16307860	1	26768473	122889651	122889701	S_Shore	GTGTGTCGTTCTTCTATCCCACCCTAGGAACTCCCGAAAACTGAAGACCG	R	5'UTR;TSS1500	C1orf58		0.2045071	0.2602314	-0.055724286	0.2262525	0.2602314 -0.033979
cg16309319	11	57684337	6191243	6191243	N/A	CGTTCCATATGAGATGCTGTTTCCACAGGACTGCAGCT	1stExon	OR52B2		0.8747871	0.91569	-0.040902857			
cg16313758	7	39777390	2647039	2647089	S_Shore	AGCAAGGACCTCGGCAATTCCAGGCACAAAGGACAAGCTGGGCCAAGGCG	F	Body;Body	IQCE		0.7493814	0.7907786	-0.041397143	0.77036	0.7907786 -0.020419
cg16314899	1	53683330	68516101	68516151	N_Shore	CGCCAAGAAAGACCTGGTTCCAGTTTCAGGGACAACTCGCCCCATAAACTT	F	5'UTR	DIRAS3		0.56636	0.6106157	-0.044255714		
cg16317516	1	35806307	47294246	47294296	S_Shelf	CGTTTCCCCCGTGCACAGACTATTTCTGGTAGGCATTCTGCTGATCGCG	F	5'UTR;5'UTR;5'UTR;5'UTR;5'L	MADD		0.6056971	0.7332014	-0.127504286		
cg16318036	6	42735434	32038045	32038095	N/A	TCCTGAGGGCCAGTTCGACTCTTTTGTGGTCCAGTTCAAGGACAAAGACG	F	Body	TNXB		0.7932229	0.8398271	-0.046604286		
cg16318311	12	56714505	96113161	96113211	N/A	GATACAAACAGTGCTTATTCTATGGACCATAGAAAAATGCCCCCTTAACG	R	Body	NTN4		0.8100514	0.8902986	-0.080247143		
cg16321280	11	40792304	44332972	44333022	S_Shore	TGAGCCTCCGTTAGCTCATCAGAAATTGGGGGCGCCAATCCTCTAGCACG	F	TSS1500	ALX4		0.21468	0.1747329	0.039947143	0.2203338	0.1747329 0.0456009
cg16324725	18	66704362	44706633	44706683	S_Shelf	TCAATTGCTGTGCACAGGCGAGAGCTGAGTGATGCCGCCGCCGCCGCG	N/A	N/A	N/A		0.7858143	0.8414814	-0.055667143		
cg16328079	3	22709398	65706740	65706790	N/A	AGGCTACACTCAGGGCCATCCCATACCAAGACAGGTTAACAGCAGCTCG	F	Body;Body;Body	MAGI1		0.9157157	0.9360143	-0.020298571		
cg16328999	11	14686392	1858605	1858655	N/A	TGGGGCAAGGGCAGCGCAGGCGAAGGCGGGGCTGCAGGGCCAGCATGCG	F	Body	SYT8		0.8761257	0.9080186	-0.031892857	0.8763363	0.9080186 -0.031682
cg16337430	12	27633344	124876643	124876693	S_Shelf	TCTGACCCGCCGGGCTGCTCTGCCAACCTTGCTCTGTCTGAGGAAAACG	F	Body;Body	NCOR2		0.6382471	0.7254743	-0.087227143		
cg16340023	20	27674385	60544932	60544982	Island	CGGCCCCCTCATCGGGGCACTCGGCCCCCCGTCGGAGCACTCGCCCCCCC	F	N/A	N/A		0.8688643	0.9023614	-0.033497143	0.8829263	0.9023614 -0.019435
cg16343503	16	54711395	56963627	56963677	N_Shelf	GCAGTGACAGCGACCAAAATGGGTAGACTTGACATAAGCACCATACTTCG	R	N/A	N/A		0.9014743	0.9317	-0.034695714	0.9189813	0.9317 -0.017189
cg16347629	1	25699375	35228240	35228290	S_Shore	CGCTCATTCCTGTGATGACGATCACTGAGAACTGACTCCTGCTGGGCAC	R	3'UTR	GJB4		0.8098814	0.87802	-0.068138571		
cg16353350	10	14726488	75684090	75684140	N/A	GTGATATCTCAAGATATCCTTAACTTCACCCCACAACACCTTTTCG	N/A	TSS1500	C10orf55		0.5615286	0.7339929	-0.172462286	0.6447913	0.7339929 -0.089202
cg16353953	18	72659375	60379190	60379240	N_Shelf	CGGCTCACTGAGTCCTCCGCCTCCTGAGTGGCTGAAATTACAGGCACCCG	R	N/A	N/A		0.9214914	0.9503814	-0.02889	0.9302325	0.9503814 -0.020149
cg16355591	16	27706301	10346074	10346124	Island	CAGCCGGGTGCACAGCCTGAAACGGAGAGCAGAGGGCTGTGGGCTGCCG	F	N/A	N/A		0.8919986	0.9231986	-0.0312		
cg16356737	6	48667353	25729805	25729855	N_Shelf	ACTGAGCTGTTATGGTTAACTTCACCTTCACAAGAACCCACAGTTTTCG	N/A	N/A	N/A		0.7369314	0.8079957	-0.071062286		
cg16358576	21	20667476	46644306	46644356	N/A	TGTGGGGCCTGAGCAGCTACCTTGAGACCATGTGAGGTGGCCACCTTTCG	R	3'UTR;Body;3'UTR;Body;Body	ADARB1		0.9274143	0.9524757	-0.025061429		
cg16360668	1	1368456	19265059	19265109	N/A	CGCCCAGTGGCTCCAGCTACAAGCTCATTCATCCAGTCAGTAGCGGTTG	R	Body	IFFO2		0.8909214	0.9267371	-0.035815714		
cg16366890	4	39704501	3342111	3342161	S_Shore	GCCTGGAGGTTAACTTAGACGGGGGCTTAAAGGTCTTCTACAAGAGG	F	Body;Body	RGS12		0.8846014	0.9261371	-0.041635714		
cg16373217	3	32787468	10192855	10192905	N/A	AAGTGCCACCTGGTCCTGCCTGATAAAAAATGCTGAATCAGCCAGCACG	F	3'UTR;3'UTR	VHL		0.7800429	0.8527871	-0.072744286		
cg16375999	5	19681416	79605222	79605272	N/A	CGGTGAGTGATACAGCTCATAAAGGCAGCAGCAAGATTTATTGCAAAGAG	F	N/A	N/A		0.7591543	0.8209543	-0.0618		
cg16382077	7	25691346	171543	171593	N/A	GTGTTGAGTGCTACACTGGAAGAGAGCTGCTTCCCAGACAAGGGAGCCG	F	N/A	N/A		0.80198	0.8411557	-0.039175714		
cg16386396	1	47735438	3132508	3132508	N/A	CCTCATCTTTTATGTGCTGCATGGGCTGTTTTCTTGTGCCTGATCCAG	R	Body;Body	PRDM16		0.6312329	0.7399286	-0.108695714		
cg16387046	12	49634405	55248207	55248257	N/A	CCAATCAGGAGCTGTCAACCAGAATCCAGGTTAGGTAATGCCAGGAAACG	F	TSS200	MUCL1		0.2479557	0.1763671	0.071588571		
cg16396191	13	48761331	42184765	42184815	N/A	CTTGCAGGATGTGGAAGCACAGCATGTAATGTGATGCAAGTATGTTCTACG	R	Body	KIAA0564		0.8595557	0.9173371	-0.057781429		
cg16411857	16	40769499	57023241	57023291	Island	CGGAGCCTCAGGGTGGGGGACCCTGGGCCCTCACGGTGACCCTT	R	TSS1500	NLRC5		0.2453657	0.3140386	-0.068672857		
cg16419441	8	26711400	105478683	105478733	Island	CGGCGGCAGCCGAGCAGCCTTGGCTCAACCAGATGCCCTCGACTCCTCCT	R	Body	DPYS		0.1503357	0.1075103	0.042825429		
cg16427743	14	48683442	65210080	65210130	Island	CGGCCCCTCTTGGCTGCTGGGCAGCGGCCCACCCTGCCCGACAG	R	Body	PLEKHG3		0.81008	0.8373857	-0.027305714	0.8193538	0.8373857 -0.018032
cg16433406	17	16786325	39981729	39981779	N/A	CACCCTGGCCTCTGCTCTCTGTGTTCACGGGGGAGCAGACTCTGGGGAGCG	R	3'UTR	NT5C3L		0.8142943	0.8532543	-0.03896		
cg16433737	12	33618321	69501713	69501763	N/A	CCCTGCCCGCCGCCGTGCCAGCTGCCGCCACGAGGCTCTGCCACGCCGC	R	5'UTR	GNB3		0.8509114	0.9124071	-0.056495714	0.8729538	0.9124071 -0.039453
cg16434510	8	34749404	129800022	129800072	N/A	CCAAACGTTCCATATGGCCCCTGGCTGTGGATTCCCCAGCTCTGACTCG	F	N/A	N/A		0.7172757	0.8156771	-0.098401429		
cg16439859	5	52810465	65506660	65506710	N/A	CTCAAAATTGAGTTCAATCCATAAAGCTAAAAGAAGTACAGGCTTGGCCG	F	N/A	N/A		0.89563	0.9271743	-0.031544286		
cg16441584	14	42796483	100545421	100545471	N/A	CGGGTTTTCTCGTCGTCGCGAGTCAGCAAAGACCTTGGCAGAATGCAGCTTT	F	Body	EVL		0.6577314	0.7209157	-0.063184286	0.6808963	0.7209157 -0.040019
cg16445596	16	50696379	90075204	90075254	N/A	CGGTGTTGAGGTTCTGTCGTCGCTCGAGTCAGCAAAGACCTCGGCCAGCTCC	F	Body;Body	DBNDD1		0.7129171	0.7765957	-0.063678571	0.72933	0.7765957 -0.047266
cg16448351	11	13624346	10318065	10318115	S_Shore	TTCATCTTGAATTGTACCCCATAATTCCCACCTGTCATGGGAGGGATCCG	F	N/A	N/A		0.4983243	0.5810614	-0.082737143		
cg16448785	5	74635366	56268336	56268386	N/A	ATT

cg16774290	7	49697497	4824628	4824678	Island	CGGGAGGTGGCCTTCGAGTACTGCCGACGCCTCATTGAGCAAAGTAACCG	F	Body	KIAA0415	0.8091871	0.8503457	-0.041158571				
cg16776350	1	47784501	160549158	160549208	N/A	GATCTTGCTCCTTTGCCTGCAAACCTGTGAGTTCTGACCCTTGCTGATCG	F	Body	CD84	0.6927714	0.8095629	-0.116791429	0.7607138	0.8095629	-0.048849	
cg16777510	17	26753367	40440022	40440072	N_Shore	AGTTTTGTCTCTGAGGTCACAAAACCTGTGGCCCCCAAGACACAACATGCG	R	5'UTR	STAT5A	0.6243029	0.7421714	-0.117868571				
cg16777896	15	71729422	65669023	65669073	N_Shore	CGCGGGGGTTTGAATAAGTGCGATCCTAAAAAGTTTAAAACATTACATC	R	Body	IGDCC3	0.4988114	0.5914414	-0.09263				
cg16778451	16	20809502	31581268	31581318	S_Shore	CGCCACCACACCAAGGCTAATTTTTGTATTTTTAGTGGAGACGCGATTTC	F	TSS1500	CSDAP1	0.4434557	0.4904357	-0.04698	0.45845	0.4904357	-0.031986	
cg16784234	7	42783330	530475	530525	N_Shelf	GGATTCAGTGAGACCTCGGAACCCCTGGGGCAGGCGTGCTGGGGACTACG	N/A	N/A	N/A	0.8601757	0.8933629	-0.033187143				
cg16787199	15	38635432	52402025	52402075	N_Shelf	CGGGTTAAAAGTTTTAAAACTCATAAATAATCGTGTCCAGAGATAAATGAA	F	3'UTR	BCL2L10	0.8186243	0.8891457	-0.070521429	0.849155	0.8891457	-0.039991	
cg16793199	2	66612490	3453196	3453246	S_Shore	CTGCCTCCTCCAGCTGGGAGTGAGTCTGTAAAGAAGCACTTTGGATGAACG	F	Body	TTC15	0.7676886	0.8535857	-0.085897143	0.8229588	0.8535857	-0.030627	
cg16795830	6	13670397	31554199	31554249	N/A	AATTGTCTTTAATTTCTTTGGGGAGCAGAGACTCAGAGGATTCCTGACG	F	Body;TSS1500;TSS1500;TSS	LST1	0.6055657	0.7043657	-0.0988	0.644575	0.7043657	-0.059791	
cg16811108	17	34787356	7905840	7905890	N_Shore	CGCCTTTCTGGGGTGGGATCTGTCCTGCCTTCCAGGTAGTCAGCCAGATC	R	TSS200	GUCY2D	0.3274586	0.40544	-0.077981429	0.3613388	0.40544	-0.044101	
cg16821175	3	7365361	128080818	128080868	N_Shore	GGGTGGCAGGACCGCTGGGCAAGGCTTCGCCGGTTTCTGCTACCCCG	F	Body;TSS200	PHF21B	0.7813814	0.8536186	-0.072237143				
cg16831440	17	41623359	700672	700722	N/A	CGCTCAGGCCCTGCTGGTACTACGCTTCCCAGTGTGCAGGTTCCCAGA	F	N/A	N/A	0.8446314	0.8873157	-0.042684286				
cg16858253	3	35658314	12202995	12203045	S_Shelf	AAGAACCCTCCCAAGGGTATTCCCAAGAAAAATATGTGTAGGATTCCACG	R	Body;Body	SYN2	0.8537114	0.90391	-0.050198571				
cg16860004	8	60702356	103137229	103137279	S_Shore	CGAGTACCTGCTGGCTGCCAGCACCTGTTTCCTGTCTTGCTGTGTCGTCC	F	TSS1500;TSS1500;TSS1500;	NCALD	0.4713314	0.5982871	-0.126955714				
cg16865618	4	66737486	27123753	27123803	N/A	CGCTGAGACTCTGAGGACCACAGACACTGTTCACACACCGTGCCTGCCCGGC	N	N/A	N/A				0.85093	0.8818429	-0.030913	
cg16868095	3	51757368	197090774	197090824	N/A	TTCCTGTTCCCAGCTTCTGACTCCTGGGCTGGTTTCTGACCACAGGTCG	F	N/A	N/A	0.7174757	0.7790457	-0.06157				
cg16868500	7	45600476	75866308	75866358	S_Shore	CTCAGGTCGTGAATTAAACCGGCAAATCCAGCCAGATTCGGTGGCTCACG	R	Body	SRRM3	0.8640771	0.8932129	-0.029135714				
cg16872847	19	7369438	39893195	39893245	Island	TTTGACACCGGAACACAGACACTGTTCACACAACCGGTGCCTGCCCGCGC	N	N/A	N/A				0.1280025	0.1031366	0.0248659	
cg16874743	3	16768418	38664022	38664072	N/A	GAAGAGCGTGCGTGGGGTCAAGGAAAGCTGAGCAGCATGGGCCGGCCACG	R	Body;Body;Body;Body;Body;B	SCN5A	0.8583271	0.8846229	-0.026295714				
cg16879608	12	54624408	13356921	13356971	N/A	CGTGTTGGTCTGGTCTGTGTAGACTAGCACAGAGTCTCACATAGTCAGG	F	5'UTR	EMP1	0.62748	0.7268086	-0.099328571	0.6874425	0.7268086	-0.039366	
cg16883728	8	23661464	50729333	50729383	N/A	CGGGGGAGAGCTGCCACTTCCACGAGGTGCTCCTGCTGCCCAAGGGGCAGT	F	N/A	N/A	0.8572243	0.8967771	-0.039552857	0.8704025	0.8967771	-0.026375	
cg16886882	18	33796393	47014260	47014310	S_Shore	ATTCTATAAATTTTCTGAAACATTGGAGTACAAGATACAAAACAACG	R	TSS1500	C18orf32	0.6881243	0.7526629	-0.064538571				
cg16896134	19	28808502	21305635	21305685	N/A	CGCTTATCAATATAACCATTCAGATTAGTTAATTAAGATAAAAGCCAGGTG	F	3'UTR	ZNF714	0.6765971	0.8417229	-0.165125714				
cg16900102	7	41712301	98283412	98283462	N/A	CTGGACTTTGTGGGTACTGGTGTAGGGCCTGGAGCAGCTGCAGCCATACG	N	N/A	N/A	0.5993086	0.6735443	-0.074235714				
cg16904585	16	52786413	10276119	10276169	Island	CCGCCGCGCACTCCGAGGGCTCCTCCGCGCGCGCGCCTCAGGTTGGCC	F	5'UTR;5'UTR;TSS200;1stExon	GRIN2A				0.1386013	0.1240629	0.0145384	
cg16908215	7	49604407	150440016	150440066	N/A	CGAGAGTAACTGGGCATACAAGGCGCTCCTCAGAGTCAAACACTTGATGC	F	Body	GIMAP5	0.8510529	0.8968071	-0.045754286				
cg16921789	3	49787420	88031773	88031823	N/A	TGCTTCTGATTTGGTTCTCTAATTCACTGCACTCCACGGCTCTTGAAACG	F	5'UTR;1stExon	HTR1F	0.6402943	0.7256514	-0.085357143				
cg16936289	17	64669231	29148918	29148968	N_Shelf	CCGTGTGTGAATATACTCATATAAAAAAAGTTCACATGCCAGGCAGCACA	F	Body	CRLF3	0.6904614	0.8137086	-0.123247143				
cg16936421	10	71731399	729226	729276	N/A	AGAAGGCAGGACGGTTGTGCAGGCTCCGAAGAGGCGGAGCCCCTCGTTCCG	R	Body	DIP2C	0.8529086	0.90785	-0.054941429				
cg16941302	18	65675393	55108947	55108997	S_Shore	GTGACTAAGCCCAAGTTTGAAAATGACGTGGCTAAAGCTGCCTGCTAACG	R	Body	ONECUT2	0.3209029	0.4350543	-0.114151429				
cg16945186	12	55627366	115103960	115104010	Island	ACGCAATACTCTTAATTAAAATGCCTGCGGCGGGGCACTGAAGCTGATCG	F	N/A	N/A	0.6399729	0.7523	-0.113237143				
cg16950800	4	52660420	100528307	100528347	N_Shelf	AACTCTTAATGATGCTTTGGAGTGGCTCTATTCTAAATATCCACGGTAACG	R	Body	MTTP	0.8637071	0.9175114	-0.053804286	0.8817825	0.9175114	-0.035729	
cg16952918	12	44695451	69078072	69078122	N_Shelf	CGTGGCTAATTTTTAAAACTTATGTTAGAGACAGGGACTCCCTATGACAT	F	N/A	N/A	0.8413929	0.8798757	-0.038482857	0.8579288	0.8798757	-0.021947	
cg16955889	3	13766359	181445647	181445697	S_Shore	CGCTTTAATGATGATTTGTAGCTCGGCGAGGGGCACGGACAGCAAACACC	F	Body	SOX2OT	0.1118557	0.0772849	0.034570857	0.0997543	0.0772849	0.0224694	
cg16960046	7	61724381	55053046	55053046	N/A	CAAAATGAGAGTCTGCTTGGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	N	N/A	N/A	0.8529957	0.9015729	-0.048577143	0.8672175	0.9015729	-0.034355	
cg16961269	6	17649415	27838269	27838319	N/Shore	TTAGTGATCCTGTATTTTAGGTGTGGCCCAAGACAATTCTTCTTCCAACG	N	N/A	N/A	0.64311	0.6838786	-0.040768571				
cg16966496	12	54608401	115172598	115172648	N_Shore	CGTGCCTGTACCCAGACAGATGGAAGCCAAGGTCTACCCAAGGGACAGAA	F	N/A	N/A	0.6915057	0.7821686	-0.090662857				
cg16967578	1	35635502	218575437	218575487	N/A	CGAGAGTGTGGTAAAAACTGTCAACTGAAGAACCAACTACCCTTCCAGG	R	Body;Body	TGFB2	0.7800729	0.8636186	-0.083545714				
cg16970492	2	28743382	27575819	27575869	N_Shelf	CCAACACCTCTTTCTTGAAACATTCACTTTTCTTGAGAAGCAATTGCAAAC	F	5'UTR;5'UTR	GTF3C2	0.8635429	0.9191671	-0.055624286				
cg16981027	2	50796392	39193891	39193941	N/A	CGACTTAGAATCTCGAAGGACCACAGGAGGAAAATGCCTTATTTTGCCC	R	Body	LOC100271715	0.8089143	0.8694314	-0.060517143	0.8242675	0.8694314	-0.045164	
cg17001153	1	29655469	206742216	206742266	N/A	CGGTGAGCCAATACGTAGCTCCTAGCTCTGGAGCACCAAGAGTTGCCGT	F	Body;Body;Body	RASSF5	0.8209757	0.87988	-0.058904286	0.8568488	0.87988	-0.023031	
cg17006443	11	21665420	70628938	70628988	N/A	CAGAAGTAATAAGGAACGCGAAATGGCAATCACGAATATCATCATCGG	N	Body	SHANK2	0.8678314	0.8933714	-0.02554				
cg17006506	14	22695412	60383037	60383087	N_Shelf	CGTCAGACCAAGTGCAGACCTGATACCTGAGGAAGGAGGAGGAGGAAGGA	N	N/A	N/A	0.8586943	0.8960571	-0.037362857	0.8757963	0.8960571	-0.020261	
cg17010522	8	69691443	1893977	1894027	Island	TCACAACATGCTGCCAGGTAATGGGGTGGGACAAGGCCCAGGGACAGACG	R	Body	ARHGEF10	0.7423814	0.80469	-0.062308571	0.78784	0.80469	-0.01685	
cg17015994	8	46724303	143961391	143961391	N/A	CGGTCTCTCAGGCAGATCCAGGGCCAGTTCTCCCATGAGTGATCCCTCT	R	TSS200;TSS200	CYP11B1	0.4543271	0.5677314	-0.113404286				
cg17018082	8	59674335	119428270	119428320	N/A	CGCTAGATATTTAAGTCAACAGCTTTAATCTTTAAATGTTGGCCTTGCTG	R	Body;Body	SAMD12	0.6829843	0.7852886	-0.102304286				
cg17021880	1	23698391	964506	964556	Island	AGCACTGGGGCTCTCTGGCAATTGGCAGGCCCCGAGAGGGGCTGGGGCTCG	F	Body	AGRN	0.8434214	0.8849886	-0.041567143				
cg17043230	12	55758300	3427729	3427779	N/A	AATTTTTAAACCCATTTAGAGTCAAGCGTGTGGTTAAGGCAGCATAACG	F	N/A	N/A	0.76327	0.8290429	-0.065772857				
cg17045635	10	15786476	80998130	80998180	N_Shelf	TCTGGGAGGGCTGGGTGCTGGGAGCAGTGCTGCTGCTGTTGTTCTCG	N	Body	ZMZ1	0.7810857	0.8427443	-0.061658571				
cg17046586	12	42677356	50665774	50665824	N/A	GTTCATTAAGGAGCCTTCTTTACAATCTCAAAGCAAAAGAAACACATACG	R	5'UTR;5'UTR	LIMA1	0.5153929	0.6125214	-0.097128571				
cg17048073	8	19744505	23102091	23102141	N_Shore	AAAAGACCCAAGAAGAGCCAACAAATATTGAACAAATAAGTCAGAGGACG	F	5'UTR	CHMP7	0.6667129	0.7333471	-0.066634286				
cg17059994	11	54777330	71958854	71958904	S_Shelf	AATTGAGAGGGCATCAGGGCAACAGGAGTCAAGGGTTTGTTTCTG	N	N/A	N/A	0.47733	0.5365557	-0.059225714	0.480095	0.5365557	-0.056461	
cg17063143	3	73716445	194343015	194343065	N/A	CGGTCTGGCAGTGTAAACAGTTTTCACCCTTGCTCTATTTGAAGAGCTAG	F	Body;Body;Body;Body	TMEM44	0.8810671	0.9318514	-0.050784286	0.9136488	0.9318514	-0.018203	
cg17066254	11	48643406	45824647	45824697	N_Shore	GGGAGGGCTGCAGGCTGCAGTGAAGTAAACAGCTGCCCCACAACGAGCCG	F	TSS1500;TSS1500	SLC35C1	0.8609443	0.9053006	-0.044364286	0.8842275	0.9053086	-0.021081	
cg17072519	22	14744456	2132063	2132113	S_Shelf	TGCTGGAGCTGCTCTAGGACCTGCAGGGGAGACTGGAGCCATCGAGACCG	F	5'UTR;5'UTR;5'UTR;Body	AIFM3	0.6735157	0.7546414	-0.081125714				
cg17079328	6	14652368	3337487	3337437	N_Shelf	CGGGAGCAGAACTCAACCTGCTGCAGAACGTCTCTGGGTGGTAGTGC	F	Body	KIFC1	0.9035757	0.9344571	-0.030881429				
cg17080138	3	25603418	115524190	115524240	N/A	CGGAAGAATTACGACTAAAGCTCCAAATATGAGGTTGCCTTAGCCAAAGG	R	3'UTR	LSAMP	0.8000743	0.8461157	-0.046041429	0.7925275	0.8461157	-0.053588	
cg17080893	8	63777471	82192535	82192585	Island	GTGACCCCTCTGGCTTCCTGGGCCTCGCAGAGGGGCGCGAAACGTGCAGGCG	R	TSS1500	FABP5	0.1906814	0.1419843	0.048697143	0.1634825	0.1419843	0.0214982	
cg17085123	1	71607500	54943183	54943233	S_Shelf	CCGGTACACACCTGCTTATTAAACTATGCAAAGCTGGCTACAGAACG	N	N/A	N/A	0.6900929	0.7888657	-0.098772857	0.74755	0.7888657	-0.041316	
cg17087907	6	35671411	167104677	167104727	N/A	CGGCCCCGGGTTCTAGCCTCCACTAAGAGTGCTGCCAGGACTTTGACCTCA	F	Body	RPS6KA2	0.6781057	0.74893	-0.070824286				
cg17091301	2	15770472	133171381	133171431	N_Shelf	AATCCTCACAATAGTGCAAAGTGGAGATTATTACCCCCATTTTACAGGCG	F	N/A	N/A	0.8452914	0.8822686	-0.036977143				
cg17091893	17	10635339	37756091	37756141	S_Shelf	AGAGGTTTAAATACCGAACACCAGACACACACTCTGGTATGGAACTCCG	R	N/A	N/A							
cg17094146	8	5364148	669161	669211	N/A	TGGGGGGCTCTCTCTCACGGTTGAAACGGCCTCCCTGGAGGTCTCCTCG	F	Body	ERCH1	0.8617271	0.8940186	-0.032291429				
cg17095652	15	24645389	40161645	40161695	N/A	TGATGGCTCAGGGCTGCACCTCTGGGAGCTGAGACACCTGCCCGAGGTCG	F	Body	GPR176	0.7123414	0.7864671	-0.074125714	0.7341738	0.7864671	-0.052293	
cg17099048	8	26666451	139734443	139734493	N/A	AGTTGTTTCAAACCAGGAGCTGTTTTTGCTTGCAGCCAGAATGCAGGAGGCTCG	R	Body	COL22A1	0.5935557	0.66602	-0.072464286	0.609155	0.66602	-0.056865	
cg17102325	1	58691468	35223005	35223055	N_Shelf	GGCTGAGATGTTGCAGTCGAAGTCCTTGTTGTTCCACACACG	F	Body	JAK1	0.80635	0.8579929	-0.051642857				
cg17102648	1	54618349	61401827	61401877	N/A	AACCATTACACTACATTCAATATTTTCTTGCTGTGGAAATTTAAGATTCG	F	N/A	N/A	0.7585257	0.8565371	-0.098011429				
cg17121828	19	26807318	56125916	56125966	Island	CGGTGTCCTCGGGCCCTCCAGCCACGCCCGTGGCGCCTGCCCCCTCCGCA	F	N/A	N/A	0.8347729	0.8796686	-0.045195714	0.8552725	0.8799686	-0.024696	
cg17126533	19	65617385	18303927	18303977	Island	CGCAGGCAGCCTCGGGAGCCACATTGCCCGGCCCGAAGAGTATTGACCA	R	TSS200	MPV17L2	0.1062821	0.0804891	0.025793	0.0952966	0.0804891	0.0148075	
cg17130251	19	3945936	3945986	3945986	S_Shelf	CGTTCCTGGTTTGTCCACTCAAGGCTCTGTTGTCCAAGGAAACAGAGG	N	N/A	N/A	0.4162814	0.5256857	-0.109384286	0.4798538	0.5256857	-0.045812	
cg17141735	1	70713486	149890572	149890572	N/A	TATATATCAGCATTCTGAAGCCTCCACATTTAGTAAGGCAGAATCACACG	F	TSS1500	SV2A	0.90991	0.9401529	-0.030242857				
cg17148503	6	52756418	136227579	136227629	N/A	GCTCTCCCTTTGTCCTACTGTTTGATATTTAGCTATTATCCCATCAGTCG	R	Body	PDE7B	0.8782414	0.91964	-0.041398571				
cg17154092	18	52778359	77675567	77675507	Island	CGAAGGATCCCAGGGCTCTCAGCGGTCCCGCCATTGAAAGCTGGCTGACCTC	F	Body;Body;Body	CPZ	0.9072143	0.9329886	-0.025774286				
cg17155978	17	39681324	80960169	80960219	N_Shore	CGCGGGTCGGAGCTGGGCTGAAACTCAACATGTGTCCAGACTGCTGCAGT	F	Body	B3GNTL1	0.8197029	0.8971843	-0.077481429	0.8607438	0.8971843	-0.036441	
cg17156100	8	40749322	145910685	145910735	Island	CTGTCCAGAGTGAGTTGTGTCCTGCCCTAGGTGGGGTGTGAGTGTGCCCG	F	N/A	N/A	0.2605886	0.3037429	-0.043154286				
cg17156828	2	14745326	240020174	240020224	N/A	CGGCACCAGAGGGCACCTGCTGCGAGGGGCCACGCTCTGCCGCGCGCCGC	F	Body	ITGA4C4	0.8880229	0.9251614	-0.037138571	0.9006813	0.9251614	-0.02448	
cg17162981	15	19775472	45248744	45248794	N/A	GGCCCTCAGATAAGGGACAGTCACTACCAGACTGAGCTGACTGGTTCTCG	F	TSS200	C15orf43	0.8888257	0.9239543	-0.035128571				
cg17171539	1	13806427	59398690	59398740	N/A	GCATTTCTTCAGAGCCCTCTCAGGCCCAGGAACTGGACTGGGCTGGTCCG	R	N/A	N/A	0.6877586	0.7752943	-0.087535714				
cg17173369	6	37685417	169224099	169224149	N_Shelf	GTGATGTTATGGCTAGCACTGGCTGAATTCTCCCTCCAGTTCCCTCCTG	F	N/A	N/A	0.3699286	0.4446886	-0.07476				
cg17173423	11	72743479	59823963	59824013	N/A	TTGCGGGCCCTCTCTCTCACAGTGTCTCAATCACACTGTTCGGGGCCATG	F	TSS200;TSS200;TSS200	MS4A3	0.6907829	0.7598543	-0.069071429	0.6950713	0.7598543	-0.064783	
cg17177602	1	16645377	1196457	1196507	N/A	CGTCAGCAGCATCAGATACCAGAGGCTAAGAAACTGAGGACTGAGAACAG	F	Body;Body;Body;Body;Body	UBE2J2	0.7295429	0.7795729	-0.05003				
cg17182184	22	30703498	27014006	27014056	N/A	GCCACAGACTATAGGGCCTGATGTCTGCCAGACTATAAAATGGGGGGTCG	F	TSS200	CRYBB1	0.55558	0.6220843	-0.066504286				
cg17187433	2	16755365	8118191	8118241	N/A	ATGACAACACATCAAGAGCAATTGTGTTTCTTTATACCCCG	F	TSS1500	LOC339788	0.8508957	0.9043029	-0.053407143				
cg17195706	4	27774434	100488671	100488721	S_Shelf	CGGCGTCAAAACTGGCAGGTTGTTCAGCAGACTCTAAGCTCAGCTAAGTG	F	5'UTR	MTTP	0.7859471	0.84173	-0.055782857				
cg17199481	16	49650369	123676	123726	S_Shore	CGTCCCTATGGGTCCCTAAGGACCCCTCTACAGGGTGCCCCCCATCCTAG	F	TSS1500	RHBDF1	0.8312914	0.8686257	-0.037334286				
cg17203447	13	44677387	112999748	112999798	S_Shore	CGGCCCCTGTGCTGGAAGCAGGTGCGTCTGCCTTTGACTAGAAAGCCTCT	F	N/A	N/A	0.8343757	0.8585586	-0.024182857				
cg17210837	5	63649345	35954233	35954283	N/A	AGGGGGAGCCACCTCTGGTCCTTTGAAGGTTCCCACCCCACCACACG	F	3'UTR	UGT3A1	0.7238586	0.7960686	-0.07311				
cg17212502	12	22710492	121093709	121093759	N/A	GTGCACAGGCATCAAATTGGTCCAACAGACAGAGTCTCAATCCTTGACG	F	Body;Body	CABP1	0.8650029	0.9029943	-0.037991429				
cg17214754	11	57748377	3168993	3169043	N/A	CGCCCGGCCTTCCCTGCCCCGACGGACCCACGCGTCCCTGGACACGCTCA	R	5'UTR;5'UTR;5'UTR	OSBPL5	0.8668314	0.8926257	-0.025794286	0.86986	0.8926257	-0.022766	
cg17231677	10	40614439	102672043	102672093	N_Shore	CCCTTAACATCAAAAAGTGAAAGCTGACCTTGTGTGTTCCTTAAAAAATT	F	TSS1500;TSS1500;TSS1500	FAM178A	0.2773814	0.3747657	-0.097384286				
cg17237063	3	45654501	29323182	29323232	N/A	CATCCAGTTCCCTGCCTCTCGGAGATAAAGATTCAGCTACATGGGCAAACG	R	1stExon;1stExon;1stExon	RBMS3	0.0609109	0.0941834	-0.033227571	0.0600118	0.0941834	-0.034172	
cg17240133	15	11725441	57977245	57977295	N/A	CGGCCTGCAGGTGCTCTTTCCTCTTGGTCCCAAGCATCTGTGCAGGGTCG	R	3'UTR;Body;Body;3'UTR	GCOM1	0.7574857	0.8375586	-0.080072857	0.8122763	0.8375586	-0.025282	
cg17244485	2	70682412	103443515	103443565	N/A	CGGGTCGCTCTCATCACAGCACGTAGCATGCTGCCAGCCGCCACATGGCT	F	N/A	N/A	0.3830229	0.5482443	-0.165221429	0.4441788	0.5482443	-0.104066	
cg17249782	11	38784443	44488287	44488337	N/A	AATGTGGTGTCCTCATAAATGTCACATGATGCTGCTGCTGCTGCTGCTGA	N	N/A	N/A	0.90316	0.9522314	-0.049071429				
cg17250770	8	73759456	22500401	22500451	N/A	CGCTGGAGATGGAATTGTGGTCCTCTGATTATGGCATCTGCTCTCTGATA	R	TSS1500;Body	FLJ14107	0.8828771	0.9226271	-0.03975	0.8945	0.9226271	-0.028127	
cg17254386	5	50722372	70897346	70897446	N/A	CAGGGTAGTGTTGAGCTTCTCATACTAGGATATGTGGCCAGCAGGGCTCG	F	Body	MCCC2	0.8818686	0.9252571	-0.043388571				
cg17256760	2	31751403	16035877	16035927	N/A	CGGTGCTCAGATGTAAGCGTTGAGAGGGGGAAGCTGGCGACTGGAGA	F	N/A	N/A	0.85089	0.9084643	-0.057574286				
cg17262868	17	44803326	1127152	1127202	N/A	AAACCACCAGATCTCATGAGAACTCCCCTCGTGATCAGGACAACAGCCCG	R	N/A	N/A	0.7298771	0.7978671	-0.06799				
cg17267681	10	56759439	134071651	134071701	N_Shore	CGGCCCTGACCTGACCTAGAGAGGGGGGCAGCTGCCTCTCCTGGATCTGC	F	Body	STK32C	0.8568571	0.8886386	-0.031781429	0.8492588	0.8886386	-0.03938	
cg17269596	1	71700329	244995112	244995162	N/A	TTGCTTTGGCCTCTCAAATTGTAAGGGATCGCAGGCCTGAGCCATCACG	R	N/A	N/A	0.6932614	0.8131729	-0.119911429				
cg17270081	9	67736343	139092974	139093024	Island	CGGGCTCAGCAGGACAGATCCCCCTTGGGGGCTTTTGGTGTTCATGCCC	R	Body;Body	LHX3	0.5161157	0.6834071	-0.167291429				
cg17279887	7	73626500	97735625	97735675	N_Shore	GGTCAATAGGATACTGCAGCTAGGATAGCAGTCCACACAGGGCCAGGGCG	R	TSS1500	LMTK2	0.8482886	0.8839686	-0.03568				
cg17284326	13	63638311	98749760	98749810	N/A	CGCCCTGCTGAGTCCCTGAGTTTTGAGAGTCATGAATATGGTGGCAACAC	F	N/A	N/A	0.85444	0.8907986	-0.036358571	0.8602763	0.8907986	-0.030522	
cg17287974	2	70642406	145876521	145876571	N/A	TTCTTACCCCCTCTCACACAAGAGTCTTATTGTTTTCTTTCACCG	R	N/A	N/A	0.8938685	0.9213357	-0.027467143				
cg17293973	2	24637439	39948248	39948298	N/A	AAAGGGCAAGGCCCCAGAGAAATTCATATGCAATTTAAATGTGTTCTTCG	F	N/A	N/A	0.8919443	0.9131171	-0.039372857	0.9068813	0.9131171	-0.02446	
cg17298516	1	60688488	94131533	94131583	N/A	CGAGATATAGTTTGCAGGTACAGTCTGCCATATCTGCTGGAGGTTTGGATA	R	Body	BCAR3	0.7503957	0.8144971	-0.064101429	0.76778	0.8144971	-0.046717	
cg17298543	7	15683504	79802066	79802066	N/A	CCGAGCAAAAGGTGTTACAATTCGGAAGGATTCTACATTCACGTTGCTT	R	Body	GNAI1	0.8239943	0.8875286	-0.063634286				
cg17303756	6	16787388	99279108	99279158	N_Shore	CACAGCTCCTCGAGATCACTCGCTAGGACAATGGCTGAGCAGGCGATTCG	N	N/A	N/A	0.1269021	0.0825777	0.044324429				
cg17316030	14	25609447	64430230	64430280	N/A	GTTCACACCCTGCAAAAACACTGACATCAAAAATAACTCAAACACTTTCG	F	Body;Body	SYNE2	0.8945886	0.9321014	-0.037512857				
cg17330176	4	26746458	2389058	2389108	N/A	AAGTGATGGGTTCTGGCCAAGTAACGGGCAAGCAGAGTTGCGTCACTTCG	F	Body	ZFYVE28	0.8511857	0.91006	-0.058874286	0.8785	0.91006	-0.03156	
cg17333783	11	31640492	8706792	8706842	N_Shelf	CGGGGGTTTGGTCTGTGTCATGGTCTTAACTCTATGAAGGTA	F	Body;TSS200	RPL27A	0.8153486	0.8606843	-0.045337143				
cg17355719	17	10706421	37893764	37893814	N/A	CCTCTGAGGGGCCAGGGCGCAGCCACCACCGTAAGGGTGACTGCAGATCG	R	TSS1500;TSS1500	GRB7	0.4779186	0.4045057	0.073412857				
cg17356750	7	26706411	114329849	114329899	N/A	AGGACATTGGGCAGTCTTCATCCTGTCTGCAATCACTGGCTTCTTCCTTGACG	F	Body;Body;Body	FOXP2	0.7074186	0.7938229	-0.086404286	0.7566463	0.7938229	-0.037177	
cg17357548	15	54765393	50429829	50429879	N/A	CGGCACACACATCCTTGTGCATGTCACTCCTGCATGAGCACTTTGTGA	N	N/A	N/A	0.8279229	0.8826457	-0.054722857				
cg17369513	5	22772300	98121165	98121215	N/A	GGTGTCAAGAAGAGCCAGAAGAGTGGGCTGCTACAAAGGCCTGTCCCACG	R	Body	RGMB	0.88021	0.9155614	-0.035351429				
cg17377066	19	23755345	1481726	1481776	N_Shore	GCCAGCCTGGGGAGCGACGATGGCAGCAGTGCCTGTCAGGGACCCAGGG	R	3'UTR	PCSK4	0.8033986	0.8562143	-0.052815714				
cg17378509	4	38626345	4557712	4557762	N/A	CGGATATCTTCAACGTGAAGGATGAGTCTCAGTCAACCCCAAACCACTG	F	N/A	N/A	0.9258529	0.95982	-0.033967143				
cg17382629	19	19674479	10169553	10169553	N_Shelf	CGAGAGAGCCCGTTCCGGCAATGCTGCCCGCTGCCCCATTCACCTAGTCA	F	Body	C3P1	0.5407788	0.6833743	-0.142595714				
cg17384214	6	71788508	31801701	31801751	N_Shore	TATTGAAACTCATAAGTCATTTAAATCCTTTCTGGACCCTTTCCTATCG	F	TSS1500;TSS1500;TSS1500	C6orf48	0.9028714	0.9380629	-0.035191429				
cg17384647	10	62735413	88717435	88717485	N/A	GGGCCAGCCAGGGTAGTTGGGGGGCAGGACAAGACCCACCGGGTAGGCCG	F	TSS200;TSS1500	MMRN2	0.6305414	0.6963329	-0.065791429				
cg17391877	6	64645446	41714182	41714232	N/A	CGGTGATTTATGCAACTCCAGAGCTGATGGTTTGGGCACCCTCCCTCG	F	Body;Body	PGC	0.8990143	0.9289186	-0.030904286				
cg17412005	1	61679391	45806886	45806936	S_Shore	CATCCCTCCTGCTAGCCAATAAAGACAGCTAATTTCGTGCTGTGGACACG	R	TSS1500;TSS1500;TSS1500;	MUTYH	0.6404129	0.7156	-0.075197143	0.67215	0.71561	-0.04346	
cg17419461	1	31793410	204

cg17863274	19	23725496	49399704	49399754	N_Shelf	CGCCTTTTAGGTGACAGAGGTGACCAAAGACCCCTGGGGGCGTTCGCCTG	R	Body	TULP2	0.3438714	0.4156871	-0.071815714			
cg17872407	15	32764506	75972447	75972497	N_Shelf	CGGGTTCTGCTCCTAGAGTCTTCACAGGTTAAGACCCTGTTAAGTTTCCA	R	Body	CSPG4	0.7788214	0.8307243	-0.051902857	0.8016813	0.8307243	-0.029043
cg17872658	17	47748461	78856861	78856911	N_Shore	CGGTCCTGCAATCAGGGGTTTGGCAGCAAAAGGCATGGAGGCAGCGCTC	R	Body;Body	RPTOR	0.9115257	0.9341729	-0.022647143			
cg17873708	6	62727366	39011018	39011068	N/A	CGGGTGCACAGCTGTGCCAGGTCTCATCCAGGCAGCAACTACAGCTGCT	R	N/A	N/A	0.8178671	0.87965	-0.061782857	0.8232238	0.87965	-0.056426
cg17875028	2	56702423	233321828	233321878	N_Shore	GCAGGTGAGCTGGGGCCCGCTGTGGGGTCAGGACCAGGCCCAAGATCTCG	R	Body	ALPI	0.7636886	0.8055214	-0.041832857	0.783075	0.8055214	-0.022446
cg17875320	1	41681324	110307912	110307962	N/A	AGTCCCTGCTGTGCTCACACTGACTTGGGGAGGGTCCTATGGGAAGGACG	F	TSS1500;TSS1500;TSS1500	EPS8L3	0.78552	0.8298343	-0.044314286	0.8092838	0.8298343	-0.020551
cg17881945	7	18706423	2539410	2539460	N/A	AACAGGGGTCCAGGGTGGGGCGTCGCTGGGGGCAGTCCTCATTGTGGACG	F	N/A	N/A	0.8934129	0.9252414	-0.031828571	0.9084325	0.9252414	-0.016809
cg17883068	15	67673459	57277634	57277684	N/A	TGAGTCAGAAGCCAAACTAATTTTGGCTACTAAATTAGTTACTTCCTTCG	R	Body;Body;Body;Body	TCF12	0.6707757	0.7823429	-0.111567143			
cg17892259	1	71783345	42149829	42149879	N/A	CGGGAGGACCCAGGTCTCCTCTCACTGTCTGCCTCACCACTCTGACTTCCTG	F	5'UTR;5'UTR	HIVEP3	0.6432686	0.7273243	-0.084055714			
cg17892328	1	36682338	182360794	182360844	Island	GCGCGCCTCGCGGGGTAGCAGGGGCGGCGCGCCTCGCTTGCGTGACACCG	R	TSS1500;5'UTR;5'UTR	GLUL	0.1354314	0.1028499	0.032581571			
cg17894069	3	50796359	12885066	12885116	S_Shelf	CGGGCAAAGTTGTAATTTCTTCTCACTTCACGCATTGCCGATGCCCGAAGGCCAG	F	N/A	N/A	0.7918414	0.8268114	-0.03497			
cg17896965	17	32602453	39728425	39728475	N/A	TTGTTCTGTGCCAGCCTCCCCCCACAGACCCGAGGGAGGTCTGGGATACG	R	TSS200	KRT9	0.7104271	0.7791271	-0.0687	0.736	0.7791271	-0.043127
cg17898124	1	41768316	112528161	112528211	N/A	TGTATCACAACCCAGGAGGCAGCATAGTGAACTGCATCAGTAGGTGCTCG	R	5'UTR;5'UTR	KCND3	0.81797	0.8681243	-0.050154286			
cg17900199	10	41650466	1156548	1156598	N/A	CGGGTTTAGTTCCTGAGAGGAATTGGCCAGGTTGTGTGTGTGTTCCGTT	F	Body	WDR37	0.6796186	0.74525	-0.065631429			
cg17901038	17	40634300	74385813	74385863	S_Shelf	TTCTCAACAACATACCAGTCTCTCCTCCTCAAATGCACCAGTCTGGTCCG	R	3'UTR	UBE2O	0.9193471	0.9578114	-0.038464286			
cg17903506	10	46677482	88395453	88395503	S_Shelf	CGGGGAAAGGTACATTTTGCATTTTTTACAGAGGATGCAATAGTCATGTT	F	N/A	N/A	0.73164	0.8005557	-0.068915714	0.7553788	0.8005557	-0.045177
cg17914835	18	50691457	46387191	46387241	S_Shore	GGTGAATTCACTGGGTTGATGAAGGGACAGTCAGGTGACCAGCGGGGTCG	R	3'UTR;3'UTR	KIAA0427	0.9032943	0.9392386	-0.035944286			
cg17917837	15	32861397	74703304	74703104	Island	CCAGCACGAGGGAGGGCGGCCAGGGCACGAGGCACGAGCATGACCTCGCG	R	Body;Body;Body	SEMA7A	0.8405086	0.8771943	-0.036685714			
cg17933764	17	27702301	27069671	27069721	N_Shore	TCAAGGGATCCTCCTGGCCAAAGCACTGCCTATGCAGGTGTGAGCCACCG	F	TSS1500;3'UTR	TRAF4	0.8960557	0.9236357	-0.02758			
cg17939977	3	49743443	186170664	186170714	N/A	ACTGGGCTGCAAATGAGAACCGCCGGGGTGCCTAAACCCACCCTGCACG	R	N/A	N/A	0.8484643	0.8977443	-0.04928	0.8739025	0.8977443	-0.023842
cg17941247	6	45751420	158094798	158094848	S_Shore	TGTCATCACTCAGCTTACTGGGCTGAGGCGTCTGTGGAGAGGTGGCACCG	R	3'UTR;3'UTR	ZDHHC14	0.86038	0.9185157	-0.058135714			
cg17942096	19	28645307	19301711	19301761	N_Shore	CGCTGGTCTGGACCTGGAGCTGCCCTGCCTGGGCACAGCTGCTGGATTTCAGA	R	Body;TSS1500;Body;5'UTR;Bo	ZNF729991	0.73928	0.7917014	-0.052421429	0.7576163	0.7917014	-0.034085
cg17967260	6	12710478	166242715	166242765	S_Shore	CGCTGCTCCCCCAGTGGAGCTGCCCTCCTGGGCACAGCTGCTGGATTTCAGA	N	N/A	N/A	0.8301771	0.86864	-0.038462857			
cg17972572	8	64703373	109257741	109257791	N_Shelf	CGCTCTTCTGGGACAGAGTGAGTACTCCTTAATGTTTTGTGTTTTGAGAC	R	Body	EIF3E	0.92489	0.9563686	-0.031478571	0.9362225	0.9563686	-0.020146
cg17996892	17	10770313	26832584	26832634	N/A	CCTGATGTGTGCACAGACATGGTTCTTCACAGACATGCAGCACTGGGACA	R	N/A	N/A	0.79388	0.8406886	-0.046808571			
cg17999865	3	64800505	72004944	72004994	N/A	CGGTGACAAATGGGTTTTATAATGAGGACTTGAAGCCAGGGCAGGGCAGAG	R	N/A	N/A	0.1355369	0.0951314	0.040405429	0.109965	0.0951314	0.0148336
cg18001869	22	41733458	39966711	39966761	N/A	TTGGTGGAGAGGCAGGTTGGGGAGCATGTACCAGGCCTGTCCCCACCACG	R	TSS200;TSS200	CACNA1I	0.6972671	0.7629957	-0.065728571			
cg18009322	6	60753423	168417574	168417624	N/A	CGCCGGGCGCTGGCGTTCCGTACATTGCCTGAGTTGCCTGCCCACTG	F	TSS1500;TSS1500	KIF25	0.4208614	0.5322429	-0.111381429	0.4209875	0.5322429	-0.111255
cg18023674	1	65668416	2424003	2424053	N/A	CGGGAATCCCCCCTGATGAGATGACTCCTTGCCTGGTGTGGACACACAC	F	Body	PLCH2	0.68627	0.7458071	-0.059537143	0.678105	0.7458071	-0.067702
cg18040181	10	18763385	76588616	76588666	S_Shore	CGCCCGGCCATTCATAAGTTCTTTACACATTTATCAGAATGAATTTGGAC	F	5'UTR	MYST4	0.8553429	0.8954786	-0.040135714			
cg18047961	6	60732412	33878466	33878516	N/A	GATGCAGACCTCCATGGCGGTTCAGGCCAGCTCAGGGAGGCTGAGGGACG	R	N/A	N/A	0.8145314	0.8515357	-0.037004286	0.8154138	0.8515357	-0.036122
cg18050634	17	25675327	79420145	79420195	Island	CGCGGGCTTGCACCTGGGTCTGGTCTGGGCATGTCCATCGCGGGGCCCCTG	F	Body	BAHCC1	0.8744514	0.9082543	-0.033802857	0.8908225	0.9082543	-0.017432
cg18058048	6	68654329	31690949	31690999	N_Shore	GCAGGCAAACTCGGAGTCTTCAAATGGTTCTCACTTAAAATGTGTGCTCG	F	TSS1500;TSS1500;TSS1500;	C6orf25	0.8160971	0.8854857	-0.069388571			
cg18063278	3	60770326	12328740	12328790	N_Shore	CTTAGCAGTGTTTCTGACACCGAGGGACTCAGACAACATGGGTGGGAGCG	F	TSS1500;TSS1500	PPARG	0.7056471	0.77356	-0.067912857	0.7268488	0.77356	-0.046711
cg18079948	10	38657504	20009271	20009321	N/A	CGATGCCAAGATGTCTTCTCTCATCTGATAAGGTTCTGCAAGGGTCAGCG	N	N/A	N/A	0.4404129	0.54729	-0.106877143	0.4316438	0.54729	-0.115646
cg18081313	12	66653347	132378192	132378242	N_Shore	CGCTGCTTGGCCTAAGTGATGAGTTAGCTGTCATTTATAGTTAGGAACGAC	F	TSS1500	ULK1	0.9159429	0.9481114	-0.032168571			
cg18081375	11	12652498	2323938	2323988	N/A	CTGGGGCGTCTGCAGTGAAGGCCTCCTGAGACCACTCCACGGAAACACCG	R	Body;TSS1500;TSS1500	TSPAN32	0.6136614	0.6710	-0.057408571	0.6221713	0.6710	-0.048899
cg18085627	11	10706374	64107672	64107722	N_Shelf	GGAGGAAGCTGCACAGGGTGTCTGTGGCTGGCCCCGGGATCCCCCACTCG	R	TSS200	CCDC88B	0.66097	0.7701657	-0.109195714	0.7144888	0.7701657	-0.055677
cg18090202	11	11791412	1300959	1300909	S_Shore	GGAGACAAGTGCCCCAAATGTGGGACAGCAGTATGGGAGACGCCGG	R	Body	TOLLIP	0.8187	0.8507629	-0.032062857			
cg18096933	6	11701352	30924505	30924555	S_Shore	TGTGGCATTTATAGTTGCCACCAGGCAGGGAGGGCGGTAACTTCTGGACG	F	N/A	N/A	0.8779457	0.92702	-0.049074286			
cg18096939	14	22698408	101513572	101513622	N/A	GCTCAAGGTTAGATGGTGACTGCTTCGTGGCAAACCCAGTCACACACTCG	F	TSS1500;TSS200	MIR889	0.77966	0.8245529	-0.044892857	0.8018525	0.8245529	-0.0227
cg18097327	8	10738507	126626177	126626227	N/A	CGCTGATGTTCTTGGAGTGTGCCTGTGTGAACATCTGGGCATATTG	R	N/A	N/A	0.85071	0.9199857	-0.069275714			
cg18106507	2	39629448	72401302	72401352	N/A	CGGCCCAAGGCCTTGTCCAGAGAGGGACCAGCAACCCTGTGGGGTGCTCT	R	N/A	N/A	0.8431657	0.8848357	-0.04167	0.8640938	0.8848357	-0.020742
cg18116968	7	49644508	25900668	25900718	N_Shore	CGGCCCCTGTCAAAGGTGAACGGCCCAGTACAGCCCCTTAAATATTCCTA	R	N/A	N/A	0.5980214	0.6586371	-0.060615714			
cg18128536	17	10761360	47092178	47092228	Island	TCCTCATCAGGGGCACTAAGGAGCCGGGACCTCGAGCACGGGATGTCTGCCG	R	Body;Body	IGF2BP1	0.4732943	0.3620829	0.111211429			
cg18132787	1	49743502	232862075	232862075	N/A	GCCTCTGGGTCCGGAACACAGGGCTCAGAGGAACTACATCCAGAGAACG	R	N/A	N/A	0.66972	0.7590957	-0.089375714			
cg18135489	11	49602351	120874859	120874909	N/A	CGCTCTGGGTCATAATGCTGAATTATGTGCACTCCTCTTAGTCAGGGACA	R	N/A	N/A	0.7975643	0.8623457	-0.064781429			
cg18145393	4	21773330	520203	520253	N/A	CGCGGGTCGGGACTCCGGGCTTGTGCCCTCTGACAGGCCGTCCAACCTCTGCA	F	Body;Body	PIGG	0.8431671	0.8787171	-0.03555	0.846215	0.8787171	-0.032502
cg18150584	1	15619995	23887816	23887866	S_Shore	TCCTACGCCTCCATTTTGCCTTCTCCTCCTCCTCCTCCTTGACTG	F	TSS1500	ID3	0.6917886	0.7476814	-0.055892857			
cg18165251	10	48643366	85961024	85961074	N/A	TGAAAACTACATATGTGTAAAGTCCCCAATAACAGCACCTGGCACAAGCG	R	Body	PCDH21	0.7628157	0.79978	-0.036964286			
cg18167340	1	12808477	44679636	44679686	S_Shore	CATCAAGGATGACACATATTCCCTGTCCTCTGTTATGTCACCCCTTTATCG	F	Body;Body;Body	DMAP1	0.1826057	0.2183114	-0.035705714			
cg18173726	15	70639412	95713150	95713100	N/A	CGCCAACAAGATCTGTTTACATGCCGACAAGCCCATCAACGTTCATCTT	N	N/A	N/A	0.8675114	0.9081114	-0.0406			
cg18174530	11	67766483	67786085	67786135	N_Shelf	AGGGCGAGGTCACCCTGGCCCTCAGGAACTCCGGGCCTGGATGAAGGACG	R	Body;Body;Body	ALDH3B1	0.7437971	0.7943	-0.050512857			
cg18183240	3	41664483	127373569	127373569	N/A	TAGATTTTCTTTGACTTAAAACTCAAGTGCTTAGGCTTTAGTTACATTCG	R	Body	PODXL2	0.9044129	0.9360586	-0.031645714			
cg18183247	5	39782330	140368417	140368467	N/A	ACATAATAGAAGAATTTCTTCCGTAACAGTAGCCCCAAACAGAGATCACG	R	Body;Body;Body;Body;Body;B	PCDHA7	0.7311586	0.8006243	-0.069465714	0.7289538	0.8006243	-0.071671
cg18185648	1	34755433	94561065	94561115	N/A	CGCTGTTATTGCAGCTGGTTGGCCGCAGTCCATTAAGCTGCAGTGCCG	F	Body	ABCA4	0.9544443	0.6744414	-0.119997143			
cg18188150	10	17610356	103895431	103895481	S_Shore	CGGCCTGTAAGCTATTAAAGAGTTTAAACCTAATGCTAAGAGCAGTAA	F	Body	PPRC1	0.8726243	0.9092929	-0.036668571	0.8887413	0.9092929	-0.020552
cg18204145	6	22792378	43475846	43475896	N_Shore	CGGGTGGTGACTGATGTTTTGATCTATTTGTTGGTCACCTGGTCCGGCCAC	F	Body	C6orf154	0.5949786	0.6353443	-0.040365714			
cg18209359	17	39698449	80159955	80159845	N/A	CAACCTTCAGGTGCTGGAGGAGCGGGACCTCGAGCTGGAAGCCGCTACG	F	Body	CSDC5	0.8782057	0.9295986	-0.051382857			
cg18210026	2	71626509	121495096	121495146	Island	AGAGTTGATCCCAGCTGGAAAAGTAGACCTGTCCCTACTGTCTGGTCCCG	R	N/A	N/A	0.3290957	0.4042	-0.071324286	0.3616538	0.4042	-0.038766
cg18211633	12	59650385	122205609	122205659	N/A	CGGGGCTTGGGCTGGTTGTGTGCACATGTGTTTATGTAGCCATTTTACT	R	Body	TMEM120B	0.6144286	0.73562	-0.121191429	0.6728138	0.73562	-0.062806
cg18213653	12	39728447	112605734	112605784	N/A	CGTCTGTCTACAGGCGGCTCTTTTCCGCCACTTCCTGTGGCAGGTGTGTA	R	Body	C12orf51	0.7367043	0.7888186	-0.052114286			
cg18217252	9	73807439	133027841	133027891	Island	GGCAGGCAGGGCAGGGATGGGGCGCGCAGAGTGACTGTGCCCGCTGCG	F	N/A	N/A	0.1678414	0.2163829	-0.048541429			
cg18217874	7	44664482	133531244	133531294	N/A	AGAGTCCTTGCATGCTATGTGGGTGGCGTTCATCCTGTAGTGTTCCTACG	R	Body	EXOC4	0.8251543	0.8847429	-0.059588571			
cg18219522	11	67758380	95870414	95870464	N/A	AAAGCCTCCTCATTTCTCCCCAGAACCAAGTGCAAGGTAATTTGAATTCG	F	Body	MAML2	0.70835	0.76317	-0.05482			
cg18219994	8	52775444	140826657	140826607	N/A	AGCTTGGAGTGCTGCTGCTGCAGCAGGTGACTGTCATCTCATCCG	F	Body;Body	TRAPPC9	0.8774371	0.9182071	-0.04077			
cg18221076	6	49804475	31442934	31442984	N/A	CGTGGGTACAAGGGTGTTGGGAAGTGTCATCCTCCAGTGCTGACTTGAGT	F	N/A	N/A	0.6884214	0.7450657	-0.056644286	0.6749238	0.7450657	-0.070142
cg18224761	1	39785331	19576921	19576971	N_Shore	CGGGTGATATGTGTATCTAATTTTGCAGAATACTTGATATATGCAATTTT	R	TSS1500;Body	MRTO4	0.8961529	0.9362043	-0.040051429			
cg18231054	1	32800410	1858037	1858087	N_Shore	CGCCTTCCCCAGCCCCACGGCCCACCCCTGGCAGAGACGCTGCCTGGGGC	R	N/A	N/A	0.7696029	0.8515414	-0.081938571	0.8189013	0.8515414	-0.03264
cg18233497	18	22695305	58039968	58040018	N/A	CGGAAACTTTGTTTTCGCCTGAGCTGGTTTGAGGGGCTCTT	R	1stExon;5'UTR	MC4R	0.2758843	0.44142	-0.165357143	0.3626763	0.44142	-0.078744
cg18244157	15	46709465	65622965	65623015	N/A	CGCCCAGCAAGCAAGACCTCCTTCACCGGCCCCATCCTGCTGCCTGGAAC	R	Body	IGDCC3	0.86885	0.9189114	-0.050061429	0.8943338	0.9189114	-0.024578
cg18247897	10	21605323	445215	445265	S_Shore	ACAGGCCCAGACGGGTCAGCATTAACGTGGGGTCCTGGCTTCCTAAGACG	R	Body	DIP2C	0.8682271	0.9011457	-0.032918571			
cg18249380	20	10648396	47253188	47253218	Island	CCGCCACCACGGCCTGCCACAGAAGATCCGCGTCTCTGCGCACAGCTCCC	R	Body	EPE1	0.8417343	0.8680686	-0.026334286	0.8394988	0.8680686	-0.02857
cg18255166	17	15714453	13504399	13504449	Island	CAGGGAGCAGACATCCTAGCAAGAACTTCCGGAAGATGCTGCGGGACAGCG	R	1stExon	HS3ST3A1				0.1941838	0.1551586	0.0390252
cg18258916	2	50689414	45506158	45506208	N/A	CGCAGACTGAAGTTAGAAGTGTTCAAATGTGGGTTCTGCCTCTCCCACAG	R	N/A	N/A	0.8832371	0.9062557	-0.023018571			
cg18258980	2	38635352	200304211	200304261	N/A	GATATGCAGAGCTGCCTTCACAGTCTTTATAACTCCTCAAGCCCTCG	R	Body	ATB2	0.8322129	0.9107414	-0.078528571	0.8670013	0.9107414	-0.04374
cg18264519	2	61718340	97214296	97214346	N_Shore	ACAGGCGACAGCCATGTGTTCCAAAAATATTTGATCCAGCTGGGCACG	F	Body	ARID5A	0.7500657	0.8219886	-0.071922857			
cg18266530	22	29795349	42671409	42671459	S_Shelf	CGGGAAGCCCGTGCAACCTGAGCGCACAGATCACCCCCACCTGCCCGGCA	F	N/A	N/A	0.8727086	0.90711	-0.034401429			
cg18277815	4	14642398	6643729	6643779	S_Shore	GGAATTAGGGCCTAGATTGATTGTAAGCTCTTGCAGCAGTCACATTTGTTCCG	R	3'UTR	MRFAP1	0.4722057	0.6135714	-0.141365714	0.4878563	0.6135714	-0.125715
cg18278184	10	1267964	70847480	70847530	N/A	CGGGGAGTAACATACCTCTGGCTGGGCGCGGCGCGCGCGCGCGCGCGAA	R	TSS1500	SRGN	0.6776257	0.7913029	-0.113671714	0.7128475	0.7913029	-0.078455
cg18280195	1	70784429	28929859	28929909	N/A	ATGACTGAGAGGATCTGCCAAAAGAATAAAGCCTCCTACCCCAACTTCCG	F	3'UTR;3'UTR	TAF12	0.5692057	0.7026529	-0.133447143			
cg18283221	7	24738303	50629542	50629592	N/A	CGGGGCAGGGGCACCTGCAGGCTGCTCGTCATCTGAGTGGACCCTGTTCT	R	5'UTR;TSS1500	DDC	0.7881714	0.8460629	-0.057891429	0.8099538	0.8460629	-0.036109
cg18284523	14	10803398	24711562	24711612	Island	GGAGTGAACTCGGGAAGCGATATCACGCCGCTCTGCTCGAGGGGATCCG	F	1stExon;5'UTR;1stExon;5'UTR	FRI2	0.1398729	0.1715357	-0.031662857	0.1433125	0.1715357	-0.028223
cg18287066	1	22682420	240671647	240671697	N/A	CGTCTGGGAGGTTAGGAGAATCAGTTCTTGGCCTTTTTATTTTGGAAATA	F	5'UTR	GREM2	0.5498829	0.6758586	-0.125975714	0.5978938	0.6758586	-0.077965
cg18290775	14	72665399	69954135	69954185	S_Shelf	TGCTCCAGCCAGGGCATTGATCGCCCTAATGGCAAGGCTCGGGTGGCG	F	Body	FLJ44817	0.8382171	0.87686	-0.038642857			
cg18291422	6	14638508	147171560	147171610	N/A	CGGAGTGCCGTGACTCAGCTGAGGCTGGGTCTGTTTCTTCAGAATGAAGT	R	N/A	N/A	0.73541	0.8231543	-0.087744286	0.7821925	0.8231543	-0.040962
cg18298115	11	50728315	126608944	126608994	N/A	CGGTATAAATGAAGAGTGCCTTTCAGAAGACCAAGTGACCTTGTCTCAA	F	Body;Body	KIRREL3	0.7698571	0.8240843	-0.054227143	0.7819963	0.8240843	-0.042088
cg18305031	19	22705314	3982603	3982653	N_Shore	GACCCAGCCCTTGATCTTTGGGCAGCTGGAAGAAGCGAGCTCAGGGAACG	F	TSS200;Body	SNORD37	0.7315143	0.7974286	-0.065914286			
cg18310515	2	50754345	85921529	85921579	N/A	AAGCTGCAGGCTCCCTGCCCATAAAACAGGGTGTGAAAGGCATTCCAGCG	R	5'UTR;1stExon;1stExon;5'UTR	GNLY	0.8678614	0.9043257	-0.036464286			
cg18320356	12	40781481	10103862	10103862	N/A	CAGGAGGACACTGTCCTTGGCTTGCTGCTCACCAGTTGAGGAAATTTCCG	N	N/A	N/A	0.7421471	0.8353057	-0.093195571	0.782985	0.8353057	-0.052321
cg18320766	19	22772449	55598782	55598832	Island	CGGTGACCTGGCTGTACACACGTGCCCCCTCCTCGGGGCTCACCGCCCGC	R	Body;Body	EPS8L1	0.1436381	0.0810454	0.062592714	0.1440963	0.0810454	0.0630508
cg18329753	19	67607464	33727145	33727195	S_Shore	CGCCACCCAGGGGCCACATCCAGCTGGGCCTCCACCCACAGGGTCCCGTG	R	N/A	N/A	0.8894971	0.94103	-0.051532857			
cg18334799	8	31631479	28165791	28165841	N/A	AATGTTCTTATTTGCATTCCATAGCTCTGTGCATGTGTATACTCTAAACG	F	N/A	N/A	0.3469886	0.4788686	-0.13188			
cg18347762	13	35656470	91499567	91499617	N/A	CCGGGCAGTGTTCATTCATAGCCAAACAGTGTCCTTTGGTTCGGA	R	N/A	N/A	0.7761214	0.8537514	-0.07763	0.8049463	0.8537514	-0.048805
cg18352882	10	66631480	22725345	22725395	N_Shore	TGGACATCAGACCGACTATGGCTTTTTGGGTTCTTCCCCCCACAGCATCG	R	N/A	N/A	0.6257	0.7133471	-0.087647143			
cg18358126	19	15692421	46119636	46119686	Island	AAGACTCCTTGCTGATCAGGGCAGAATCAGGTTGAGTGTGAAGCTGCG	R	Body	EML2	0.8416943	0.8782671	-0.036572857	0.8974425	0.8782671	0.0191754
cg18380742	1	70733455	61674366	61674416	N/A	CGTAGTGGCTTGCATTATTTCTTGTATTATCCACAAGTTTCCTGCATTCG	F	Body;Body;Body;Body	NFA	0.7750629	0.8492457	-0.074182857			
cg18391467	17	69612383	72376791	72376841	N/A	CGGTGCTCCCTGGTCAGGGGTCCCAGCCATTTCAATAGGTGGTAGAAGCT	R	N/A	N/A	0.7531971	0.8437714	-0.090574286			
cg18395632	1	50735359	165345040	165345090	N/A	CGACATGAGCATAAGACCATTGTCAGGGTGAGGCAGCACAGAATTACA	F	N/A	N/A	0.8469714	0.9138829	-0.066911429	0.8851425	0.9138829	-0.02874	
cg18406010	14	29724485	51137626	51137676	S_Shelf	TAGCAGTAAACAGACCCCAAACGGAAATTGAGGCTGGCCTGGTGGCTACG	F	N/A	N/A	0.87594	0.91822	-0.04228			
cg18408209	2	46772449	193509	193559	N_Shelf	CGGTTAGCTGCTTTAAATTCTGCCAGGCCTTGCTGCCCAAAGACCT	R	N/A	N/A	0.8315529	0.8920314	-0.060478571	0.8555825	0.8920314	-0.036449
cg18409196	20	70627442	30179130	30179180	S_Shelf	TCCATCTACTTGAAGTAAGGAGTTCCTTTCTCTAATTCCTACAAAGTACG	R	N/A	N/A				0.9090375	0.9338714	-0.02834
cg18426551	17	31606439	42147617	42147667	N_Shore	CGCCTTTTAGGGAAGACCCCTCAAAATCAAGAGACTTATCTGTCAGCCT	F	TSS1500;TSS1500;TSS1500	G6PC3	0.4565	0.5635057	-0.107005714	0.537065	0.5635057	-0.026441
cg18428193	2	30714345	27665007	27665067	Island	CGGGTGGGCTCTGGGTCCTGGTCCTCTCTCTCTTCTTCCACA	R	TSS1500;3'UTR;TSS1500	KTCAP3	0.6841943	0.7419514	-0.057767143			
cg18434354	2	51674322	121224009	121224059	N/A	GGGCGTGGCTGGGGACCTGGGCCTGGGCCAGGAGGGGCCTTTCCCTCTCG	R	TSS200	LOC84931	0.6760214	0.7469029	-0.070881429			
cg18434367	6	59653335	45891455	45891505	N/A	CGGATCGTGAACTGATTTGATCACCATTTCCTAAATGACACACTCTTGTT	F	Body;Body	CLIC5	0.7090186	0.7831171	-0.074098571	0.737885	0.7831171	-0.045232
cg18436491	2	63790404	23865767	23865926	N/A	TCTCAACGTTCCAGAGGCTGCTCTCCTCCTCGGACGCCAGCCTCTCCTG	F	Body;Body;Body;Body;Body	LRRFIP1	0.8993614	0.91762	-0.018258571			
cg18436788	1	21771378	3704244	3704294	S_Shore	CGTGACCTCATGTCTGGGACCTAGCCAGGACTGCTCAGGTGAGAAGCAGGT	F	Body	LRRC47	0.8282186	0.8857429	-0.057524286			
cg18437602	2	35808314	75681243	75681293	N/A	ATCTTTGAGTTTTACTTTCCCTTCTATGCTGCAAGACCCCCATTCTCATCG	F	N/A	N/A	0.60839	0.65506	-0.04667			
cg18438345	6	40602474	41009313	41009363	N/A	CGGACAGTCAGGAGCACAGAAAGACAAGTAGAAATATGCACAGGTGGGCA	F	TSS1500;TSS1500	TSPO2	0.72097	0.7741714	-0.053201429			
cg18442992	13	66749462	24614476	24614426	N/A	AGGAACTTGTTCTAAATGATCATTCTCTCTCTCTCTCTCTCCAAAACCG	F	N/A	N/A	0.8964529	0.9337729	-0.03732			
cg18445292	11	69775454	68610381	68610431	N_Shore	TTGTTCATAACATCGGTGCATTTATGGAGCACCTGCTGTATGCAGAGCCG	F	TSS1500;TSS1500	CPT1A	0.5046129	0.65447	-0.149857143	0.593475	0.65447	-0.060995
cg18446472	7	23655414	44253807	44253857	N/A	CGCCAAATGATTTACAACAGAACACAACAGGAGCAGGGGATCTGTGGGTG	R	3'UTR	YKT6	0.86013	0.91528	-0.05515			
cg18452449	3	33663500	52260671	52260721	N/A	GTCAACCTGGAGCAGGCCAGTGGGGCCTGCAAATGCACAGGCAACGCG	R	TSS1500	TLR9	0.7647686	0.8367857	-0.072017143	0.8041338	0.8367857	-0.032652
cg18463876	7	69800345	75906035	75906085	N_Shelf	TTGGCCTTGGATCTTCCCAGGAAGCATGAGACCCAGCCAAGCTGAGGACG	R	Body	SRRM3	0.7247071	0.76599	-0.041282857			
cg18473137	17	32692482	30815034	30815084	Island	TGGTGGACGCTGGACGATGACCCGTTTGGGCGTCCTCGGGAGGTGACG	F	Body	CDK5R1	0.8999071	0.9310929	-0.031185714	0.9040875	0.9310929	-0.027005
cg18479322	6	20741324	163587135	163587185	N/A	ATGAAAGACAGATGCATTGTTTGGAGTAACACAGAAGCTCCAATTCCTCG	R	Body;Body;Body	PACRG	0.8682443	0.9100957	-0.041851429			
cg18480790	19	71626348	38893255	38893305	N_Shore	CGCTTGGCAGCAGTTGGAGCACGAGCTGCCTGCAGAAACCTTT	R	TSS1500	FAM98C	0.8936629	0.9235667	-0.029872857			
cg18483459	2	73807338	203294144	203294194	N/A	CGTGTTAAGTTCCAGTAACCATAAATAGTTCAGTGTTACTGGAATGCAGA	R	Body	BMPR2	0.6887729	0.8211257	-0.132352857			
cg18484958	3	30747388	149420985	149421035	N/A	CGCCAGGATGTGAGCTGAAATGAGTCAATATAAGGCCTTGTGTTTGGGAG	F	1stExon;5'UTR	WWTR1	0.8390714	0.9130671	-0.073995714			
cg18495563	11	48719449	33061907	33061957	N_Shore	CAAGGAGTTGTGCCAGGGCCTTTCTACAACGTCTTTCTGGCTCTAATTAAAG	F	5'UTR;5'UTR	CFTR11	0.24227	0.3369143	-0.094644286			
cg18503234	11	16727426	68847839	68847889

cg18929335	10	33800420	30336504	30336554	N/A	CGGGGAGCCCCAGACGCTTCTGCTTCCAGAACCTCGGAGGCGGGGTAAG	R	Body	KIAA1462	0.8159086	0.8568443	-0.040935714			
cg18930444	2	2374329	239974723	239974773	Island	CGGGGAAGTTTCTTGGCTGAGCTTCAAGACAGAGACAGACAGACAAGAGA	F	3'UTR	HDAC4	0.8282086	0.8750214	-0.046812857			
cg18948877	2	49629348	242904738	242904788	N/A	CGGCAGCCCGGTTACTCCTCACGCACGGAAGGCGCAGCAATGAAACAAAACG	F	N/A	N/A	0.8439957	0.9085857	-0.06459			
cg18949192	12	12605303	115134280	115134330	N_Shore	AAGAGCTTCTGGACAGAAAGGTCAAACTCAATCACCCTTAGCTCTTCCACG	R	N/A	N/A	0.6148071	0.7006843	-0.085877143			
cg18951537	17	51702392	11950516	11950566	N/A	AACAGCCATGATTCCTAAAATATTAAACATTTTCCTTCATCTGACAGGATCG	F	Body	MAP2K4	0.7530643	0.8579914	-0.104927143			
cg18953011	17	59725504	65040616	65040666	N_Shore	CGGCCCCAAGGCCAGGCCCACTCTGGCTCAGCCAGGCACACTAAACTTAGT	F	TSS200	CACNG1	0.8582514	0.9010886	-0.042837143	0.8727775	0.9010886	-0.028311
cg18953104	6	68719374	139613145	139613195	N/A	CGGGCTGCTGTGTTCTTACAAGGGAGAGAGAAACCCAATACACACACAC	F	5'UTR;1stExon	TXLNB	0.4412743	0.5531614	-0.111887143			
cg18956355	17	7279472	63534340	63534390	Island	CTGGAAAAGCTGAAGCTGGAGTTGGAGAGCCGCCACAGCCTGGAGGAGCG	F	Body	AXIN2	0.75377	0.8259043	-0.072134286			
cg18959161	2	20741356	168725535	168725585	N/A	CGTGTTCTCAAGACAATGGCTTCAAAGGTCTCCTGTTTGTATGTTTTGAC	F	5'UTR	B3GALT1	0.8212371	0.8663571	-0.04512			
cg18961546	7	31620320	1363437	1363487	Island	CGGGGCTCACCGCAGCCAGGACACCCAGGGACTCACCCCCAGCACTCACA	R	N/A	N/A	0.6186843	0.71524	-0.096555714	0.6685163	0.71524	-0.046724
cg18961788	14	29730437	102019326	102019376	N/A	CGGGGAGGCTGCTTGGGCCATCACAGACAGGGGCTGCACGCTTCCG	R	Body	OKSOS	0.8017314	0.8645971	-0.062865714			
cg18987103	11	26690303	134338443	134338493	S_Shore	CGCCTCCTTTGTCACACTCTGCTCAGGCACAGACTCTGTGCTCAGGTGCT	R	N/A	N/A	0.7949057	0.8768029	-0.081897143	0.8201263	0.8768029	-0.056677
cg18991240	2	50604371	71298920	71298970	S_Shelf	CGGTGGTGATTAAGTAGCTTTCACTCAGGTAGGGAAATCGGTCCCTCAGC	R	Body	NAGK	0.6788229	0.7607529	-0.08193	0.7051413	0.7607529	-0.055612
cg18997188	20	7065956	57463270	57463320	N_Shore	GTAATCAGGCTAAGAGTGGCAAGTGTCTTGGATGGGACACAGGCCTACG	F	3'UTR;3'UTR;TSS1500;Body	GNAS	0.5024471	0.56265	-0.060202857			
cg19003390	10	72697429	123948441	123948491	S_Shelf	TTTGCAATCCCGAGCACCGCTCCGGGAGCAAAGACGCTCCCGGGGACGCG	F	Body	ANKMP3	0.90048	0.9359357	-0.035455714	0.92424	0.9359357	-0.011696
cg19004285	12	35784378	95468616	95468666	S_Shore	CGCAGAGTACTTTGCACACAGGGCAGTTATTCCTGCCCACCCTTGCCACT	R	TSS1500;TSS1500;TSS1500	NR2C1	0.8535243	0.9266971	-0.073172857	0.903075	0.9266971	-0.023622
cg19007948	6	51670510	2731676	2731726	N/A	CGGCCAGGCAGAGGGAGAAGCACCTCCAGCAGCCATGGCTCAGTGACCAG	R	Body	MYLK4	0.9102157	0.94063	-0.030414286			
cg19012958	7	13796330	150479502	150479552	N/A	CGTGAACCTCGGGGAGGACGCATCTATGATTTGTTTCACTCATTTGCTGA	R	Body	LOC100128542	0.8577843	0.8845743	-0.02679			
cg19022476	8	38774362	145745884	145745934	Island	CGGGACCTGCGAGCTGAGGACCTGCCCATGCGCAACACTGTGGCCCTGCT	F	Body	LRRC14	0.8551029	0.88681	-0.031707143			
cg19023046	5	69772375	93446954	93447004	Island	GGAGCGACGTGTGTGTTCCCTGGATGACTTTCCTTATGTCGGGGCGTACG	F	Body;5'UTR;5'UTR;5'UTR	FAM172A	0.0397596	0.0660304	-0.026270857			
cg19023320	3	33648445	13033587	13033637	N_Shore	ACCCAGTCATCCTGAGAGGGCTGCTTCCTGGGGAATGCTCGGAGGACTCG	F	Body	IQSEC1	0.7658143	0.8194814	-0.053677143			
cg19024575	17	66683313	76794560	76794610	S_Shelf	CGTGACCAAAAAAAAAGTGTTAAGGACTCACAGACAGGGGTTGAAGTTAT	R	Body	USP36	0.8548943	0.9075843	-0.05269			
cg19031085	5	13796403	135228288	135228338	N/A	GATGTAGAGCCAAGCAGCCCCGAAGAGCTACCTGCCAAGAGCCAGAGTCG	R	Body	IL9	0.7127014	0.7858429	-0.073141429			
cg19037884	7	21723401	150517346	150517396	N/A	CGGTGGCACGACATCTGATTTCCTACAGAAGAGAAAACCCGAGACATGGG	F	N/A	N/A	0.53125	0.6268514	-0.095601429	0.5434863	0.6268514	-0.083365
cg19042390	6	26665322	166261046	166261096	N/A	CGGCCCTGGGCCATTTTCTTCTTCTTCTTCTTCTTCTATATGCTAA	F	N/A	N/A	0.5446429	0.6247286	-0.080085714			
cg19046642	7	12783474	138141133	138141183	N_Shelf	CCGGTTAACAATACAGGTTTGTTTTCGTTTTTTAGAGACTGAATCTCG	N	N/A	N/A	0.8061786	0.8632771	-0.057098571	0.8363588	0.8632771	-0.026918
cg19054785	10	55626422	131264145	131264195	N_Shore	AAATACGAAGGTATGAGCATTGGCCGAATCCCAACAGGGAAACTTCACCG	R	TSS1500	MGMT	0.8996229	0.9270329	-0.02741	0.9089763	0.9270329	-0.018057
cg19062112	14	47727486	103059954	103059984	Island	GGCGATGAGACGCGAAAGTTGGCCTCGGCTCGTCGCTGGGGAGCTGAAGCG	F	TSS200	RCOR1	0.1520629	0.1199997	0.032063143	0.1376563	0.1199997	0.0176565
cg19062258	7	24616422	1052779	1052829	S_Shore	CGGGCCGACACTGTGCAGGCCAAGCAGAGCAAGCAGCAGGTCCCCGGCAT	R	Body;Body;Body	C7orf50	0.8661843	0.9162986	-0.050114286			
cg19088503	10	18705409	86910486	86910536	N/A	CGCCAGAGCAGATATGCTTATATATTAAGATTCTGGGTAAGAGTTCATTA	R	N/A	N/A	0.80826	0.8865371	-0.078277143			
cg19093295	11	52602489	45715517	45715567	N/A	CGACCTAGACTTGCTGAGTGGGCCCTGCTGAGTGAGCCCTGCTCACGCC	R	N/A	N/A	0.7569257	0.8066614	-0.049735714			
cg19095000	1	56790399	11711141	11711191	S_Shelf	AAGAGGATCTTCACGGCAGTTCCTCTCTGGACCAGAAACCCCACACG	R	Body	FBXO2	0.79319	0.8390643	-0.045874286			
cg19100996	12	40614392	133138586	133138636	N_Shore	CGGCTCCCCAGAAAGGCCTCGGCACCTCCTTGGCCGTGCCCATCCCCCAG	R	Body	FBRSL1	0.66837	0.7411886	-0.072818571			
cg19107120	17	67611470	42430376	42430426	N_Shore	CGGGGAGGGGATGGCAGCTGTAATGTGGCTTTTGCCAACACCCCCTTCT	R	3'UTR	GRN	0.7619486	0.8168643	-0.054915714			
cg19107655	13	40628052	112838828	112838878	N/A	TCAGGAACTGGGCCTCTGTCTGTCTGTTCTGTGGGGTCTCCTTGGGCCG	N	N/A	N/A	0.7715486	0.8089386	-0.03739			
cg19110982	20	63647365	32662344	32662394	N/A	GCCCACCCCAGGCAGCCCAAGAAGAACAGTGCCTCTCTGAGCATGAGTCG	R	Body;Body	RALY	0.8444729	0.8891429	-0.04467			
cg19123345	2	60618349	235976249	235976299	N/A	GGTCAGCCCCAGGCCTTAGCCTGGCCAGGGGCACATGCTGTCCTGTTTCG	R	N/A	N/A	0.8797729	0.9165271	-0.036754286			
cg19133023	11	14743487	891017	891067	S_Shore	CGCGCTGCTGCAAAAGCACCAGGGACAGGGATTTACGAGGCTCCTTGCTA	F	Body;Body;Body;Body;Body	CHID1	0.8898771	0.91532	-0.025442857			
cg19137288	3	11679435	132754249	132754249	N_Shelf	CGGTCTTCAGAAGTCTTGGAAGTCACATTATTATTGTCA	N	N/A	N/A				0.8235475	0.8786843	-0.055137
cg19150842	3	69686400	141877942	141877992	N/A	CGAGGCTGCAGTGAGATATGATCCAACTGAATTGTTTGCTTAATGAGCCATAT	R	3'UTR	GK5	0.5434014	0.6477914	-0.10439	0.5952888	0.6477914	-0.052503
cg19165249	1	16709479	1558097	1558147	N_Shore	CCACAGAGCCTTCTCTGGAAAAGTGGCCCTGGCCACGCAAGGCACTCACG	F	Body;Body;Body;5'UTR;Body;(	MIB2	0.7959414	0.8401743	-0.044232857	0.8228175	0.8401743	-0.017357
cg19170009	10	59675327	17277806	17277856	N_Shelf	CGTGACCAAAAAAAAAGTGTTAAGGACTCACAGACAGGGGTTGAAGTTAT	F	Body	VIM	0.7120557	0.8073386	-0.095828857			
cg19175123	10	43689364	103411746	103411796	N/A	GGTCACAATGTGTAAATTCTTTTGACCTGCACCTAATCAAAGATTCACCG	R	Body	FBXW4	0.8793414	0.9087886	-0.029447143			
cg19175386	12	56710448	115134496	115134546	N_Shore	GCAGTACTACCCACTTGTAGGCAAGGTGTGTGCTCTGAGTGCAAGAAACG	F	N/A	N/A	0.5788157	0.67345	-0.094634286			
cg19185146	2	19754368	134880302	134880352	S_Shore	AGCTCCAAACCAGGACTGCAGATTCCTTTCTCCTAATGACTCCAGTTCCG	R	N/A	N/A	0.7612814	0.8244743	-0.063192857	0.8020275	0.8244743	-0.022447
cg19192377	11	55613448	62209356	62209406	S_Shelf	CGTCCTCTCCGTTGAGATGCTAATATGGGGCCGCTTGGGTCCTGGTCA	F	Body	AHNAK	0.8243729	0.9013771	-0.077004286			
cg19200953	13	57715418	100470738	100470788	N/A	CGGACACCACACTGCCACACTGCCACTGATCAGATTCGACATGAACAGGAA	F	Body	CLYBL	0.6511029	0.7750057	-0.123902857	0.708965	0.7750057	-0.066041
cg19202618	2	59636462	8021551	8021601	N/A	CGTGGGGGTCTTTGTACTGAGACTCATCAGCATCTCGGAAAGGAGAAG	F	N/A	N/A	0.5310543	0.6246071	-0.093552857	0.5559975	0.6246071	-0.06861
cg19209355	4	66607418	8345155	8345205	N_Shelf	GAAGGGCTTTCTCCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	R	N/A	N/A	0.7190971	0.7773443	-0.058247143			
cg19210342	10	20772487	23640730	23640780	N/A	TAACAGGCATGAACCTAATGTGTTGGGATTACTGGCATAGTTTCCCCACG	F	N/A	N/A	0.79963	0.8650343	-0.065404286			
cg19212550	10	66675364	101767908	101767958	N/A	CGTTCCATCAATCTCTTCCTCTTTTCTGGCTCCTGACTTCAGGTGATCCG	F	5'UTR	DNMBP	0.4682929	0.5664014	-0.098108571			
cg19213808	17	44604398	49336082	49336132	N_Shore	CGCTGATTTTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC	F	5'UTR	MBTD1	0.6048143	0.7376443	-0.12283			
cg19219435	19	37605313	15354051	15354101	N/A	CGGCGTAGGGGGCTGCACCTTCTGCAGCTGCTGCAGGTAGCAGCTGCATCT	F	Body	BRD4	0.84993	0.88177	-0.03184			
cg19220825	12	16698307	50353951	50354001	N_Shore	CCTTAGCACAGTGCCTGGCACAGAGTAAGGCTCAGTAAAGTCTCCTTACG	F	TSS1500	AQP5	0.6240343	0.70593	-0.081895714			
cg19225688	2	59674340	218990043	218990093	N/A	CGGCTGCATATTCTCAGCTATCACCACTGCTTACAACACCCTGGCTAACC	R	TSS1500;1stExon;5'UTR	CXCR2	0.5886729	0.67074	-0.082067143			
cg19230787	7	61667309	4049967	4050017	N/A	TTCCAGCAGTGTGCAAGAGGAGCTCTGCCACATGCACTTCTTGCCCG	R	Body	SDK1	0.8654629	0.90076	-0.035297143			
cg19234613	12	17648305	107832552	107832552	N/A	TTGTTGCCCTCACTCCCCCTCTCAGGTTCTTGGAGCCATTCAATTTAACG	R	Body	BTBD11	0.8024114	0.8822671	-0.079855714	0.8482775	0.8822671	-0.03399
cg19235974	12	46772361	1063197	1063247	S_Shelf	ATGTCCACACCCCTGCCAATTCTTGACATCATGCTGATTCACAACTTTCG	N	N/A	N/A	0.6960914	0.8121757	-0.116084286			
cg19237600	7	36704401	99564474	99564524	N/A	GAATGATTTGGGTGCCAAGTGCTACTCAAGACGCGCTCCCAGTTTCG	R	3'UTR	ZASP1	0.8833014	0.9219286	-0.038827143	0.8989225	0.9219286	-0.023006
cg19239041	20	36808446	4795444	4795494	N/A	CGGGGGGTTTCCAGACCGTTTCCAGGGGAAGTTTGCCACAGTAGCACATT	F	5'UTR;5'UTR	RASSF2	0.6170243	0.7022129	-0.085188571			
cg19240678	11	59681466	132582550	132582600	N/A	CGCTGACAAGCGTGGCCTTCCAATTCATCTCTGAGCTGCCGCTTCCCACT	F	Body;Body	OPCML	0.7003457	0.7836571	-0.083311429			
cg19242851	17	48706317	143233	143283	N/A	CGTCTGAATACCCCGATTTCCCTGAGAGCTGACACTCGCAGAAGGCACGAGT	R	Body	RPH3AL	0.6919186	0.7895157	-0.097597143			
cg19244655	11	61785343	17755937	17755987	N_Shore	CCGGGCGGTGTCTCTGATGACAAAACTCCGGGACGACATTTGTCTCCCGC	F	N/A	N/A				0.3215813	0.2707743	0.050807
cg19248395	1	22730337	64660725	64660775	N/A	CGAAGATGGGGGTTCAAATCCACACGACGTTAGCACTTTGTACTGCTACA	F	N/A	N/A	0.7304871	0.8165914	-0.086104286	0.7846525	0.8165914	-0.031939
cg19251719	1	42620340	203055479	203055529	N/A	CGGCCTGCCTGCTGTCTCCTTGCAGTCCCGAAGAAGCTGGTGGGTATAGG	F	TSS200	MYOG	0.8137686	0.85652	-0.042751429			
cg19255818	11	70682357	66330936	66330986	N/A	CGGGAAGAGCACCTCTTTATTGCTGTTAGAAGATCTTTGTTCTAACAGTT	F	3'UTR	CTSF	0.8680486	0.9175714	-0.049562857			
cg19256368	15	15777493	83619037	83619087	N_Shore	GTAAGAACACAAACTCACTGGAGAGGCCACACTTAACACAGAACACTTCG	R	Body;Body;Body;Body	HOMER2	0.7816857	0.8521114	-0.070425714	0.8101638	0.8521114	-0.041948
cg19269956	6	62649453	30524408	30524458	Island	TCCCGGGAGAACCTACCACTACCCTGGAGGGGGCGGCGGAGCGGAGGGCG	R	TSS200;5'UTR;TSS200;1stEx	PRR3	0.4177914	0.46875	-0.050958571	0.4399725	0.46875	-0.028778
cg19272663	12	18612479	57646177	57646227	N/A	TCGTCGTTAGGGATACAGCTACTTGGACCCAAGAGATTTCCAGGGCAACG	R	TSS1500	STAC3	0.6971286	0.7955343	-0.098405714			
cg19280785	3	64618309	134340995	134340995	N/A	CGATGCTTTGGAATTGTAAAATTGTGCAGCTGCTGTTGAGAAATTTTCCG	N	Body	KY	0.66317	0.78608	-0.12291	0.7251188	0.78608	-0.060961
cg19283298	13	19605491	98090226	98090276	S_Shelf	CGGAGGTATGTACACTTACAGACACTTAAGGGAGTATGGGTCAGTTTCAC	R	Body	RAP2A	0.80294	0.9010943	-0.098154286			
cg19285752	17	63651355	17699461	17699511	N_Shore	CGGGGCTCACTCAGGGCCGTGAAGAACGAGTACACATCCTGGGGAGCCC	R	Body	RAI1	0.8796971	0.9045	-0.024802857			
cg19286667	2	41662416	220282243	220282293	N_Shore	CGGTGCTGGACAACACAACCCCTGCTGTGTGTGGCGTGGGGTGGTGGT	F	TSS1500	DES	0.7109171	0.7985214	-0.087604286	0.7494588	0.7985214	-0.049063
cg19289355	7	14650300	127260012	127260062	N/A	CGGGTTTGGGGCTAATTGTCCCCTTCATTAGCTGGGCCCAGGCCCCGGGCTG	F	N/A	N/A	0.1455414	0.1195514	0.02599			
cg19293468	17	38721388	1973400	1973450	N/A	CTCTCCGGGAACTTCCCTGAGAAATGTGAAAGTCCACAGGGAAGGCAAGCG	F	Body;Body	SMG6	0.6439286	0.7068586	-0.06293	0.6357863	0.7068586	-0.071072
cg19303005	4	27792302	8277610	8277660	N/A	CGCGTCACTTCTTCTGAGCCCAGGTGCTCTGCCGTCCCCTG	F	Body	HTRA3	0.7415557	0.79821	-0.056642857			
cg19304800	5	66684484	153853057	153853107	Island	AGAAACTTTGATTTTCTCTCTGCTCTCCCCAAGGGCCCTGGGGCCTCG	R	N/A	N/A	0.1417957	0.1857014	-0.043905714	0.153945	0.1857014	-0.031756
cg19308375	2	46777369	228324937	228324987	N/A	CGCCGCCCCCCAGGAGACCTGGGGAGCGTGGCCTTGTCTCCCATAAGCATT	R	N/A	N/A	0.5795257	0.6863314	-0.106805714	0.6283113	0.6863314	-0.05802
cg19310162	18	57615351	74836070	74836120	S_Shelf	GAGCAGGGCTCTCTGGGAGCATCCCGTGTCACCAGATGCCCCCAAAAGACG	R	5'UTR;5'UTR	MBP	0.7971586	0.8456186	-0.04846	0.8209163	0.8456186	-0.024702
cg19311253	7	25704493	65971710	65971760	S_Shore	CCCAGTTTAATAAAAACATTGTAGGCAAAGTGGGGGTGGGGGTGGGGG	F	Body	ZNF804A	0.4516071	0.5402657	-0.088658571	0.49103	0.5402657	-0.049236
cg19320261	1	45626317	64409138	64409188	N/A	CGGACTTCCTAAAGAGCAAGGCTGTGAAGCACAGGGGCTTGCCCTGAGCT	R	Body;Body	ROR1	0.7138786	0.7765614	-0.062682857	0.7386488	0.7765614	-0.037913
cg19324997	2	45781413	240169161	240169211	N/A	CGCCCCGCACGTACTGTGTGCCTCGTTCTTTATCTGTGTTCGTTTATTCA	R	Body	HDAC4	0.8967786	0.9345214	-0.037742857	0.9105475	0.9345214	-0.023974
cg19328485	10	51690424	5060318	5060368	N/A	CGGTGGACGCAGACACCAATCATATTGGATTTGGATATTCCACAATTTCTG	F	TSS200;TSS200	AKR1C2	0.7932314	0.8569457	-0.063712286			
cg19350870	2	58770453	73008384	73008434	N/A	CGGTTTGCTTAGAGAGGAGAAAACCTTGTGTAGAGGAACAGTATGAAGAA	R	Body	EXOC6B	0.5486229	0.65602	-0.107397143	0.582735	0.65602	-0.073285
cg19356624	1	18781468	2386965	2387015	N_Shore	ACAGAGCATCCTTCACACTCACTGAGTCTAACTCCACCTGCAGGAAGCGG	F	N/A	N/A	0.7755414	0.8239886	-0.048447143			
cg19357369	4	30711481	2429884	2429934	N_Shore	CTGGGCCTTCGCTATTGTCTGTTTTGGACGTGCAAGGCCGAGGGCAGGCCG	F	N/A	N/A	0.8698814	0.90883	-0.038948571			
cg19364784	7	12623382	149416873	149416923	Island	TGTTCATTTCCAGGTGGAAAAGCTAAGACTGAGCCCTCCAGGGACTCCG	F	Body	KRBA1	0.8735971	0.9010471	-0.02745			
cg19375224	19	65690344	39802921	39802971	N_Shore	CGGTGAAGATCTGACAGCCAGGAGCTGGGGCTCTCCACAGGTAGGGAAAC	F	Body	LRFN1	0.87706	0.9170571	-0.039997143	0.8941313	0.9170571	-0.022926
cg19375458	11	50728367	77024568	77024618	N/A	CGCCCTCCGCCCTAAGGGTTCGTGGCCCACCGCTCCTTCGCAGTCCCTGC	N	N/A	N/A	0.8355171	0.8709171	-0.0354	0.8514763	0.8709171	-0.019441
cg19378892	11	33605502	159283586	159283636	N/A	AAGCCTTCACAACGCTTCTTAAGGAGACAGGTATCTTGCCCCACCG	R	1stExon	OR10J3	0.8859957	0.9157757	-0.02978			
cg19384448	1	36810430	10977926	10977976	N/A	GTGCTCACGTTATGGAATCATGTCTATTTGGGATGTGTGGCTTCCAGGCG	R	N/A	N/A	0.7634357	0.84717	-0.083734286			
cg19384905	6	58677434	153299788	153299838	N_Shelf	CGTGGTAGTCATTTTAACTCCTTAAGTGCTAATTTCGTGAGGAAGGATAC	R	5'UTR;Body	FBXO5	0.5307214	0.6157043	-0.084982857	0.5623313	0.6157043	-0.053373
cg19390317	21	57612369	43347995	43348045	N/A	CGTGGGGCTCCTGCGTCAACCTGACTCCAACCCGCGCCCCCAGCAACACTC	F	Body;TSS1500	C2CD2	0.7023714	0.7914971	-0.089125714			
cg19391675	6	36695492	40345594	40345644	N/A	CACCACCCTGGAGAACCACTTTGTTGTTGAGCAGGATACCAG	F	TSS1500	TDRG1	0.8560143	0.9026429	-0.046628571			
cg19400179	3	58697474	108321607	108321657	N/A	AGTGGTGACATTTCAGGCTGACTGCTTCCTTTTGGTTGCTAGGCACTTCG	R	5'UTR	DZIP3	0.7905129	0.8797829	-0.08927			
cg19411729	17	34726353	34207663	34207713	N/A	GACTTCTGATCCTGTCCTAACTGCCAACTCCTTGTTGTCCCCAAGAAGCG	F	TSS1500	CCL5	0.7165543	0.7897414	-0.073187143			
cg19418273	7	25662427	137562490	137562540	N/A	CGAGTGCAGGCCTCCTCCTCCTCCGAGCCATAAAGATGCATCTTCTAATTAT	R	3'UTR	CREBL2	0.9327588	0.9589414	-0.026182857			
cg19450840	7	25724505	134540954	134541004	N/A	CGCTAAAGCACTATAGCTCTGTACTATACGTGGAAGGCAACAGTTCAGGG	R	5'UTR;5'UTR;5'UTR	CALD1	0.7062186	0.8009971	-0.094778571			
cg19454081	7	17641414	152593653	152593613	S_Shore	TGCAAGCCTGGGGTACGGCAGTCGCTCCTGGCTGGACCTCTCCTGACG	R	N/A	N/A	0.6831957	0.7650714	-0.081875714			
cg19458787	5	61796489	173116776	173116826	N/A	CCTGCTCTTGGCTTTCATTATTGTCCTATGTTTTCAAAGTACCAGCTCCG	F	N/A	N/A	0.24214	0.1714086	0.070731429			
cg19463193	15	69779335	68564546	68564596	N/A	AGCTGGACTTTAGCCTTAAGATGTGCTGTGGTCAGTGCATGGCTTTTCG	R	N/A	N/A	0.6217886	0.7307171	-0.108926571	0.6243413	0.7307171	-0.106376
cg19468534	15	30706322	41623761	41623811	N_Shore	CTACAATCCTTTTAGATATTAGAACTTTTTGATACAGGGTCTTGCTCTCG	F	Body;TSS1500;TSS1500;TSS	OIP5	0.7366729	0.8620174	-0.125398571			
cg19472590	10	15613309	102753828	102753878	N_Shelf	CGGGGACTTTCATGCGAAACTCCAGCCTAGGCTTTCAAAGTCAAAGGGTGA	F	3'UTR;3'UTR;3'UTR	C10orf2	0.8957771	0.9165057	-0.020728571			
cg19474725	14	53796450	102394473	102394523	N_Shore	TGAAAGAATTTGGGTGAGCAACACTGGTGTTTTGAGCAAACCTGCTTCTG	R	N/A	N/A	0.4423014	0.6326457	-0.190344286	0.495565	0.6326457	-0.137081
cg19475258	17	44686354	77082464	77082514	N/A	TTCAGCCCCTGCATGAGCGGATGCTAAGGCCGGGTGGTCTCCTGGCCTCG	R	3'UTR	ENGASE	0.8471114	0.88958	-0.042468571	0.8700488	0.88958	-0.019531
cg19476426	14	38733494	88630031	88630081	N/A	CGGGACTGGAAGCTCTTTTTACAGTCACGATATGGCTCTGGTCTGTGGTC	F	N/A	N/A	0.8828143	0.9231714	-0.040357143			
cg19488505	12	10735328	6477001	6477051	S_Shelf	TGAAGAACTCTGTATCACGGTGGTTAATGTAGCTTAGCACGTTAGGACACACG	R	Body;Body;Body	SCN1A	0.2237343	0.32515	-0.101415714			
cg19493651	2	4474367	62428082	62428132	S_Shelf	CTTTATCTTCCCCATTTTACAAGTGAGAAAATTATCCTGAAATAGTTCG	F	5'UTR	B3GNT2	0.7619529	0.8364243	-0.074471429			
cg19494742	12	47741323	123058028	123058078	N/A	TTGGCAAAATAAACTCCCTAAATTAACTGAGAACTGTCTCAGATTTTCCG	F	Body	KNTC1	0.8661414	0.9157671	-0.049625714			
cg19497798	17	57746391	73910342	73910392	Island	CGCTGTCTCCAGGAGCAGGCTGAGCTGAAGATCAGGGCCAGCGAGCTCCG	F	Body	FBF1	0.8066786	0.8500343	-0.043355714	0.83466	0.8500343	-0.015374
cg19498110	22	3361500	17590041	17590091	Island	CAGCAGCCTGGAGGCCATCCTGCACGCCGCCGCCGCCGCCGCCGCCGCC	R	Body	IL17RA	0.81322	0.8465729	-0.033352857			
cg19509763	14	17679306	50320632	50320682	S_Shore	CATGTGTAGCCTGCAAGCCTCTAGCAGCTCTTTTGCAGCGACGCCGAGCG	F	TSS1500	SDCCAG1	0.1227571	0.0803104	0.042446714			
cg19513232	5	62808412	149623972	149624022	N/A	CGCCAGGCAGGGCTCTGAGCCCAGAAAAAGGCAGGGTCTCAAGAAGAGGAT	R	Body;Body	CAMK2A	0.7724371	0.8277929	-0.055355714			
cg19514182	12	67773486	48419492	48420002	N_Shelf	TCAGAAGGGGGCCTGTCTGTCTGTCAGAGATCTTGTCCCTGTTTTCCG	F	N/A	N/A	0.8627357	0.9008957	-0.03816	0.8773288	0.9008957	-0.023567
cg19522511	3	35757407	105073077	105073127	S_Shore	TAATGGATGCTCTCCAGGCCAGCCAGAGTCGCGGCTGATTCTGTTTTGCG	F	Body	AIP	0.7142743	0.8170257	-0.102751429			
cg19528654	11	33682479	67251154	67251204	S_Shore	CGTCCCAGGGTCTTGGTTTTCCACTCTAAACAGCGGCAGTTGGTCTAAGT	R	Body	AIP	0.7746386	0.8475014	-0.072862857	0.8160575	0.8475014	-0.031444
cg19534906	14	56627469	104098457	104098507	S_Shelf	CGCCGGCCAACAGTGGCTCTTTTATCAAGGTATCGCTGACTACTCAGCA	R	5'UTR;5'UTR;5'UTR	KLC1	0.9000686	0.9421643	-0.042095714	0.915165	0.9421643	-0.026999
cg19535096	4	68751711	68751761	68751811	N/A	GGAAAATTCATGCTCTGAAAGTGATCCTCTGTTTGAGCTCACAGCA	R	N/A	N/A	0.7864771	0.83925	-0.052772857			
cg19536922	2	4968235 7	3292956	3293006	S_Shore	GGAGACAAGCGAGGATTTGTTTCTGTATTAATTGGCAAACCTCTTTGCCG	R	Body	TSSC1	0.8940743	0.9301514	-0.036077143			
cg19536929	12	42745318	115134594	115134644	N_Shore	CGCTCTGCACAAACAGAAAACTTTGGGATAGACAACTAGGGAGTCTTGCG	R	N/A	N/A	0.6558614	0.7314814	-0.07562			
cg19541916	2	36642304	19674105	19674155	N/A	CAACTCAATGTTTGTATGTGGTGAACAGACCACCAACTTGCTCTCTCAG	F	N/A	N/A	0.6491086	0.7537057	-0.104957143			
cg19544707	14	70760429	103746266	103746316	Island	CGCCCGAGGCCTGAAAGCTGTCTTTACCTTCGCAGCTTTCCAAGTTACT	F	N/A	N/A	0.73422	0.8067	-0.07248			
cg19556337	11	28706366	511660	511710	S_Shelf	GTCTTGGCTTTGAGCCTCCAATTTCAATCAGACAGAAAGCAGACCAGTCG	R	N/A	N/A	0.8341171	0.8819729	-0.047855714			
cg19559984	7	59631418	28848933	28848983	N/A	GTAGACGAGATCCGAGACGAGGCGGCGGAAATTTTGGAACGGAACCG	R	Body;Body;Body;Body	CREB5

cg19909117	14	53666417	96219318	96219368	N/A	GAATGGCAGCAACATGATCTGGGGATGAATTAGCACATGAATGCATCTCG	F	N/A	N/A	0.4822957	0.5690814	-0.0867854	0.513135	0.5690814	-0.055946		
cg19909613	8	50796355	109487153	109487203	N/A	CTGTTTCACACATGTATACTAATAATAGCTTTTACTAAATGCTTATTTACG	F	Body	TTC35	0.8815357	0.9199743	-0.0384385					
cg19910940	1	43616509	91605041	91605091	N/A	CGGTGCAAGAGGGCAATTCTGTGATTGGAATGCCAAGTTGTGAAAGCAA	R	N/A	N/A	0.9034429	0.9327071	-0.0292624					
cg19911494	5	34779417	9169758	9169808	N/A	ATCATTTTCACTCTGCTTGTTGAACAAATAAATCCCTGCATAGTCAGACG	R	Body	SEMA5A	0.87211	0.9062843	-0.0341726					
cg19911566	17	41768433	28164614	28164664	N/A	CGGCTGGTCAGGACCCACTCTCCCAGGCCCAGAGCCCTCTGCTGTGCCTC	F	Body	SSH2	0.8765714	0.9063771	-0.0298057					
cg19917530	2	57748470	133855847	133855897	N/A	AGTTTCTGCAACATCTGCAAACTTGAATGCTATTGTTAATGTGCACAACG	R	Body;Body	NCKAP5	0.7565343	0.8313614	-0.0748271					
cg19918549	14	7280325	100531800	100531850	N/A	AGGGTCTGTGGTCCTCTGATCAACATAGGCTGGTGGGAGTACAGGACTCG	R	1stExon;5'UTR	EVL	0.7147829	0.82007	-0.105287143	0.74891	0.82007	-0.07116		
cg19919989	5	11787323	66492464	66492514	N/A	CGCCATCACAGGCTAGGATTGCTTGGTGGGTTTACCTAATGCTTGGAGCT	F	1stExon	CD180	0.8525329	0.9045014	-0.0519685					
cg19923360	1	62610493	25667109	25667159	S_Shore	GTACATATTTAAAACATCCTGCAGAATTCAAAACCCATAAACACAAAGG	F	Body	TMEM50A	0.7645071	0.8229457	-0.0584385					
cg19934294	4	54613476	2933421	2933471	N/Shore	ATCTTCCCCTGCTGTAGGCTGGGAGCGGGTGTGTTAGTGCAGGGCACCCG	R	Body;Body	MFSD10	0.62904	0.68826	-0.05922					
cg19938159	3	64724489	50196278	50196328	N/Shore	CGGCCATTCCCGCTCCAGAACTCCGCCATAGCGGTTGCAGGTCCAAGTTTC	R	5'UTR	SEMA3F	0.7162714	0.7633571	-0.0470857					
cg19939178	12	66600485	107976961	107977011	S_Shore	CGTGCAGTATCCATTCAAACAATGCCTGAAAGGAAATAAGTGCCTATAAA	F	Body;Body	BTBD11	0.7960386	0.8444671	-0.0484287					
cg19942383	3	54703380	42979226	42979276	S_Shore	CGCCAGAAAAGGCATCTTGGAAGTTAACAGGGAGTCCAGTAAGGAGAAAT	R	N/A	N/A	0.7292057	0.7988886	-0.0696828	0.753155	0.7988886	-0.045734		
cg19944656	17	10723336	76876040	76876090	N/A	GGCCGGTTGTGACTGTCGAAGTCTGACCGTAGCCCATCCTCTTTGATCG	F	Body	TIMP2	0.5310586	0.6474843	-0.1164257					
cg19945535	5	72607496	137968163	137968213	N/A	CCCCCCCTTCTATTTTAAATGTTCCGTTCTCTGAGTTACTCAACAGTGTGAAG	R	N/A	N/A	0.8913686	0.92115	-0.0297814					
cg19951006	12	39718407	56732615	56732665	N/A	CGGGCCTTACAATGCAGGGACCTTAAAAGACTCAGAGACAAAGGGAGAAA	F	TSS200	IL23A	0.6488529	0.7646243	-0.1157714					
cg19955849	4	49657473	140095286	140095336	N_Shore	TTAGCCAGGTGTTGGTGCATGCGCCTGTGGCAGGAGAATCGCTTGAACCG	R	N/A	N/A	0.7325629	0.7667243	-0.0341614					
cg19963544	2	72723492	106483700	106483750	N/A	TATCTTAATTCTTTTAAATGTTCCGTTCTCTCAACAAATTGTTATACG	R	Body;Body;Body	NCK2	0.8070657	0.8908314	-0.0837675					
cg19968840	15	44679497	45409319	45409369	Island	CGTGCTGCTCTCCACGCCGGCCCCGCTCTACGGAGGCCTGGCACTGCTGA	F	Body	DUOXA2	0.1605557	0.1251429	0.035412857	0.1542838	0.1251429	0.0291409		
cg19971102	14	49782486	100135277	100135327	N/A	CGTGTCTTTGTGCTCATTTCCACCACTGTAAAATGAACGGCTGAGACGTC	R	3'UTR;Body	HHIPL1	0.69739	0.7747971	-0.0774071	0.7290625	0.7747971	-0.045735		
cg19972822	7	26696500	138778744	138778794	N/A	AGGGACCAAATTTTCAGCATCGCTAGCTTAGCAAACCCCAAGAGGCCACG	F	Body;Body	ZC3HAV1	0.7027543	0.7715214	-0.0687674					
cg19973647	14	24733381	65323517	65323567	N/A	TTCACCAGGTCACCTCTGTTGGAAGCTGATGGCTGTCCCAGGTGTCCG	R	N/A	N/A	0.7745157	0.8502814	-0.0757674	0.8156163	0.8502814	-0.034665		
cg19977179	3	20624411	128779500	128779550	N/A	CGGGCCCCTGGAGGGCCTCCTGCCTCTGGAAATAGGCCCCAAGGCTGCACT	F	TSS200	GP9	0.5514429	0.6233643	-0.0719214					
cg19980718	5	33761408	121704136	121704186	N/A	CGAGGTTCAAAAACTGGAAATCTGGTAGCAGAGAAGGATGACAGAATTTG	R	5'UTR	SNCAIP	0.8874386	0.9234786	-0.03604					
cg19982230	17	3368374	27045302	27045352	N_Shore	CTCCTCCAGCTGTTTTGGACCTCCTCTGTTCTCCTCCTCTCTCG	R	TSS1500;TSS200;TSS200;TS	RAB34	0.4795871	0.6025514	-0.1229642086					
cg19983527	10	73630310	95389073	95390023	N/A	CGCCAGATGCTCCCAGGAATCAGCTTCTGTATGTGCTACTCTACCTGACC	F	Body	PDE6C	0.8871114	0.9212557	-0.0341446286					
cg19987349	8	64741437	98993142	98993192	N/A	GCCATAGCATAATCTTGAATACTAAATGAGGCTGGGCACAGTGGCTCACG	R	Body;Body	MATN2	0.5244171	0.5907629	-0.0663454					
cg19991948	10	43714334	121335173	121335223	N/A	CCGCTCACTGTGTTTGGTAACTTGCCACATACATCCGGCTTGGTTAGGA	F	3'UTR;3'UTR	TIAL1	0.5072757	0.6677029	-0.1602743					
cg19994159	13	65712408	22794813	22794863	N/A	CGCTGGGGCTCCTGCCCAGCGGACTTACTGCACCCTCACCGGCCTTGGC	F	N/A	N/A	0.9133286	0.9397014	-0.0263728 57	0.9225375	0.9397014	-0.017164		
cg19998294	10	11677453	18629497	18629547	N/A	AAGGATTCTCGAGCAGGGCTGGAGTCCTGGCTGCCTGGAGGGACCTGTCG	R	Body;TSS200;Body;Body;Bod	CACNB2	0.61666	0.7701429	-0.153482857					
cg20006618	4	23765461	186652504	186652504	N/A	CTTCATGCAAATGAGGAAGCTCAATTGGCTTCTTATTGAAAATACCTCACG	R	5'UTR;5'UTR;5'UTR;5'UTR;5'L	SORBS2	0.6750571	0.77491	-0.099852857					
cg20007844	8	51774397	126374301	126374301	N/A	CGCTGCACATCACAGCACAAATGCAAGGGACTGCGGATTTCTCGGAACCG	F	Body	NSMCE2	0.7769157	0.8208086	-0.0438925857					
cg20012848	12	17756498	52435420	52435470	S_Shelf	CGGCCCCCAGGCTCCAATGCCTAACCCGGGGAGGTCCTTGGGCGCTGGCT	F	N/A	N/A	0.8312829	0.8760943	-0.0448114297					
cg20012920	17	44645480	80809645	80809695	N/A	CGGAAGGGAGCCTCCTGCGAGCCACCGTGGAGATGGAAAATGGCATGTTA	F	Body	TBCD	0.8753114	0.9021086	-0.0267971143					
cg20022869	20	17749343	57267943	57267993	N/Shore	GCCAGGGTGGTTCTCTTTACAGTTCTAGCAAGCACCTCCAAGGAGCCCG	R	TSS1500	NPEPL1	0.7035243	0.7611729	-0.0576485571					
cg20026673	7	18754384	6389919	6389969	S_Shore	CGGTGCTCAAGGAGGGCATGCAATGTGCACTGAAAGGAAAAAATAGCTTC	R	TSS1500	C7orf70	0.6338457	0.7200343	-0.0861885571					
cg20031845	7	61742302	50306663	50306713	N/A	ACATTAAACTGTGTGCATGTTTCAAAGCACACCCAGGACAGAGGCTCTCG	F	N/A	N/A	0.6879457	0.7834286	-0.0954828571	0.721205	0.7834286	-0.062224		
cg20036706	10	2869362	131711529	131711579	N/A	TGCAAAGAAAACAGCATAAAGATAACAAAACATTGTCATTACCATCTTCCG	R	Body	EBF3	0.75764	0.8264043	-0.0687642857					
cg20036711	13	64789425	21622707	21622757	N/A	CGTGAGCCCCCAGTCTGAGTAGGTATTTAAATAATGTTTGTATT	R	5'UTR	LATS2	0.7187857	0.7734457	-0.05466	0.7369288	0.7734457	-0.036517		
cg20039814	8	13668424	95962383	95962433	S_Shore	AGAACAGAGGGCTAAGTTCCGTGGGTCACATGAGAGCTAGGCTGCAGCG	F	TSS1500;TSS1500	TP53INP1				0.3128063	0.1695571	0.1432491		
cg20041873	7	62734419	94286669	94286719	S_Shore	CGCAGCTCATGTCCCACTACGGCTGCTTTATTTGTAGCGCAAACGGTCTG	R	TSS1500;5'UTR;TSS1500;5'U	SGCE	0.5185343	0.5778214	-0.0592871 43	0.5446975	0.5778214	-0.033124		
cg20047677	12	67705391	113865876	113865926	N/A	TTCACCAGGTGCAACCTCTGTTGGAGAGCTGATGGCGTGTCCCAGGTGTCG	R	Body	SDSL	0.8823186	0.9162886	-0.03287					
cg20050828	12	21758349	131303094	131303144	Island	ACACAGGGATAACCGGTGGGACAGGATCTGAATCCAGAGCCACAGAGGCG	R	Body;Body	STX2	0.7000671	0.7754486	-0.0753814297					
cg20052933	14	11743310	69995128	69995228	N/A	AAAGTGATGGGCGCTCCTCCCCTGCTTCCCAAGTCTCCCCTGGATGGGCG	R	3'UTR	FLJ44817	0.8182171	0.85864	-0.0404422857					
cg20062492	7	16754356	55248572	55248622	N/A	ACAGCCACGCTTCGATGTGCAGGGTCAGTCATTACCCAGGGTGTTCCG	R	Body	EGFR	0.8040014	0.8662929	-0.0622914297	0.8400375	0.8662929	-0.026255		
cg20066227	10	66638319	16564622	16564672	S_Shelf	CGTACTTGGTGCTTACAGTTCTAGCAGCTCTGCAAGCAGCTCCAAGGAGCCCG	F	TSS1500	C1QL3	0.9238443	0.9526086	-0.0287642857					
cg20066792	20	69666428	4664695	4664745	N_Shelf	CGTCAACAGCATACAGTGGAAGTGATGCTACCTGACTACTGAGCCCAGGC	F	N/A	N/A	0.8822157	0.9221543	-0.0399385571					
cg20075114	14	42752363	95822738	95822788	N_Shelf	CGGGAACCTGGTTCTGGCCTGTCTCCCCAAAGCTTATCCACTAGGATGAG	F	N/A	N/A	0.7142843	0.7648286	-0.0505442857	0.7442688	0.7648286	-0.02056		
cg20076039	14	1669246	50448968	50448718	N/A	CGGTGCCATCTGCGCCAGAAATGCAGGGCTGCGGATTTCGAGGACA	R	3'UTR	C14orf182	0.7502671	0.7937271	-0.04346	0.7668488	0.7937271	-0.026878		
cg20091297	2	24800377	37572423	37572473	S_Shore	GACTGTAGGGACACTTCAGCGCCCCCAGCAGCATCCTTGGATGAAGCAGCG	F	Body	QPCT	0.30038	0.4194886	-0.119108571					
cg20095674	2	56660395	21067324	21067324	N_Shore	CGGGCCCAGGCTGCTACTGCGCGAGCCCAGGCCAGGCCGGCCCACTTGCT	F	Body;Body	UNC80	0.8980529	0.9287614	-0.0307085571					
cg20097268	1	63676371	110950612	110950662	S_Shore	CCCCTTGGTTTCAACTGCCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC	F	TSS200	HBXIP	0.0668828	0.0880224	-0.021139857	0.0603928	0.0880224	-0.02763		
cg20098015	22	30763312	50971140	50971190	S_Shore	GTGTGGATTCTGTGGCACGGGTGGGATAGTAGCCTGGGCCACCCAGAACG	R	TSS200	ODF3B	0.4671871	0.5406743	-0.0734871 43					
cg20098910	17	73770424	26643841	26643891	N/Shore	GCTGCCCGGCTCTGTGGTCCTGGGCAAGGCTGACCTGGAGACTTGGGGGACG	R	N/A	N/A	0.86608	0.9028386	-0.0367585571	0.885565	0.9028386	-0.017274		
cg20100801	12	38749342	95987054	95987704	N/A	GTCCTTCATTGAAGACGCCTCTGAGTGGTTATCAACAATGCCTACCTCACG	R	N/A	N/A	0.8086586	0.8982357	-0.0895771 43	0.8574888	0.8982357	-0.040747		
cg20111269	12	26643348	107972344	107972414	N_Shelf	AAACCACGCCCAACTGCTCAAGAGCACTCTCTGGGTATAAGTTTCAGAGGCG	F	Body	BTBD11	0.8153014	0.8765871	-0.0612857 14					
cg20120614	10	17621402	34915830	34915880	N/A	CGTGTTCCAGACTTTCTAGGCTCAGAGGATGACACGTCATCTTCGCCTGG	F	Body	PARD3	0.8545057	0.9194171	-0.0649114297	0.8944475	0.9194171	-0.02497		
cg20136100	11	17733455	63974860	63974910	Island	ACTCTCTGTAGCAGCCGCAGCCATGGCGGGGGATGAAGACAGCCTCCGG	R	Body;Body	FERMT3	0.5417686	0.6233171	-0.0815485 71	0.5889125	0.6233171	-0.034405		
cg20136609	1	20709327	2725823	2725873	N/A	CCTGGGACAGCAGGTTGGGGGAGCACGAGGGCTGTGCCCCGCG	R	N/A	N/A	0.8004071	0.8503986	-0.0499914297	0.8271475	0.8503986	-0.023251		
cg20138861	3	59727418	169775992	169776042	N/A	CGAGCTTACTTCTCTCGTGTAGCAGGCCTGGGTGGGTATTTCAGGCCACT	F	5'UTR	GPR160	0.8445271	0.8852343	-0.0407074 43					
cg20139706	2	13687486	237068750	237068800	Island	CGTGCAGCTCTGGGCCGCACACTGGCGTCCTTCGGTGCCTGTTCCAGAGA	F	N/A	N/A	0.2780214	0.20455	0.073471429	0.2623488	0.20455	0.0577988		
cg20142501	17	21760453	791118	791168	N/A	GCTAGTGGGTTGTCATAGATCCAAGGGTTTAAACTCAGGCCTCCGTGACG	F	Body	NXN	0.7508057	0.8342829	-0.0834771 43					
cg20142890	6	58802373	56637368	56637418	N/A	CGTACCTATTCTTTGTCTCACATCTGTGTCACATCTGACCTGAGTGCAC	R	Body;Body;Body;Body	DST	0.8343314	0.88668	-0.0523485 71					
cg20146177	8	39684392	122639115	122639165	N/A	TGGCTGAGAGTCCCAGGAGGCATCAGGGCCTAGTTAAAAGCTGCTGGTCG	R	Body	HAS2	0.6236443	0.7413971	-0.117752857					
cg20150565	20	42731454	47893809	47893909	N/Shore	ACCCAGGGAGCCCACGGTCCCTAATGGAAATGTTATGGGGTCAGGGAGCG	R	TSS1500;TSS1500;5'UTR;TSS	C20orf199	0.1591714	0.20997	-0.050798571					
cg20151982	11	20703437	122311658	122311708	N/A	GAAAAGCAGGGCATTGGCTCTGCTCTCCTCCTCCTCCTCCTCCTCCTCCT	R	N/A	N/A	0.1957029	0.2768429	-0.08114	0.2252138	0.2768429	-0.051629		
cg20162076	6	57676454	6588089	6588139	N/A	TATTCTGCTGCAGGACAGCAAGGTTTCTCAGTCTTGATTCCTCAACCCCG	F	TSS1500;Body	LY86	0.8094514	0.8485243	-0.039072857					
cg20162240	10	68606306	129733373	129733423	N/A	CGCGTGACTGACAGTGCTGTCTCCCCCAGCAGTCCCCTCTGAGTCTGTCG	F	5'UTR	PTPRE	0.8237057	0.87977	-0.0560642 86	0.8092275	0.87977	-0.070543		
cg20169734	3	50735449	47307826	47307876	N/A	CGTATGAGTATTTGCATGAGTATTTCAAATAAATATTTGTATGAGTGTAT	R	Body;Body;Body	KIF9	0.9143243	0.9359386	-0.0216142 86					
cg20170777	17	29716444	13972099	13972149	S_Shore	AATTACCATTTTACCGTCTATCAAATGGGAGGACCTCCTGGAGCTGTCG	F	TSS1500	COX10	0.5192343	0.6257243	-0.10649					
cg20172777	7	37641416	134004305	134004355	S_Shelf	CAGGATCACTATTCCATATGGCAGTGGTGGAAGTTCCAGAGGTGAAATCG	F	N/A	N/A	0.8059986	0.8721129	-0.0661142 86					
cg20177485	4	54795409	908414	908464	N/Shore	TGCACGCTGGGGCTGTGTGTGTGGGCCGTGCACGCTAGGGCTGAGTGCG	F	Body	GAK	0.7007057	0.7418257	-0.04112					
cg20179942	11	66727300	61912310	61912360	N/A	CACGTGGGCAGCATCAGAATGCTTCTTAGAGCACGAGCTTTATCCCCAACG	R	Body;Body	INCENP	0.8698471	0.9054786	-0.0356314 29					
cg20181209	6	21793436	166859733	166859783	N/A	CGTGCTTCTGAAGTGGCTCTGGTCACAGGACCTTCTGGACCACGAGCCTA	F	Body;Body	RPS6KA2	0.7844314	0.8545571	-0.0701257 14	0.8180813	0.8545571	-0.036476		
cg20186396	17	24714473	80275498	80275548	N/Shore	CGCCTCCAGGAAGCCCTCTCTGAGCTCTGAGCGCCTGCGGTCTCCTGTGT	R	TSS200	CD7	0.7352486	0.7901714	-0.0549228 57					
cg20191066	17	32640352	56413977	56414027	N/A	CCGGACCTTGCTCGTCTTCTTGTCTTCAAAAGGTTTTGGGTCTTATT	R	N/A	N/A	0.4004857	0.50797	-0.107384286					
cg20196537	2	42604318	171574548	171574598	S_Shore	CCGGTCTCATTTGATCTTTTCTTCTTCTTCTGGGTGGCTGTACTAAGCGGTCG	R	N/A	N/A	0.5141714	0.6837757	-0.1696042 86					
cg20212364	4	43626493	101745102	101745152	N/A	CGCAGCTTTGTTACACCTGGGAGCTTGAAAGAAATGCAAAATCTTGGGCT	F	N/A	N/A	0.8705757	0.9171943	-0.0466185 71	0.8879863	0.9171943	-0.029208		
cg20219379	6	69734397	168374007	168374007	N_Shelf	AACATGTGCTGCTGCCTCCTGGAGTGATGCTCCCTGGGGGCAGAGCCACG	F	N/A	N/A	0.8476	0.87707	-0.02947	0.85239	0.87707	-0.02468		
cg20226230	3	14736448	9743616	9743666	N_Shore	TGGCTTCTTGCTGGCTGGCTGATGCTCCCCCTCCTCCACACCACCACG	R	Body;Body;Body	TMR14	0.8396029	0.8700129	-0.03041					
cg20227471	2	55710380	25065550	25065600	N/A	AAGCATCCCAACGTGGCTCTGTGCTCAGCATCCTCGTGCCACAAGAAGCG	R	Body	ADCY3	0.8353557	0.8585914	-0.0232357 14					
cg20238525	1	43610342	95173100	95173100	N/A	ATGTTTGTGATCTCTGACGTGGATGACGGTGACCAGGGCCAGCTCCTACG	R	N/A	N/A	0.7435271	0.8462057	-0.1026785 71					
cg20239604	7	30698372	5265722	5265772	N_Shore	CGGCAGCTGAGGAGCGTGAGGCCGCCGCCGCCGCCGCCGCCGCCGCCGC	F	Body;Body;Body;Body;Body	WIPI2	0.84904	0.8784471	-0.0298071 43					
cg20241299	10	59808426	105362799	105362849	Island	CGCAGGCATCCGCGGCACTCCCAAGGTCAGGGCAAAGAAGGATGCTGATG	R	Body	SH3PXD2A	0.8552614	0.8897914	-0.03453					
cg20247455	22	12608326	49579793	49579843	Island	CGGCTTTCACAGGGCCAAGGTGTCCTCAGCCCCGTCCTGCCCCCGGAGTC	R	N/A	N/A	0.7890943	0.8459671	-0.0568728 57					
cg20253855	7	42618454	101762511	101762561	N/A	TGAAATTAACGGCCTTGGAGGAAATTGACTTTCACCGCATCACCACGACG	R	Body;Body	CUX1	0.8571743	0.9031314	-0.0459571 43					
cg20258674	10	52661346	101088861	101088861	N_Shore	CGGCAGGCTTTCCCGGGCCTGGAGCTTCCGCGAGACCACTCTTATTTT	F	TSS200	CNNM1	0.2672443	0.2357786	-0.0314657 14					
cg20263733	3	26651415	130616293	130616343	S_Shelf	CGCCAGAGCAATTGGTAGATACAGTTAACTTGGATGAATTGAGTGATGC	F	Body;Body;Body	ATP2C1	0.9293857	0.9530743	-0.0236885 71					
cg20267828	6	24704473	128222390	128222440	N/A	TTTTGCTACCATAGTAGATGCACACCTGGATTAACAAAGGACAGAATGCG	F	5'UTR;TSS200;TSS200	THEMIS	0.8297429	0.8913314	-0.0615885 71					
cg20268967	2	71646324	180730512	180730512	S_Shelf	AGCTCCAATAACTAGTATCTTTTGATTTCAAATTGTTTTTAAATCG	N	N/A	N/A	0.5399786	0.6335414	-0.0935628 57	0.5528413	0.6335414	-0.0807		
cg20271511	22	70797489	17566989	17567039	Island	TTTGTTTTTTTCCTTAAGATGGTCCTGGCTCACAGAAAGGCCACTACCCG	F	Body	IL17RA	0.4967629	0.6343543	-0.1375914 29					
cg20278154	12	44643375	104914611	104914661	N/A	CGCCACTGGCTGCAGACTGTCTGACTTCCTGAGCAGATACAAGCAAAGGC	R	Body	CHST11	0.6852657	0.7619014	-0.0766357 14					
cg20278383	13	44614386	96086098	96086148	Island	CGCCCTGGACATGTCGCCGCCCTTCTCCAGTGACACTGTCCGGTCAGAA	R	1stExon;1stExon	CLDN10	0.9184529	0.9447957	-0.0263428 57					
cg20278854	3	34753434	195929942	195929992	N/A	CCGGCTTCCTGGGTGCCTGGGCCCTTCTCCAGGTGCCCTCTCCTGCCTCT	R	Body	ZDHHC19	0.5705914	0.6568857	-0.0860942 86					
cg20282158	8	55654324	13425120	13425170	N/A	CGGAGCTGGCCCTGTCTGCCTTTCTGAAACAAAAGAAGACTTTACTGGAG	F	1stExon	C8orf48	0.6421343	0.7138914	-0.0717514 43					
cg20285745	12	66734449	117798627	117798677	Island	TGAGCTTGGGCAGAGCTACAACGGTCCCCAGGGACTGGCATCCCCCAGCCCG	R	5'UTR	NOS1	0.1304509	0.18428	-0.0538293 43	0.1572563	0.18428	-0.027024		
cg20288927	1	45714320	25243248	25243298	N/A	CGGCCGATAGAGGCATTGCTGCGCACCCCGACAGCTGACCCCTCCCGCG	R	Body;Body	ZUBX3	0.6904857	0.7354343	-0.0449485 71					
cg20291636	6	58647414	138656168	138656218	N/A	ATGCCGCATTTGCCCTTGGTCCATCAAGTGCTGGGGACGCTGAAGCAGCG	F	Body	KIAA1244	0.8102814	0.8474343	-0.0375285 71	0.8191088	0.8474343	-0.028326		
cg20296298	2	51769423	21007420	21007470	Island	GACCCCTCTTCCTGGAGCCCAAGAAGAGCTTCCAGACTCACAATTTGGCG	R	N/A	N/A	0.7388657	0.8757071	-0.1368414 29	0.719215	0.8757071	-0.156492		
cg20297017	2	51702334	21766498	21766548	N/A	GCATCTATGTGTGGGATGGGGTCCTGGCCTTGGCAACAAGGGGGGTGTACG	R	N/A	N/A	0.8034214	0.8640571	-0.0606357 14					
cg20303441	2	13742440	25496440	25496490	N_Shelf	CGTGGGCTCACGTGAACTCAGCTCTCATTTCGTTTCTCTCCAGGC	R	Body;Body	DNMT3A	0.5140257	0.5859814	-0.0719557 14					
cg20307448	11	42788405	134132814	134132864	N/A	CGGGGCTTTTCTCTAAGGTTATCGAGTACGTGGTTCTGAGGGATCCAAGA	F	Body	ACAD8	0.8669414	0.8940529	-0.0271114 29					
cg20310974	8	19750502	134846823	134846873	N/A	CGGCTTTAAGCTCTGGTCAGGGAAACGAGGCAAAAGCAGCCTGAGAATT	F	N/A	N/A	0.8872943	0.9232829	-0.0359885 71					
cg20317521	17	24714371	79026632	79026682	Island	TTGGCCCTGGTGGTGGTGGTGCAGTATAGTGAGGGTGTACCCCG	R	Body;Body;Body;Body	RAIAP2	0.75968	0.8120186	-0.0523857 14	0.7833675	0.8120186	-0.028651		
cg20325454	2	12775407	74078577	74078627	N/A	CGCTGGCACCTCTTGTGGCCTTTAGCACGTTCTGCCCCAGGTGAAGTTAT	R	Body;Body	STAMBP	0.6752271	0.76958	-0.0943528 57					
cg20331980	6	72625371	149554503	149554553	N/A	CGGTGAGCTTTCAGGATCAACTTTCTTGGCCTACAGTAGAGGCGTCTAG	R	N/A	N/A	0.8072743	0.8720943	-0.06482					
cg20333292	14	42664417	105532062	105532112	N/A	GCCAGGCCTCCGAGCTCCAATAGGAGGTCCTGGGGCCTGGGCCTGGCG	F	TSS1500	GPR122	0.6824886	0.7639457	-0.0814571 43					
cg20336222	7	69787429	64164953	64164953	N/A	GCACATAATCATGAAAATATATGACTTTCAGCCAGGCGCGGTGTCTCG	F	Body;Body	ZNF107	0.8263586	0.8540729	-0.0277142 86					
cg20337996	12	28626323	124780809	124780859	S_Shore	CAAACCCAGACAGGATTCCTTCCTTCCCGGGATGTTAAGGCATGTTGACG	R	5'UTR	FAM101A	0.4897114	0.6605857	-0.1708742 86					
cg20351495	1	69605330	2408494	2408544	N_Shore	TGAAGGGGTGCCTTGTGCTCTGGGGGTCAGTGGTGCTTGCAGCCCAGGCG	R	Body	PLCH2	0.8275786	0.8814214	-0.0538428 57					
cg20355401	17	61604488	4311576	4311626	Island	CGCCCCCGCCCCCGCACCCCTGCCCCCGCCCCCGCCCCCGCCCCCGCCC	F	Body	DCAKD	0.8326457	0.8615429	-0.0288971 43					
cg20359413	3	32611355	50316909	50316959	S_Shelf	GTTAGGAGTGGGTCAACTACAGGCTGTGCTCAGGTGGGTGTGGGCATCCG	R	Body	C3orf45	0.8790457	0.9174543	-0.0384085 71					
cg20360285	7	49674415	47989345	47989395	N/A	GTTCAAGGGGTCTGTGTTCCCATCTGAGAAAGAGCTTGTGCCTGAAAACG	F	TSS1500	PKD1L1	0.7444443	0.7977243	-0.05328					
cg20365566	13	31621354	24616658	24616708	N/A	CATTGCCTGCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCC	R	N/A	N/A	0.8873371	0.9240243	-0.0366874 43	0.9027088	0.9240243	-0.021316		
cg20372666	10	39611497	71149910	71149960	N/A	CCTTCCAGGTGCCAGGAAGAACTTTTCATTCATTGTTAAGCCACTTTTCG	R	Body;Body;Body;Body;Body	HK1	0.9135729	0.9484257	-0.0348528 57					
cg20375844	5	56725371	87986922	87986972	S_Shore	CGGCCGCCTCCCGCTCCTGAAGCTCAAATTCAAGTCGCGTTAATTAACACCCG	N	N/A	N/A	0.0998053	0.1389929	-0.0391875 71					
cg20382418	20	31726410	6020535	6020585	N_Shore	CGGAGCCTCCAAGAGGAACCAACCCCACTGATGCTTTGATTTGGGATTTC	F	3'UTR;3'UTR	CRLS1	0.8160743	0.91074	-0.0946657 14	0.8769988	0.91074	-0.033741		
cg20386404	1	54662337	214577721	214577771	N/A	CGGACTTGGTGGTGGTCTACAGAGTGGCTAAAGGTTCTCCTGTGCACAGG	F	Body	PTPN14	0.6449986	0.7544629	-0.1094624 86	0.7022225	0.7544629	-0.05224		
cg20389653	1	55779487	16766715	16766765	N_Shore	CTAAACTTTACTTCTTTGAATACAACTTGTTGTTGAGGTTTGGCCACACG	R	TSS1500;TSS1500;TSS1500	NECAP2	0.76795	0.8524614	-0.0845114 29					
cg20390119	15	37688501	37161314	37161364	N/A	AAGTTAACAGAATGATGGATCTCAAATGCAAACACTGAATCTCTACCACG	R	Body	LOC145845	0.8776043	0.9199757	-0.0423714 29	0.8992988	0.9199757	-0.020677		
cg20398880	6	45636373	41068772	41068822	Island	GATCGGCTGGGCGACCTCAATAGGGCGCCTCATGGATTTGGCTGCTCACG	R	3'UTR;3'UTR;TSS200	PEYA	0.7324143	0.83625	-0.1038357 14					

cg20814312	2	69649412	133339746	133339796	N_Shelf	CGGATCACCTTGAGCTTTGACTCACAGCCCAGACGTGGCCACCTGCAGAT	R	Body	GPR39	0.7327114	0.8202414	-0.08753	0.765115	0.8202414	-0.055126
cg20820876	2	65721336	98365143	98365193	N/A	CGCCCAGCTAGCATATGGCAGTGAACAGGGAGTGAGGGGATGGCCCAGAA	R	N/A	N/A	0.8440557	0.8964329	-0.052377143	0.8561663	0.8964329	-0.040267
cg20825216	11	71772410	2274400	2274450	N/A	CGCTTTTGTCTTGGGTTTTCAGCAGTTTAAATGTGATATGCCTTCAGTTT	R	N/A	N/A	0.8024829	0.84257	-0.040087143	0.8151688	0.84257	-0.027401
cg20843202	3	40708442	99903438	99903488	N/A	CGGGAATTTTCAGCATGACATTTGAACTAATTTGAGGGTGGCAACTAG	R	TSS1500;TSS1500	TMEM30C	0.7389971	0.8255643	-0.086567143			
cg20843650	17	40611446	422568	422618	N/A	ATATCCAGATACTGCGCTGTCCCCCGTGGGCCATTCTGGCCCAGACTTCG	F	Body	VPS53	0.9067429	0.93892	-0.032177143			
cg20851317	18	10614303	47792341	47792391	N_Shore	ATGTCTGTCCCCCATGCAGTGGCGAGTGTGTGTTATGGAAAGGGCACCCG	F	Body	CCDC11	0.5505429	0.6387514	-0.088208571			
cg20860806	15	17733408	49267825	49267875	N_Shore	TGTTGCTAAATCCTTCCATACAAAATGCTAATTGCAGACGCCAGATAGCG	R	N/A	N/A	0.5683643	0.6842257	-0.115861429			
cg20861607	15	23643346	32323114	32323164	S_Shore	AGGGATTGTAGTTCTTGACCAGCTCCTTGTAAAGCTTCCTCTGGAACTCG	F	Body	CHRNA7				0.1100286	0.0749297	0.0350989
cg20865082	3	42690449	139557385	139557435	N/A	TTTGCATAATTCTACCTGCCTGCCTTTGGTTTAATTCAGGAATGGCTGCG	R	N/A	N/A	0.8536843	0.8918086	-0.038124286			
cg20870000	8	42610415	38584896	38584946	N/A	CGCAATGCAGGTGTTCTTGTTCTTAAACTGTGGGCGGTAGGGTGCTGCCT	R	TSS1500	TACC1	0.7920814	0.8518371	-0.059755714	0.8200063	0.8518371	-0.031831
cg20871964	2	14771406	234844925	234844975	N_Shelf	CTTGGGCTGCCTGAAGGTGTCCAGGCGTGACCTCAGAGTGGATTTCG	R	Body	TPPM8	0.8213557	0.90347	-0.082114286			
cg20872472	1	74775385	36600284	36600334	N/A	CCAGCATGGGAGTTTGAAGTATGTATGCGGCCAGACATCCTTGGCCAACG	R	N/A	N/A	0.9134143	0.9497443	-0.03633			
cg20896431	7	73665366	142879966	142880016	N/A	CGCTCTAGTTGTGTGATGTTGGCCAAGTTATTTAACCTCTGTATGCCTTA	F	TSS1500	TAS2R39	0.6704357	0.7500271	-0.079591429	0.695345	0.7500271	-0.054682
cg20908789	8	40782418	11551964	11552014	S_Shore	GCTGGCGTGGCCTCTCAGGGATCCTTTCTTTTCTTCCCCCAGAACATTGCG	R	N/A	N/A	0.7378971	0.8138757	-0.075978571	0.77501	0.8138757	-0.038866
cg20909017	12	73895469	54805345	54805395	N/A	CCTGGGCTGTTGGGCTATCTGGGTGATTCAGGAATTAGAGAGGCAC	F	Body	ITGA5	0.6480271	0.7095157	-0.061488571			
cg20924735	2	71649323	202565040	202565090	N/A	TTCTAGCAAAGAGCAAATTAACTTTCTGACCCCAATAACCCAAGGACACG	F	3'UTR	ALS2	0.73081	0.8217186	-0.090908571	0.77687	0.8217186	-0.044849
cg20935223	7	40765400	6208238	6208288	N_Shore	CGCCAGCTGGACCAGCCCCTCCAGGGCCCCTGCGCTTGGCACCCGGCGC	F	Body	CYTH3	0.8631486	0.9014286	-0.03828			
cg20940398	5	64720335	150000103	150000153	N/A	CGAGGGTTGTGCCTTGGCCACCCTGTTCTTCTGGAATTATAGGAGTAAA	F	Body;Body	SYNPO	0.84827	0.8889314	-0.040661429	0.8613488	0.8889314	-0.027583
cg20944315	1	64655509	200839460	200839510	N_Shelf	GATGTGGGCACCGCTCACCAGCAACCACATGCTCAGACATTAGAAAAGCG	R	N/A	N/A	0.7614086	0.8288157	-0.067407143			
cg20946041	3	32779462	126753478	126753528	S_Shore	CGGGCCGAGGCCGGAGCACCACATCCACCTCGCCCCAGAGAGGCTCTGCTC	F	3'UTR	PLXNA1	0.8818443	0.9134629	-0.031618571			
cg20951054	14	19712319	2157056	2157106	N_Shore	CTTGTCACCATTCAGGGTCTCCTCACTGGGACTGTCACTCTGGAGCTTCG	R	5'UTR;Body	ZNF219	0.8651771	0.8996857	-0.034508571			
cg20955839	2	47639415	108922863	108922863	N/A	CGTGGATTATGGAGTTGGGCCGCAATTAATCTAGCCGGATTTTATTTAA	R	Body;Body	SULT1C2	0.6671729	0.7434814	-0.076308571	0.68252	0.7434814	-0.060961
cg20956738	18	50802326	55108537	55108587	Island	CGCCGGATCAAGTTCCAGATCAATGAAATCTGGGTCCACACGTTTACGTT	R	Body	ONECUT2	0.3486014	0.4939129	-0.144551429			
cg20969822	19	66796489	41787138	41787188	N/A	CTATGGAGGCACTGGGAAGAAGTCCACCAATAGCCGGTTTGAAAACTACG	R	Body;Body	HNRNPUL1	0.7541614	0.8266186	-0.072457143	0.786125	0.8266186	-0.040494
cg20972199	11	18733466	69065333	69065383	N/A	TTCTGGGTTCTGGGGAAGTCTACGGTTGGGAAGTCTCCCTTGG	R	Body	N/A	0.56733	0.6474071	-0.080077143			
cg20975414	1	13605318	145715571	145715621	S_Shore	CGTGAGCCCCCAGTCTGAGAACAAGAAAGAAGAACTTCTGTCTCGAGGTA	R	TSS200	CD160	0.6579129	0.7411543	-0.083241429	0.7040875	0.7411543	-0.037067
cg20975835	11	49681371	64107374	64107424	N_Shelf	CGCAAGGCCCAGAGCCCTTTGAGGCCCTCGAAGGTCCCAGGCTGGGGTC	F	TSS1500	CCDC88B	0.6063629	0.6849943	-0.078631429			
cg20983854	3	54727451	111315344	111315394	N/A	CGAAGCAACTGTGGCAGTCTCAGAACTCTGGTTAACGTCTAAAAATTTTG	F	Body;TSS1500;Body	CD96	0.7176029	0.78482	-0.067171143	0.7312225	0.78482	-0.053598
cg20985521	1	57602506	55168880	55168880	N/A	CGTTGCCCTTAATTCAGGGCACCGACACCCCTCAGTTAGGCTATTGGCCC	F	Body;Body	C1orf175	0.78871	0.85336	-0.06465	0.81637	0.85336	-0.03699
cg21000999	21	50732309	27253974	27254024	N/A	CGGGGGTCTAGTTCTGCATCTGCTCAAAGAACTTGTAGGTTGGATTTTCG	F	3'UTR;3'UTR;3'UTR;3'UTR;3'U	APP	0.79138	0.8486014	-0.057221429			
cg21006526	21	52765392	38574643	38574693	N/A	ACAGAAGCTGCTAAGGAAGGCAGCGGAGTTCAAAGAGCAGGCTCCAACCG	F	3'UTR;3'UTR	TTC3	0.7751014	0.8246143	-0.049512857	0.7897288	0.8246143	-0.034886
cg21013710	11	46686496	15128655	15128705	N/A	GTGCACTTTCTCCCACGGCGCAACCTCTGACCTTGTCTGAAACTCCG	R	N/A	N/A	0.7591857	0.8153971	-0.056211429			
cg21024969	6	45766337	163994355	163994405	N/A	TACATGTCAGCTGTACGATAACATACAAGCGACACTCCCATCTACCCACG	F	3'UTR	QKI	0.8084586	0.8600657	-0.051607143	0.833625	0.8600657	-0.026441
cg21028785	13	25718313	51946399	51946449	N/A	TTGTTAGGCTTGCCCCTTTACTCCACAGAAACTGCTCTTGCTAAGATCG	R	Body;Body	INTS6	0.8897114	0.92216	-0.032448571			
cg21033494	10	42739447	51550114	51550164	N/A	TTTAAATAATGGTGCTTTGGGCCAGCTGTGTGCTGGTGCTGCTCTCG	F	Body;Body	MSMB	0.8976914	0.9301357	-0.032444286			
cg21038264	4	47713450	780856	780906	S_Shore	GGGCAGGAGGGTCAGCTGCGGGTTGACTGTTTCTCCCCACCTCTGCCACG	F	Body	CPLX1	0.4882057	0.6343586	-0.146152857	0.5672313	0.6343586	-0.067127
cg21038740	2	56640485	155390332	155390382	N/A	CGATAGTGGCTGGTAAATAAAGGATCCAGGACTTCCCTGACTGAGAACAC	R	N/A	N/A	0.74204	0.8232871	-0.081247143			
cg21048260	6	53613347	32039911	32039961	N/A	CCCTGAGGGTGAATTCGACTCCTTTGTGGTTCAGTAGCAAAGACAGGGACG	F	Body	TNXB	0.8748714	0.9087671	-0.033895714			
cg21052656	11	10691452	67250046	67250096	N_Shore	CGGAAACTGAGTACTATGCTTTGTCCAATTAATATCTCGATCAA	F	TSS1500	AIP	0.64316	0.7372871	-0.094127143			
cg21060736	15	19784473	73618666	73618716	N/A	CGCACAACTGCTGCACAGAAACCCCACGGGCAAATGAGGGCTGAGAAT	F	Body	HCN4	0.53155	0.60996	-0.07841			
cg21069005	8	18710345	11537430	11537480	Island	GGTAACAGTATTGTTAACTGGCCATGAATTTTAATCCCTGTTGTGTGTCG	R	N/A	N/A	0.4362943	0.5437271	-0.107432857			
cg21073212	20	10709401	30866501	30866551	S_Shore	CGAAGCTCCAGGTAGAAAATGTAGACATGACCCCAGGTATCTACAACGGGT	R	5'UTR	KIF3B	0.7662829	0.8557429	-0.08946	0.8012575	0.8557429	-0.054485
cg21073511	8	72647400	143373628	143373678	N/A	TCGCTTCCACGGGGGAAGCTCGTGGGTTCTGTGGGTCAGAACTTCCAACG	F	Body	TSNARE1	0.8138443	0.8597229	-0.045878571			
cg21074877	14	10735510	23481968	23482018	S_Shelf	CGCCCGGCCAAAAAAAATTTATTTTTAAGTGGCACGATCTCAGCTCACTG	R	N/A	N/A	0.9005429	0.9394171	-0.038874286			
cg21078322	6	40670388	134491163	134491213	N/A	CGCTCGTTCAGAGATAGCACCACGTTGGAAGGAAGAAATAAAATGAAAA	F	3'UTR;3'UTR;3'UTR	SGK1	0.6615886	0.7517329	-0.090144286			
cg21080533	6	48693445	49755105	49755155	N/A	CGAGATTGACGGTCTTGGAGCACATAGACCAATACAAAACTTGCTTTCCAG	R	TSS200	PGK2				0.7168113	0.7973114	-0.0805
cg21092462	1	23709499	211307761	211307811	S_Shore	AAGAGAGTTACATCAGCACGCTCCCCTAAGACTTGTTGGGGGTGAATCCG	F	TSS1500;TSS1500	KCNH1	0.2396943	0.2853114	-0.045617143			
cg21097733	17	55607508	46623729	46623779	S_Shelf	CGGATGGAGAGGAGATGAGGCGATCAATCTTAGCCCCCTGACAGCTCCCT	F	TSS1500	HOXB2				0.573875	0.5271286	0.0467464
cg21099332	5	67614347	39270715	39270765	N/A	ACTCTCTGGTCTCCTCTTTCACTCTCAAGCTGCACCATCTCTTCCCG	R	N/A	N/A	0.7068143	0.7719029	-0.072288571	0.7243375	0.7791029	-0.054765
cg21099575	13	37627412	99092226	99092276	N/A	CGCTCTCCTCAATCTGTGGGCAAGAGAAGATAACGTCACCATGAGGACG	R	Body	FARP1	0.8319243	0.8697786	-0.037854286			
cg21100077	13	45635359	100627366	100627416	S_Shelf	CGCCAGCTCGAGCATCCCCAAGAATCGGGTCCCGTGGCCTCCAGGCAGCT	F	N/A	N/A	0.2370857	0.1966214	0.040464286	0.2367125	0.1966214	0.0400911
cg21104449	3	36766452	196485238	196485288	N/A	CGGCTTGGTTTGCACAGGATCTGGGCGCATGTGAGGGAGTGTATGT	F	5'UTR	PAK2	0.8496586	0.8996843	-0.050025714			
cg21106136	3	47808503	194405973	194406023	N_Shore	CGGACGGGGAAAAGCCTTATTCATTGACGGTATTCTACAGTAGTCACCCC	F	TSS1500	FAM43A	0.7597614	0.8022786	-0.042517143	0.7439875	0.8022786	-0.058291
cg21107579	18	64708372	74728959	74729009	N/A	TGTGGCCAGGTACTTGGATCCGTGCCTCTGGGAGGGTCTCTTCTGTGACG	R	1stExon;1stExon;Body;1stExo	MBP	0.8879843	0.9309	-0.042105714			
cg21113768	6	51748328	144386848	144386898	S_Shore	CGAAGACAACAACATAAGGAAAGGAACTTTCCTGTTCAAGGCACTTCATT	F	TSS1500;TSS1500	PLAGL1	0.8889614	0.9308871	-0.041925714			
cg21113846	7	16692460	837536	837586	N/A	CGGGACGCCCTGCCTGTCCAGGTGGTTCACTGTCATATCTGCAGCAGGAT	R	5'UTR	KIF3B	0.7850257	0.8642243	-0.079198571			
cg21122466	6	47759506	99323548	99323598	N/A	CGGACCCTGGATCTGTGGAGATGTAAGAATTATACTGAAGTGAATAGC	R	Body	FBXL4	0.8576471	0.8843343	-0.026687143	0.8553338	0.8843343	-0.029001
cg21142904	1	41759324	158047439	158047489	N/A	GCTCATGTCTGTGCTGCGATGCCCTATATTTCCTGGCGGCCCACACATCG	R	Body	KIRREL	0.72104	0.7558357	-0.034795714	0.7382913	0.7558357	-0.017544
cg21147203	5	74664385	134529059	134529109	S_Shelf	GCCAGGCCTGGTCTCGGCCTCAGAGAGACTGACCAGGAGTCATTCTCCCT	R	N/A	N/A	0.6065571	0.7026714	-0.096114286	0.6650075	0.7026714	-0.037664
cg21149708	8	21643387	21549935	21549985	N/A	GAAGACAGCAGGAAGCTTGAGGGCCCACGGTGCTGCAGACACACACCCG	R	3'UTR;3'UTR;3'UTR	GFRA2	0.5948429	0.6527771	-0.057934286	0.6103075	0.6527771	-0.04247
cg21150901	17	50749327	34957586	34957636	N_Shore	TTCCTGCCTTCCTGGATCGCTGGGGGGCTGAGTGCTGCGCAAGGAGTCTCG	R	TSS1500	MRM1	0.4089843	0.53033	-0.121345714			
cg21151355	1	59618326	35246607	35246657	N_Shore	CGTGCAGAAGAGTGTAGATAGACATACTTCCACAGGTTAAGACTATATAGT	F	TSS200;TSS1500	GJB3	0.4003271	0.5600357	-0.159708571	0.4844375	0.5600357	-0.075598
cg21155852	7	22736469	2048760	2048810	S_Shelf	CGAGCTGGGTGTCACACACGCCTTTTCCGGGTGCAACGTGTCCCCGG	R	Body;Body;Body	MAD1L1	0.8778186	0.9046743	-0.026855714			
cg21157107	9	74642378	110399894	110399944	Island	CGGACCCCGACCCTGACCCCGAACTTGACCTCGGGACCCAGGCCGACTCA	R	N/A	N/A	0.2414086	0.1934671	0.047941429	0.2244663	0.1934671	0.0309991
cg21158528	1	47721459	211501629	211501679	S_Shore	CGCCTAGCTTCTGTAAAGGTTTTTGATTTTGTTTACAGTTTACTGTTTTTGT	F	5'UTR;5'UTR	TRAF5	0.8050729	0.88589	-0.080817143			
cg21167985	13	58740467	113540421	113540471	Island	GCCCTGGCTCTGCCAGACACAGCCTGCTGCCTCCTCCTTCCTTCCTTCG	F	3'UTR;3'UTR	TP11A	0.2219929	0.131772	0.090220857	0.2282875	0.131772	0.0965155
cg21170304	9	19778466	138879603	138879653	N_Shelf	CAGGATGACCTTGGGTCACTCTGGGATGTAAGGGTTTTCCAGACTCCACG	R	N/A	N/A	0.8389214	0.8763443	-0.037422857			
cg21182416	8	15746374	86065151	86065201	N/A	GGGCCGCGGAGCAGGGGCTGCCGGCGCCTGTTGGGGAGGCTCAGGCCACGG	F	N/A	N/A	0.8083271	0.8499157	-0.041588571			
cg21195376	1	55605357	204449827	204449877	N/A	TGACTTCCTTTGGCCCTTCTCAGAGCTGAGCAGGTGGCTGTCAGCTCCGG	F	5'UTR	PIK3C2B	0.7705729	0.8332029	-0.06263			
cg21199854	3	40778483	52724044	52724094	S_Shelf	TTGAATTGCCTGCTTTGCTTGAAAACTTTCCACCTTCTCAACCG	F	Body;Body;Body;TSS1500	GAL3	0.75077	0.8137486	-0.062978571	0.7796638	0.8137486	-0.034085
cg21207636	8	43751475	142232992	142233042	S_Shore	CGCTCCAGTCACGCGGTGCCAATTCATCCCACAGGGGACTTGAGATCTGT	F	Body	SLC45A4	0.8977886	0.9337257	-0.035937143			
cg21210529	5	74806466	137588237	137588287	N/A	CGAGGGGGCAGGAGCCTTCTTCACAAAGGAGAATGACTTTCTAGGCTGCC	F	3'UTR	GFRA3	0.8002157	0.8676471	-0.067431429			
cg21222743	6	21543356	31543395	31543395	N/A	CCTCCCCCTGCTCCATCGTGTCCTTTCCAGCGGGAGAGGA	F	1stExon	TNF	0.4992629	0.5633214	-0.064058571	0.530315	0.5633214	-0.033006
cg21225548	9	67791393	100864335	100864385	N/A	CTCAGAACGTTCGCTCCCCACTGCTGTTGTTTCTGTTTTCTGCTAGTGACG	F	Body;Body;Body;Body	TRIM14	0.69855	0.7918929	-0.093342857			
cg21228760	4	11744361	160322259	160322309	N/A	CGCCTCAGAAATGCACCTCCCAGGATCAGAACAGTAGCTGCAGCATCTCC	R	N/A	N/A	0.4929371	0.6339329	-0.140995714	0.559245	0.6339329	-0.074688
cg21230231	9	48801373	138823290	138823340	Island	CAGGCCTTTGGGGCTGGTGGGCCGTCCCGGCCGTCCCGCTCTGGAGCACG	F	N/A	N/A	0.9193629	0.9470414	-0.027678571			
cg21234032	6	44734473	143607364	143607414	N/A	CGTGGACTGATTCTACCCACAATGGAAGACAGGCCATCAGAAAGTACATA	R	Body	AIG1	0.8798971	0.9271143	-0.047217143	0.9027425	0.9271143	-0.024372
cg21235754	2	35656469	23747094	23747144	N_Shore	CGGGCACTTGGGCCTGGGTGGCTCTGCCACTCCCTAGCACAGCACTGAGC	R	5'UTR	KLHL29	0.75126	0.8037371	-0.052477143	0.7764225	0.8037371	-0.027315
cg21237591	11	61625409	2162510	2162560	S_Shore	TGCAGTGGGTGGCGGCGAGCCGGGAACATGCCCAAATTTTGGGGAACG	R	Body;Body;5'UTR;Body;TSS2	IGF2AS	0.6013586	0.6765157	-0.075157143	0.616665	0.6765157	-0.059851
cg21238254	4	38777417	1988851	1988901	S_Shore	CGGCACCGGGCCAGCCCAGGATCTCTCCACGTCTTCTCCACCAG	F	TSS200;Body	MR043	0.9059157	0.9453171	-0.039401429	0.9282475	0.9453171	-0.01707
cg21241675	9	72635328	93925541	93925591	S_Shelf	CTTCAGCATGCTGGCATGCATGTGCCCTGCTCTTTCTCCTGTGATCATCG	F	N/A	N/A	0.6887214	0.7626571	-0.073935714			
cg21242009	6	57660387	6894182	6894232	N/A	CGCTGGTCTACAGTCATGTTTTCTAAGCTTGAATGCACATCCGAATCCCC	F	N/A	N/A	0.92863	0.9582843	-0.029654286			
cg21243150	15	74704492	40751171	40751221	N/A	AGCCGTGGTCTGCATCGTGCTACCTGGGGCTGCTCCCCTGCAAGAAGCG	R	Body	FAHD1	0.8926288	0.9260829	-0.033434286			
cg21243951	2	62627465	235951579	235951629	Island	CTACCAGGGCAGGGTGGGCCCTCGTGCACCAAGAACGTGCTGGTGGTCG	R	Body	SH3BP4	0.8932486	0.9281214	-0.034872857	0.9100413	0.9281214	-0.01808
cg21244116	9	18638476	140729241	140729291	Island	CGCTCTCCATAGTCAAACCTGGGGAGGGAACAGAACCAAGGCTCCAAGTC	R	Body	EHMT1	0.9286186	0.9501871	-0.021568571			
cg21253130	13	20766316	32609104	32609154	S_Shelf	CAGGGCCAAATGGGCTTCAGATCTCTTGCTCCTGCACTTTGCATGGCTTCG	R	Body	FRY	0.87455	0.9070557	-0.032505714	0.8849	0.9070557	-0.022156
cg21253742	15	14769355	85305079	85305129	N/A	CAGGCCTTTGTTGGATCCTGGAGCAGCCGGCCGTCCCGCTCTGCCCTCG	F	5'UTR	ZNF592	0.47895	0.6456329	-0.166682857			
cg21268578	22	73764382	38029428	38029528	N/A	GTCTCCTTCATTCATTGGCCCTCTGCTGGGGCCTCCTATGGGTGTCTTACG	N	3'UTR;2'UTR	GGA1	0.4595057	0.6020686	-0.142562857	0.547985	0.6020686	-0.054084
cg21276022	9	3669034	136390236	136390286	N/A	ACCAGCATTTGTCTCTGATTTTTCTTTCTTTTTCTGAGACAGAGTCTCG	R	TSS200	TMEM8C	0.6954229	0.76283	-0.067407143			
cg21295295	1	54789468	156256449	156256498	N/A	ACACCTCCCCCTGTCTATATGGTTATATGTGCCTTTCGAAATCTG	F	Body;Body	TMEM79	0.9100786	0.9390671	-0.028988571			
cg21302480	1	49642409	50486893	50486943	N_Shelf	TCCATTTATCTTGAAACATTCCTTTAGCTGTGCTCTAATCTCTCCAGTCG	R	Body	AGBL4	0.4708957	0.5693514	-0.098455714	0.49862	0.5693514	-0.070731
cg21336300	12	50802312	25204332	25204382	N/A	TGGCATTCTGACTAAATGTTAACGTTTGAGAGGCATGCACAAGGCCTACG	R	TSS1500	LRMP	0.7223371	0.82772	-0.105382857	0.7671513	0.82772	-0.060569
cg21337881	17	61649406	5138645	5138695	N/A	GGGGACCCAACTGCAGTCAAAATGCTCCACTGGCCACATTTCTCAAGGTCG	F	TSS1500	C17orf87	0.7668814	0.8332529	-0.066371429			
cg21341889	8	71613306	17773367	17773417	N/A	CCGGCCGGTTCTCCTCTCTCTCTCTCTCTCTCCTTCTTACCC	N	N/A	N/A	0.8903657	0.9154614	-0.025095714			
cg21347347	8	58699461	123446268	123446318	N/A	CGTGCTTAAAGCATTTTGTTCTACTAAGGTTCTGTTGGGAAAACTTTGGG	R	N/A	N/A	0.8816829	0.9210729	-0.03939			
cg21348357	2	63648412	171574592	171574642	S_Shore	CGGTCGGGTTCCCCGGGAATTTGATGGTTCCTATAGTTGCCTGTGTCG	N	N/A	N/A	0.2940729	0.5280671	-0.233994286	0.4252575	0.5280671	-0.10281
cg21354212	2	56795311	28584981	28585031	N/A	GTGATGGCCACCGGGGGACTATGGAGACGGGGCTCTCTTCTCTCTCTCG	R	N/A	N/A	0.9033514	0.9332157	-0.029862286			
cg21356229	12	13702400	2885886	2885936	N/A	CGGTGCTCTTACACCTCTGTCCTCACAGCAGTCCTGGAAGGAGCATGCAC	R	N/A	N/A	0.9130629	0.9322829	-0.01922			
cg21364828	13	64739399	114825658	114825658	N/A	CGAGGCCTTCGCACCTGGTGTCCCTTCTGCCTAGACCCCTCCTGCGCTCTC	R	Body	RASA3	0.7796757	0.8139829	-0.034307143	0.7830263	0.8139829	-0.030957
cg21386992	21	67766366	44724719	44724769	S_Shelf	AGGGGTCAGCAGAGCCCCCGTGGTCCAGACAGGCAGAGCCTCTGTGTCCG	R	N/A	N/A	0.8868029	0.9132871	-0.026484286			
cg21399203	4	27732348	57623913	57623963	N/A	AGACCTTTGAACCTTAGTTGAGTATCTGTGGCCCTGTGAGATCTCTGG	R	N/A	N/A	0.7765929	0.87131	-0.094717143			
cg21404980	8	74747422	144599027	144599077	N_Shelf	CGGCAGCCCGACAGGGCCATAAGTCACCCTAAGCAGCCATCCGCAGTGCA	F	Body	ZC3H3	0.6469343	0.7253414	-0.078407143			
cg21405799	16	31757360	84002843	84002893	Island	GGTAGGGGTTGTTAGGGGTCTCAGAAAAGTATCGCTCCCGGACAGGATCCG	F	Body	NECAB2	0.5413986	0.7146357	-0.173237143			
cg21408813	13	34738319	52736898	52736948	S_Shelf	CCGTGAATTTAAACCAAATGCCTCCTTAAAAGGAGTTGCTGCCCTCCCG	N	N/A	N/A	0.5835143	0.7105986	-0.127094286	0.6190988	0.7105986	-0.0915
cg21410120	7	60785362	540775	540825	N/A	CGGATTCAGGCTTGTGGCTGCGCAGGCGCACTCCAAATGCTCCCTGAACT	R	Body	PDGFA	0.8740929	0.90926	-0.035167143	0.8889063	0.90926	-0.020354
cg21413219	1	39752385	6299374	6299424	N_Shelf	CGCAGACCCCATGCAGGGACCTGCTTTCCCGCCACAGAGGAAAGCAATCT	F	N/A	N/A	0.5200986	0.6489586	-0.12886	0.5676638	0.6489586	-0.081295
cg21422361	7	60728398	1884392	1884442	N_Shore	CCGCTGCAACCGTGTGCCGCCGCTGTGCCAGCCTGTGCCAGCAGCC	F	Body;Body;Body	MAD1L1	0.8688257	0.91176	-0.042934286	0.8818288	0.91176	-0.029931
cg21429394	12	16602411	100750899	100750949	N/A	CGCTCTGCAGCAGCCTGTGGCAGCTGTCTCAGGCAGCCACTCTCAGACTG	R	1stExon;5'UTR;1stExon;5'UTR	SLC17A8	0.4350086	0.5261786	-0.09117			
cg21441868	12	30613509	133125416	133125466	N_Shore	TGGACGGGGGTGAGGGCCCTGCCGATGTGCCAGGGGAATGGTCACCCCG	R	Body	FBRSL1	0.8980786	0.9245871	-0.026508571			
cg21445527	4	18741402	737453	737503	N_Shore	GGGAATCCCTGCATGAGGCCTTTTCTTAAAGAGCTGGCGCTGTCTGCCG	R	Body	PCGF3	0.6490814	0.7961729	-0.147091429	0.7265	0.7961729	-0.069673
cg21449520	19	53716399	42878863	42878863	N_Shelf	CGGTGTTGCCATATATACTGGGTGCTCAATGAATCTTGCCTGATGAACGT	R	Body	MEGF8	0.8940171	0.9262371	-0.03222			
cg21452538	4	71713498	870773	870823	Island	GGCTGGGGCCACAGTGCGCTCACTTCTCACCGAGGGTCCAGGGTGCTCG	F	Body	GAK	0.9248129	0.9511343	-0.026321429			
cg21454485	1	42791353	160546243	160546293	N/A	CGGAAGTTAGGCAGGGAGTGAGGCAGAATACCCAGAAACAAACCATC	R	Body	CD84	0.7318386	0.8115686	-0.07973	0.7585638	0.8115686	-0.053005
cg21466415	3	27753381	133294854	133294904	S_Shelf	GTCAAAGCAGATTTTCAGGTTAAGGAAGGATTCCTGGGCACCCAAGTCC	R	Body;Body;Body	CDV3	0.7042571	0.80367	-0.099412857	0.7636025	0.80367	-0.040068
cg21469505	18	63801503	47085749	47085799	N_Shore	CGCCTGGAGGAGTTCCAGCTGAGGAGTCTTGATGGAACTTCTGCTGTGTT	R	N/A	N/A	0.2995171	0.3740771	-0.07456			
cg21473786	2	55708324	44311918	44311968	N_Shelf	ACAAGAATCCTGTCAGGTCAGTTTAGCCAGAATTTCCCCTAACCCACTCG	N	N/A	N/A	0.8642557	0.8975114	-0.033255714			
cg21483311	7	19746374	1793123	1793173	N/A	CGGCTTGCACCTGGGTGTAATTTTGTTAACTAGACTAAGATCTGATTCAG	F	N/A	N/A	0.7626743	0.8317471	-0.069072857			
cg21490161	5	16626320	180647246	180647296	S_Shore	CGTGCTTCCCCGCTCTGCTGGCTTCGTCGCAAGCGCTTGCCGCCGACCT	F	Body	CAMK2G	0.8362829	0.8805386	-0.044255714			
cg21505923	3	55676347	72226668	72226718	N/A	CGGACATGTGTGGGCAGGTCCCTTCTGACCCATGGCAGGTCCCTGTTGAT	R	N/A	N/A	0.3354014	0.4397914	-0.10439	0.319895	0.4397914	-0.119896
cg21509385	22	73633310	50729419	50729469	S_Shore	ATTCATGCCCCCTGACCTGTGACCCCAAGGAGCTCCAGGTGGTCGGGACG	R	5'UTR	PLXNB2	0.7549829	0.7903571	-0.035374286			
cg21514529	5	19628327	168885285	168885335	N/A	TCAGCCACACTGTTTTGGCTTTGATTAATGTTTTTTGGCACCTCTCTCG	R	N/A	N/A	0.6288988	0.7003843	-0.074154857	0.65911	0.7003843	-0.041274
cg21516305	17	35656310	5788714	5788764	N/A	CGGGCCAGTGGCTGGGATAAGAGAGCAAAAGCTCATGCTGGAGAAACACC	R	N/A	N/A	0.7842743	0.8672071	-0.082932857	0.82605	0.8672071	-0.041157

cg21886042	13	26787312	112076036	112076086	N/A	GAGACTCTCGCTGCTGGGCACGGGGGCTCGGAAGTCTTTGTTGAATGCACG	R	N/A	N/A	0.7973771	0.87899	-0.081612857				
cg21890423	3	49701439	55395559	55395609	N/A	CGAGGTCACTAGCCAATGCAGTGTAAGAGTGTGATTGATTGCAATGCTAT	R	N/A	N/A	0.4756443	0.5849586	-0.109314286	0.5149163	0.5849586	-0.070042	
cg21898708	6	56733339	31802157	31802207	N_Shore	CGCCTGTAATCTCAACACTTTGGACAGGCCCAGGCAGAGGATCATTTGAG	R	TSS1500;TSS1500;TSS1500	C6orf48	0.39673	0.4257986	-0.029068571				
cg21904074	13	50758381	30075712	30075762	N_Shore	CTTGGCTGATAATCCAACTTCCAGAAATTCACAATTTCCATCCAGGTCTCG	R	Body;Body	MTUS2	0.8577914	0.8903429	-0.032551429				
cg21913528	1	10734403	185283071	185283121	N_Shelf	CGGGCTGTGAACTTCTGGGTGTTATTAAAGCAGTTTAATTACTCATTTAT	R	5'UTR	IVNS1ABP	0.7301871	0.8093643	-0.079177143	0.7708588	0.8093643	-0.038506	
cg21923959	11	18768455	111250566	111250616	N/A	TATTGCTTTTCTGTTTATTCCATTTTGAAACACAGTAGCCCCTCCCCTCG	R	TSS1500	POU2AF1	0.70018	0.7728557	-0.072675714				
cg21929472	8	43614410	27527865	27527915	N/A	CGTTGTGAGTCTTTTCATTGACACATACAAAGAGAAGTCACCTCACAGTG	R	Body;Body	SCARA3	0.8641443	0.9077929	-0.043648571				
cg21931174	14	21664496	20977318	20977368	N/A	GTAGTGCAGTGGCACCATCTTGGCCTTCTCACGGGTTCAAGCAATTCTCG	R	TSS1500	RNASE10	0.7920429	0.8505214	-0.058478571	0.8331625	0.8505214	-0.017359	
cg21934504	19	2380373	4445085	4445135	N_Shore	CAGTGGCTGCACCTGGCACTGGGCTGCTCTGTGGATGTGGGTGACAACG	F	3'UTR;3'UTR	UBXN6	0.8154471	0.8657286	-0.050281429				
cg21938521	13	59614304	52006267	52006317	N/A	CGTGGAAAATGCAGAGATTTAAACTGGGCCTTAAGGAATGAGTGGCAGTT	R	Body;Body	INTS6	0.8803243	0.9009171	-0.020592857				
cg21938522	20	17794500	57426931	57426981	N_Island	CTTGGAGGCAGTCTGTAGTGGGCTAAAGGAATGACTGACCGCCGCCTGCG	R	TSS1500;TSS1500;3'UTR;TSS	GNAS	0.4773529	0.5150371	-0.037868286	0.4766325	0.5150371	-0.038405	
cg21942150	18	52715387	19784572	19784622	S_Shelf	TATTTCAACCCAGAAACAAAATGCATTTTAGCCAGGTGCCAGTGGCTCACG	F	N/A	N/A	0.6067643	0.6849414	-0.078177143				
cg21946967	15	65771493	82340505	82340555	S_Shore	CGGCAAGAACCCTCATTCCCAAGTTAGTTGGATTCCAAGTCCATAAACCG	R	N/A	N/A	0.5562314	0.46689	0.089341429	0.5442688	0.46689	0.0773788	
cg21952646	5	27713412	134734561	134734611	Island	AAGTTGGTTTCCAGGTTTCTTTTTTGAACAAAACCAAAGGGAATCCCCGCG	R	5'UTR;5'UTR;5'UTR;5'UTR	H2AFY	0.993548	0.1268014	-0.033253429	0.1050803	0.1268014	-0.021721	
cg21954370	15	26688452	45018720	45018770	N/A	CCTGCGTGTGATCAGGATTGAGTGTGAGCACGAGGATGTCTCTGAGGAGCTGTCCCGG	F	N/A	N/A	0.64893	0.7406557	-0.091725714				
cg21961149	15	19668314	37396505	37396555	S_Shelf	GGTCAGTCTGCTGAATTCAAAACACTATTACCTTTAATCAGCAACTTGCG	R	N/A	N/A	0.8834329	0.9245471	-0.041114286				
cg21962324	5	16651321	2547252	2547302	N/A	CGCTGATGGCTGAGGCACTTCCACCGTCATTTGCATTTCGATTCATCATCT	R	N/A	N/A	0.8271129	0.9072	-0.079907143	0.8661238	0.90702	-0.040896	
cg21964084	4	55644403	7772496	7772546	N_Shore	CCTGCGTGGAGGGTGGTGGCAGGACGAGGATGCTCTGAGGAGCTGTCCCGG	F	Body;Body;Body	AFAP1	0.8349443	0.8898229	-0.054878571				
cg21964564	1	25637396	204941271	204941321	N/A	CGGGGAATCAGCAGATGGGAAAGGAAGACAAAGTTAGCACCCTTATCATC	R	Body;Body;Body;Body;Body;B	NFASC	0.4362929	0.5516371	-0.115344286				
cg21967790	6	14644399	10430644	10430694	N/A	CAGAGCTGTTGAGGTGTTGAGGCACCTGCTACTGATACACACTATAAACG	F	Body	C6orf218	0.6747386	0.7848429	-0.110104286	0.7316975	0.7848429	-0.053145	
cg21983178	1	67693407	45120676	45120726	Island	GGAGCGCTGTCAAAGATGGTGCCCACCACACGCAGGCGGCAGAAGCGACG	R	Body	TMEM53	0.7823486	0.8246257	-0.042271143	0.8005513	0.8246257	-0.024074	
cg21997465	1	72786301	203055662	203055712	N/A	TACTGAGTGCCATAGGTGCTGCAAGAATCTAATGCTCTTTCCAGCATTCG	R	TSS1500	MYOG	0.8863171	0.9197943	-0.033447143				
cg21998983	2	52715325	154727925	154727975	Island	CGCCCTCCGCAGAAAGGACGGAGGTTGGCCTCTTGTTGGTTACAGTATCT	R	TSS1500	GALNT13	0.1034149	0.068517	0.034897857				
cg21999229	6	65786381	3154014	3154064	N/A	CGCTGCCACTGCCGCTTCCTCTTAAAGGGACCTGAGCGTCCGGGCCCAG	F	TSS200;1stExon;5'UTR	LTA	0.7901514	0.8549971	-0.064845714	0.8293938	0.8549971	-0.025603	
cg22013719	5	14656404	124144760	124144810	N/A	CCGCTCTGGTTCTTGTCGGTGGTCTTGCGGGAGCCCTGTCTTTTAG	N/A	N/A	N/A	0.7499686	0.7803914	-0.030422857				
cg22014112	6	31741504	138192658	138192708	S_Shelf	ACTCAACTGGTGTCGAGAAGTCCGGAAGCTTGTGGCGCTGAAAACGAACG	R	Body	TNFAIP3	0.7770429	0.8653943	-0.088351429	0.8125338	0.8653943	-0.052861	
cg22016870	2	22615368	237980832	237980882	N/A	AGGTCGTGATCAGCCCGAAGCATCCGTGGAAAAACTGGATGAAGTTCCCG	F	N/A	N/A	0.8639414	0.9011957	-0.037254286				
cg22017309	11	14737468	61685549	61685549	S_Shore	CCGGATATAACTCAGAGAGTAGGACTCAGAAAACTTGTTTCGGGTTTGTC	R	TSS1500	RAB3IL1	0.2276129	0.2976657	-0.069992857				
cg22032366	6	66645404	79911416	79911466	N/A	CGAGGGAGAATGAATTGTCATGAAAAATTGGGGTTGATTTTATGTATCTC	R	Body;3'UTR	HMGN3	0.9220857	0.9532557	-0.03117				
cg22032789	5	56605390	149512529	149512579	Island	CGGGGCCCTGGGGGCAGGGCACCAACTGAATCCCAAAGGAGGCCAGCCTG	F	Body	PDGFRB	0.8243014	0.8743043	-0.050002857	0.851105	0.8743043	-0.023199	
cg22032870	15	66733505	44398964	44399014	N/A	CGGTGGCAGAACTTTGCCTCACAGTTTAGAGGTGAAGACATACTTCTCAA	R	Body	FRMD5	0.7784114	0.838	-0.059588571	0.8081025	0.838	-0.029898	
cg22034968	19	54662320	47724582	47724632	N/A	CGTGACCCAGCTTGGAGCCGTGGAGCTGGGCTGGGCTGTTTGCCGGTTG	R	3'UTR;3'UTR;3'UTR;3'UTR	BBC3	0.6808957	0.7733457	-0.09245				
cg22039960	2	31761335	218416812	218416862	N/A	ACCAGATCACTTACCATGTAACCAGTTATTTAATGTCCATCTCCCCTTCG	F	Body	DIRC3	0.7589043	0.8366343	-0.07773	0.7792663	0.8366343	-0.057368	
cg22040158	1	44656371	112527540	112527590	S_Shelf	CGAGTCAAGAGCCCAAAGGAAGAAGAGAATCTCATAGTGAGGAGAGGAGG	R	5'UTR;5'UTR	KCND3	0.6970757	0.7800286	-0.082952857	0.7448163	0.7800286	-0.035212	
cg22045975	1	39763325	2304160	2304210	Island	CCAGGACGTGTGGAGGCTGGGCGTGGGCGGACGGGATGCGCACCATCGG	R	Body	MXRN1	0.8469343	0.8846171	-0.037682857				
cg22071610	22	74690423	24086732	24086782	N/A	TGGTGTTGCGTGAGGGCTGAGCTCTGGCGGAAGGCCTTCCCACACTCCCG	R	Body	ZNF70	0.8368014	0.8720429	-0.035241429				
cg22076160	1	25779434	235805690	235805740	Island	CAACTGAGCAAAACATAGAACAGAAACTCCCTCTCGAATAGAGACCCACG	R	5'UTR;5'UTR;5'UTR	GNG4	0.6180414	0.7056429	-0.087601429				
cg22076474	21	21610501	30677172	30677222	N/A	CGCTGGCACACTTTAGAAAATGAATAAGGCAATAAGCATGTGAAGATATC	R	5'UTR;TSS1500;5'UTR	BACH1	0.7090771	0.8038657	-0.094788571				
cg22089361	17	53618357	52600604	52600654	N/A	CGGAGGCAGTTCTCCAGTTGCAAAAGTAATTCTGAGAGAAGGGGAAG	R	N/A	N/A	0.7689243	0.8536443	-0.08472	0.8057125	0.8536443	-0.047932	
cg22089701	11	39800459	124253666	124253716	N/A	ACCCTATAGGAGACCCCTGTCTAGGAAACAGAATATCAGATGTGCTCCG	F	TSS1500	ORI8B2	0.8049814	0.8704	-0.065458571				
cg22090404	13	26787333	51489972	51490022	N/A	CGGGGACAGATAATGAAACAGGGACTAGAACATGCAGCCCCAAATCCCTT	R	Body;Body	RNASEH2B	0.9007214	0.92605	-0.025328571				
cg22098511	17	2361446	7947651	7947651	N_Shore	CGAGGGCCTCACCTGGTGTAAGAGGCTCAGGAGTGCCTTTGCTATTCCA	N/A	N/A	N/A	0.1498043	0.1752786	-0.025474286	0.1321263	0.1752786	-0.043152	
cg22102996	2	11751430	238888645	238888695	N/A	CGAGTGTCTCCCAGCTGTGAGGCATGCAGAAAAGGTGGATTTGAAGGATTT	F	Body	UBE2F	0.8423743	0.8561	-0.043235714	0.8714988	0.88561	-0.014111	
cg22107535	15	23775313	45028083	45028133	N/A	AATGACCACAGCTCTTTCCCCAGTGTTTGGGATCGCCCAAATATGTCACG	F	TSS1500;TSS1500	TRIM69	0.6076329	0.7197529	-0.11212				
cg22109787	2	42739305	152108040	152108090	N/A	CGGAGATTCTTCCATTGGGTTTCAAAGGACTGAAACTTGAAGCTTGGGGATT	F	Body	RBM43	0.8203014	0.8883743	-0.068072857				
cg22118112	20	71609301	62657367	62657417	N_Shelf	CCGGCCGGTCTCGTACTCATCATTCTTCGACTTCTCGGACTTCCTCCAG	R	Body	PRPF6	0.9046714	0.9334271	-0.028757143	0.9143425	0.9334271	-0.019085	
cg22127773	17	49632396	7754785	7754835	N/Shore	CGCCCCAGCAGCAGCGCACCAGACCCGAAGAACCATCACATCATCAAGTT	F	Body	KDM6B	0.91987	0.9525257	-0.032655714				
cg22136363	11	40620367	1911511	1911561	N/A	GGGTGTGCGGGGAGCGGGGAGGGCAGCCACCATGCGGGGGATGCGCCGGCG	R	3'UTR;3'UTR;3'UTR;3'UTR	LSP1	0.77323	0.8341771	-0.060947143	0.7868313	0.8341771	-0.047346	
cg22143352	14	52735340	75897891	75897941	S_Shelf	CGCCAACTTGTAGCCTTGGAGCTGGAGCTGCCACACCTA	R	5'UTR;5'UTR;5'UTR;TSS1500	JDP2	0.6671057	0.7487 6	-0.081654286				
cg22143387	5	57754373	176759081	176759131	Island	CGCCTCCGGCGGGGCCTGTCCCTGGGCCCAGGAGCCAATGTGAACTTTTT	R	3'UTR	LMAN2	0.8232914	0.8530557	-0.029764286	0.8397363	0.8530557	-0.013319	
cg22154545	20	15730452	17944526	17944576	N/A	CGGGCAGCCTGCTCTCCATGCTGCCATTTGTATTTCAAACTGAGATGACC	R	TSS1500;Body;Body	SNORD17	0.8703571	0.9083429	-0.037985714	0.8919738	0.9083429	-0.016369	
cg22153463	1	53762354	85462885	85462935	Island	CGGGGCAGTGTTCTCCGCCAGTTGGGGCGCCGCCGCCGCCGCCGCCGCC	F	TSS200	MCOLN2	0.1241129	0.19724	-0.073111	0.1246608	0.19724	-0.072579	
cg22153728	1	74715509	25291584	25291634	N/A	GGTACGAGGGCGGCCGGGGGTGGGGAGCACCAGGAGCCAACCAGCTCCCG	R	TSS200	RUNX3	0.61654	0.67911	-0.06257				
cg22158175	6	32779392	32809475	32809525	N_Shelf	CGGCTCTCAGGAAATATGTTCTCCACGGGTAGTGGGAACACTTATGCCTA	R	Body;Body	PSMB8	0.88434	0.9327557	-0.048415714	0.9117513	0.9327557	-0.021004	
cg22167660	19	37769435	40885241	40885291	N_Shore	TATTGAAATAGACAGAGGCAGCAGGGCCAAGGGCGAGCGCAGGGCCAGCG	R	3'UTR	HIPK4	0.5115957	0.5657329	-0.054137143	0.5257413	0.5657329	-0.039992	
cg22181303	19	37601498	38940209	38940259	N_Shelf	CCCGGGTACTCACGTGGTGTAAGAGGCTCAGGAGTGCCTTTGCATCATTA	R	Body;Body	RYR1	0.9115629	0.9415	-0.029937143				
cg22189823	15	58720323	90815996	90816046	N_Shelf	CGGGATTGCTACACCATGGCACCATTGTAAAAATCTGGTTAAGTAAACT	R	N/A	N/A	0.8147271	0.8790457	-0.064318571	0.8331675	0.8790457	-0.045878	
cg22193276	2	40809320	11965198	11965248	N/A	AAAGCATTCCTCAGTTGTGGCTTAATGCCAGTTACGACGCTGCCTTTCCG	R	3'UTR	LPIN1	0.7497714	0.82418	-0.074408571				
cg22206745	11	38731408	69484607	69484657	N/A	CCGGGCAAGAAGTGCACGTTTACCGGAAGCTGTGTTCACTCAACGGA	F	Body	ORAOV1	0.8718271	0.8999386	-0.028311429				
cg22219379	3	58741454	140541305	140541405	N/A	CGCCATTAAAAGCAGACAGATCTTTGTATTTGTGAAGGCTCACAATTAA	R	N/A	N/A	0.6025071	0.70973	-0.107222857				
cg22232269	4	58725392	10105548	10105598	N/A	CTGACATCTACACAGAGCACGCCCATCAGGTGGTGGTGGCCAAGTATGCG	F	Body;Body	WDR1	0.9187814	0.9476043	-0.028822857	0.9364038	0.9476043	-0.011201	
cg22235522	6	53618427	17169462	17169512	N/A	TAGCCCTTGCTTTTTCTACTAAGGCCAATAATGAATAGACTCCAATCG	R	N/A	N/A	0.8267071	0.9041286	-0.077421429	0.8795538	0.9041286	-0.024575	
cg22246218	17	53756370	7366270	7366320	Island	CCGCGCCCTGCGCCACGCCCACTCCCGCCCGCCCGCCCGCCCGCCAGC	F	Body;Body	ZBTB4	0.8235614	0.8592729	-0.035711429	0.8361025	0.8592729	-0.02317	
cg22266967	4	41609347	6695698	6695748	N/A	CGTCTATGATCATGCCCATGGCTGTCTCTAGTTCCGTCATGGTGCTAGAT	R	1stExon	S100P	0.8790029	0.8997629	-0.02076				
cg22284311	11	10757397	3169027	3169077	N/A	CGCCTTTCATGCCCCTGTGCCCTGTCTAGGGCCACGCCCGGCCTTCCCTG	R	5'UTR;5'UTR	OSBPL5	0.7804729	0.84197	-0.061497143	0.8143925	0.84197	-0.027577	
cg22299191	17	68735443	7991169	7991219	N/Shore	CGGAAGCCCCGCCCGCCCGATCGTGCCGCCGCCGCCGCCGCCGCCGCCG	F	TSS200	ALOX12B	0.7568514	0.8172957	-0.060444286	0.7892538	0.8172957	-0.028042	
cg22301128	4	34709313	77011716	77011766	N/A	TACATGGCTTGATGTTAGACAGAAGTCTACAGTTAGAAAACATTAGACG	F	Body;Body;Body	ART3	0.7401557	0.8281914	-0.088035714				
cg22310648	3	63709469	58603077	58603077	N/A	GGAGCTCAGCCAGAAATGGGGCAGTGTCTGTCCTTTTGAGGGACCATCCG	N/A	N/A	N/A	0.7446543	0.79919	-0.054535714				
cg22312249	17	74681345	72779428	72779478	N/A	CGCAGCCCACGGCCACAGTGAGCTTCATATTTAGTAACAGGGAAAAGAGA	F	Body	TMEM104	0.8631514	0.9034414	-0.04029				
cg22312782	17	31736497	80931612	80931662	S_Shelf	CCGGCACAAGCCACACCCTTGATCTTAATCTTACCAGTCCGGAACTTGGG	F	Body	B3GTA1	0.9257543	0.9469	-0.021145714				
cg22328746	4	68644462	186578455	186578505	N/A	CAACAGCTTCTTTCCTGCCACACACAGCATAACATTCATGAGAAGTCG	R	Body;Body;TSS1500;Bo	SORBS2	0.8560929	0.9185986	-0.062505714				
cg22329021	4	43759406	1573282	1573332	S_Shelf	GCAGGTGAACCAGACCTGGTGCCGGGTGCTGGTGCTGCCAGGGAAGACG	R	N/A	N/A	0.6678786	0.7422443	-0.074365714	0.6823275	0.7422443	-0.059917	
cg22329743	2	20713310	208688874	208688924	N/A	CAAGGTCCAGGTCAATGCCTGTGCCTGTGCGGTTAATGTAAA	R	3'UTR	PKHM3	0.8988829	0.92224	-0.023357143				
cg22334684	1	33702311	9666668	9666668	N_Shelf	GGACAACGTGCTGGTGAGCGGGCAGGCTGGCCCACGCCCTGCAGGAGCCG	F	Body	TMEM201	0.8618243	0.9016757	-0.039851429				
cg22338446	19	19687481	42390475	42390525	S_Shore	TGACCACGGACTGGAGGGTGCATGCTCATCCCACTCAGAGGTAGAAACG	F	5'UTR;Body;5'UTR	ARHGEF1	0.58618	0.7299229	-0.143742857	0.6527763	0.7299229	-0.077147	
cg22339219	7	10745376	104530561	104530611	N/A	CTGGCACCTGTTTCTGTGCCACGTAATCCCAAGTTTTGGAGATCG	R	Body	LHFPL3	0.7770543	0.8357871	-0.058727857	0.7994013	0.8357871	-0.036386	
cg22340807	1	17752363	61378118	61378168	N/A	CGAAAAAGTTAAGTATACTGAGTGCAGGGCTTGAATGCACAGTTTGGCT	F	N/A	N/A	0.7364814	0.800671	-0.063585714				
cg22341471	12	65690325	123451323	123451373	S_Shore	CGGAAAATGGTTTCACCTGAAGGAGGCCAGCTTTTTAACTGGCCTTTTTCC	F	5'UTR;TSS1500;TSS1500	ABCB9	0.43234	0.49518	-0.06284				
cg22341513	18	52802346	54785289	54785339	N_Shelf	GCGGGAAAGGCCCAGCTATTCTAAGACTCAGGTCTGGCTGGCTGAGACG	R	N/A	N/A	0.6164657	0.7011357	-0.08467				
cg22348345	11	57675456	1857477	1857527	N/A	CGCTCCCCCCGTTGTTTGACGAGACCTCGCTGGATCAGGGTGGCTGCG	F	Body	SYT8	0.84567	0.8814	-0.03573	0.861525	0.8814	-0.019875	
cg22351924	1	17623404	27994914	27994964	Island	TCTGGAGGGCGAGGATCTCGGGCAGGCGGGGCGGGCCTCTGCCGCGGACG	F	Body;Body;Body	IFI6	0.7763	0.8487314	-0.072431429				
cg22356061	1	34678505	227954102	227954152	N/A	CGCTCCGCAGAAGGTGCCCCAGTGTGCCTCTGCCTGCAGAGGCCAACCTGCCT	R	Body	SNAP47	0.6936557	0.7760043	-0.082348571	0.7115488	0.7760043	-0.064456	
cg22358291	4	16674314	10101553	10101603	N/A	TTCTCTTCTGCTCCAGCCCATGTTAACGCCAATTGTAACACACACCG	R	Body;Body	WDR1	0.8150371	0.8800971	-0.06506	0.8468188	0.8800971	-0.033278	
cg22361543	1	24690319	7757378	7757428	N/A	CGGCCGGGATGAAGTTGGATAATAAACTTAAATAGATAGCCCAGGGCCTG	R	Body	CAMTA1	0.9019014	0.9287343	-0.026832857				
cg22367886	19	41637317	13218670	13218720	S_Shelf	GGTCAAGGAGTCCGGCATCTCCCTCATAATCCCTGCTGTTCCCCAGGTCG	F	Body;Body;Body	TRMT1	0.8686529	0.9017671	-0.033114286	0.8855413	0.9017671	-0.016226	
cg22368413	2	50789369	21875627	21875677	N/A	CAGACCTAGAGCTGGGTCAAGTCAAGCATCCCACCTTGGAGTTCGCCACCG	R	Body	TNS1	0.1714029	0.1986757	-0.027272857				
cg22372070	3	39691444	11861650	11861700	N/A	GCTGTAAGATTTACACAGTTTAACCTGCTGTTCTCTCTCTCATTTCA	R	Body	C6orf31	0.7692314	0.8746229	-0.105391429	0.8421075	0.8746229	-0.032515	
cg22374165	2	67654453	39199273	39199223	N/A	CGAGGCAAAGATTTCAAGTTTTGAGTAATGACTTTCTGATGAGAAACTGT	F	3'UTR	LOC100271715	0.8823157	0.9122557	-0.02994				
cg22376214	7	20628323	4836291	4836341	S_Shelf	CGGGACTCTGCTATTTTTGCAGCTTCCTTTGGATCTATAATTATGTAAA	R	3'UTR	N/A	0.77573	0.8391114	-0.063381429				
cg22378717	8	59681390	143200334	143200334	N_Shelf	CGGTCCAGACAGTGATGGCCCAGCCAAGGCCCTGATGAGGGGGCCTCGAACG	F	N/A	N/A	0.7214	0.7670643	-0.045664286	0.7348325	0.7670643	-0.032232	
cg22379708	1	47692369	982918	982968	N_Shore	CGGCCCCCCAAGTCCTTGCCTACTCCCTGCCACAGCTGGACGACCTCTTC	R	Body	AGRN	0.7674829	0.8322786	-0.064795714	0.800865	0.8322786	-0.031414	
cg22383292	7	40748356	11412105	11412155	N/A	CGGTGTAGCTTAAGTGAATTTAAAAAGAGTGCATAAAAGCTTGTTTTTAA	R	3'UTR	THSD7A	0.9042243	0.9423971	-0.038172857				
cg22386757	4	54712359	8126646	8126696	N/A	CGGATCTGTAATCGCGTCTCACTGGGATTCTGATGTGCCGTTCCCTGTGG	F	Body;Body;Body;Body;B	ABLIM2	0.8829957	0.9068914	-0.023935714				
cg22386774	2	48731471	209029690	209029740	N/A	CGGTCCTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	F	TSS1500	CRYGA	0.8192143	0.8690029	-0.041688571				
cg22387998	11	15798346	66628642	66628692	S_Shore	CGAGCCCCTGCTTTCTCTGCTAGGACCCCTGGCCAGGCCCGGGCAGCCTCC	F	Body;Body;Body	PC	0.7871743	0.8295871	-0.042412857				
cg22396119	8	39766341	122419020	122419070	N/A	CGTGCATGGATACATCACCTAAGGACAAGGGAGCATGTTCATGCATATAT	F	N/A	N/A	0.6634686	0.7241914	-0.060722857	0.6706688	0.7241914	-0.053523	
cg22399111	8	17708367	142295325	142295375	Island	ACCCGAGGTCGCGCGCTGGGGTGCGGCGCGTTGCGCGCGCGCGCGCGCG	R	N/A	N/A	0.8249043	0.9065757	-0.081671429	0.8491163	0.9065757	-0.057459	
cg22404856	11	17674407	18750217	18750267	N/A	CGGGCTCCAGTTTTAACGATGGTTCCATCAATACCTGATCCAGAATGTT	R	3'UTR;3'UTR;3'UTR	PTPN5	0.8079129	0.8631557	-0.055242857				
cg22405226	6	72631327	82616606	82616656	N/A	CGGTAGCCACTTCTTTGCATATGAAAGCAAGTGCATAAATATGCGGTGGA	R	N/A	N/A	0.82444	0.8970214	-0.072581429	0.8715125	0.8970214	-0.025509	
cg22413090	6	11635323	29986760	29986810	N/A	ATTTGACATGGTCCTTTGCTGCCCCTGTAACCTTACACAATAATCCAGCG	R	Body	NCRNA00171	0.8778743	0.9137543	-0.03588	0.8850163	0.9137543	-0.028738	
cg22414525	8	27626361	27946669	27946669	N_Shelf	CGTGGTGGCTGGTCTTCTGCTGCAAGCTGTTGGCAAGGATTCAACGCCAT	R	N/A	N/A	0.7199514	0.8172486	-0.097297143				
cg22416721	4	40769391	88570574	88570624	N/A	CGGCAGGATGGCCACTGAACAAGAATTTAGAGAATATCAGCTGCTGGACC	R	TSS1500;TSS1500	DMP1	0.8216571	0.8971671	-0.07551				
cg22432982	1	43798344	2886676	2886726	Island	TCTAACCCACGGCCACAGCAGCTGCTGCTCACAGGGCCTGGTGTCTCGG	F	N/A	N/A	0.7446557	0.8067757	-0.06212				
cg22444116	7	53658490	17081421	17081471	N/A	CGAGGTGGCAACTTCTTTTTGATTGACTATCTTCTTTTTGCTTTT	R	N/A	N/A	0.7271971	0.8103229	-0.083125714				
cg22446208	2	67608431	61388665	61388715	N/A	CGTTGGTTGGTTTTTGTGTACTAAACTATCTTTGCATTCCAAGAATAAGT	F	TSS1500;5'UTR	C2orf74	0.85414	0.9174071	-0.063267143	0.8895363	0.9174071	-0.027871	
cg22451887	20	20687493	60969143	60969193	Island	TTTTACGTGGAGTGAAGCACAGCTTCACGTGTGCTCGTGGGCACTGAGG	R	Body	CABLES2	0.8921786	0.9250543	-0.032875714				
cg22464865	19	39808440	35620827	35620877	S_Shelf	TTCCGGCTATAAACCTGTTACTGAAGCATAGTCTGTTTACTGATAGAAACCG	R	Body	LGI4	0.6811543	0.7560571	-0.074902857	0.710145	0.7560571	-0.045912	
cg22468751	6	71677362	136824489	136824539	N/A	CCCCCTCAGAAATCCTTGTTTGGACAGATTCTTCTTTTGGAACCACATCG	F	Body	MAP7	0.5973214	0.6887371	-0.091415714				
cg22482801	22	14638427	29724443	29724493	N/A	AGGGTCCATCCCATGAGAGGTGGCAGTGGAGGGCCCTTTAACACCAACCG	R	3'UTR;3'UTR;3'UTR	AP1B1	0.7639957	0.8301386	-0.066142857				
cg22497969	1	19664334	3143018	3143068	N/A	CGCTCAGAGACAAACAGAAATGCCGTTTGGCAAAGGCGGCCTAAAAC	F	Body;Body	PRDM16	0.7621986	0.8343643	-0.072165714	0.78454	0.8343643	-0.049824	
cg22501690	5	46682347	125932790	125932840	N_Shelf	TGTTGCGAGCTGGTTCCGCACCTCCTCGGCGTCCTCTCGGCTTGCCTCG	R	N/A	N/A	0.7857457	0.8352	-0.049454286				
cg22501922	19	49691416	7928773	7928823	S_Shore	GGTACAGACCAAGATGGGTAAACACTGCTGGGGATAGAGAGCCTGCCCCG	F	3'UTR;3'UTR	EVI5L	0.7877114	0.8656529	-0.077941429				
cg22504024	12	43602450	111710593	111710643	N/A	GATGTGAGCCCACCACACCAAGGATGACAGCTAACTTTAGAAGGCAGTGTCG	R	Body	CUX2	0.8040871	0.8621629	-0.058075714	0.8351913	0.8621629	-0.026972	
cg22518157	4	17619380	36210723	36210723	N_Shelf	CGGCTGGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	R	Body	ARAP2	0.6288457	0.7195971	-0.090751429	0.680515	0.7195971	-0.039082	
cg22537597	7	42777438	149530984	149531034	N/A	CGTGGTCAGTGCTGCTGAGTCCCATGATCACAAGAGGGACAGCTGTGGAC	R	3'UTR	SSPO	0.7182829	0.7920429	-0.07376	0.7563838	0.7920429	-0.035659	
cg22542901	12	65797448	68052319	68052369	N/A	CGGGGAGAAAACGTCAGTGAAAAGGATAACTGAGAGCACCGGTGTTGCA	F	Body;Body	PYGO2	0.8676214	0.9104386	-0.042817143	0.8958038	0.9104386	-0.014635	
cg22546775	12	46617501	66697281	66697331	N/A	AAACAACAACAACAACAAAAACTACAAAATTAGCCGGGCGTGATGTCG	R	Body;Body	HELB	0.7411443	0.7982414	-0.057097143	0.76786	0.7982414	-0.030381	
cg22549626	12	16727406	121343003	121343053	S_Shore	CGGTAAGAACACCAGAGACCAACAAGTGATCTGGCATTTGGCAAGTCGA	F	TSS1500	HPLI3	0.6245243	0.7079771	-0.083452857				
cg22557725	10	67620413	60368369	60368419	N/A	CGACAAGACTAAAACATTACAGAAGGTCACAGATGATTAAGCACAGGAA	R	Body	BICC1	0.56687	0.6667457	-0.099875714				
cg22571065	12	50785393	1949503	1949553	N/A	CCAGC

cg23010236	1	41609434	113259865	113259915	N_Shore	CGGACAGCTTGCAGCCACACCATGGTGGGTGCTAGAAAGGGCAGGGAATA	R	N/A	N/A	0.8674086	0.8963986	-0.02899			
cg23014221	1	56602417	44833461	44833511	N/A	TCTGCTATTCTGCTCACAGGGAGGGCCACCTGGACCTCAGTGGAATACCG	F	N/A	N/A	0.8757486	0.9159143	-0.040165714			
cg23015991	12	41616416	20556313	20556363	N/A	TAAGACTATAACCTGACAAGCATGGTTAAGTGCTCTCCCTGCAAAGTCG	F	Body	PDE3A	0.8198929	0.8637657	-0.043872857	0.8378863	0.8637657	-0.025879
cg23020660	11	21665405	73581438	73581488	N/A	TGAGGGAAAGGCTTGGATGGCAAGGTCTCTTTTGCTGATCAAATACG	N	N/A	N/A	0.83628	0.90074	-0.06446			
cg23024326	6	43713450	36761843	36761893	N/A	CGGTGGGCCAGCCTCACTCCACCACCCTGACCATCTGGCTTCGGCTGGCC	R	Body	CPNE5	0.7332971	0.7946857	-0.061388571			
cg23025459	1	10768336	3134420	3134470	N/A	CGCTCACTCCCAACTCTGCTCCCCCACACGAGGTTTTGGGGTGCCCCCTTG	F	Body;Body	PRDM16	0.7966786	0.8482714	-0.051592857			
cg23027715	19	64771388	1045096	1045146	N_Shore	TTGGGTGCTCTGTGGGGTCTGAAGAGTCCTCAGGTCCCAAGAAGACGACG	F	Body	ABCA7	0.8293629	0.8639614	-0.034598571			
cg23029292	14	2661759	22982777	22982827	N/A	CATCTAGAAATCTCCCCACTTAACCATAGTTTTTGTTTTTCCTTAGCACG	F	N/A	N/A	0.8636686	0.91149	-0.047821429			
cg23031196	12	60761365	46664096	46664146	S_Shore	TCATCACCACTGGAAAAGCAAGATGATAACCAAATTTGAAACTCATCAG	R	TSS1500;TSS1500	SLC38A1	0.6635943	0.7673057	-0.103711429			
cg23032215	1	57773420	7154850	7154900	S_Shelf	CGCAAGTCCTCTCACCAGAAATATGAGGTTCCTCTTGGAGTTTTAGCAG	F	N/A	N/A	0.89687	0.9268657	-0.029995714	0.915315	0.9268657	-0.011551
cg23037111	19	62719428	55857159	55857209	N_Shore	CAGAGGACGCCAGGATTGGGCTCTGGAGTGAGGGAGGCCTTCACGAGCG	R	Body	SLV420H2	0.8182629	0.8837914	-0.065528571	0.8572375	0.8837914	-0.026554
cg23043937	13	32651475	59893019	59893069	N/A	CGGAGAAGGCATATTAAATTATGCTAGTGCTGACTGCGCCTCCAAGGACT	F	N/A	N/A	0.6306629	0.73493	-0.104267143	0.69402	0.73493	-0.04091
cg23044929	8	35620401	145706567	145706617	S_Shelf	GTTTTATATTTGGATTATGACGTTGTTCACAAAACCCATCAAACAGGCCG	F	N/A	N/A	0.7982057	0.8423057	-0.0441	0.8122475	0.8423057	-0.030058
cg23046934	18	16715419	77154321	77154371	Island	TCCCCAGGCCTGGGGCCAGGATTTGGCGGGAGGATTTCCGTCCCCCCCG	F	TSS1500;TSS1500;TSS1500	NFATC1	0.2312129	0.3447643	-0.113551429	0.264505	0.3447643	-0.080259
cg23054188	5	37698413	115887070	115887020	N/A	CCGGCCATATTTGGCTGTTATTTATCCTCTCTTCTACTCTCCCC	R	5'UTR	SEMA6A	0.77679	0.83629	-0.0595	0.8079638	0.83629	-0.028326
cg23065732	6	72777321	31701808	31701858	S_Shelf	CGTGGGATAAGAAAGGGACTCCAGGGGGAGGGCAAAAATGTTCATGACAG	F	Body	CLIC1	0.6645314	0.7767829	-0.112251429			
cg23065757	14	46648365	70313141	70313191	N_Shelf	TGGTGTGTGCTACCATGCCTGGCTAAATTTTGTATATTTTGTAGAGTCCG	R	N/A	N/A	0.89865	0.9215314	-0.022881429			
cg23066414	5	30781309	149337641	149337691	N_Shelf	CGGCTCACGTCACCTCTTCTGTTCTTCTGAGACCACAGGGGAAAAAAT	R	N/A	N/A	0.8880357	0.9098514	-0.021815714			
cg23071690	6	30747362	30232015	30232065	S_Shelf	TATGTCCTTCAAATATTTCATCAAAGGTCACCTTCCCAACAAGGCCCACG	F	Body	HLA-L	0.8148557	0.8472514	-0.032395714			
cg23072161	1	56810499	16489115	16489165	N/A	CGGCCACCCGGTAGCTTGGGCGGGTTCCGCCCCACCTCCCGCCTGTATTTA	F	N/A	N/A	0.51769	0.6147971	-0.097107143			
cg23074762	15	59711366	101781259	101781309	N/A	CGGTGAATCTTTGGGGGTGGAGTTGTACGTTATTTTATTTTTGTATATG	R	Body	CHSY1	0.7113986	0.8272671	-0.115868571			
cg23080559	14	28622312	88790542	88790592	Island	GGAACCACTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCC	F	Body;TSS1500	KRNK10	0.1459871	0.1745514	-0.028564286	0.1503138	0.1745514	-0.024238
cg23089643	12	45695306	52262163	52262213	N_Shore	AGGTTTTCTGGGTCCTGGGCAGCACGGCTGTCTGTGTCACCAGCGGACCG	R	N/A	N/A	0.8377	0.87646	-0.03876			
cg23092086	16	3580736	55909573	55909623	N/A	GCCGGGCTGCTTGTCTGAGCTGGCAGTGCTTGTGCCTTCAGAGCCACTCG	F	TSS1500;TSS1500	CES7	0.8886229	0.9276986	-0.039075714			
cg23093404	2	37740306	97599787	97599837	N/A	CGGTTGGGCTAATTGATGAGGAGCAGCCTGTGCAGAATATTG	R	Body	FAM178B	0.8022114	0.8552986	-0.053087143	0.8318788	0.8552986	-0.02342
cg23098038	2	19614427	242435173	242435223	N/A	CGGCCTCTTGGGTGTGCAGTCTGCGGTGGCAGCCCTGACAAGCCACCGCA	F	Body	STK25	0.7478471	0.7771914	-0.029344286	0.758185	0.7771914	-0.019006
cg23111276	8	50706449	700734	700784	N/A	CGCCGTCTGCAGTGTTTCAGGCTGATGGGAGAACAGTGTTTCCTGTCTTT	F	N/A	N/A	0.688	0.8029029	-0.114902857	0.74687	0.8029029	-0.056033
cg23119977	15	23715305	44213357	44213357	N/A	ACTCATTATGCCACCTCAATGTGGTTAAGAGGCCCTTCTCACATTACACG	R	Body	FRMD5	0.7192943	0.7865014	-0.067207143	0.75151	0.7865014	-0.034991
cg23120243	6	40677302	1663171	1663221	N/A	GAGCACAGATTCAGAAGCAAAACTTCCATAGTGCATGAATCCTCCCAACG	R	Body	GMDS	0.6438	0.7364814	-0.092681429			
cg23123621	4	27665379	1343375	1343425	S_Shore	CGCCGAGATCCGTCTCTCAGCCTTCCAGATTGTGGAGGAACTCTTCGTCA	F	Body	KIAA1530	0.9060643	0.9391386	-0.033074286			
cg23126203	12	15616395	117036972	117037022	N/A	TTTTTAAGCCCAGGACTGGCTACTTGGTTAACAGATGTGGCCTGACCTCG	F	N/A	N/A	0.7953514	0.88803	-0.092678571			
cg23144899	2	22681409	208994373	208994423	N/A	CGGCCCTGGAAGGCCCTTCTCCTCATAGAAGTGTGATCTGCAAAGGAGAAT	F	Body	CRYGC	0.8285143	0.8668629	-0.038348571	0.8548138	0.8668629	-0.012049
cg23147373	14	19754316	64954212	64954262	N/A	CGTTCCCCACAGTAATGGCATAAGTGTATTTTGACACTGTTTTCAGTAAA	F	Body	ZBTB25	0.7448214	0.81986	-0.075038571	0.7755738	0.81986	-0.044286
cg23164218	11	50679466	28569134	28569184	N/A	CGACAAGAAAATAGACAACACTTTCTTAAAGTGCTGCTATTTAGGGTATT	N	N/A	N/A	0.7786857	0.8687471	-0.090061429	0.8287	0.8687471	-0.040047
cg23165166	2	16603481	189914501	189914551	N/A	CGGGGAAAGGATGGAGGATGCAGTCCTCTGCTGCTGCTGCCAACGAATC	R	Body	COL5A2	0.8903043	0.9257557	-0.035451429	0.90522	0.9257557	-0.020536
cg23168192	14	39752334	23624788	23624838	N/A	CCAGGGTGGCATGGCAGGCCACCCTGGATTTCTTGGTGTCCAGTTTTTCG	F	Body;TSS1500	SLC7A8	0.5530657	0.7146043	-0.161538571			
cg23169051	3	42774369	107921136	107921186	N/A	CGGCATAGCCACTGTGAACATGCAAGCAGTGCCCAACTGACATATGCAAA	F	Body	IFT57	0.8891629	0.9227186	-0.033555714			
cg23169111	20	50758385	3065582	3065632	S_Shore	TGAATCCAGAGCGCTGCAGTCACAGTAGAGGGCAATTGCTGTCATTCCGCG	F	TSS1500	AVP	0.6557257	0.7094471	-0.053721429	0.673875	0.7094471	-0.035572
cg23170988	10	35789403	88720216	88720266	N/A	CGCCGCCGAGGACCCCATTTTATAAGTGAAACCAGGATCCCACACCG	F	Body	SNCG	0.4073586	0.4699	-0.062541429			
cg23173910	2	30647397	74120274	74120324	N/A	GGCCTCCTGGGTGCGGGAGGTGCCTCCAGATTGGCCTGGCTTCTGTGACG	R	5'UTR	ACTG2	0.8320914	0.8741429	-0.042051429			
cg23180600	3	46659388	10780722	10780772	N/A	CGGTGCCAGCTGTCGAGTGATGGCGCCCCCTGGTGTCCAATGAAAGAGGC	F	N/A	N/A				0.2438763	0.2179929	0.0258834
cg23186787	4	43800687	4380004	4380054	N/A	CACACTGAGGTCAAGCAAGTGACCACGCGTGGCCGGGGTGGAGATAAATAACG	F	N/A	N/A	0.8217157	0.8752186	-0.053502857			
cg23190190	11	69680494	70031725	70031775	N/A	CGGAAAACAAGTACGACATCTCCAAGGACTTCTGGGCCGTCCTGGCAGCC	F	Body;Body	ANO1	0.8885329	0.9175457	-0.029012857			
cg23195373	19	12634354	45954891	45954941	S_Shore	TCCATTCACACTGTCACACACTCAATTTCTTCTCTCTGCTCGGAGATTCG	F	N/A	N/A	0.1795514	0.2784643	-0.098912857	0.2235713	0.2784643	-0.054893
cg23196630	8	65743387	144362100	144362150	S_Shore	GCTGCCTCGAGAGACCTCTCCCTGCAGCTCCAGTGCTTTGAGGTTCAGCG	F	N/A	N/A	0.8608371	0.8969143	-0.036077143			
cg23198793	15	19622443	42694406	42694456	N/A	CGACGAGCTCGTCGCAGCACAGACTCGTGCACGCTCGCACGCCCGCCAAC	R	Body;Body;TSS200;Body;Body	CAPN3	0.7346743	0.7990814	-0.064407143	0.756705	0.7990814	-0.042376
cg23199907	13	41663423	33305966	33306016	N/A	CGGCGTTAACGAGAGAGTGTGAGTCACCAGCCTGTTAGTGTTTGCTATTG	F	Body	PDS5B				0.6350775	0.6050257	0.0300518
cg23202496	20	27622392	35488318	35488368	N_Shelf	ATTCCACAGATGGGAAACTGTGGCCAGAGGTGGGTCCCAGAGCAGGGTCG	F	Body;TSS200	C20orf117	0.7800357	0.8435214	-0.063485714			
cg23208294	1	43751335	186175724	186175824	N/A	CGTGGTTTTCCTCCTCCCCAAAGATTTTTTGCTGCTGCTGCTGCTGCTGC	F	Body	MR548F1	0.71327	0.7786157	-0.065345714			
cg23210278	2	10636391	220439623	220439673	S_Shelf	CGGGAGGACCCGTGGCTGTGCCCATGTCTTTGGGCCATGCTCCCCCTCAC	F	Body	INHA	0.8163686	0.8429371	-0.026568571	0.8222713	0.8429371	-0.020666
cg23212796	1	17739320	3089597	3089647	N/A	TCACGATGCCAGATCTTAGCTCGTGGAGCTAGTGCTTGGAGCCAACACCG	R	Body;Body	PRDM16	0.9272029	0.9565971	-0.029394286			
cg23217940	15	18687466	22954817	22954867	N/A	CGGAGCAGCTCCGCGCCGCCGCTGAGCGCGCGCCGCAGTAACG	R	Body;TSS1500	CYFIP1	0.8065157	0.8519957	-0.04548			
cg23218957	14	58717327	59109856	59109906	N_Shelf	CGTGGACCTGGCAGTTAGGCCTGAGCTTAACTTCTGCCTCTGCCACTCAC	F	Body;Body	DACT1	0.5529729	0.6729843	-0.120011429	0.6124863	0.6729843	-0.060498
cg23222278	3	19625431	8623867	8623917	N/A	AAGGCACACTCCAGGGGCCCTGGGTGCTTGTTTATTTCACTCAGACCG	R	N/A	N/A	0.8682286	0.9108557	-0.042627143			
cg23232773	6	60788449	31431902	31431952	N/A	GGGTGGAAGTGATGTGGCTCCATATCCCATTCCTTCAACTCACCTGTCG	F	3'UTR	HCP5	0.6730843	0.7538171	-0.080732857	0.7134363	0.7538171	-0.040381
cg23240589	2	42682390	55217063	55217113	N/A	CCGGGAGTGATGATAAGACAGCCTTGGTAGGATCACCTCTTTCCTGTGA	F	Body;Body;Body;Body;Body	RTN4	0.8930686	0.9309943	-0.037925714			
cg23240617	14	29757352	105742034	105742084	S_Shelf	TTTAGGAGTCAACATTCTGACATAGCAGCCCTGCATGCTGGGGACACG	F	Body	BRF1	0.7219571	0.8003114	-0.078354286	0.77175	0.8003114	-0.028561
cg23247068	21	38722503	45144343	45144393	N/A	GGGACCTCAGCACTTGAGCAGCATGTGGACGCGAGCACGCGAGTAACCCCG	R	Body	PDXK	0.9011614	0.9294757	-0.028314286			
cg23251296	17	59629349	62011004	62011054	N/A	GATAAGCTGGGGCGCCACTCTCAGAGGGTGCAGGCCAGGCAGTCTGAGCCACG	F	TSS1500;TSS1500;TSS1500	CD79B	0.8012186	0.8406657	-0.039447143	0.8125425	0.8406657	-0.028123
cg23253053	12	50768437	111558736	111558786	N/A	CTTGTGCCTCCAGTAATGAACAAAACCAAACCAACCACTGAAACCAGCCCG	R	Body	CUX2	0.6193471	0.70909	-0.089742857	0.6495575	0.70909	-0.059533
cg23253961	14	68746307	62394494	62394544	N/A	CGTACCCCAACTGTGCAAAACTGCAGTTCCCACCTAGCAGGGGTAAAGGA	R	N/A	N/A	0.6741843	0.7877043	-0.11352			
cg23254316	11	29754368	12200844	12200894	N/A	CTGCAAAGGTGGAGGATCTCCAAGGACAGGATTTCACAGACTAACACCG	F	Body	MICAL2	0.8368829	0.8911357	-0.054252857	0.8624688	0.8911357	-0.029667
cg23256579	12	41700448	11002403	11002453	N/A	CGTGCTTTGTTGTATGTTTGTAGGTCCTGTCTTTAAGCCAGAAGT	F	TSS1500;Body	PRR4	0.82718	0.8835414	-0.056361429	0.8567825	0.8835414	-0.026759
cg23258400	14	41801349	72113798	72113848	N/A	TCATTCTATCTGGGAGCATGGCTGCTAAGGATTCTAGGAGCCTGAGTTCG	R	Body	SIPA1L1	0.8762157	0.9103986	-0.034182857			
cg23270712	2	15704444	206349708	206349758	N/A	TTCAATTGTCAGCAGCAGAGTGCCTAATTTTCCTTCTTCTTTGATATTCG	R	Body;Body;Body	PARD3B	0.8981829	0.9317971	-0.033614286			
cg23277328	17	34695310	211482	211532	N/A	TGGCCCCATTGCTAAGTTCCCATTTGTCCCGCGGGCCTGACTCTCG	F	N/A	N/A	0.8538114	0.8886571	-0.034845714			
cg23287004	8	63655356	35979325	35979375	N/A	ATAAGGTGCGCGCTGTCCCATGTGATAAGATCCGAGGTCCGGGCAGGGCG	R	N/A	N/A	0.8440743	0.8797886	-0.035714286			
cg23295647	14	41680348	34269637	34269687	Island	GTCCCCGCAGGGCGGCGGCGGTGGGGGTGGCGGTGGCGGGGGCTGCACG	R	Body;Body;Body;Body	NPAS3	0.45501	0.3167829	0.138227143	0.4141175	0.3167829	0.0973346
cg23296572	7	14678422	142583836	142583886	N/A	GGAGTCAGGGCAGGCCCATTCCCAATGTTGAGGACTCCCAGGAGGGACGG	R	TSS1500	TRPV6	0.7326214	0.7817429	-0.049121429	0.7516663	0.7817429	-0.030077
cg23315423	10	38715326	88718164	88718214	N/A	CAGGGCAGCAGTTGGAGGTGCCCGCCTCCATCATGGAGGGCACCG	R	TSS200;TSS1500	SNCG	0.7154886	0.77134	-0.055851429			
cg23317859	20	73744373	34742329	34742379	N/A	CGCCCCCGGCTGCCCCCACCCTGGTCCTAGCCAGCCCCGGGCCTCCTTGCT	R	TSS1500;5'UTR	EPB41L1	0.1710986	0.24109	-0.069991429			
cg23318523	8	29759415	144597448	144597498	N/A	TCATCTATACACCGAGCAGGGCAGGATGGAGCCAGCCTGTGGCGCATACG	R	Body	ZC3H3	0.8851014	0.9044314	-0.01933			
cg23318703	7	49791393	76895968	76896018	N/A	CCGGGTTATCACTATGGGGCCTGATGATGTCATCTCTTCATTAGAATAAA	F	Body	CCDC146	0.8032357	0.8649243	-0.061688571			
cg23319289	14	62732354	82292196	82292246	N/A	CGAGTTGTTATTTGCATTAGTGATATAAATATACAGAAAGAGATTATA	F	N/A	N/A	0.8691671	0.9186771	-0.04951	0.8898688	0.9186771	-0.028808
cg23324101	19	47766353	17444399	17444449	Island	CGAGGGGGCCCAAGGCCTCCTACGTATTCCCGTTCTGGGAAGCCGAGCTC	F	Body	ANO8	0.8832971	0.9153286	-0.032031429			
cg23328556	12	15771338	123374731	123374781	N/A	CTGTGCCAGGTGAAATTCTCCGCTAAGTTGTAGCAGCTTGCATGTTTCTA	F	Body	VPS37B	0.6970357	0.8056471	-0.108611429	0.73848	0.8056471	-0.067167
cg23334662	2	59648472	198540518	198540568	N/A	CGTGGCATGGAAATTCTCCGCTAAGTTGTAGCAGCTTGCATGTTTCTCTA	R	1stExon;5'UTR	RFTN2	0.4635643	0.6110171	-0.147452857	0.5297238	0.6110171	-0.081293
cg23335356	12	48750347	63547716	63547766	S_Shelf	AGCAGCTATCTCCTTCACTTACTAGCAGTAAGACTTTGTTTTCATCTTCG	R	TSS1500	AVPR1A	0.9048471	0.9445386	-0.039691429			
cg23339693	6	24763372	10738257	10738267	N/A	CGTTCTGTCAAGTGCTGTATGTGGGCCAGTGCCCATAAGCCCTGATGGTGA	F	N/A	N/A	0.4826414	0.6047757	-0.122134286	0.5461	0.6047757	-0.058676
cg23342105	4	22726475	10147038	10147088	Island	CGCTCGGGCATGCACCGAATACTGGCTGGTCCTCGTGCCACCTCGTCGA	F	N/A	N/A	0.9026571	0.9282371	-0.02558			
cg23349767	19	14661365	15482099	15482149	N/A	TGGTGTCCTCATCCTTCATCCTCACAACAAGGCACAGGCAGGCAGCACG	F	Body	AKAP8	0.8253071	0.8590957	-0.033788571	0.8394688	0.8590957	-0.019627
cg23350747	13	29651315	111774082	111774132	N/A	CTGCGGGAACGAAGCCAGGTGTGCCTGCTACCTGTGAAGCACGCAAGGACCG	F	Body;Body	ARHGEF7	0.8243614	0.8799543	-0.055592857	0.8363863	0.8799543	-0.043568
cg23352695	17	54709300	29648861	29648911	N/A	CGGGGAGTTTGGTCTCAAGGCACAGTCTGCTGCACCACTACTAGAGA	R	Body;TSS200;Body;TSS200	NF1	0.7462114	0.8359386	-0.089727143	0.78873	0.8359386	-0.047209
cg23353000	17	45651350	42120896	42120946	N/A	CGGGGTTTTTTGGTGCTTGAGTAAGCGTTGCTTGTTGCTGCTTAAAATA	Body	LSM12	0.4528843	0.56003	-0.107145714				
cg23354735	17	14635391	37077918	37077968	S_Shelf	TTGTCTCATTTTGGTCTGTTTTGGTCCCCTCCCTCCGTGGGCTTGTGCTCG	R	3'UTR	LASP1	0.7650686	0.8684686	-0.1034			
cg23356309	5	24627383	140344620	140344670	N_Shore	CGGACAGTTAAAGGAGCCAAGGTTGTGATCCTGACACCCAGAATTCAAAG	R	Body;TSS1500;Body;Body;Bo	PCDHA7	0.6473643	0.7490743	-0.10171			
cg23364656	10	30707481	72362715	72362765	S_Shelf	CCGCTTGTGTCCCTGAGTCCCCGAGGTCCTACCTGGGAGATCTACCGAG	R	TSS200;TSS200	PRF1	0.7294	0.7892229	-0.059622857	0.7564375	0.7892229	-0.032785
cg23367358	2	49746455	106043573	106043573	N/A	CGCCCTTGGCACTGTAAGAATCCAGGCGAAAGGAAAAAGAAAACCTGCAA	F	5'UTR	FHL2	0.7700557	0.8417757	-0.07172	0.7970838	0.8417757	-0.044692
cg23370328	14	23755447	47121132	47121182	Island	GACGACTCTCTTTCAGGACGTCCCAACCAGAGACGCAGGGACGTCTGCG	R	TSS200	RPL10L				0.791465	0.8680614	-0.076596
cg23370394	17	18708484	79410520	79410520	N_Shore	CGCGACCACCTCGTGGCATTGCAGTGCGCCTGGCCGAGAAGGAGCACAC	F	Body	BAHCC1	0.8610386	0.8975914	-0.036552857			
cg23373850	11	37709361	75898132	75898182	N/A	CGGTACGCTCACACCTGCGGCAGGTGACGTAGCAGCACCAGTGGTACTTA	F	Body	WNT11				0.850245	0.9059657	-0.055721
cg23383189	5	25655374	176560116	176560166	Island	CGGGGCCTGAGGCCTGAAGACCCCAGCCCAAGCCCCCAGGTGAGCCCTG	F	1stExon;TSS1500;5'UTR	NSD1	0.1620271	0.2176957	-0.055668571			
cg23390619	10	64789404	49687769	49687719	Island	GCATGATTACCTGGGAGCAAGGGTTCTAGAGGGTGGGCATGCGATCTACG	R	Body	ARHGAP22	0.79893	0.8440343	-0.045104286			
cg23402920	2	45743475	3176003	3176053	N/A	CGAGGCCTCTCTGTCGCGCGGCGGAGCTGCTGCTGCTGCTGAGCT	N	N/A	N/A	0.8669186	0.90489	-0.037971429			
cg23411043	17	44788505	78157950	78158000	Island	CCTTCTCCTGCAGCGCATTGCTATAGTGCAGCGAGAGGCTGAGCATCTCG	F	Body	CARD14	0.75989	0.8340186	-0.074128571			
cg23414387	1	40611378	47264866	47264916	N/A	CGTCTGCCTCCGCAGCAGAGTGCCAGTGGATGAGCTTGAGAAAGCCTAAGACCA	R	1stExon;1stExon	CYP4B1	0.6950786	0.7767086	-0.08163	0.72644	0.7767086	-0.050269
cg23418510	10	17676369	25240960	25240710	N_Shore	CGTGGGCACAAGGTCACAAGGAGCTGGATCCTGAGAGAATTGGAGAGG	F	Body	PRTFDC1	0.6670029	0.7655829	-0.09858	0.7140085	0.7655829	-0.051498
cg23419490	11	59794510	2904746	2904796	N_Shore	TACTAACTTATATTTTCTATTTATGTCCAGGCGTGGACCGCTCTGCCACG	F	3'UTR;3'UTR;3'UTR	CDKN1C	0.89923	0.9378871	-0.038657143	0.9222413	0.9378871	-0.015646
cg23419606	17	25627495	79914671	79914721	Island	CGGGGCTCCCCACCCACAGATGCCACTCACCCAGGCCCTTCTGGGGCAA	F	Body	NOTUM	0.8801457	0.92395	-0.043804286	0.9034063	0.92395	-0.02544
cg23428143	14	54685417	57385648	57385698	N/A	AGCTTCTCCATGATAGTTTCAGTTTTTACACACACACACCTGTAATCTCG	R	Body	OTX2OS1	0.5634371	0.6534957	-0.090058571	0.5806788	0.6534957	-0.072817
cg23429457	14	44753450	35135441	35135491	N/A	CGACACACAGGTGTTTATGAAGCATTTATGGAAGACTTTTCTTCTCCTCG	N	N/A	N/A	0.3408029	0.5181471	-0.177342286			
cg23430652	1	63648423	1565027	1565077	Island	AGTTTCTTGCTGACGACCACCTGGCACCTGATGCACTTCTTCATCCTGCG	F	Body;Body;Body;Body;B	MIB2	0.5978857	0.6854443	-0.087558571	0.63946	0.6854443	-0.045984
cg23433345	12	29649364	77059628	77059678	N/A	GGTGTGTACTATGCTTCCTCTTTCCTGACATTGCCTCTGAGCCACATCCG	R	N/A	N/A	0.6908514	0.7388557	-0.048004286			
cg23434815	10	65705370	75839302	75839352	N/A	CGTAACCAGGTGTTGTTGGATCATGCTTTGTAACAATTATTTTCTTAACG	F	Body;Body	VCL	0.6742014	0.7991471	-0.124945714			
cg23438040	20	60762303	32319291	32319341	N_Shore	GGCTGTACAACATGGTCCTGGCACCTGGCACCTGATGCACTTCTTCATCCTGCG	F	TSS1500	ZNF341	0.7627914	0.80574	-0.042948571			
cg23439460	10	31620340	102809954	102810004	Island	GACTGAGCGGGCTCCCCCGGCCTTAATGAGATAATCAATACTTGTTCTCG	R	N/A	N/A				0.2393025	0.1954829	0.0438196
cg23439621	14	25802336	102228266	102228266	Island	GGACTCAGTGTGCCTGAGTTCCCTCTGTTTTTATTCCGCCATGAGCGGCGCCG	R	1stExon;1stExon;5'UTR;5'UTR	PPP2R5C	0.1247043	0.1710629	-0.046358571	0.1402325	0.1710629	-0.03083
cg23445945	10	20793456	4822998	4823048	N/A	TTTTAGCCAGAGGTCTCTATAGACATGCCATCAAATAGTAATGGCAACCG	F	N/A	N/A	0.8022743	0.8673357	-0.065061429			
cg23448803	3	72735480	36754544	36754594	N/A	CGGGAAGTTCCAGTCACTCTGCATCCTCGCTAGTAGTTGGTAAGGTCAGT	F	3'UTR	DCLK3	0.8704043	0.8968071	-0.026402857			
cg23451678	3	74666321	112323619	112323669	N/A	CGGGGTCCAGGAATTCCTACCAGAATCTGGCACTGCAGCCAAAGGCGAT	R	3'UTR;3'UTR	CCDC80	0.4284957	0.5820386	-0.153542857	0.500015	0.5820386	-0.082024
cg23459386	12	74602314	123834919	123834919	N/A	CCGGGGTGGCATTTGGAGTTTGACGCCCTGCATCTGTCAAGCTCAAAGG	F	1stExon;1stExon	SBNO1	0.8647043	0.9224943	-0.05779			
cg23462129	5	21784324	185589	185639	S_Shelf	CCTGGGCGGCCTCTGGGGCTGTGTGATGGTGGCTGTCCATACTCAGGACG	F	3'UTR	PLEKHG4B	0.84087	0.8962071	-0.055337143			
cg23465685	7	21616402	155617333	155617383	N/A	GAGATGACTTCTCCAGCCCTTGGTGGTGATGGAATGTTGGGAACCGTAGATCG	F	Body	CLIC4	0.8776757	0.90922	-0.031544286			
cg23471293	17	32808453	79797038	79797088	N_Shelf	GCTGCCCAGAAGGAAGTGCTGCTGGCCCAGCACAGGATGCCTGGAAACCG	R	N/A	N/A	0.7007029	0.7800629	-0.08227			
cg23474890	12	45710506	122467179	122467229	N/A	CACTGGTATAATAAGAAAAGCCGGGCCGTAGCGTCCTCTGATGGAACACG	R	Body;Body	BCL7A	0.8146957	0.8802729	-0.065577143			
cg23475489	8	11719434	16142299	16142249	N/A	CGGAGTTTAATTACACAAGGAAAAAAAAATCATGAATTGGGCAGCACCC	F	N/A	N/A	0.5058171	0.60873	-0.102912857			
cg23477168	2	28796502	192750645	192750695	S_Shelf	CGTGTGGCCTTACTCACGACTCACCACTGCCAATCGCGGAGGTGCCAGT	R	N/A	N/A	0.8928257	0.9249614	-0.032135714			
cg23481873	20	42628322	464150	464200	N/A	CGTGCTTTCCAGATTTGCTGCTTTCTGCTGCTTCTGCTGCTGCTGCTGCG	N	3'UTR;3'UTR;3'UTR	CSNK2A1	0.73023	0.8177529	-0.087522857			
cg23497020	12	56808379	50616562	50616612	N/A	CTTTCTTGTTTTTTCCCCATTAACTTTTGGGTAAAAATCTCTTGTTTCG	F	Body;TSS200;Body	LIMA1	0.5515957	0.7196914	-0.168095714			
cg23498494	7	53702389	90095672	90095722	N/A	CGGGGTTCTCCTGAGAGGACACCTATTAAGATACCCTTATTGTGTTTTCC	F	N/A	N/A	0.79421	0.8504871	-0.056277143			
cg23499133	3	58746498	50189428	50189478	N_Shelf	GGAGGTAAGGCCAGTAGGAAGGCCAGCCTGTGCCTCCTCCAGTTCACG	F	N/A	N/A	0.78401	0.8547443	-0.070734286			
cg23513211	7	37740324	72726717	72726767	N_Shore	CGGCCCCCAGGCCTTGGCAGCCAGGGACACACTGAAATCCCCATGGTTCC	R	3'UTR	TRIM50	0.8114143	0.8395757	-0.028161429			
cg23517677	11	38645416	62528272	62528322	N_Shore	ATGCTATCCATTACTACTTTCTTCCTAGATGCCAGACACTGTGCTAAGCG	F	TSS1500	POLR2G	0.7

cg23921838	6	69749389	151941727	151941777	N/A	CGGAGCTTGAGTGGCTTCTGCCCCACCCTGAATCATGCACCCAATAATGCA	F	3'UTR	C6orf97	0.8074771	0.86611	-0.058632857			
cg23922520	2	59626384	236580152	236580202	Island	CGTCTCCCTGTTAGTGCTACCATCTGTCAGTGTTGTGATGTGGACTCAGC	F	Body;Body	AGAP1	0.5831657	0.6782871	-0.095121429			
cg23924137	6	74794327	157263588	157263638	N/A	CGCTGCCTCTGTGGCCCAGGCATCCAGACCACAGAAGAGCTCCGTGGCCT	R	Body;Body;Body	ARID1B	0.8707257	0.9103886	-0.039662857	0.884595	0.9103886	-0.025794
cg23924647	12	57763346	122227872	122227922	N_Shelf	ACATCCTCTGAGGCAGGAAGCTCGAGTGAAGTCTGAACTTTCCTGGGCCG	F	Body	RHOF	0.6476657	0.7468757	-0.09931	0.6946525	0.7468757	-0.052223
cg23933339	15	58649483	57731055	57731105	N/A	GAGTTTGTGGATGACGAGGAGGACCTCCGGGACCGAGCTCCATCCAGGACG	F	Body	CGNL1	0.7429757	0.7982814	-0.055305714			
cg23938543	6	74721317	30036994	30037044	N_Shore	GAAGAGGGCTGTGGTCATACACACTGTGTACGTGGCCACCGCAAAGGACG	R	Body	PPP1R11	0.85139	0.8831086	-0.031718571			
cg23941963	7	22798388	204401	204451	N_Shelf	CGCAGTGGTCCAGGGCACTGAGCCCAGCCCCAGTCTTGACCATGGCCTGT	F	Body	FAM20C	0.8846114	0.9066557	-0.022044286			
cg23948452	5	62716418	1077231	1077281	N_Shore	CGCGGTTCCCCAGACCCTGTGGTGACCTTTCTCATCAGGCCACCCTCACC	F	Body	SLC12A7	0.8360243	0.8658614	-0.029837143			
cg23949524	12	63752448	96588205	96588255	N_Shore	ATTATTCCCCAGGCGGTGTGCAGTCTGTGTAAACAGGCTTTTCCGCCCCG	F	TSS200	ELK3	0.1757957	0.2080114	-0.032215714	0.1889825	0.2080114	-0.019029
cg23951190	3	14795361	131538721	131538771	N/A	CGCAGGGCCCAGCTGCTCCCTCTGGGGAAGAAAGTTGTTCTTTCAGACTA	F	Body	CPNE4	0.7150086	0.7731357	-0.058127143			
cg23951296	5	53645345	7512782	7512792	N/A	AGCCGATACCTGCAGTACAGTGACCACGCCAGCGTTCTTGAGGATCCACA	N/A	N/A	N/A				0.8540063	0.8945886	-0.040582
cg23953052	19	50767462	55586493	55586543	N/A	CGTCTCACAGATGAGAAAATGAGGAAGAGAAGGGTTAAGAAACTTGCATG	R	TSS1500	EPS8L1	0.63326	0.7269686	-0.093708571			
cg23966795	2	67734340	160068465	160068515	N/A	GGGGCATCAGAGAAACCACAAGTTGGAGCAACTGACAAGGGGCGAGTGCG	F	Body;Body	TANC1	0.8908386	0.9131786	-0.02234			
cg23977256	6	18643354	30123461	30123511	N/A	CGGAAAGGAGAGAAAATTTTGCAGGATTTGCACTATGACTATGTTATGAC	R	Body;Body	TRIM10	0.8983314	0.9396129	-0.041281429			
cg23978004	4	17702340	142144580	142144630	S_Shelf	CCGGGGCAATTTGGAAATCTGGTACGGTCAACCAATTGTTTTTGTCTTTTG	F	Body	ZNF330	0.8919543	0.9227457	-0.030791429			
cg23978062	1	63789413	26357956	26358006	N_Shelf	CGCCCTGAGGGCAGATTCAGCGCCCTGATCTGGGTGGGGCCCCCAGGCCA	F	Body	EXTL1	0.8544343	0.8891843	-0.03475			
cg23997911	6	47716500	161575382	161575432	N/A	TCCTCTTTTTCTACTTCAGTCTCCAACAGCCCCGGCAGGTGGCTCTGACG	F	Body	AGPAT4	0.88464	0.91382	-0.02918			
cg24010658	8	27717488	144544041	144544091	N/A	TGGTTCTGTGGGCTCCTGGTGAAACTTGAGTGGTACGCTGCACCACAGGG	F	Body	ZC3H3	0.8214057	0.9096914	-0.088285714	0.8624025	0.9096914	-0.047289
cg24018633	14	26706473	22971114	22971164	N/A	GAATAGACCGCCATAATAAACAGTCTTTTCCGCTGCCTCTTTAGCCAACG	R	N/A	N/A	0.7529171	0.8170043	-0.064087143	0.78058	0.8170043	-0.036424
cg24020650	7	64808475	152564119	152564169	N/A	CGGTGGGGACTTCTGGTGGTCTTGCTGCCCCCCCTGGCTATTTTGCTTCAT	R	N/A	N/A	0.8502186	0.8882443	-0.038025714	0.8646638	0.8882443	-0.023581
cg24026619	14	63737348	59027109	59027159	N/A	CGGCATACATGAGAACCAGCCTGTGAAAGAGGAGGGCAATTTACCATGTG	R	N/A	N/A	0.6466229	0.7433571	-0.096734286			
cg24034746	1	35693328	1175851	1175901	S_Shore	AGCCGTACTCCGGCTAGACAGCAGTGACCAGCGCTCCTGGCCTGGCACCG	R	N/A	N/A	0.8556671	0.9019814	-0.046312286			
cg24037820	17	20750301	79639690	79639740	N/A	CGCTCCCCGTGCAGCTGCTGCTGCCGCTGCTTCAACGCTCTGTAGGCCTG	R	Body	CCDC137	0.6648371	0.7241043	-0.059267143			
cg24052246	12	49608408	64554454	64554504	N/A	CGGCCCCAGGACCCAGCCACTGCGAACAGAGTCTGGGCTTCCTTGTGAA	R	N/A	N/A	0.88181	0.9167271	-0.034917143			
cg24060475	4	56628497	85801119	85801169	N/A	TAACAAGGTTTATACCACCTCTGTGAGGCAGAATACGGCTCTAAAGACG	R	5'UTR;5'UTR	WDFY3	0.8457814	0.8912386	-0.045457143			
cg24064224	10	13671485	1156594	1156644	N/A	GTGTGCTCTTACAAGTCATGTTCAGAACGTCCCAGACAAGTGACCAAACG	F	Body	WDR37	0.8196329	0.8750557	-0.055422857			
cg24067911	6	65690372	16729610	16729660	N/A	CGCTCGGCTTTCTTTGAAATGTTTTCTCATCTAAACTTGGGAGCTGCTGGC	F	5'UTR;5'UTR	ATXN1	0.74698	0.8496857	-0.102705714			
cg24076537	4	73700502	139859030	139859080	N/A	GCCTTTTGCTCTCAAGGCAAGACCAAGATTTAACCCAGAAACCAGAGGACG	F	N/A	N/A	0.6424757	0.7406614	-0.098185714			
cg24078695	1	30794405	230882977	230883027	N/A	CTGCAGACTCAGAGGCAGCTCTGGGGCCTGGCACATTCCACTCAGAGGCG	F	TSS200;TSS200	CAPN9	0.8616271	0.8995	-0.037872857			
cg24082799	12	18627324	27930472	27930522	N_Shelf	CGTGTCTCACTGCACCCTCATAGAGAATGGAAGTGTGAAGGGTTGATGTG	F	N/A	N/A	0.7864571	0.8355829	-0.049125714			
cg24083274	7	44782412	121977191	121977241	N/A	ATGGTCTGCTGCCCACCTAATTTTGCCTTATTGTCAGTCACTACTTACCG	F	Body;Body;Body	CADPS2	0.92075	0.9398014	-0.019051429	0.9120113	0.9398014	-0.02779
cg24086124	2	43804486	45487797	45487847	N/A	CGTCTCCAATGTGTTGTTCTCAGGTCAGAGTGCAGACAATTTTGGGGT	R	N/A	N/A	0.9143743	0.9443557	-0.029981429			
cg24089936	14	32785456	49341594	49341644	N/A	TACACTCAAACCCATACTGATTGCCTCTGAAGCCTACGCTCCATTAGTCG	R	Body	AGBL4	0.7779471	0.8247157	-0.046768571	0.7896213	0.8247157	-0.035094
cg24092939	12	33719465	49181106	49181106	N/A	CCAGGGGGCTTGGAACATGGCCAGAAACTAGTCCTTTGGGAACAGGTCCG	F	5'UTR	ADCY6	0.5823457	0.71136	-0.129014286	0.6576188	0.71136	-0.053741
cg24095583	12	13632477	14975112	14975162	N/A	TCCAAAACTGCCACCTCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCG	F	5'UTR;5'UTR	C12orf60	0.8730471	0.9159586	-0.042911429			
cg24104608	6	14718446	170461816	170461866	N/A	TGGTGTGGACACACTGCTCTTTAAAAGTGCAACAGCCTCAAAAACAATCG	R	N/A	N/A	0.7892414	0.8547729	-0.065531429			
cg24105933	4	66605502	8270795	8270845	N_Shore	AGGGTACTAGGAACACACACAGTGTGAAGACCGCAGCTCCAGGCTGTGCG	R	TSS1500	HTRA3	0.8483157	0.88728	-0.038964286			
cg24110396	10	19636464	35589246	35589296	N/A	TCTGTCTCATCAAAGCAGCAAGGCTGCCACGCCCTGCCTGACATGCCACG	R	5'UTR	CCNY	0.7178343	0.7927886	-0.074954286	0.7592013	0.7927886	-0.033587
cg24114458	7	45685452	92380449	92380499	N/A	TAACTAGAACCTCTGGAGGTGCTTTCTGAATTGCAAACAGGGACAACAG	F	Body;Body	CDK6	0.7157714	0.8285243	-0.112752857	0.7835913	0.8285243	-0.044933
cg24119469	4	50705439	1625181	1625231	Island	CGGGGGCCTGGTGGCCTGGACCGTGGGCCAAGCCTCACAGCTGCCATCCC	R	N/A	N/A	0.8022986	0.8540214	-0.051722857			
cg24127115	3	31767408	40341035	40341085	N/A	CGGACACTGTTCAGCCCAGTTATTTGCTACTTTATAACAAGGGTGGCCTT	F	N/A	N/A	0.8538557	0.9058786	-0.052022857	0.8820038	0.9058786	-0.023875
cg24130476	13	59761439	113893787	113893837	N/A	CATCTCAGGGCTCGACCACTTACTGGATGAGACCGCCGCCTGGCACCTCG	R	Body;Body	CLL4A	0.8453888	0.88632	-0.040931429			
cg24137448	17	27718440	46189113	46189163	S_Shelf	CGCAGCCAGAACAGGCGGGTCCAGATGTAAAACTTTTGCCTTGAAGAATG	R	5'UTR;5'UTR	SNX11	0.8550943	0.9102971	-0.055202857			
cg24143221	6	69788469	31780526	31780576	N/A	AGTTCAATCACAGCGGTGTTCAACCAATTTCCAGAATTCTGTTCATCTCG	R	5'UTR	HSPA1L	0.9204014	0.9492186	-0.028817143			
cg24145486	19	13612426	1054884	1054934	S_Shelf	CGCCTCACCTGTGGAGCTATGCTGCACTGGGGGCTCCTCCAGTCCTGCC	R	Body	ABCA7	0.9130771	0.9427186	-0.029641429			
cg24150244	22	21785409	28402194	28402144	N/A	CGGAGTCTGGGTCAGCTGCCAGATGCGTGCAGGGTGGTCAGCACTGGTT	F	Body	TTC28	0.7833629	0.8425529	-0.05919	0.8097475	0.8425529	-0.032805
cg24150528	5	19620403	43125550	43125600	S_Shelf	GGCCACTTATTTTTTAAGACTTAAAAATTCTGCTCAGACTTGGCCAGTCG	F	Body	ZNF131	0.90717	0.9515586	-0.044388571	0.9265063	0.9515586	-0.025052
cg24158045	2	33748502	202707626	202707676	N/A	CGGGTATCTCCACACAGCAGAAATCCTCAGAGAAGCTTAAAGATATGTAG	F	Body	CDK15	0.7579471	0.8378486	-0.076841429	0.7673538	0.8378486	-0.067435
cg24158482	17	35706485	55715302	55715132	N/A	CGGGAGATGTAGTGTATTTTGGGTTGGGGAAGGTTATGGGAAGG	F	Body	MS2	0.8800971	0.9125614	-0.032464286			
cg24159253	17	16644302	78475908	78475958	N/A	CGGGCTCTGCCAGTGTGTTCCTGCACCACGGCTCTTGCCTCAAAGCCACC	F	N/A	N/A	0.7084529	0.7826	-0.074147143	0.7274075	0.7826	-0.055192
cg24165121	20	24686373	23398291	23398341	N_Shelf	CAACAAACTAAAGGACAAGACAACTTCCTTTGGAAGTAGTTTTACTAAACG	R	Body	NAPB	0.7886171	0.8487429	-0.060125714			
cg24166149	19	27715430	42449148	42449198	Island	GAGGCCCCCAAGTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC	N/A	N/A	N/A	0.2951571	0.3717171	-0.04202			
cg24170465	4	33654391	159094277	159094327	N_Shelf	TCTAATTGACACCCCAAGGTCATCAGCCCCTGCCTTTGTGCTAGGACACG	F	TSS200;TSS1500;TSS200	FAM198B	0.4891657	0.6082629	-0.119097143	0.530885	0.6082629	-0.077378
cg24184737	21	38774452	31655982	31656032	N/A	TGTTGCTAAGCAAACCAAGCATTCTGTTAAATCCCTTCTTAAAGAGTGTCG	R	TSS1500	KRTAP24-1	0.8443329	0.7845057	0.059827143			
cg24190139	3	36695486	48951829	48951879	N/A	CCAAGTGGAAGCCATGTTGCCCTTTGTGGCCTAACCTTCAAAGTCACACG	F	N/A	N/A	0.7964471	0.8553829	-0.058935714			
cg24200083	22	13755416	19279295	19279345	Island	CCGCGCACGCCGCAGTGCCCGAGCTCCCGGTCTGGCACCTCCGCCCTCCTC	F	N/A	TSS200;TSS200	0.2347543	0.30986	-0.075105714	0.26803	0.30986	-0.04183
cg24201173	15	60655341	96389108	96389158	N/A	CCTGGAGCATGTTACAGTAACATCTGCTTGTTAAGAGTCTTTAGGGAGCCG	F	N/A	N/A	0.7513943	0.7993643	-0.04797			
cg24201362	6	22671406	467681	467731	N/A	TTCAGGGCTGAAAGTCGCCGTGGTCCCCAAGGAAGGTGCGGTGCCCGACG	F	N/A	N/A	0.8755314	0.9244829	-0.048951429	0.9022425	0.9244829	-0.02224
cg24215525	12	16702476	122931412	122931462	S_Shore	GCCTAGCTGCGGGAGCGATGCTGCACTGGGGGCTCCTCCAGTCCTGCAC	R	N/A	N/A	0.7618988	0.8341157	-0.072217143			
cg24216596	3	62602412	55518142	55518192	N_Shore	CGCCTATTTGGCGTCCCTCATCGTTTCACTCCCAGAAACTTGGGGCCTAA	R	Body	WNT5A	0.5833686	0.6439843	-0.060615714			
cg24216966	6	39754341	31540121	31540171	N/A	CGTGCTTTGGACTACCGCCCAGCAGTGTCCTGCCCTCTGCCTGGGCCTCG	F	1stExon;5'UTR;5'UTR	LTA	0.7969129	0.85751	-0.060597143	0.8301813	0.85751	-0.027329
cg24218620	17	56752312	27229069	27229119	N_Shore	CGCAGCCACAAAGGAGTTCCTTCCAAAGGCTATTTCTGACAGTCCGGAGCC	F	Body	DHRS13	0.6833443	0.7538471	-0.070502857	0.6960788	0.7538471	-0.057768
cg24221639	4	16678471	62778452	62778502	N/A	CACATTTATGCCAGAAGTACACGAAAGTACCTGGATCCAGTCCTCCTCCG	F	Body	LPHN3	0.9123271	0.9376729	-0.025345714			
cg24221738	4	15665463	166125552	166125602	N_Shelf	CCTCCTCTGGGTTAGTTTTGTCTTACATAATTCTTTGCTTAAGGGGTTCG	F	N/A	N/A	0.84229	0.8831414	-0.040851429	0.8305063	0.8831414	-0.052635
cg24227984	19	64724393	4474970	4475020	S_Shore	CCCTCTTTGGGGAGGGGTCCCCAGGAAAGGTCCTGGGAGTCCATAGACG	R	Body;Body	HDGF2	0.4989657	0.5839271	-0.084961429			
cg24233332	6	54623237	31673800	31673850	S_Shelf	AAATTAGCCGGGTGGTGGCGGGCGTGCCTGTTGTTGAACG	F	TSS1500	LYSGF	0.91172	0.9336471	-0.021927143			
cg24235466	11	12647490	64521142	64521192	N/A	CGGCCGCCACCCGCTGTGCCCAGAGAGCCCAGAGCTAGAACCAGACCCAG	F	Body;Body	PYGM	0.8995229	0.9268571	-0.027334286			
cg24240077	11	23617396	77574320	77574370	N/A	CGCCCATTGCGCTCCCGATTGGGCAAATAAAGCCTTGCCATTGTTCCT	R	Body	C11orf67	0.6409157	0.7117771	-0.070861429	0.6828125	0.7117771	-0.028965
cg24242051	6	30694509	3270566	3270616	N/A	AGTGAGCAAGGTGGCAGGAGCCCACCCAAGCCTGATACGCATCTGGGCCCG	F	3'UTR;3'UTR	SLC22A23	0.8764986	0.9120443	-0.035545714			
cg24250588	1	68808457	43203008	43203058	N_Shore	GGCCTTCACCAGGAGAAGATTTTGTTCCTATTGGAGGCAGCCAGCCAGG	F	Body;Body	LDN19	0.5697986	0.7191586	-0.14938	0.6446138	0.7191586	-0.074545
cg24256810	3	62717435	195750746	195750796	N/A	CGCTGAGGCATCTGTGATGTCTGCTGTAAGTGCCACCAGGCTCTCCGCTG	N/A	N/A	N/A	0.6225171	0.6753629	-0.052845714			
cg24258108	8	20749300	38236714	38236764	N_Shelf	TGCCCAGCTGTCATAAGTATCCTGGTTCCTTGGACAGGTATTCATATACG	F	5'UTR;5'UTR	WHSC1L1	0.7808714	0.8754471	-0.094575714	0.8242675	0.8754471	-0.05118
cg24262691	11	57763342	7547326	7547376	N/A	TCCTGCCACACGAATGCCAGGGCCTGACGCCACCTGAGAGCACCTGAAGCG	N/A	N/A	N/A	0.8523486	0.88708	-0.034731429			
cg24266624	12	58611303	133220636	133220686	N/A	CGTCACTGGGCGTAAGTGGTAATGTCTGTGGTACACACAAAGCACACG	R	Body	POLE	0.8897843	0.9207643	-0.03098			
cg24269377	12	54631333	3580189	3580239	N/A	TCTCTGAGCGCTGCGTCACTTGGTTCCAGGCCCCTAGAGCTTTAGACACG	F	N/A	N/A	0.6873243	0.76891	-0.081585714			
cg24271203	12	19745410	122658897	122658947	N/A	GATTTAGCTGCATTTTCTCCAGAAAACACTCAAAAGTTGGCCACCACCG	F	TSS200;5'UTR	IL31	0.77953	0.8528571	-0.073227143			
cg24274164	12	37681347	123734136	123734186	N/A	AGTGAGGGCTTGGCGGGCCCCGACCTAGGAGTGGCCGGCTGGTGCCGCCG	F	5'UTR;5'UTR	C12orf65	0.9040057	0.9395529	-0.035547143	0.92093	0.9395529	-0.018623
cg24278165	8	67608476	23083551	23083601	S_Shore	CGCAGGCAGGACCGTGACTCGCGTGGCTTTCGGGAGGCTGATTACCCACG	F	TSS1500	TNFRSF10A	0.9102943	0.9458886	-0.035594286			
cg24290299	12	49711385	121813316	121813366	N/A	TTTTTCGCTGTTTGGGGCGATTGCTTTTTATGAGCTGTGACACTCACCG	R	N/A	N/A	0.7218529	0.7749614	-0.053108571			
cg24296900	12	41689363	49657587	49657587	N_Shore	CATACTAAATGCCTCTCTGACCATCTCTGCCACAGCCTCTGAGAGCCCG	F	TSS1500	TUBA1C	0.8822486	0.9239	-0.041651429			
cg24310395	3	49761405	39309435	39309485	N/A	CCAGGAGGCTGTTTTGAAGGGTTTCTGAGGGACCCATCTGTGGTATCACG	F	Body;5'UTR;5'UTR;5'UTR	CX3CR1	0.7179414	0.8086643	-0.090722857			
cg24313572	1	71733458	56050060	56050110	N/A	CGGCCCCTGAAAGTGGCAGAGTGGGGGCAACCCTCAATACATATTGGTTG	F	N/A	N/A	0.83942	0.8794457	-0.040025714	0.8566363	0.8794457	-0.022809
cg24317310	17	13673430	72363656	72363606	N/A	CGTGGTTGGTCTGCTGCTGCTGCCACCACCTGCTGCTGCCACATCTCCAG	F	TSS200	GPR142	0.6278686	0.68515	-0.057284429	0.6539225	0.68515	-0.031228
cg24331786	17	64645407	76895244	76895294	N_Shore	CCCAGGGATGCTGATGCTGCCATCTGGGGGACCACGCTTGGAGTACTGCG	R	Body	TIMP2	0.85389	0.8828543	-0.028964286			
cg24331824	11	61688416	64458869	64458919	N/A	GGGCTGGGTACCTGGAAGCCAGGTGCTGAGTATATAGGTTCACTGGAGCG	F	Body;Body	NRXN2	0.91599	0.9526943	-0.036704286	0.9396825	0.9526943	-0.013012
cg24336219	12	38753415	128998713	128998763	N/A	AAAGTGCTGTACTTACAATGCTAAAGAAAGCATCACAATCCAAGTTGGCG	R	Body	TMEM132C	0.8370643	0.8933514	-0.056287143	0.8489613	0.8933514	-0.04439
cg24339597	3	59745384	127199198	127199198	N/A	CCGGAACTGTTCTATACCACCACCATCTCTAAAATGCCTAAGACTCAGCTC	N/A	N/A	N/A	0.7743114	0.8241514	-0.04984			
cg24345551	6	56737411	33360652	33360702	S_Shore	CGCCTAGCATGTAGGTGCTCAATTCAATGCATTGAATTAATAGATCGAG	R	Body	KIFC1	0.5149	0.6185043	-0.103604286	0.5687325	0.6185043	-0.049772
cg24346429	20	13738334	57428032	57428082	N_Shore	TCATGCCCCCAGGCTGCCCCCCCAGCCCCTCTTCCTTGGTCTATCCTTACG	F	TSS200;TSS200;3'UTR	GNAS	0.3799814	0.48413	-0.104148571	0.423875	0.48413	-0.060255
cg24356700	7	19799367	100482725	100482775	N_Shore	AGGATTGGAGAGTTTCCCCTAAAAGCACCCCTAACGTCAATGTCG	F	Body;Body;Body;Body	SRRT	0.6357986	0.7211286	-0.08533			
cg24366105	7	29749486	2296929	2296979	Island	CAGCTCTGTTCCAGACACAAGGAGCCAACCCAGGGGAGCCCACCAGGACG	R	Body	SNX8	0.6604571	0.72873	-0.068272857			
cg24368400	2	13772436	122210472	122210522	N/A	TATTTTTGTATGAATAAATCCTAATAGTCCTAGGAACCCATTCAAGAACG	R	Body;Body;Body	CLASP1	0.8934971	0.9215271	-0.02803			
cg24368876	1	30729497	170899295	170899335	N/A	TCAGACTGTCCCACTTCTACTTGTAAAACGGAATTTATATTTTGCTCG	N/A	N/A	N/A	0.5282914	0.6625243	-0.134232857			
cg24371534	1	71788418	3384929	3384979	N/A	CGTGCTCTCCAATCGAGCCACACTCCCGCGCGTCATTGTTGAACG	F	Body	ARHGEF16	0.9291357	0.9626871	-0.033531429			
cg24376776	10	65639340	101297245	101297295	Island	ACTTGTAGCAATAATGACCCAGCATTCAGGCCGCCGACTCCCGCTGAACG	F	N/A	N/A	0.1300143	0.0683921	0.061622143			
cg24387126	8	40713401	11617293	11617343	N/A	ATCCCTTCCTTTCTCAGCAGAGCTGTAGCTGACTGTGGCATTACTACG	R	3'UTR	GATA4	0.78332	0.8360343	-0.052714286	0.8138788	0.8360343	-0.022156
cg24415793	12	31687507	51818443	51818493	N_Shore	TGCAAATAAGACAGAGATTTCTAGCAAGCACTTGTGTACGCTTTCTCCG	R	TSS200;TSS200	SLC4A8	0.199469	0.2662286	-0.096795571			
cg24418941	19	32725451	2062522	2062572	S_Shore	CGGGCCTCCAGCCTATCATGCCCTGAGGGCTGCCACTGGGACACTCCAG	N	N/A	N/A	0.76639	0.8177543	-0.051364286			
cg24419108	7	14773421	155971387	155971437	N/A	CTTCCTTGCTGTTGTTGAAATCTGGCCCCTAGTGTTGCTGACGATGCGG	R	N/A	N/A	0.8982871	0.9305414	-0.032524286	0.90971	0.9305414	-0.020831
cg24422732	4	36685456	117522933	117522983	S_Shelf	ATTGTCTATTCTGCTTATTATGTTTATATACCTCCCCACTTTCCAGTTTCG	N	N/A	N/A				0.84027	0.8854971	-0.045227
cg24425705	19	60631337	18704214	18704264	N_Shore	CGTGGGCGTTGGCGATCGTTATGGGCGTTGATAGGGCTTATGGGGCGCCAGC	F	3'UTR	CRLF1	0.8036357	0.8518543	-0.048218571			
cg24432295	17	37701383	70101836	70101886	N/A	CGTCGGGAGCTCAGTAGACAATCAAACAAAAATTCCCTGAATACCAGAAG	R	N/A	N/A	0.85183	0.8885071	-0.036677143	0.8625038	0.8885071	-0.026003
cg24433016	6	12726401	80713408	80713458	N_Shore	CGCTAGCTGGGTGGCTATCCAGAGCTGGGAATGTGAGGGTTCTAAGGATA	F	TSS1500;TSS1500	TTK	0.7232014	0.7849414	-0.06174			
cg24442766	1	34735332	62270328	62270378	N/A	CGTAGAGATTTGCTCTCTCACTGCTCCTAACGGTATAAACTCT	N/A	Body	INADL	0.7443457	0.81775	-0.073404286			
cg24451653	10	63604499	104375165	104375215	N/A	CGCTCACCTTAGGCAGAGAGGAATGAGGGCTCCGGACTCCTGGTTGAATT	R	Body	SUFU	0.8614971	0.8868414	-0.025344286			
cg24459563	17	38644405	65040609	65040659	N_Shore	TTAGTGTGCCTGGCTGAGCCAGAGTGGGCTGGCCTTGGGGCCGAGGGACG	F	TSS200	CACNG1	0.78714	0.8459386	-0.058798571			
cg24459792	1	19657336	31230896	31230946	N/A	CCGTCATCTGCCTTCTCTGCAGGCCACGGGTTCCACCCTCTTCACCAG	F	TSS200	LAPTM5	0.6611557	0.7396171	-0.078461429			
cg24460268	13	22733417	51995368	51995418	N/A	CGACCTGATCCTGGATGTCACTTCAAGCAGTCAGATCGTGGGGAAAAGCC	R	Body;Body	INTS6	0.7168643	0.7999514	-0.083087143			
cg24478966	19	70733401	42460930	42460980	N_Shelf	CGGCTCTGCTGCTCGGGCCCACACGGCCGTCCCATCACAAGCCCGGGGAG	R	3'UTR	RABAC1	0.8618671	0.89192	-0.030052857			
cg24480926	12	17660331	131919579	131919629	S_Shore	ATGAAGCGTGCACTGCGGACACTCACTTTCGGTTTCATGTATTGGCTTCG	R	N/A	N/A	0.7096286	0.7692	-0.059571429	0.7375663	0.7692	-0.031634
cg24487251	19	62667450	66038483	66038533	S_Shore	CGGGACTTTGGTGGACAGCCTTGGTGGACAGGTTCTGAGAAGCCTGTCG	F	Body	RAB1B	0.8848271	0.9115714	-0.026742286			
cg24486037	1	28648377	151345181	151345231	N/A	ACTTTGATCCCGGCGGGTTTGCTGTGCTGGTGTCAGAGGCCGCTGTTCCG	R	TSS200	SELENBP1	0.3955357	0.3110857	0.08445			
cg24487489	6	40625485	33384337	33384387	N_Shore	CGGGATTATTGGGGCCAAGTCATCACCTGGAAGTCAAGGAGCGTTGAA	F	3'UTR;3'UTR;3'UTR;3'U	CUTA	0.6488043	0.7352629	-0.086458571			
cg24512303	8	16741457	76452203	76452202	N/A	GGATTAGCACTCACAGACCATCACAGTTGTGTGCTGTCACATCACCG	N/A	TSS200	HNF4G	0.7916857	0.85156	-0.059874286			
cg24517501	1	60670481	92952702	92952752	S_Shore	GCGCCATAAAAGCACCACTTGGATGACTATTGCAAAGTAAGCCTTCTTCG	R	TSS1500;TSS1500	GFI1	0.82749	0.8801671	-0.052677143	0.84462	0.8801671	-0.035547
cg24531401	7	21730316	1513791	1513841	Island	GTGGGACTGCCTTCTGTCCTTCATCCGCCTGCTGCTGGTGTGTGCTCCCG	F	Body	INTS1	0.3202971	0.3719514	-0.051654286			
cg24535130	17	26671310	79917287	79917337	Island	GGCTGGGCATGATGTGCGGGGTGGGGGCCTGGCTGGGGCTCCAGGAGGCG	R	Body	NOTUM				0.1895338	0.1355848	0.05349
cg24544512	6	57682451	100836966	100836916	N/A	CGCTGGGACTCTCACTCAAACCAGGAAACTGTGACCTGGGCTTCCTCCG	F	3'UTR	SIM1	0.7574014	0.8095143	-0.052112857	0.7495138	0.8095143	-0.060001
cg24545125	2	70665465	21772866	21772916	N/A	CGGGGCTCTACTGTGCTGTCACTCACCTTTGCTGCACTTTGGTCACATTT	F	TSS200	TNP1	0.8339329	0.8714629	-0.03753	0.8554413	0.8714629	-0.016022
cg24551917	2	68633358	206568291	206568341	N/A	CGGGGAGGCAGACAGCACAAGAGTAAAGCAGAGATTGAAAACTAGGGTAT	R	Body;Body;Body;Body;B	NRP2	0.9066571	0.9327457	-0.026088571			
cg24555089	2	51636478	240187690	240187740	N/A	CGCTCCCCATACGTTGGTGTATGAGGATGGGCTCCTCCTGCCTTTG	R	Body	HDAC4	0.8656986	0.9125771	-0.046878571			
cg24563967	17	24725330	74009962	74010012	S_Shore	GGACTCAGGGCGAGGGCGACCAGATGGGCAGACCACACAGGCCCTTCCG	F	Body	EVPL	0.7722686	0.8157071	-0.043438571	0.7875875	0.8157071	-0.02812
cg24576026	17	13769503	75290917	75290967	N/A	GCGCAGAATCAAAAATCACAAGACACGAACATATCCTGCGTGCCTGGCG	F	5'UTR;Body	09-sep	0.8913714	0.9231429	-0.031771429	0.8918375	0.9231429	-0.031305
cg24583704	13	48782361	21047671	21047721	N/A	CGCCCGCCACCCACCTCTGGCCAGGTCCGCTGAGATCACA

cg24976638	7	40796418	101615743	101615793	N/A	ATCAGAATTTTCCTTGCCTGCTGCGGACGGCATCTGCGACTGGCTAGGTTGCG	R	Body;Body;Body	CUX1	0.9311786	0.9567943	-0.025615714			
cg24977891	2	60737489	201733454	201733504	S_Shelf	TCTTAATTTCAGAATGTAGTCTTGTTAAAACCGTTTCCCTCCCTTTCCCG	R	N/A	N/A	0.9054986	0.9404586	-0.03496	0.9249575	0.9404586	-0.015501
cg24979161	14	52690496	94567367	94567417	N/A	CGGGGTTGCATGGTTTGTACTTGGTGGAAGCTGAGAGTAGCCCCAGCTCT	R	Body;Body	IF27L1	0.8707643	0.9129857	-0.042221429			
cg24987293	12	16620343	121792270	121792320	S_Shelf	GCATGGGCACTGCATGCAGCCTCATGCCTGCTTTTTGTTTTCTCAATCG	R	TSS1500	ANAPC5	0.9169529	0.9562029	-0.03925	0.9211763	0.9562029	-0.035027
cg24996605	2	48684371	128381653	128381703	Island	ATCATGTGGTCGCGCCCGCTGCCCAGGGACCAGAACTGAGGCCAGAGTCG	F	Body	MYO7B	0.7200471	0.7578929	-0.037845714	0.7341288	0.7578929	-0.023764
cg24997231	1	52614425	209527535	209527585	N/A	CGCGCTGCCTAGGGGAACTCACAGATCAAGACTGAATAAAATTACACGGC	F	N/A	N/A	0.3440157	0.4270971	-0.083081429	0.353295	0.4270971	-0.073802
cg24997744	17	36625490	79433049	79433099	S_Shore	CGGCGGAGCAGAGGATCCAACCTCCGTGGCTGCACCCTCCTCCGCCCTCT	R	3'UTR	BAHCC1	0.8598357	0.89504	-0.035204286			
cg25008614	15	68611481	44956192	44956242	S_Shore	CGCTTTTCTTATTGTGCTGTTCGCTTACAGGCTCTGGGGTGGTGCCATTT	F	TSS1500;TSS1500	SPG11	0.6035429	0.6827	-0.079151743			
cg25012257	13	35656453	94792894	94792944	N/A	AGTTAAAGGAGCCACATTTCTGAATAAAATTGCTGAAGACAGTGCCTTCG	F	Body	GPC6	0.8265343	0.9015	-0.074965714	0.8730913	0.9015	-0.028409
cg25019486	10	20675407	133728830	133728880	N/A	TGAGGTGGCAAACAACGGAGCCTCCCGTACACAGGTTACTGCAAAGGACG	F	N/A	N/A	0.8968643	0.9390786	-0.042214286			
cg25023165	1	23603331	229275061	229275111	N/A	CGGAGAGCTTGCACGTGTGCTCCAGACCTGCTCAGAGCCCCCCACTGT	R	N/A	N/A	0.82205	0.8813286	-0.059278571			
cg25024195	17	12700434	46144968	46145018	N/A	ATGGTCTCTGTCACCTAGTCTAGAGTGCAGTGGTGCTACCATGGCTCACG	F	N/A	N/A	0.30066	0.4415114	-0.140851429	0.3797138	0.4415114	-0.061798
cg25028293	1	43775312	6528261	6528311	N_Shelf	GTGTCCCATGGGTGCCAGCCCCTGCCAGCAGCTGGAGGAGGCTGGCCTCG	R	Body;Body;Body;Body;Body	PLEKHG5	0.8539871	0.8973186	-0.043331429			
cg25030018	4	67796348	70866995	70867045	N/A	CGAGAAAACTGAGGTTCAGGAGCATTAGGAGTAGTTCAAAGTCATGAAAC	R	3'UTR;3'UTR	STATH	0.49116	0.5674157	-0.076255714	0.4994288	0.5674157	-0.067987
cg25032991	2	56649495	159981152	159981202	N/A	CGATCTCTCTAGAAAAAGTCCCTGTGCTCACAGATTTGTGCTGAAGACGC	R	Body;Body	TANC1	0.5228414	0.6886657	-0.165824286	0.5826088	0.6886657	-0.106057
cg25044765	11	17764457	8084497	8084547	N/A	CGGTAACCTTTTCCTGAGGCACAGGAAAGCATGGAGCACAGAGTGGGC	F	Body	TUB	0.84868	0.8961643	-0.047484286			
cg25044817	2	55783472	24233259	24233309	Island	CGGGAAGCCTAGCCCTAGCCAAGGAAGTAACTTGGGGATGCGTGGTCATT	F	Body	MFSD2B	0.20205	0.25333	-0.05128			
cg25046584	21	46768338	32932066	32932066	Island	TTTTTCTCCTGGAAAAAGTCCCTGTGCTCCCCTAGAGCCAGGGCAACG	F	TSS1500	TIAM1	0.1733929	0.3340471	-0.160654286			
cg25046772	15	17632450	75527224	75527274	N/A	CGTGTTTGCCACCTGCTTCTGAAGCCTTAGAAGCCTTGAGAGCCTTCAGC	R	N/A	N/A	0.6830257	0.7586186	-0.075592857			
cg25063864	18	32654314	77489374	77489424	S_Shore	CATGACCATGAGTGCCTCCAGACCCCGTCCATGTCCTTGGGGTGAGCCG	F	Body;Body	CTDP1	0.8951886	0.9250671	-0.029878571			
cg25064552	1	24716434	153938859	153938909	N/A	TTGAGAAAGTTACTTAAACTTGTCAGCTCGGACGGGCGTGGTGGCTCACG	R	5'UTR	SLC39A1	0.8091071	0.8512957	-0.042188571			
cg25065689	13	38618474	111113462	111113462	S_Shelf	GAACAGCACAGCTTCAAACCTAACACAGCTTAGACGCACAACCG	R	Body	COL4A2	0.8883029	0.9316543	-0.043351429			
cg25066772	14	51635414	93136682	93136732	N/A	GGACCAGAGATCACGCCCATTTGGCTGTGCATTCAAATGCCCTGCTGGCG	F	Body	RIN3	0.74244	0.8210557	-0.078615714			
cg25066972	14	23619482	82002568	82002618	S_Shelf	ACTCATTGCTGGCTAAAGGCAAAAGCTGTAGCAGCTCTAAGCCCTTTTCG	F	N/A	N/A	0.9107914	0.94541	-0.034618571			
cg25071349	18	21602419	24237843	24237893	S_Shelf	CGCTGGTCCTCCTCAATGGATGTTTTTGTTTTGTTGCCAAGGAGGAAA	F	N/A	N/A	0.1429849	0.23722	-0.094235143			
cg25072766	11	10737445	3073488	3073538	N/A	AGCTTTACAGGGCTGATGTTATGAGCGTGTTTTACCGTGAAGGAAATGCCG	F	Body;Body;5'UTR;Body	CARS	0.7108757	0.7673257	-0.05645			
cg25102349	1	2267333	20064059	20064009	S_Shore	TTTATTGATGGGAACCACACAGACTAAATGTATCAGACTTCCCAAGTTCG	R	TSS1500	DDX59	0.7887471	0.8344743	-0.045727143			
cg25105522	17	10669302	43355199	43355139	N/A	CCGCCACCGGAGCTCTGCAGGAGACACCGCGTGAACTATCTCATCGACAA	F	Body	MAP3K14	0.1049727	0.0719579	0.033014857			
cg25105561	1	66658302	91316318	91316368	Island	TGGGCACCGGGGGTGGGGGCTACGCTACGCGTGAAGGGCCTCAGTCCTCG	R	N/A	N/A	0.1538071	0.1271757	0.026631429			
cg25113123	2	28659366	3464991	3465041	S_Shelf	CGGACCCTGCAGCATCCCCAGAGGTGACTGTGACCCCGGGCACTGCTCCG	F	Body	TTC15	0.8687771	0.9075029	-0.038725714			
cg25116200	5	24725482	156698854	156698904	N/A	TCTCAGATGCACCTGCTAAAACTCAACAAGGGAAGCCATGCATCTGCTACG	F	5'UTR;5'UTR;5'UTR	CYFIP2	0.73147	0.80302	-0.07155			
cg25117895	6	72644371	5003999	5004049	S_Shore	CGGGGCCCTCGCCGGCTTTGGGAGTTGTACCTCTCTTAACTCTCTTAA	F	Body	RPP40						
cg25120405	14	50807414	105033924	105033974	N/A	CTGAGGTGGGAACCAGGAGAGGCCAGCACTTCTAGACAGCAGCTCAGTCG	R	N/A	N/A	0.6562671	0.7473629	-0.091095714			
cg25120705	17	53806381	73739874	73739924	S_Shore	CCATCCTGTGTGCGGTAGGAGACCTGGGACTTCCCCGCCGTCCAGGACACG	F	Body;Body;Body	ITGB4	0.81713	0.8658386	-0.048708571			
cg25123881	4	42725474	187510001	187510050	N/A	ATTCAAATGGTTCTCTGGTTGTCTGCCAATACCTGTCATACCCCG	R	Body	FAT1	0.84292	0.8851771	-0.042571143			
cg25125298	5	38605502	71853215	71853265	N/A	CGCCTGTGTTCCTGTAGGACGTTTACAGTTCACACGATGTCTCATCTCTC	F	N/A	N/A	0.5209743	0.5746257	-0.053651429			
cg25127011	13	17651380	32526883	32526933	Island	CGGGATGTTCTCTCTGGCTCTGGCAATATCATGGAGGATCATGCTGGCCT	R	Body	EEF1DP3	0.8784171	0.9077886	-0.029371429	0.8907963	0.9077886	-0.016992
cg25129097	10	47643403	8420138	8420188	N/A	CGCCTCTGAAAAGGCTATGAAGGAAGTTATCCACTTTAAATACGTGAGTG	F	N/A	N/A	0.5449243	0.64288	-0.097955714			
cg25131632	10	53633408	94549040	94549090	N/A	ATCTCCGGCCTGCTCTCCAAGCAGTAACCGCTGCCCACGCCCCGCTCCG	R	N/A	N/A	0.8772571	0.9048771	-0.02762	0.889705	0.9048771	-0.015172
cg25133951	1	53763501	178575267	178575317	N/A	CGGCCTAGTGAGCTGAGGTGTTGCCACCCACTAGGCACAGCTGCTCTGCT	F	N/A	N/A	0.8511243	0.8935586	-0.042434286	0.8582575	0.8935586	-0.035301
cg25134567	17	7062724	64782369	64782419	N/A	CGGTGGCCCCGTGGGACCTTGTGGCTTTGAGTCAGGTGGATCTGGACCA	R	Body;TSS1500	PRKCA	0.67673	0.7296229	-0.052892857	0.68987	0.7296229	-0.039753
cg25135145	3	67681479	16233024	16233074	N/A	CGCGAAACCAAGGGACCCAGAAGCTAAGCAACTTTCTGGTCCAAGGTCATTCGACG	R	Body	GALNTL2	0.8669057	0.8989329	-0.032027143			
cg25146100	22	73636438	50158060	50158110	Island	CCCGAGGGAGCCCTGGGAGGAGGCCGTCAGCCCAGGCAGTGGGTGGAGACG	R	N/A	N/A	0.7431671	0.7972214	-0.054054286			
cg25152942	19	30790492	41281080	41281130	N_Shelf	CGGAGGAGCCTGTAAAGAAAACCACCTTGGAATTTCCTGTGCTGTGGGGC	R	TSS1500	MIA	0.9145986	0.9542471	-0.039648571			
cg25160190	17	28725378	65026636	65026686	N/A	CGGGTCACCTGTGTTGCTGGAAATGTAGACGATGATACCGATGATGTTAC	F	Body	CACNG4	0.8459329	0.8786814	-0.032758571	0.9007525	0.8786914	0.0220611
cg25182165	17	47649488	51916142	51916192	N/A	CGACAGCCTGTTGGTGTTGTTGTCTGTCCAATACCGTGTGTGAAGCAGCG	R	Body	ARAP1	0.7997929	0.8477429	-0.04795			
cg25191596	6	46768388	29455126	29455176	N/A	ACAGAGCGGTGTGTGTGTGTCCTCTTCCCCATCTGGTACAGATGCCACCG	F	1stExon	MAS1L	0.7003686	0.8060971	-0.105728571	0.7490938	0.8060971	-0.057003
cg25198340	3	44757507	57186283	57186333	N/A	CGGCCGCTGGGCAGAGGCTGCACACCATTCTGCTGCAGCATCTAAATCGC	F	Body	IL17RD	0.7457771	0.8348586	-0.089081429			
cg25202141	2	21610305	113735454	113735404	N/A	CGCTGAACAATGGTCTCTGTGCCAATTTCCACCACCACAAGGAA	R	TSS1500	IL1F9	0.8965257	0.9328686	-0.036342857	0.9057525	0.9328686	-0.027116
cg25232725	22	58631302	51175515	51175565	N/A	AAAGAAATAACAACTCTGTTTTTCCACTTCAGTGCCAGAGGCCCTCATCG	F	TSS1500	ACR	0.84727	0.8868571	-0.039587143	0.8505113	0.8868571	-0.036346
cg25237894	2	73666320	233734115	233734165	N/A	CGCCCCCCTACTTCACCCATTGATGGTTTCCCACCGCGCTAAGGGCTTGCC	R	TSS1500	C2orf82	0.6741471	0.76919	-0.095042857	0.6981575	0.76919	-0.071032
cg25246062	4	35721469	39034094	39034154	N/A	CGCCCCCGCCGCTTCTTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	R	TSS1500	TMEM156	0.8184457	0.8883371	-0.069891429	0.837915	0.8883371	-0.050422
cg25247177	19	11678418	3698223	3698273	Island	CGGCACGACAATCACCAAGCACGAGCGCCAACTCATCCCAGGCTCAGCCC	F	Body	PIP5K1C	0.91656	0.9596557	-0.043095714	0.94203	0.9596557	-0.017626
cg25247520	8	19750441	128808067	128808067	S_Shore	TTCGCTATGACCACAGGACTGTGTCAAGTTGAACAAGTCTCAACTTGTCG	F	TSS200;Body	MIR1204	0.7534129	0.8189829	-0.06557			
cg25248445	2	63729392	68880245	68880295	N_Shelf	CCCTTCATTAAGATCGCGGTGCTCCTGATGTAACCAGAGCCTCAAACTCG	F	Body	PROKR1	0.8818671	0.9119829	-0.030115714			
cg25250082	12	33718487	115272264	115272314	N/A	CCATTAACTTGGTACTTCCTGTGGTGCTTTACTGTGCTCAGCATTCAACG	R	N/A	N/A	0.8496514	0.9039429	-0.054291429			
cg25255893	17	45612477	14427896	14427946	N/A	ACACTCTGTGAGCTCAGACAATCCTAGTTGCTTCCCATTTAGTACTTTTCG	N	N/A	N/A	0.9073186	0.95054	-0.043221429			
cg25256924	11	16702369	67205739	67205789	S_Shelf	CGCAGGGGTCAGTTCCCACCCCCACCCGTCCCAGGCCCAGGCCGAAGCCA	R	3'UTR;2'UTR;TSS1500	CORO1B	0.6956014	0.7742114	-0.07861	0.7226263	0.7742114	-0.051585
cg25259479	7	62786456	157408682	157408682	N_Shore	CTGTGCTCCCTGGATCAGCGCCTCCACCTTATCCACCAGAAGTTACG	F	Body;Body;Body	PTPRN2	0.7267514	0.7997257	-0.072974286			
cg25266621	15	43777353	86284469	86284519	Island	CGCCTGCGCTTCTCCTCGAGGTACTGGGCCTGCTGCTTCTGCAGGTTGGC	R	Body;Body;Body	AKAP13	0.8583243	0.8849843	-0.02666			
cg25273005	12	47624448	109181848	109181898	N/A	TTCTGGGGCGGGTTTCCCTGATGGTTTGGAGGTTGCAGCTGGGTCCCTCG	R	Body	SSH1	0.9002886	0.9292314	-0.029942857			
cg25273707	11	21682373	76037166	76037116	S_Shelf	CGGTCAGAGGATGCTTCCTGGGTCTCAGAGCTGTGACTTTGAGAATTGAGT	F	N/A	N/A	0.5288843	0.6243	-0.095415714			
cg25276694	1	43723359	117089999	117089949	Island	AATACCTTGGTCCTGCAGAAACCGAGTGGGGGAGCTTGCAGGGTGTACCG	F	Body	FBXO2	0.1687486	0.1246686	0.04408	0.1539513	0.1246686	0.0292827
cg25286393	19	17693443	50869138	50869188	N/A	CGGTGGAGGAGACCCCACCACCACTGCCACCCAAGTAGGGAGTGAGGAGC	R	TSS1500	NAPSA	0.6836943	0.7753357	-0.091641429			
cg25287153	1	51741490	78408890	78408940	N/A	CGTCTATGGGAAATACAGTCTTTTAATAAGTGTTGATAGAATAATTGAG	R	3'UTR	NEXN	0.8055086	0.8870829	-0.081574286			
cg25287372	7	34687451	115910291	115910241	N/A	CGCAGACATTAGGGGCTTTGGTTTTTGTTTTGGATTTGGTTCACCTCCG	F	N/A	N/A	0.8893486	0.9219686	-0.03262	0.8953875	0.9219686	-0.026581
cg25287591	6	40720378	33149777	33149827	N/A	CGCCCGGCCTAGCTTTTATCAGGTTCTCATGTGGGTCCATGCCCTCCTCT	R	Body;Body;Body	COL11A2	0.8583357	0.8944671	-0.036131429			
cg25292663	17	63702342	79386969	79387019	N/A	CGGGACCCCACCCGTGGCTGTGGCTGCCTCCCCTGTGCTGACCATGCCCC	F	Body	BAHCC1	0.7011071	0.8056786	-0.104571429	0.7773975	0.8056786	-0.08281
cg25323360	13	20602327	111935681	111935731	Island	CGGCCCTCAGCTGCTCTCTGCTACAAGGAGGTGAGGTGCCTTGACCACTC	F	Body;Body;Body;Body;Body	ARHGEF7	0.83889	0.86968	-0.03079			
cg25325588	2	37948345	145281672	145281672	N_Shore	CGGCTTCAGGGTTTTGCCAACGTCTCCACTGACGACAAGCTTGGAACCT	F	N/A	N/A	0.0828213	0.1123429	-0.029621571			
cg25334575	13	37723480	100641744	100641794	Island	GGGACAGCCAGGTATGGGCGTGCGGCTCTGGGACGAGTTTCTTCCCTCG	R	N/A	N/A				0.272565	0.2277443	0.0448207
cg25336892	2	1280221	30887962	30888012	N/A	CAGGCACAGACGGGCAGAGGGTGTGGGCCAGGCTGGGCCTGAGTCACACG	R	N/A	N/A	0.7920614	0.8600614	-0.068			
cg25338972	6	57667458	152011128	152011178	N/A	AAAGCCGCTTGCACCTTCTTGTTACCGATTAACTGAGGTTTGTGACTTCG	F	TSS1500	TGFB1	0.7620671	0.8550671	-0.093			
cg25339966	3	21629505	49031969	49032019	S_Shelf	TGTTTCTAAAGACACTTGGCAACTGGGACCTGGGCCACAAAAGGCCCACG	R	Body;Body	P4HTM	0.79027	0.8435429	-0.053182857	0.8192875	0.8435429	-0.024165
cg25340906	8	21620385	600940	600990	S_Shore	TGGCTTCGGTGATTCGTATCTGCTGTCATTTGTAAACTGTTTATACACCG	F	N/A	N/A	0.9159414	0.9465129	-0.030571429			
cg25344964	2	45668455	202897387	202897437	Island	GGAGAGCCCCTCTGGCCCTCCTCCTCAGGAGTAACCACGAGAGCG	R	N/A	N/A	0.4229871	0.4783086	-0.055321429			
cg25345520	7	34617467	116210196	116210246	N/A	CGAGGCAGGGTGCAAAAGCAAGATATATTTTGAAGAAGGAACTGATAGA	R	N/A	N/A	0.7455557	0.8165843	-0.071028571	0.7805675	0.8165843	-0.036017
cg25345722	3	36687396	169656700	169656750	N/A	CGGGCAGAAGTACAGAACAGAAATGGAGAAGCTGACCACGACTCCATCTC	F	3'UTR	SAMD7	0.7579414	0.8595143	-0.101572857	0.8201625	0.8595143	-0.039352
cg25351763	5	28764450	71724363	71724413	N/A	TCTTTTTGAGCCAGTTCCCTCCCCTACAATAATTCAGGGTGGTGGTGACG	F	N/A	N/A	0.82605	0.8792686	-0.053218571			
cg25357825	3	43792352	11697188	11697138	N/A	CGGGGAACTTAAGGGGTCCTTGGAGAGGATGGGCTGGCAGGGCAAGT	F	Body	VGLL4	0.7905586	0.8476871	-0.057128571			
cg25366639	5	72725391	64330915	64330965	N_Shore	GCTTCGGGGGTAACCAGAAGGCTCTCTGCGCCCGCTGCTGGGAGGTGGCG	F	N/A	N/A	0.8530929	0.8898886	-0.036795714	0.8761625	0.8898886	-0.013726
cg25367334	10	45772374	134928457	134928507	S_Shore	GGCCCCTGGGGGCCTTCGATGCACTGAGGTCATTTTTCACAGGAAAGAGG	F	Body	GPR123	0.8261257	0.8756557	-0.04953	0.8466713	0.8756557	-0.028984
cg25368667	1	28744463	26675790	26675840	S_Shelf	CGGTTTCTTCTTCAGGAGCAAATCACAGACCACCAATCCGAAGG	N	N/A	N/A	0.8744214	0.92939	-0.054968571	0.8999763	0.92939	-0.029414
cg25384897	6	71743389	32813544	32813594	S_Shore	GGTGCTGGGTGATGAGAAGCACTGAGCGGGAGTACCGCTCAGGGCTTTCG	R	Body;TSS1500	TAP1	0.6317657	0.6959386	-0.064172857	0.6620988	0.6959386	-0.03384
cg25385819	18	30678416	3445098	3445148	N_Shelf	CGTCAATGGGCTGTGGTTGAGAACTCCTGAGCCACACGATGGCAGCGGG	F	5'UTR	TGIF1	0.6714286	0.7393757	-0.067947143	0.702685	0.7393757	-0.036691
cg25390325	12	10784397	133234688	133234738	N_Shore	TTTCCAAACCAGGTCATATTCTAAGGTTCCGGATGGACGTGAATTTGGCG	R	Body	MMP17	0.8857671	0.9099514	-0.024184286			
cg25393613	6	30739504	32055068	32055118	Island	CACACTCCCTGGTGGTGATGAAGGCGTAGGACTTGTCTGCCCCG	R	Body	TNXB	0.6089657	0.755514	-0.146585714	0.6839188	0.7555514	-0.071633
cg25397818	7	69742302	1863962	1864012	N_Shore	AGCGTGCAGACCAGGCTCAAGGAAGGGTGTGTCGGTGTGCCCAGGGTCACG	F	Body;Body;Body	MAD1L1	0.8439829	0.8864586	-0.042475714			
cg25402787	15	31616371	53084679	53084729	N_Shore	CTGCCTTTTGGGAAGATAGTTGTCATAAGGGCAAATCAATCACTTCAGCG	F	N/A	N/A	0.4020757	0.4991286	-0.097052857			
cg25403416	19	22648313	30193119	30193119	N/A	CGGGCCCCTGCTGAGTGAAGCACAAATACCACCTCTGCACCCCGCGG	R	3'UTR;3'UTR	C19orf12	0.8355871	0.8864129	-0.050825714			
cg25407876	10	74738328	75005362	75005412	N_Shore	CGGGTTCCACTAACTTTATCTCCTGAGGAATGCCTCAGGAATGCTACAAG	F	Body	DNAJC9	0.6277514	0.7010743	-0.073322857			
cg25424488	3	11691392	128848784	128848834	N/A	CGGAGGGTAGGGGTCTGTCCCTGGTCTTTCCTGGTAGGTTTTGTACACATA	R	3'UTR	ISY1	0.7748257	0.8143543	-0.039528571			
cg25426203	10	61658359	88600793	88600843	N/A	CGGTGACACTTTGCCTGTCTGCCAGAGTAAGGAGACGATTCCTCTAATTTT	F	5'UTR	BMPR1A	0.7422929	0.8311471	-0.088854286			
cg25427871	11	58729377	2920735	2920785	N_Shelf	CCCTGGGCTGCTTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	F	Body;TSS1500	SLC22A18AS	0.6064557	0.66173	-0.055274286			
cg25439496	6	23630453	85484627	85484677	Island	GAGGTGCTGGGCTAGGCTGCGCCTCCCCAGGCAGGACGCCAGGCAGTGCG	F	N/A	N/A	0.1807557	0.1441943	0.036561429	0.18376	0.1441943	0.0395657
cg25446789	2	21770471	25810393	25810443	N/A	CGGTCCAGGTCATTCTTGGTTGTGGCACAGTCCAGTGTGCAGT	R	Body;Body;Body;Body;Body	DTNB	0.7488743	0.8208914	-0.072017143	0.7734725	0.8208914	-0.047419
cg25448861	12	50727472	119447524	119447574	N/A	CTTGGAGTTGTTGGCAAATGGAAGCACACAGACACCTACTATTCACCG	R	Body	SRRM4	0.8377543	0.8923814	-0.055027143	0.8627575	0.8923814	-0.029624
cg25449765	4	72735317	81254292	81254342	N_Shelf	CCACTGCTTCTCTGTCCTGGAGACACAATGTGTTCATGTGTCATAATCCG	F	N/A	N/A	0.7375571	0.8075486	-0.069991429	0.7350775	0.8075486	-0.072471
cg25468681	1	47700319	9428106	9428156	S_Shore	CGGGGCCATGCCATGGCAGTAAAGAAGCTCAGGACGTCAAAAACTCACCATG	F	3'UTR	SPSB1	0.9317029	0.9515614	-0.019858571			
cg25474399	18	13740445	3067624	3067674	S_Shore	CGGCTGGTGGCTTGGCATGACCAAAGGGAGATAAGTAAAAGCCTCCCGG	F	Body;Body	MYOM1	0.6906343	0.7784471	-0.087812857			
cg25475999	11	27669467	35282046	35282096	N/A	CGCTGCTCTTGCTCATTTTCCCAAGTCCTCCTGGTGACACTGCTCCTG	F	3'UTR	SLC1A2	0.8619029	0.8932929	-0.03139			
cg25484252	3	45612347	72184399	72184449	N/A	GAGCAGCAACAGACATGTGGCTTAAAGACGGTCTTTCTCCCTTTCTCTG	F	N/A	N/A	0.7902829	0.8497129	-0.05943			
cg25492383	10	33644412	134837664	134837714	S_Shore	CCAGTCACGTCTTTCACACTTTCATCCTGGCAATGAGAGCGAAGACCCCG	F	N/A	N/A	0.7751986	0.8189371	-0.043738571	0.7875075	0.8189371	-0.03143
cg25493992	19	41781332	8503800	8503850	N/A	CGCGACACCCCGCTCCTCCTCCTCCAGCTTTATAAAGTTTCACTTTCTG	R	3'UTR;3'UTR;3'UTR	MARCH2	0.7750643	0.8268243	-0.05176			
cg25495534	10	31759334	65431222	65431272	N/A	CGCCTTGTATGGGCAATGAAAGCTTTTAAAGGAGACACACAGAATACAAA	R	N/A	N/A	0.7196957	0.7886386	-0.068942857			
cg25521338	2	67770320	196549184	196549234	N/A	GGGTAAAACCAAAACTATTTTTAAATTTCTTAGGTCTTTTTTCATCG	R	Body;Body	SLC39A10	0.8560986	0.9192257	-0.063127143			
cg25523477	17	11610436	79410752	79410752	N_Shore	AGCTGGGGGGCCCTCCGCTGGTCTGGTTGAAATCGCCTGGTCCTCGGCC	R	Body	BAHCC1	0.8253271	0.87428	-0.048962857			
cg25537797	5	17719470	171408	171458	N/A	CTGGGCCAGGCCACAGCTGGCCTCCTTGACGAGCTCCTGGAGTAGCAGCG	F	Body	PLEKHG4B	0.7489114	0.8141757	-0.065264286			
cg25538883	18	18719364	48191042	48191092	S_Shore	ATCAAAGCCACATAGCAGAGCCAAGACCAAGAACCAGATCTCCCTCCACG	F	Body	MAPK4	0.7652514	0.8208629	-0.055611429			
cg25539979	15	27628468	74415439	74415489	N/A	CAAAATATTCAGTGATCAGATTTTAACCTCAAATAGCAGTTCCCCAACCG	R	N/A	N/A	0.4852614	0.6134471	-0.128185714			
cg25541528	7	71711473	1545869	1545869	S_Shore	CCGACCTCTCCTTCCCACCAGGGTCCGGGTGTGCCCACAATGGGCTCTG	R	N/A	N/A	0.7607071	0.8086857	-0.047978571	0.740025	0.8086857	-0.068661
cg25551545	17	48800461	46106286	46106336	S_Shelf	CGGGGAGAGGACAGGAAGATTTCTTCCATTAACTGGCATCCCACCCAGAA	F	Body	COPZ2	0.8405057	0.8761614	-0.035655714			
cg25560831	4	31748372	152666626	152666676	N/A	CGTTCAAGCTAGGTGAAATCTGCAGCATTCCGAATCTGAACATAGAGATA	R	Body	PET112L	0.8715629	0.9302886	-0.058725714	0.9192963	0.9302886	-0.010992
cg25591301	17	18780441	56156944	56156994	N_Shelf	CCATGTTGCAGAACTATCTAGCTCCTGCAGCAACTCTACATCACCCG	R	N/A	N/A	0.7528571	0.8155967	-0.062728571			
cg25592021	6	12683351	169248433	169248483	N/A	GGTTCCATGAAAACACATCCTTTGTTTTATGAGCAGAATCAGAGATTCCG	R	N/A	N/A	0.8213171	0.8729957	-0.051678571			
cg25592858	14	47769435	105183652	105183702	N_Shelf	AGGACGGCAGCGCACCCTGCCCGGGGGGCGGCTAGGAGGACGGCAGCG	F	Body;3'UTR	INF2	0.83251	0.8736271	-0.041117143	0.837245	0.8736271	-0.036382
cg25599521	14	17676378	94981685	94981735	N/A	GCTGTCTGGGTGGTCCGGGAAGGCTTCCTGGAGAAGGTGGCCATAAAACG	R	5'UTR	SERPINA12	0.71496	0.78535	-0.07039	0.7636738	0.78535	-0.021676
cg25600410	1	36625472	205550469	205550519	N_Shelf	GGGGTGGGCTCCCACCCTGTCTGCACACTCTCTGGCCAGTCTGGGCTAACG	F	Body	MFSD4	0.7573286	0.8303157	-0.072987143	0.7611125	0.8303157	-0.069203
cg25602692	12	24780413	123998085	123998135	N/A	GCTATGAGACCGAAGGCAGAAGCCTGGCGCCTGACTCCTATCCCAGCTTCG	R	Body	RILPL1	0.8290571	0.8830243	-0.053967143			
cg25628740	1	22773339	11866499	11866549	Island	CGGGCCCAGATTGGCCCGGCCCCACCCCCGGCAACGCCTCTCTCAGTCCC	R	Body;Body;Body;TSS15	CLCN6	0.107264	0.0817149	0.025549143			
cg25639082	11	13744463	6655429	6655479	S_Shelf	TTGAGGCCGGTCACGGTCCACGGGTCCGGGTTGTGCACACATCACCCG	R	Body	DCHS1	0.90509	0.93456	-0.02947			
cg25653204	19	20709438	52264429	52264479	N/A	GCTAAGCTCCTTTTCCTGTGTGCTTCTTGGCTTTCCTGTGGAGCAACACCG	F	TSS200	FPR2				0.139525	0.2240114	-0.084486
cg25653336	15	43762376	85202837	85202887	S_Shore	CGGAACAGAGTGGCCGTACCAGAACCTACTCCCATCTGGCTTGATAATGG	F	TSS1500;TSS1500	NMB	0.90957	0.9357657	-0.026195714			
cg25655084	20	24684489	4666494	4666544	N_Shore	CGCTCCGTTAAAAACCGTGTTTGTCACATTACCTGAGATATCTTCTATG	R	TSS1500;TSS

cg26054764	1	72680350	214152805	214152855	N_Shore	CAGATCTCGGAAACCTCAATTAAGAAACTTAGTCTAGAAGGATCTGGACG	F	N/A	N/A	0.7049171	0.8024657	-0.097548571	0.74824	0.8024657	-0.054226
cg26060971	3	48626440	52407402	52407452	N/A	GCTTTTGGTGATTCTTTCTCCTTCTTGTTTTATTCGGCATGGCTGGAGCG	F	Body	DNAH1	0.6011229	0.7070929	-0.10597			
cg26067259	5	20750415	92927796	92927846	N_Shore	CGAGGCCATAGCCTTGTAGATGAAGGTGTTAGAATGCTTTGTAAATCCCA	F	Body	NR2F1	0.5730414	0.6417314	-0.06869	0.6099038	0.6417314	-0.031828
cg26067361	8	12785401	38010768	38010818	N/A	GGTGATGCAGTCGGGGAATCCTGTGAGCAGAGGCTCTGGCCTAGAGGTACCG	R	N/A	N/A	0.8772686	0.9045329	-0.027264286	0.88809	0.9045329	-0.016443
cg26070636	18	13628371	12703072	12703122	Island	GCAGGGAACGAACATGGTCGCAGTGGGGGTGGCCAGCAGGGACTAACCGCG	F	5'UTR;1stExon;TSS1500	PSMG2	0.1551043	0.1261063	0.028998	0.1395525	0.1261063	0.0134462
cg26085385	2	45660382	235756391	235756441	N/A	CGGGGTCCTGTAGCTGATGCTGGTGGTGGCAGGGGCCACACATGCATCCT	R	N/A	N/A	0.8511357	0.8847543	-0.033618571	0.8722625	0.8847543	-0.012492
cg26091747	6	56646307	30113696	30113746	N/A	CGGTAGGGGGCCTGATCCCAGAATGCAACTAATGTAAAATTCTGCCTAAA	R	Body	TRIM40	0.5782486	0.64127	-0.063021429			
cg26101277	17	44788429	32690412	32690462	N/A	CAGCGACCATGTGGTAAACTCCTTTCCCCACCTCTCCTGGCTGGTATTCG	R	TSS200	CCL1	0.4258629	0.5137786	-0.087915714	0.4255725	0.5137786	-0.088206
cg26102475	19	57623380	39826821	39826871	N/A	CGCTCAGACCAGGGTTCCAAAGCTTCCTTGCTGTGTGACCCTAGCTAAGT	F	TSS200	GMFG	0.4486771	0.6021571	-0.15348			
cg26103845	8	23775430	49283175	49283225	N/A	TTCGGACCCCAACAGGCATAGATTAAAAAGCTTTTATAGCCTGCTCTCG	F	N/A	N/A	0.8849543	0.9166729	-0.031718571			
cg26106370	2	66614494	37554707	37554757	S_Shelf	GCGCAAGGGCCTTGAGACAAGGACATTTGATAACCTATATCACCTTAT	R	N/A	N/A	0.8844229	0.9297829	-0.04536			
cg26113233	5	57604376	174673622	174673672	N/A	CTGTCCTGTGGCTCCAGATGCTTTTCTTGAGAGGCAGTGTGATGTGGTCG	F	N/A	N/A	0.5680429	0.6889786	-0.120935714	0.6366588	0.6889786	-0.05232
cg26113962	1	72645424	23546304	23546354	S_Shelf	CGCCCTGACCAGGGCAGCTTCTGGGGCTGTCAGGGTCTTTTCATTGAGGA	R	N/A	N/A	0.8883614	0.9208629	-0.032501429			
cg26124526	5	49786403	60618932	60618982	N/A	CGGCCAGGCTTTCCTAAGGAAGTGTGATTAAGCCGAGCAGGAGGAAACTA	F	N/A	N/A	0.6847614	0.7385957	-0.053834286			
cg26130242	11	60687404	94600954	94601004	N/A	CGCAGGCAATCGACGCTGAGAAAGCAGCGGTGTTGACCGTGGATGAAGTG	F	Body	MAOTL1	0.84214	0.8868157	-0.044675714	0.8590175	0.8868157	-0.027798
cg26139953	2	16622367	23797305	23797335	N/A	TTGTTGACCCAGTTTCCTCGAGGTTGGCTCCCTCTCAGACAGGCCCTCCG	F	N/A	N/A	0.90026	0.9260786	-0.025818571			
cg26145096	1	23670487	11398738	11398788	N/A	CCAGGCCTGAGGAATGCTCAGCTGCTTTTGTGTGCATACACACACACAGG	F	N/A	N/A	0.7004929	0.7416571	-0.041164286	0.7277975	0.7416571	-0.01386
cg26156085	14	20601484	81609957	81609967	N/A	CGCTTGCAAAGACAGTGAGAAAAGCAGCGGTGTTGCCCCAGGGCCTGTC	R	Body	TSHR	0.9082114	0.9321329	-0.023921429			
cg26159601	7	74723393	1248693	1248743	N_Shelf	CGGACCACCGACCAGGCTCCAGCTAAGCTGTCTTAAGGTGAAATAAGGA	R	N/A	N/A	0.8575771	0.8972414	-0.039664286	0.8803375	0.8972414	-0.016904
cg26159933	1	18747472	111832593	111832643	N/A	CGGAGCTATAGTGGGAGTCTACCCAGAAGTTCGGTTAGTTCAATCAGCCT	R	TSS1500;TSS1500	CHIA	0.8669171	0.9169714	-0.050054286			
cg26161997	4	40705499	124281050	124281100	N/A	CGGAGGCTCTTGGGTCAGCTTCTAGAAAGATTAGGTCATACACCCGGAAG	R	N/A	N/A	0.8564314	0.8941929	-0.037761429	0.86903	0.8941929	-0.025163
cg26164907	8	42794488	155616247	155616297	N_Shelf	ACACACTTCTCCTGGGTCTCAATTCTGGGCAGTCTCTCTCTCTCACG	R	N/A	N/A	0.8271643	0.8823557	-0.055191429			
cg26170660	6	72725394	28493601	28493651	N/A	ACTTATGAGTCCCAGGTCCTCATTGCAGTGGTAAGCGCTGAGTGCTCACG	R	TSS200;TSS200	GPX5	0.4242543	0.5553929	-0.131138571			
cg26172195	11	10791345	68972651	68972701	N/A	CGGCCCACAGGGCTCCAAATTCAGCCTTTTCCCAGGCCAGTGACGAAACC	R	N/A	N/A	0.7790414	0.8508329	-0.071791429	0.797325	0.8508329	-0.053508
cg26173417	7	48775323	672515	672565	N_Shelf	GCCGCAGGCACTGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	F	Body;Body;Body;Body;Body;B	PRKAR1B	0.8097486	0.8483671	-0.038618571			
cg26174807	4	35690349	159992037	159992087	N/A	AACGAATGGTTCCAGCATGCTATCAAGCGTCCTTAGAGGATGAGTTCTCG	N/A	N/A	N/A	0.8942	0.9417771	-0.047577143	0.9214088	0.9417771	-0.020368
cg26177311	17	60743494	17449166	17449216	N/A	CTACCAAGGCAGGATGTACTGGAATCTAAGGGCTGATGTTTGGAAGTTCG	R	Body;Body;Body	PEMT	0.8054786	0.9084971	-0.103018571			
cg26188814	4	18741413	1292205	1292255	N/A	CTGTGGGTTGCGCACAGTTAAGAAGAAGGGCGCGTGTGCCTCTTCG	R	Body;Body	MAEA	0.9154314	0.9447743	-0.029342857	0.930485	0.9447743	-0.014289
cg26195358	14	17702469	34034105	34034155	N/A	AGGAAATTTACACATTTGTATGGGGTGATACCATTAGAAAATACCCTACG	R	Body;Body;Body;Body	NPAS3	0.56901	0.6684857	-0.099475714	0.6030275	0.6684857	-0.065458
cg26200484	11	10752382	107044383	107044433	N/A	ACAAACCAGTCCCTTTGCACAGAATCCTCTGCCTATCTGCAGACTAGTCG	R	N/A	N/A	0.6706229	0.7857457	-0.115122857			
cg26200826	11	28789480	113775549	113775599	N/A	CTGAGTGTTTACAAAATAGCACCAGTAAGGATAGCATCAACTGGCAAACG	R	TSS200	HTR3B	0.70327	0.7836314	-0.080361429	0.7496638	0.7836314	-0.033968
cg26207766	2	50779451	242763864	242763914	S_Shelf	CCTGGCTGCTGTTAAAAGGTGTGGGGACACCTGCCCAGTTGCCAGTTCG	R	N/A	N/A	0.7810029	0.85174	-0.070647143	0.828265	0.85174	-0.023475
cg26213224	7	19631324	55254659	55254709	N/A	CGGCTCTGGAGGGTGAGGGGCCATCTGGCTTGTTCACTGCTATCTTCCCA	R	Body	EGFR	0.80614	0.8538871	-0.047747143			
cg26220725	6	14665493	296538	296588	S_Shelf	CGTGTTCCTGTGGAGCCTTTGAAAACTCCTAGTTGACTCAAAGTTCTCTC	F	Body	DUSP22	0.3860914	0.4470029	-0.060911429			
cg26224781	7	61713360	95470278	95470328	N/A	CGAGCCAGGGCTGCTCTCAAAACCCTTCTTAGAGGATGCTCCAGGAACG	F	Body;Body;Body	DYNC1I1	0.7843714	0.8330843	-0.048712857			
cg26227310	10	59787355	102884087	102884137	S_Shore	GTGCTTCAGTGTGTAGTCAGGACACCATGGGGAACATGTTAACCTCCCCG	R	5'UTR	TLX1NB	0.7560243	0.8262029	-0.070178571			
cg26228558	8	67614446	71527496	71527546	N/A	CGCACCACATACCACAGAGCCTAGGGGTGGAATGGGTGTCTTTCATGGTC	R	N/A	N/A	0.8359243	0.8905471	-0.054622857	0.8489488	0.8905471	-0.041598
cg26230076	11	61657483	6493798	6493748	N/A	CGCCTGCCTCTCTGCCAGTGAGTCCAGTCGGCACCCAGCTGTGGCTCCCC	R	TSS200	SPDYC	0.8855929	0.92139	-0.035797143	0.9059375	0.92139	-0.015452
cg26237003	5	55607329	43413209	43413259	N/A	CGTTGCCTGTTGTACAACTTATAGTAGATGAGCAGAACAATTAGAACTC	R	TSS1500	CCL28	0.8017086	0.8801729	-0.078464286			
cg26239233	16	18703447	10970801	10970851	N_Shore	ATTGGCAGCTGGCACAGTGCGGTTCCATTGTGATCATCTTTCCTTTCAA	R	TSS1500	CIITA	0.4123814	0.5120457	-0.099664286	0.42874	0.5120457	-0.083306
cg26240939	16	40732356	20913414	20913464	S_Shore	CGGAGTGAGACTCCGTCTTAAGAAAAAGAAAAGGCCCTCAGTCACAGTG	F	5'UTR;5'UTR;5'UTR	LYRM1	0.67788	0.7442486	-0.066368571			
cg26244164	8	49604448	12987449	12987499	N_Shore	GCGAAATGAGGCATTGCAAAAATAAAAGACCTCAGAAGACTCCAGACAAT	F	Body;Body	DLC1	0.6071214	0.7189286	-0.111807143	0.6669463	0.7189286	-0.051982
cg26246840	18	65756380	67625063	67625113	N/A	TGGGCCAGAGGTAGCCAGAGTAGCCTTCTCAAACACCTGCCTGACTCTCG	R	TSS1500	CD226	0.90127	0.94514	-0.04387			
cg26251585	7	33790464	11456440	11456490	N/A	TTACATAAGCAGCCAGTTCTGTTTCAAATGACTCTCTTCCCAGAGTCTCG	R	Body	THSD7A	0.6158229	0.7109714	-0.095148571			
cg26262900	3	12706493	46768322	46768372	N/A	CGGTTCTGAATTTGCAATTACACAAAAGAAGGAAATAAGAGGAAGACT	F	N/A	N/A	0.8413157	0.90215	-0.060834286			
cg26266528	14	20782460	72886557	72886587	N/A	CACTGCACATTCTATGTTTTTAAATTCCTACTTCACTGGGAAACG	F	Body	RGS6	0.89816	0.9277971	-0.029637143			
cg26266618	1	37656454	208085043	208085093	S_Shore	CGTGACTATAAGTATTCATTTTGGCTGTCCAAACCATTCTTGGAGACTTT	F	TSS1500;TSS1500	CD34	0.6186229	0.6883357	-0.069712857			
cg26270847	2	53690418	22474324	22474374	N/A	CGCAGCTCCACAGCACAGAGCCTAGGGGTGGAATGGGTGTCTTTCATGGTC	R	3'UTR	WDFY1	0.9021571	0.9260463	-0.024457143			
cg26272125	1	38690402	27662075	27662125	N/A	TTTTTTCTCTGTCCCAAAAATGTTTCTCTTGTTGGTGACCCG	R	3'UTR	TMEM222	0.9012286	0.9307929	-0.029564286	0.9174963	0.9307929	-0.013297
cg26275799	6	10622324	150255758	150255808	N_Shelf	CTTCCTGGTATCCTTGGCTCTGGGATGAAGCAGCGTCCTGTGGGTTTCG	F	N/A	N/A	0.5972871	0.7114257	-0.114138571	0.60735	0.7114257	-0.104076
cg26280097	6	52635321	33177714	33177764	S_Shore	TCAAAGTTGGGTCTGGCCTGGAGGATCGCTTGTGGACACCAGCTTCTTTCG	F	Body	RING1	0.9142257	0.9460157	-0.03179			
cg26291675	19	41630338	41084435	41084485	S_Shore	CGAGAGGAGGATCATCTTGTGGAAAGTTGTGGTGGTTA	F	Body	SWKBP1	0.8625629	0.8983829	-0.0358			
cg26309983	1	10799352	89588880	89588930	N/A	AATATATGCCAGGCTTATCTAATATTTTTTCTGCTTCAGCCTTAGAATCG	R	5'UTR	GBP2	0.8779414	0.9017686	-0.023827143			
cg26312965	1	50652396	1152547	1152597	Island	CGGCCCCTCCCGGGGCCGCGGCTCCGGTGGGAAAAACAGCTCCTCCATTT	R	3'UTR;3'UTR	SDF4	0.7963229	0.8390186	-0.042695714	0.80944	0.8390186	-0.029579
cg26313301	19	35618468	11219615	11219665	S_Shelf	CGGTCTCTGGTGCAGTTTCTCAACATGGCTGTTGGGTGAACCAACCACG	R	Body	LDLR	0.86353	0.9221557	-0.058625714			
cg26315261	1	16649363	20697328	20697378	S_Shelf	CGGGCCTTGGGCTCTAATATCTGGGGAGAGGGCGGCTTACCATTGC	R	N/A	N/A	0.74296	0.8137557	-0.070795714	0.7826888	0.8137557	-0.031067
cg26328150	8	16642383	140749377	140749427	N/A	GATAGAAGCCGAATGCTGGGGGAGCCAGGAGTAGAGCCAGCCCCTGCGCG	F	Body;Body	TRAPPC9	0.8653314	0.8998914	-0.03456			
cg26329047	4	33774334	105492888	105492938	N/A	CGTGAAGGGTACACTGGAACACACAGAGATGAAGCCATTGCTAGAGAAAC	R	N/A	N/A	0.8928743	0.9181329	-0.025258571			
cg26329992	4	72735319	56719419	56719469	N_Shore	CCGGTGCCCACAGACATCAGTACTTTTAATCTCCTCCAGATGATTCTC	R	TSS1500;TSS1500;TSS1500	COX1	0.8715386	0.9206414	-0.049102857			
cg26333513	11	34621363	62477082	62477132	Island	GAAGCCCTGTACGGTAAACTCCGTGACGTGGGGGCTGCCATGTTGGTACG	F	TSS200	BSCL2	0.0492353	0.0629157	-0.013680429	0.100064	0.0629157	0.0371483
cg26336955	1	74698446	227751018	227751068	N_Shore	CGCCCTTTATTAAAGATGGTATGCATGGAAAGACATGGAACAATTTTGGA	F	TSS1500;TSS1500	ZNF678	0.8687329	0.9207229	-0.05199			
cg26340149	11	65799429	69988497	69988547	N/A	CGTCTGCGGGAACTAACCTTGTTCCAGGCATAAATAGGTAGGGTGCCCGG	F	Body;Body	ANO1	0.5764429	0.67102	-0.094577143			
cg26345203	14	24719508	23005866	23005916	N/A	CGGCTGTGTCGCTGTCATACCTGGTCTGTCTCCACCCCGAAACCCCAC	R	N/A	N/A	0.6662143	0.7793214	-0.113107143			
cg26346167	3	61704456	131004472	131004522	N/A	AATGACTCAGGTGCCCGCATGAGAAAAGTTTGTTTTGCTCTTGAGAAACG	F	Body;Body	NEK11	0.6337971	0.7225871	-0.08879	0.6817963	0.7225871	-0.040791
cg26346210	8	60756416	98610507	98610557	N/A	CGCGGGTCCTTCTACCAGAGCCCTGCGGGGCTAAAATGGGATCCTCCTAT	F	N/A	N/A	0.6667543	0.7629457	-0.096191429			
cg26348243	6	60759502	31540461	31540511	N/A	CCGCGGCGCCGCCGTGGGGCGCCTCCCCCCCGACCCCC	R	5'UTR;5'UTR	LTA	0.6729214	0.7891586	-0.116237143	0.7067375	0.7891586	-0.082421
cg26349964	8	74738408	144262934	144262984	N/A	CGCCCCATCGAGAAGCTCCACACTGCGGCATTTTGTGTGTCGGGGCTACG	R	N/A	N/A	0.8882829	0.91462	-0.026337143			
cg26351229	8	54777446	132053780	132053830	Island	CACCGCGGGTGTCTGACCACTCTGACAGGTCTCCAAATTTCTCCCAGTCG	F	TSS1500	ADCY8	0.1629686	0.1183459	0.044627714	0.1464588	0.1183459	0.028129
cg26354908	12	34631415	49610040	49610090	N/A	CGAGGAGCCTAGACCAGAAAGTGGAGTGACCATGCCAAAGAGGCAGAGCC	F	N/A	N/A	0.8169643	0.8611471	-0.044182857			
cg26361327	19	34758457	37892209	37892259	N_Shelf	CGAAGTGTTTGGATTAGAGTGGCATCTGCACACGGCTGTGAATGTTAC	R	N/A	N/A	0.6802386	0.7665314	-0.086292857			
cg26363363	12	63711453	7060386	7060436	N/A	CGGGGCCCACTTCCCACACGTCTGCAATCAAAGGCTCAGGACATGGCAT	R	TSS200;Body;TSS200	PTPN6	0.7081586	0.80198	-0.093821429			
cg26363759	1	33676428	9377984	9378034	N/A	CGCGGAGCGAATGGTGTGCCAAGGAAGCAAGAAACTCCCACCAAAGCGAC	R	5'UTR	SPSB1	0.7634029	0.8651543	-0.101751429			
cg26371501	3	29725486	153003079	153003129	N/A	CCACCACTCTGTGTGAGAGTGCTGGTGTACTCTATTACGCCAGCCCT	F	N/A	N/A	0.6565571	0.7041557	-0.047598571			
cg26377557	19	38679492	18667464	18667464	N_Shore	CGTTTGAGGCCAGGAGGCAGAAGTTGCAGTGAACGAAGACCCCACTCCAG	R	TSS1500	C19orf50	0.6866214	0.7330929	-0.046471429			
cg26389392	10	46697421	110326562	110326612	N/A	AAGTGGGAGCCTGGGCACGCCCCTGAGCTCTGAGGCCATGGAGGAAGCTCG	N/A	N/A	N/A	0.8783214	0.9101886	-0.031867143	0.891645	0.9101886	-0.018544
cg26390889	5	69659380	33936652	33936512	Island	CCGCCCCTCGGAATGCTAGTGTGCATTTCGCGCGGCTGGGCGCCCCCGT	N/A	TSS200	EXFP3				0.1850588	0.14637	0.0386888
cg26394191	3	27756300	123459423	123459473	N/A	CGGAGCCAGCAGCTCCTGCAGAATCTGCAGTGCTGCCACACTGAAACACTG	F	Body;Body;Body;Body	MYLK	0.8585829	0.8986114	-0.040028571	0.87694	0.8986114	-0.021671
cg26400954	13	39753318	76291075	76291125	N/A	GATGGGAGGTACAGACTGACTAACCACTGACACACCCAATCAGACTATCG	F	Body	LMO7	0.8080871	0.8756571	-0.06757	0.844535	0.8756571	-0.031122
cg26411222	12	17678361	115104352	115104402	N_Shore	CGGTTTGAATCCTGGCTCCATAATTTCCCCCAGAAGGATCTTGGGTAAGTG	F	N/A	N/A	0.61133	0.6854229	-0.074092857			
cg26416887	12	39675326	116618975	116618975	N/A	CAAAAGTCTGGTTGCTGATTGAAATAACCTGATTGAAATAACGGGTGAG	R	Body	CUX2	0.6898814	0.8154529	-0.125571429	0.7427238	0.8154529	-0.072729
cg26424967	1	20689368	31197383	31197433	S_Shelf	GAAGCCACCTACATCAAGCTACACTGAGACAGCAGCATGGCTGAGAGCCG	F	TSS1500	MATN1	0.8671057	0.8994	-0.032294286	0.8728388	0.8994	-0.026561
cg26425321	8	68679413	142428317	142428367	Island	AGGAGGCTGGGAGCCCGGGGCTCAGCGGGTCTCAGGGAGTAAGCTGCG	F	N/A	N/A	0.5987071	0.6858271	-0.08712			
cg26427487	7	27672470	105987358	105987308	N/A	GACACCCTTCACACTTCAGCCTTCTGTGACATCTGAAAAAACCG	R	N/A	N/A	0.7956557	0.8666243	-0.070988571	0.8168775	0.8666243	-0.049747
cg26429266	5	39807399	126648067	126648117	N/A	CGGTGCCAAAAAGCTCCCCATAAAAGCAGCTTCCTGCTCACTGCCTGAAT	R	5'UTR	MEGF10	0.8510557	0.8947571	-0.043701429			
cg26429499	11	59672324	70563792	70563842	Island	CCGAGTGAGATGGTCACACCCAGGTTTGGAAAGGATGGCGCAGAATTACG	F	Body	SHANK2	0.7962729	0.8439786	-0.047705714	0.8135063	0.8439786	-0.030472
cg26430059	14	34714455	89770384	89770434	N/A	CGGCTGCCTTCAACTATCAACAGTGGAAAGAAAGGATCATTTATGGACTG	R	Body;Body	FOXN3	0.4241057	0.5357471	-0.111641429			
cg26430081	12	32788507	130529394	130529444	S_Shelf	CCGCTCCTGGAAATGCTAGTGTGACTTTTCTTTTTCAAGAGCAC	N/A	N/A	N/A	0.6115386	0.7191943	-0.107655714	0.6724775	0.7191943	-0.046717
cg26434370	16	23662412	10909361	10909411	N_Shelf	CGGGGGCAAGTTTGCCCCACAGAGGATATTTGGCAATGCCTGAGACTTTA	F	Body	FAM18A	0.8812357	0.9103586	-0.029122857			
cg26435149	3	59773370	55605611	55605661	N/A	GAAATTATTCAAGCTAGTCAGTTCTAAACCTGCTCACCCTGCCTTGCTCG	R	3'UTR	ERC2	0.6685257	0.7350271	-0.066501429			
cg26442607	16	13746348	2129814	2129864	S_Shore	CGGCCCCTGGGCTCGGGGCGTTCCTGAACACGGCGACGACGACTGA	F	Body;Body;Body	TSC2	0.7612757	0.8035357	-0.04226	0.77313	0.8035357	-0.030406
cg26442740	12	59739347	55613318	55613368	N/A	CGTAAGTTTTTATGAATATACCAGGAATATGATGTTGTTGTTTCTATTCC	F	TSS1500	OR10A7	0.81899	0.8721629	-0.053172857			
cg26442890	10	27770379	79289545	79289595	N/A	TTAGGATGTCATGGTTCTCAGCCCCTGACTTTCCTGACAAAGGCCCACG	F	Body;Body;Body;Body	KCNMA1	0.8307343	0.89145	-0.060715714	0.8662113	0.89145	-0.025239
cg26448489	2	25693438	238600469	238600519	Island	GGAGCTGCGGCCGGAGCCTGAGGGGTCTTTTCCTCCAGGTCCTCTTTCCG	N/A	TSS1500;TSS1500;TSS1500;	LRRFIP1				0.1861463	0.1246643	0.061482
cg26454666	15	38779462	61111795	61111845	N/A	TTCTGTGCCTCTCTAGAGAATTTTCTGTGCAGTGCTGCTGGCG	R	Body	TRIM9	0.9095786	0.94236	-0.032781429			
cg26460678	3	50739459	50360667	50360717	S_Shore	ACACATTGTCCTGTCACACAGGATGCGGAAGCTCTCAGTGGAAAAAACG	F	TSS1500	HYAL2	0.5569743	0.6150929	-0.058118571	0.589695	0.6150929	-0.025398
cg26471790	2	54631487	203044722	203044772	N/A	CGCGCCCACCGCGGCTGGCAGCCAAGTAATCTTAACTTCAGTTGGAGTAAG	N/A	N/A	N/A	0.8595671	0.91456	-0.054992857			
cg26471982	8	69717311	10701203	10701253	S_Shelf	CGGAAACCAAGAACTCGGAGGTCTCACTGAGGTGCACAACAAT	N/A	N/A	N/A	0.8667343	0.8959286	-0.027194286			
cg26479374	4	51736346	1243980	1244030	Island	CGCGTCCTCACGAACCACAGCGAAATTACAGCAGGTATCTCGCGGATAGG	R	TSS1500;TSS1500;TSS200	CTBP1	0.5006757	0.6228557	-0.12218	0.4623625	0.6228557	-0.160493
cg26491844	2	13751423	23929717	23929767	N/A	ATATTCTCTACATTGAATGTAAAAATCATCCTCGCCTTTGGATGAAACG	R	3'UTR	GALT	0.9366657	0.9624043	-0.025738571			
cg26495711	2	57705413	240169280	240169330	N/A	CGTTGCTGAGTCACGTTTGGTGAGCAGCTTGTTCGGCTCAGATGCCCTGG	R	Body	HDAC4	0.7815229	0.8308329	-0.04931	0.7766638	0.8308329	-0.054169
cg26496293	2	46682336	237412439	237412489	N_Shelf	GGACCCCTCCTCCACCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	F	Body	IQCA1	0.7431929	0.8147967	-0.071602857			
cg26503038	19	62717418	2699659	2699709	N_Shelf	TTGTCTATAACAAGGGTTCCACACTGGAGTATCTCTGTCCCTACAAGAC	R	5'UTR	GNG7	0.73538	0.8190829	-0.083702857			
cg26510473	2	24628476	1553797	1553847	N/A	CCACCCCAGCCACGTAAATAGGGAACAAGTTCCACCTGCCATAGGACACCG	R	N/A	N/A	0.78548	0.8186114	-0.033131429			
cg26511585	22	54627497	43810812	43810862	S_Shelf	GGACCCCTCCTCCACAAGGGCAGCACAACAAGTATTATTGCCCTTCCGC	F	5'UTR	MPPED1	0.8130314	0.8712343	-0.058202857	0.8454675	0.8712343	-0.025767
cg26514793	10	20723303	73769127	73769177	S_Shore	CGGGCAGGGGCTTTGAACGCTGCAGTTCTGAATCCCAGTTCCAGGCAAA	R	3'UTR	CHST3	0.54556	0.6695243	-0.123964286			
cg26525147	17	51753404	19641484	19641534	N/A	CGGACCACCCTCACTGGCTCTCCTGGCCCTGGGAGAATCGCTCCTGCAGC	R	3'UTR;3'UTR;3'UTR	ALDH3A1	0.8942043	0.9343771	-0.040172857	0.9099225	0.9343771	-0.024455
cg26531906	11	57735468	71135066	71135036	N/A	GCACAGACTCTGCCTACCAAGGACAACAGCGGCCTCTAAGACTTTTGCCG	N/A	N/A	N/A	0.8419414	0.8725871	-0.030664714	0.85293	0.8725871	-0.019657
cg26532638	1	23804404	68517691	68517741	S_Shore	CGCCAGGCTAGACCTCACAGGTCTTTAGACTTCTACGCACCAGGTACCTG	R	TSS1500	DIRAS3	0.8902629	0.9285529	-0.03829			
cg26536401	12	49672430	6956432	6956482	N/A	AGAGGGCCAGGACCCTAGTGGTGCCAGAGCCATAGTCACAGGGCCAAACG	F	3'UTR	GNB3	0.8440029	0.87688	-0.032877143			
cg26539615	19	27773401	49402007	49402057	N_Shore	CGGTCACTGATGCAGCCAGGCAACCCTGCTCCGGGGGTTCTGAACACGAA	F	TSS200	TULP2	0.9247286	0.9506129	-0.025884286			
cg26553513	11	19679335	40310788	40310788	N/A	CGAGCACATCTGTAAACTGGGAGTGTGCATGTAAAACTGCTGGGCGCG	F	5'UTR	ERC4C	0.6043971	0.7060843	-0.101687143	0.64199	0.7060843	-0.064094
cg26566236	6	71656408	139459701	139459751	S_Shelf	CGGCCACCAGAGCAGGGCAATATTAGCTTTTAGTTGTTCAGTTTGTCAAG	F	Body	HECA	0.9108329	0.93999	-0.029157143			
cg26568226	15	59675389	22913326	22913376	N/A	CACCTTATCACTGTGCCCAACAGACCGTGATCTGCTGGGCTGCCGGCG	F	5'UTR	CYFIP1	0.89737	0.9395629	-0.042192857			
cg26571814	12	26687390	20589722	20589722	N/A	TGATCTTATAACGAGATTTAAGCCTCCCTGTCTGCTACG	R	Body	PDE3A	0.4714629	0.5902014	-0.118738571			
cg26591391	7	48740351	117644097	117644147	N/A	GAAGAATTCAGCCACCTGTAGAATACAACTGACTATTCTTAAAATTCCCG	F	N/A	N/A	0.7531843	0.8233314	-0.070147143			
cg26598899	11	26674458	2321800	2321850	N/A	GGTCTCTGGAGGGCCAGCCGGGGGTTCCCGTCCACCTGTCAGGGGGTTCG	R	Body;TSS1500;Body	C11orf21	0.6879214	0.7733086	-0.085387143	0.7275388	0.7733086	-0.04577
cg26599989	11	47790406	1297087	1297137	N_Shore	CGGATGTAAACCCACTGATAACGGACAGAAAGAGAATGCCCACAAGTGGG	R	3'UTR	TOLLIP	0.7810357	0.8249114	-0.043875714			
cg26604191	7	51602315	5372609	5372659	Island	CGCCCTCCTCCGGTGCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCG	F	Body	TNRC18	0.8777157	0.9077943	-0.030068571			
cg26608693	1	71743343	14027581	14027631	S_Shore	CGGCAAAGACCCCATAGTTAACCGGGAAGTCCTGATTTCCTTAACTACGC	F	5'UTR	PRDM2	0.4475929	0.6050243	-0.157431429			
cg26615853	10	11713313	79347104	79347154	N/A	CGCCTACTGAGTTATACTGCCTTGTTTACATAAGCCTATATTCAGTGGCCT	R	Body;Body;Body;Body	KCNMA1	0.8703457	0.9124329	-0.042087143			
cg26616258	16	17754496	358551	358641	N/A	CCCTGGGCGACCTGGGAGCCTTCATGGGAGCTTGAAAATCAACGAGCG	R	Body;Body	AXIN1	0.8614971	0.8895129	-0.028015714			
cg26625028	8	29801312	629589	629639	S_Shelf	CCATCTCTCCCGTGGATGCTGCTACAAATATTCCATGCAATGATATTCACG	R	Body	ERICH1	0.8915	0.9199957	-0.028495714			
cg26640672	12	21743394	59925037	59925087	N/A	CGAACCAGATCACAGGGGGTTGTACATGCCCCCGCGATAAGGGGAGTAGT	R	N/A	N/A	0.8362614	0.8881743	-0.051912857			
c

cg27032905	13	27732325	51878551	51878601	N/A	AGTGCTCTTCTGGTGTTATTAGCTGGCAGGAGCTCATTGTGCCCATCTCG	F	N/A	N/A		0.8590771	0.9156343	-0.056557143	0.8874613	0.9156343	-0.028173
cg27033973	6	53671496	149869713	149869763	S_Shelf	TTTAAGCCAAGTATTACTATATACTATAGCACCCTCAGGGTGTAATATCG	F	N/A	N/A					0.9029213	0.9277114	-0.02479
cg27035734	12	63608413	86230557	86230607	N/A	TCATGGCAAGCATGAGGGATTGCTGAGAACTCTCTTTGCCAACTCATTCG	R	TSS1500	RASSF9		0.4090814	0.4869314	-0.07785	0.4148975	0.4869314	-0.072034
cg27036936	10	50675413	30305021	30305071	N/A	CGGGGGCGACTTACCGTTCTGTTTTGTTTGTTACAGTCCAAATACATAGAAGT	F	3'UTR	KIAA1462		0.69459	0.80375	-0.10916	0.7488238	0.80375	-0.054926
cg27045723	16	44726447	1077761	1077811	Island	CGGCGGCTGGCGTCCTATTGGCTATTAAATATAATCATTACAATAATTAT	F	N/A	N/A		0.7569157	0.82417	-0.067254286	0.7913275	0.82417	-0.032842
cg27050407	6	72697501	24832728	24832778	N/A	CGCATGAGTTTTTAGTATCATCACCACATTCAGGAAGGATGAGGCTGG	R	Body	FAM65B					0.679845	0.7613886	-0.081544
cg27051318	8	52658325	42623771	42623821	N/A	TCAGGAAATGTGATGACTCATCTGACATCAGATCGAATCTTTTTTATTCG	F	TSS200	CHRNA6		0.6970786	0.7849857	-0.087907143	0.74168	0.7849857	-0.043306
cg27054144	4	61760400	185092121	185092171	S_Shelf	CGCCTAAAAGAACCTGCCTGTTTCAGAGAACACTTCTACTGGGAAGGGAT	R	Body	ENPP6		0.8129914	0.8659357	-0.052944286			
cg27057027	7	73625339	27243276	27243326	N_Shore	GCCCTGAGAGGGCAGTGCAGGCAGGACCGGAGGGTAGTTTCTGCAGCACG	R	N/A	N/A		0.44594	0.5280571	-0.082117143			
cg27058166	11	54773500	2285989	2286039	N/A	CGGGCGCTGATGGCCACCGAGCAGCCACGTTTTCCATTCAAATCCCGCACT	F	N/A	N/A		0.92607	0.9487357	-0.022665714	0.9284763	0.9487357	-0.020259
cg27061791	16	49754427	67009163	67009213	N/A	CGCATCTGAACCTCGAAGGAACCAGTTCCCGACACGCCACCTTTCAGAA	F	N/A	N/A		0.80319	0.8800614	-0.076871429			
cg27062514	11	37775317	10800841	10800891	N/A	AAGCCCCAAGAGACATTTCCTGTGCTAGAGTCCAATATTTGAGTCTCTCG	R	3'UTR	CTR9		0.7167271	0.8443543	-0.127627143	0.7768325	0.8443543	-0.067522
cg27092297	6	42795319	31116343	31116393	N/A	CGGGGCTGCAGCCAGGACTTAGGGAGGGACCCTGTCCTTTGCTGCATCCT	R	Body;Body;Body	CCHCR1		0.8784343	0.9004529	-0.022018571			
cg27096416	7	37700467	140599947	140599997	N/A	CGGTAATTACCAACAATAGATAACTAATAGTGTGTTATAAGTATCTT	F	Body	BRAF		0.7740071	0.87622	-0.102212857			
cg27101452	7	52675494	150145374	150145424	N/A	CGGGGCGCCTCCTCCTCCTCCTCCGGGCCATCGGGCCCTAAAGACAGCAGAG	R	N/A	N/A		0.9078543	0.9420114	-0.034151143			
cg27105465	17	56781420	40337623	40337673	S_Shore	CGGCGTTCAGAGGCCAGGGTTGGATCACTGTGCCCCTGATCACCCCCTTG	F	TSS200	HCRT							
cg27108147	4	30804417	2401605	2401655	Island	GGTGGGCGCCCTGCCCTGTTCTCCACCTTGTGCTGAGGAAGCTTTGACG	F	Body	ZFYVE28		0.7115371	0.7743671	-0.06283			
cg27110580	3	48643404	195463368	195463418	N/A	CGGGCTTTAAATAAATCAGTTAAATTGTCCTCGGAAAGGTTTGATACCAAT	R	3'UTR;3'UTR	MUC20		0.8619571	0.91101	-0.049052857	0.8832688	0.91101	-0.027741
cg27113548	14	62680395	106354912	106354962	N/A	CGGTCACTGACTCGGTTACTATCCAGCGACCTCCGTGGCTGTTCAGTGGT	F	N/A	N/A		0.8348729	0.8705514	-0.035678571	0.8206925	0.8705514	-0.049859
cg27121758	19	49608420	3178742	3178792	Island	TGAACATAACGAGAAATTTCAAATAACAGGAAACCAAGACCAGCAAGGCG	R	TSS200	S1PR4		0.5940614	0.68232	-0.088258571			
cg27129984	16	62669381	1538803	1538853	S_Shore	CGGTTTCCTGGGCCCCACTGGGGCGGCTTCCTGCGCATGAAGCCCCATGTA	F	TSS1500	C16orf38		0.55338	0.6247443	-0.071364286	0.558465	0.6247443	-0.066279
cg27134223	6	57662431	31465961	31466011	Island	CGTGTGCACCTTCTCAGCTGCTCAGCAGTGCCAACTGAGTGAACCCCGT	R	5'UTR;1stExon	MICB					0.092412	0.0573299	0.0350821
cg27135915	10	70631325	135373802	135373852	N/A	GTGGTGCCCCTTCTTCTTGTCCTGAGGTGGACAGTACACTAGATGAATCG	R	Body;5'UTR;Body	SYCE1		0.6533771	0.7128971	-0.05952	0.6230213	0.7128971	-0.089876
cg27143007	7	69761418	157568342	157568392	Island	ACATGCAGGGAGTCGCCCAGGACAGCAAGCCTGGGTGTGGGGCTGAGGCG	R	Body;Body;Body	PTPRN2					0.8862438	0.9038357	-0.017592
cg27147004	12	73701482	130822818	130822868	N_Shore	TGAGGCTCGAGGTGCGGGGACCGGGTTGCGGGGCGAGCGTCCCAGGTGCG	R	5'UTR	PIWIL1		0.7473	0.8139314	-0.066631429	0.7613938	0.8139314	-0.052538
cg27147306	8	70781391	99837480	99837530	Island	CGGCCTGACCTCCCGGGGCGGGAGGAATTAAATATTAAGCTACACAGT	R	Body	STK3		0.1349	0.1758729	-0.040972857			
cg27149973	17	40726435	74868725	74868775	S_Shelf	CTCATGCCTAAGTGTGCGTCATTCTGCCTTGTGGTTTCTCGTGTGGCTCG	R	Body;TSS200	MGAT5B		0.5044229	0.5681	-0.063677143			
cg27150870	16	13611510	89390609	89390659	N/A	CGCGCTCTCGGTGCTGCCACCCCCCGCCGTGATAACAGAAATGTGAGTG	R	5'UTR	ANKRD11		0.6998886	0.7640071	-0.064118571			
cg27151135	12	41683359	66412241	66412291	N/A	GGCACAGAGCCTGGCATGCAAGTCTGGTAGTTGCTATTATCAATTACTCG	F	N/A	N/A		0.8853186	0.9180557	-0.032737143			
cg27152128	7	47774373	5269245	5269295	S_Shore	CGGCAGTCTGGAAACGACCAATGAGATCTTGGACTCTGCCTCTCACGACT	F	Body;Body;Body;Body;Body	WIPI2		0.8934071	0.9205214	-0.027114286			
cg27170947	2	56801368	2640298	2640248	Island	CAGGAAACAAGGCCAACACTGGGGAAGTGGCACCATGCTCAGGGAAGACG	F	Body	FAM59B					0.0767963	0.0514601	0.0253361
cg27177415	17	44771441	79412681	79412731	Island	CGCCCATCATCACATCCGAACCAGGTGAGAGTAGCGCCTGGCCCCGG	F	Body	BAHCC1		0.9355329	0.96298	-0.027447143	0.9485775	0.96298	-0.014403
cg27185772	12	37727380	113725987	113726037	N/A	CGCTCCTTCAACTTAAACAACCTGAGCGAGGAGGACACCCGTCACCTCCA	R	Body;Body	TPCN1		0.9233743	0.9494286	-0.026054286			
cg27192248	15	57614306	65285669	65285719	S_Shelf	CGACTGTACCCTGTAAAGCTTTAAGGGGATGGTATTCCAAGAATTAGTAT	R	N/A	N/A		0.6645971	0.75296	-0.088362857			
cg27193735	7	22797363	90562815	90562865	N/A	CGAAGAAGTTATGTAACAGAGGGCTGTAGATTGTTTTCAACACTCACT	F	Body	CDK14		0.8513714	0.8936343	-0.042262857			
cg27199827	20	37645446	18567975	18568025	N_Shore	CGTGGTTTGGTTCATTTAAATCTAACAACCCAGTGAGGGGGCCAATTAGT	F	TSS1500	DTD1		0.7000929	0.7942714	-0.094178571	0.7342575	0.7942714	-0.060014
cg27203924	3	54637426	64627542	64627592	N/A	CGAGAGTGCAACGAACAGAGTAAGTCCTAGAATGTATAACTGTTATTAC	R	Body	ADAMTS9		0.8380757	0.8800071	-0.041931429			
cg27205487	21	36704499	17961996	17962046	N/A	GATTTTTCTCTTTGAATCTCCAAACTATTCAGACAGCAAATATTTCCACG	F	Body;TSS1500;Body	C21orf34		0.8826457	0.9314071	-0.048761429	0.9057663	0.9314071	-0.025641
cg27225130	1	13666495	208218009	208218059	N/A	TGGCTCGGTGAGTGTCATCCTGGGCAGCTTGCTGACCCTGCCAGCCATCG	F	Body	PLXNA2		0.8577986	0.9100014	-0.052202857	0.8531975	0.9100014	-0.056804
cg27230534	3	49642476	195267087	195267137	N_Shelf	CGTTCACAGCCGAAGGTAGCATGTTCCCAGATGGGGTCAAACAAGGCGACG	R	Body	PPP1R2		0.7368629	0.7982743	-0.061411429	0.763625	0.7982743	-0.034649
cg27235904	10	67777504	121566670	121566720	N/A	CGGGGATTACAGATGACGGGCCACCACGCCCAGCTAGTAGGGACGGGATTT	R	Body	INPP5F		0.9225014	0.9496443	-0.027142857			
cg27247736	6	21631496	160241105	160241155	N/A	GGAAGGAGATTGCTTCAGCTGGGTCACAGCTCGGTGCAGCCAGGGGCAGCG	R	Body	PNLDC1		0.7173686	0.8039357	-0.086567143	0.76501	0.8039357	-0.038926
cg27252325	12	54610351	49745406	49745456	N/A	CGCCCAGCCCCTGCAAGCAGTTTCTTTAACTCTGTTGGGATGCCATTCGT	R	3'UTR	DNAJC22		0.8337329	0.8841114	-0.050378571			
cg27257408	15	16670375	78526836	78526886	N/A	TCAGTGGGTGACTGAGCTGTCTTCAGTGGAAGCCCGAGGCAGATGCCACG	F	1stExon	ACSBG1		0.8746914	0.9080029	-0.033311429			
cg27273054	11	51743474	64621560	64621610	Island	GAGGCCGTGCACACAGGGCTGGCACACGGGGAGGCGGCGACAAAGAACG	R	3'UTR	EHD1		0.7362186	0.7852271	-0.049008571			
cg27273141	2	46647350	235701285	235701335	N/A	TGGTTCCATATTTGTGGCCAGAGTTTCCCCGCGGAACATGGAGACACAGG	F	N/A	N/A		0.8745686	0.9198614	-0.045292857			
cg27277366	6	56614463	90974476	90974526	N/A	CGAGGAAACCCCAAAGGGACAGCTTTCTGGAGAAAAATGCCTGGCTGTGA	R	5'UTR;5'UTR	BACH2		0.9201871	0.9485143	-0.028327143			
cg27279839	6	60782462	158994509	158994559	N/A	CGTCTTCTTCATCTGCTTTGGCCTGACCATCTTCGTTGGGATCAGAGGTA	F	Body	TMEM181		0.8246729	0.8602	-0.035527143			
cg27297043	3	35641350	154035092	154035142	N/A	TCAGAGATCAATTCCATATATTCATCTACGTTCAGTCATTATTACAAGTCG	F	Body;Body	DHX36		0.9266071	0.9555857	-0.028978571			
cg27302054	7	59613467	23387862	23387912	N/A	TCTTGAAGTAGAATTGCCATCTGTCCAGGTTCCATTCCTATCACTGTTCG	F	Body	IGF2BP3		0.9064714	0.9481543	-0.041682857			
cg27308386	10	26600419	1000575	1000625	N/A	CGGGTCCCATTTAGGTTCTGTGGCCTCTCGGTCCCGTGACTCCACGCAGC	R	N/A	N/A		0.6949471	0.7592471	-0.0643			
cg27310311	2	66620322	8813841	8813891	N_Shelf	CGTGGCCTCCAATGACATTGTGGGGTGGAGGCATCTTACCATTGGAAGGT	R	N/A	N/A		0.8626429	0.8974786	-0.034835714	0.8727213	0.8974786	-0.024757
cg27330006	19	14736422	6746538	6746588	S_Shore	TTGCCCCCAGAGCAGCAGCGAAAACGGCTTCAACAGCAGTTGGAAGAACG	R	Body	TRIP10		0.8649857	0.9157071	-0.050721429			
cg27333283	16	61804314	19514329	19514329	N/A	CGGAATTTGGGGAAGCCACCATGCAATCCAGTGAGGCTTCAGTGTACAGC	R	3'UTR	GDE1		0.8640271	0.9008143	-0.044787143			
cg27333426	6	34658332	28552582	28552632	N_Shelf	TCTTCAAGAACTACTGTACTTTCCACAGTGTTAAACTGTCTGTGCAGACG	F	Body	SCAND3		0.6915543	0.78364	-0.092085714	0.7349738	0.78364	-0.048666
cg27338089	16	58802326	29820515	29820565	S_Shore	CAGAGAAAGCTGCCTTCAGTCAGACTCACCCGGTTAACTCGGGTTGAGACCG	R	Body;Body	MAZ		0.89045	0.9315929	-0.041142857			
cg27342720	8	39635351	120033982	120034032	N/A	CAAGCTCAAAATTGGTTTCAGATTTTGACTCTGGTCATCTTTTTACTACG	F	N/A	N/A		0.75877	0.8208886	-0.062118571			
cg27347220	3	56706329	186860524	186860574	S_Shelf	CGTCCCCCAAACTGCATATTGAAATTTGATCCCTAATGTTAGAGGTGGGG	R	N/A	N/A		0.67019	0.74601	-0.07582	0.7068325	0.74601	-0.039178
cg27351624	6	41752390	30073797	30073797	S_Shelf	AACTGGGAGATGAAGGCACTCGGGCCTCCCCTTGCAGGAGCTCTGTCTTCG	F	Body	TRIM31		0.7847557	0.8308314	-0.046075714	0.8025125	0.8308314	-0.028319
cg27359629	6	36649475	74101601	74101651	N_Shelf	CTTCCAGTGCTTTGAAGAAACCTCAGGTGCTTGTCACTGACCTGTGTTCG	F	N/A	N/A		0.8319686	0.9035014	-0.071532857			
cg27361369	22	73628434	28311714	28311764	N_Shelf	CGGAATTTTTAGGTATAGAAGGACTTACAAAAAAGTTTATTCTTGATGGAG	R	Body	PITPNB		0.92526	0.9521214	-0.026861429			
cg27365426	2	60635374	143886372	143886422	N/A	CGGCGTGGCTCTGGGCTGTGTTTTCTGAAGTTCTAATGCAACCCTCCCAA	F	TSS1500	ARHGAP15		0.61631	0.6889086	-0.072598571			
cg27367066	15	42713457	34662635	34662685	S_Shelf	CGTTGAGAATTGATCATCTCTGGTAGCATCTGTCACTCCCTTGAAAATA	F	N/A	N/A		0.55495	0.689	-0.13405	0.648595	0.689	-0.040405
cg27377289	7	51643413	7812273	7812323	N/A	CCATTCATCTGTGAAGAATGGCAATGACTGTAAATTGTTCTTCCTGATCG	F	N/A	N/A		0.87573	0.93124	-0.05551	0.9015375	0.93124	-0.029703
cg27380459	11	44709301	66315870	66315920	S_Shore	TAGGTGACAAAGGCAAGTTACAGACTGGCACGTGTCATATGGGGGGCACG	F	Body	ACTN3		0.78722	0.8631629	-0.075942857			
cg27383174	3	37628507	148450860	148450910	N/A	TGGGTGACCTTGAAGCAATCATTTAGCTTTCCCTGGACCCCTGTATCCTCG	F	5'UTR;5'UTR;5'UTR;5'UTR;S/L	AGTR1		0.8393143	0.87339	-0.034075714	0.850515	0.87339	-0.022875
cg27384355	3	71785336	99844353	99844403	N/A	CGGGTCAAGTAATTAGCAGGCAGAATTATGATTGGGCTGTAACCTAACTC	F	Body;Body	C3orf26		0.8674257	0.89513	-0.027704286			
cg27387993	16	56724402	12373566	12373616	N/A	CGTTCCACAGCCACTTATTGGCAAATGGTAGGTGCTGCGTAACCCTTGAA	F	Body	SNX29		0.8936671	0.9279486	-0.034281429	0.9023713	0.9279486	-0.025577
cg27389290	2	74751387	196944767	196944817	N/A	CGGTCCATGATCAGCTACTCCTGAATATGGGCTTGGAAGAAGGGAGAGGA	F	N/A	N/A		0.8175543	0.8770514	-0.059497143	0.8449763	0.8770514	-0.032075
cg27402180	2	47614430	237065068	237065118	N_Shelf	ACTCCCCAGAGCTTCGAGGGACAGAGTGAAGATCCCCGGGAGCAGGACCG	F	N/A	N/A		0.7802757	0.8115914	-0.031315714	0.7798438	0.8115914	-0.031748
cg27416337	3	71665371	32748004	32748054	N/A	CTTGTGGTTACTGACTTCTTTAAATCATACTTCTGTTCGCAGTCACATCG	R	Body	CNOT10		0.70862	0.8507071	-0.142087143			
cg27424447	15	46792411	95388503	95388553	S_Shore	GTGCATGTGCACCCGGCAAACAATAGGCTCCAGGAGGCAGAGCTGCGCCG	F	N/A	N/A		0.1841029	0.2150643	-0.030961429			
cg27430293	16	17627504	89069935	89069985	N_Shore	CGAGTTATCTCCTTGCACGAACGAAACTGGGGTTCCAAGGGGGTTCTCG	F	N/A	N/A		0.4417643	0.5372043	-0.09544	0.4805725	0.5372043	-0.056632
cg27430561	7	31750381	23633208	23633258	N_Shelf	ACTTCTATGAGGATATCTGCTCAGCAATTGTCTGTCTAACCTCAGACTCG	R	N/A	N/A		0.8641943	0.8952757	-0.031081429			
cg27431500	16	71786500	1742281	1742331	N/A	GACGGGCTGTGGCGGCTCCTCACTGCAGTGCTGCGGGGCGCGGAGAAGCG	R	Body	HN1L		0.9100629	0.9332971	-0.023234286			
cg27446137	4	17666501	77723198	77723248	Island	GGCGCTAATGGCGAACACCTGGGGAACTGCCAAGTCTGGTAGGGGAATCG	R	N/A	N/A		0.4480614	0.5478757	-0.099814286			
cg27446570	1	13600332	3809532	3809582	S_Shore	CCGCGCTGAAGACCGCACTGCACCTGTGAGCTAGAGAGATTGAGAGCCACT	F	Body	C1orf174		0.8435157	0.8982414	-0.054725714			
cg27454316	4	27707445	4482158	4482208	N/A	AGTTAGCAGGGAAGCCTTTAGGAGGTGTGACACCTGAGCAGAGCCTCACG	F	Body	STX18		0.8199429	0.8911143	-0.071171429			
cg27455918	7	66719363	92370191	92370241	N/A	CGTGGCCCCTCTGCAACTCCTCAAGTCTCCAGCCTCAGGCACTAAGTATG	F	Body;Body	CDK6		0.6361214	0.7295157	-0.093394286			
cg27467787	20	53734485	36160512	36160562	S_Shelf	CGGCTTTGACTTGAGAGACCTGGAAGGTCATTCTGCCCTAAAATTTTGCT	F	N/A	N/A		0.90258	0.9268286	-0.024248571			
cg27473895	10	35611355	102497354	102497404	Island	CGCACTTCGAGGCGGCTCCGCAGAGCAGAGCTGCAGAGTCTTCCGCCCTC	F	N/A	N/A		0.1624357	0.14199	0.020445714	0.1752463	0.14199	0.0332563
cg27478659	17	13781410	39769012	39769062	N/A	TTCCCCAGCTACGATAAAGGTCTCTGGGGTTGGAGGCAGCCACAGACGG	F	1stExon;5'UTR	KRT16		0.6499871	0.72784	-0.077852857			
cg27496570	7	30779349	4804991	4804991	N_Shore	CGGCCACAAAGGCTTCCCTCTGTGCCCATCGGGCCAGCCAGCCAGCGCCTC	F	3'UTR	FOXK1		0.8098743	0.8577414	-0.047867143			
cg27499185	19	34717435	6138355	6138405	N/A	ATTGAGATCTAGCAGAACCCACAATGCGCCTGGGTGATGGGCCTCTCACG	R	5'UTR	ACSBG2		0.4579229	0.5721771	-0.114254286			
cg27504053	1	30699460	201488666	201488716	N/A	CGGACATAGGACATTTTATTATAAAGTCATCGGTGCTGGGTAAGGTGTC	F	TSS1500	RPS10P7		0.9351671	0.9604357	-0.025268571			
cg27507713	20	66665383	60587265	60587315	Island	CACCAGGGTGGATACAGAACCCTTCTAGAACGATGCTCTCACTACAGACG	R	Body	TAF4		0.7891314	0.8204743	-0.031342857			
cg27508545	1	64807330	10240017	10240067	N/A	CTTGCCTTCTTGGCTTGGCTTGGCTGTGCTCACGGATGGCGCGGCGGAACG	F	3'UTR;3'UTR	IFI44B		0.8153957	0.8840071	-0.068611429			
cg27510257	13	50670424	111305863	111305913	N/A	AGGTCTCCGGGTTTCGGTGTGGAAACACCACTCCACAAGCAGCCTCCACG	R	Body	CARS2		0.7928314	0.83765	-0.044818571	0.814745	0.83765	-0.022905
cg27511611	7	59614359	150140172	150140222	N/A	CGGCTTCATTCGCTTCAGCTGCGAGCTTTTCTCAGCGCAGAGAGCACAGG	F	N/A	N/A		0.8556414	0.8854614	-0.02982	0.8619575	0.8854614	-0.023504
cg27527798	7	70719393	1773245	1773295	N/A	AAGCAACTCTTAGCCTAGGAGGTTTCAGCAACGGAAGAGGGCTGGGACG	F	5'UTR	ELFN1		0.6223329	0.7050329	-0.0827	0.6567213	0.7050329	-0.048312
cg27528817	3	29607497	72860419	72860469	N/A	GAGGTTTTGCCAATTCTCCATCTGGAAGCCATGATATAACAGGATAATCG	R	Body	SHQ1							
cg27529240	16	29614369	89960078	89960128	N/A	ATATCGCAGAGGCCTCATCCAGAACACCACGAAGGTGAGGGCTGTGCTCG	R	Body	TCF25		0.9078457	0.9368243	-0.029878571			
cg27529911	8	35766440	33428326	33428376	S_Shelf	CGGAGTGTCTAAGAGGAAGCTGGAGTCAGGCAGTGGGAATAAAAAGAATC	R	N/A	N/A		0.8914343	0.9204743	-0.02904			
cg27531490	6	59624373	31542459	31542509	N/A	GGGGCCCTTACACTGGCGCATGAACTGTCTTCGTTAAAGGGGCTCCCCATACTCG	F	TSS1500	TNF		0.6135857	0.695424	-0.081838571			
cg27542729	1	70798300	177850564	177850614	N/A	CGTCTTCACATGCTTAGGAAGTCATTGTGAGCAAAAACAGAGTCCAAGGC	R	N/A	N/A		0.5629886	0.6431386	-0.08015	0.60821	0.6431386	-0.034929
cg27544673	10	66683447	129685902	129685952	N/A	CGGCTTTCTGAATTTCTGCCACACAAGGTCTGACAGCTGTATCTCCAGCG	F	Body	CLRN3		0.7598529	0.8343929	-0.07454	0.7934975	0.8343929	-0.040895
cg27551440	17	16738454	78617745	78617795	N/A	GACAACACAGCACACAATGCCAGCAGGGCAGACGCAGCACACGAAGCG	F	Body;Body	RPTOR		0.7800386	0.8127057	-0.032667143	0.7742838	0.8127057	-0.038422
cg27557134	1	19741381	34642345	34642395	N_Shore	AGGGCAAGCGCCCCATAAAATGGCAGTTAGGATTAAAATCGAGGTTGCCG	R	5'UTR;TSS1500	C1orf94		0.6109643	0.6886071	-0.077642857	0.5641938	0.6886071	-0.124413
cg27560182	1	50651490	26511621	26511671	N/A	CGCCGGCCGCTGGTTTGTGCTCAAGGGACACACGCTCTACTGGTACCGCCA	F	Body;Body	CNKSR1		0.8547414	0.9012657	-0.046524286	0.872755	0.9012657	-0.028511
cg27569829	18	62687456	60984485	60984535	N_Shore	CGGCTGAAAAAAATTTGCATCTAGGTATCTATGTAAAGTGTAGAAGAATT	R	Body	BCL2		0.6914571	0.7746786	-0.083221429	0.7285575	0.7746786	-0.046121
cg27576900	1	28660451	95113965	95113965	N/A	GCTCAAGGTCAGGAGGCTTGCGGAAATGCGCCAGCTGGCCTAAACAGATACG	R	N/A	N/A		0.6848414	0.7976743	-0.112832857	0.758885	0.7976743	-0.038789
cg27579359	16	32797385	55736319	55736369	N/A	AGGACAACTTCCAGGGGAGGAATCCCAAGATGGTGTCCGAGGTGGGAGCG	F	3'UTR	SLC6A2		0.8596186	0.8918129	-0.032194286			
cg27581644	20	51626461	42213729	42213779	N/A	CTGGAAAAAATAAACCTGCTTCTCGTTGAAGCCATTGTTAGTTTGAGTCG	F	3'UTR;3'UTR	SGK2		0.9361729	0.9648129	-0.02864			
cg27582180	5	29640461	35852286	35852336	N/A	CGGCTGCCCACTCACTGTCGGACACAGTGCCCCAGTGTGTTTCTGAGAA	R	N/A	N/A		0.8973757	0.9278014	-0.030425714	0.9062125	0.9278014	-0.021589
cg27582546	1	24778413	1062237	1062287	N/A	TGTGAGGTTGCTGGTTTGGGTGTCGGAAAGCCAGCACACCCGAAGGTCCG	R	N/A	N/A		0.8017043	0.8534829	-0.051778571	0.8155	0.8534829	-0.037983
cg27586885	19	42621310	33726898	33726948	Island	CGCCCGCGCCTTTCCCAGGCTCAAGGCCTCCCTGCCCACCAGGCAGGTGG	R	N/A	N/A		0.8531171	0.9005171	-0.0474	0.8724238	0.9005171	-0.028093
cg27597952	2	42644323	120284386	120284436	S_Shelf	ACCATATATTTACCACTGTCGTCGTGCTGGGGAGTCTGTTAGGAAGCTCG	R	N/A	N/A		0.7915357	0.8518971	-0.060361429	0.8206838	0.8518971	-0.031213
cg27603000	5	49690329	1834527	1834577	N/A	CGCCCACGACTTGGAGGGAGGGCACCTGCTCCGATCTTCAGCAGGAAAA	R	N/A	N/A		0.6476714	0.72894	-0.081268571			
cg27606002	17	67784484	76142461	76142511	N/A	AGAACAGCCCAGGGAGCCCCATGCCTCGGTGGGTGTAGGGCCTCTGCTCG	F	5'UTR;1stExon	C17orf99		0.7775471	0.8347229	-0.057175714			
cg27608981	7	34770445	101544969	101545019	N/A	CGGGCACACACACACTAGGTGGTTTGTTTTGTTCCCAGCAGCCCGTGTC	F	Body;Body;Body	CUX1		0.8926643	0.9218729	-0.029208571			
cg27616811	12	12661330	117484423	117484473	Island	GGTGGTCGAGGAGCTGCTGTCGGAAACCCTCACATCGAGAGGAGTCCCG	F	Body;Body;Body	TESC		0.7944514	0.8586871	-0.064235714	0.8141238	0.8586871	-0.044563
cg27619006	12	24679442	121177288	121177338	Island	GGGCCGCCCAGTCTCTGAGCCGGGGTTGGGGTGGAAGCCCCTGGCTCCCG	F	3'UTR	ACADS		0.8856243	0.9224343	-0.03681			
cg27628090	18	14806329	2538512	2538562	N/A	CTACACAGAGGCCTTTGTTCTTTCCTGGCATCAGTCTGCAGGACCAAGCG	F	3'UTR	METTL4		0.9233571	0.9651886	-0.031831429			
cg27630678	11	57701425	70565201	70565251	S_Shore	CGTGCTCTTCACATGGGCGATGAACTGTAAGAGCGAACCAAGCTCGATCT	R	Body	SHANK2		0.9019686	0.9397143	-0.037745714	0.9173188	0.9397143	-0.022396
cg27631057	1	29704325	236651140	236651190	N/A	CGGTGGCCTGGGACAGCAGCCCAAGACGTGGGCTTCTAACTGCCTCCGAA	F	N/A	N/A		0.67544	0.8035657	-0.128125714	0.7404563	0.8035657	-0.063109
cg27631638	2	61634491	138892947	138892997	N/A	CGGAAGCTGGGTAAAGGAGATCCGGGAGTTCTTTGTATTCTTCTTGCAAA	R	N/A	N/A		0.8705086	0.9015729	-0.031064286	0.88473	0.9015729	-0.016843
cg27635069	1	19668306	115880381	115880431	Island	CGCCAGGCGCGGGAGGAGTGCCGGCCAGCACCGCCGGGGGGAGCGCAGAGCG	F	5'UTR	NGF		0.2532371	0.28479	-0.031552857	0.254545	0.28479	-0.030245
cg27645065	8	41608507	144963911	144963961	N_Shelf	CGCAAAGTGGCCCTCCAGGTTCAAGTTGTGTCACGTTGGCATCCCACACG	F	N/A	N/A		0.8373514	0.8740143	-0.036662857			
cg27651238	12	18733343	52644264	52644314	Island	GCTGGTGAGGCGGCGTCGGTACAAAGTGGGGCGCTCAGGCGAAGCGCACG	R	N/A	N/A		0.4946214	0.3489714	0.14565	0.4650375	0.3489714	0.1160661
cg27655921	15	52632384	74044539	74044589	N_Shore	CGCCCTAGGGAGCCTTGGGGGCCCCCCAACTCCGTCTTGGGGCTTGGCCC	R	TSS1500	C15orf59		0.1457986	0.1818843	-0.036085714			
cg27664689	2	69792350	152830665	152830715	N/A	AGCAGTTGGTTTTGGAGTATTCAATGATTTGGCCTTTCCAAACATTCCACG	F	Body;Body;Body;TSS200	CACNB4		0.5957129	0.7027457	-0.107032857			
ch.10.655137	10	23655448	65843749	65843799	N/A	CAGGCATGAGCTGCTGTGTCTGGACAAAACTCAGTTGTTAATGGTGCCCC	F	N/A	N/A		0.1489886	0.1768486	-

Table_S2 Number of significantly changed genes or CpG-sties

	Methylome	Transcriptome	Overlay	Negative correlation
ND-obese vs non-obese	Genes: 3058 ↓ 2915 + ↑ 143 metylation sites: 5682 ↓ 5485 + ↑ 197	Genes: 713 ↓ 432 + ↑ 281	mRNA genes: 36 ↓ 13 + ↑ 23 methylation sites: 46 ↓ 45 + ↑ 1	mRNA ↑ and me sites ↓ Genes: 23 methylation sites: 26 mRNA ↓ and me sites ↑ Genes: 0 methylation sites: 0
T2D-obese vs non-obese	Genes: 1388 ↓ 1259 + ↑ 129 metylation sites: 2255 ↓ 2079 + ↑ 176	Genes: 920 ↓ 510 + ↑ 410	mRNA genes: 61 ↓ 23 + ↑ 38 methylation sites: 73 ↓ 66 + ↑ 7	mRNA ↑ and me sites ↓ Genes: 33 methylation sites: 40 mRNA ↓ and me sites ↑ Genes: 2 methylation sites: 2

Table_S3 Differentially expressed genes between any pairs of three phenotypic groups, obese non-diabetic group, the obese type 2 diabetic and non-obese

Obese non-diabetic group versus non-obese group							
Name	probe_ID	logFC	AveExpr	t	P.Value	FDR	B
PRKCE	8041763	0.885949	6.86951	2.908569	0.009259	0.311677	-2.52271
RPL13 /// S	7997940	-0.71861	8.178815	-6.62868	2.94E-06	0.097874	4.091509
#NV	7896112	0.734514	5.693303	5.809017	1.57E-05	0.123468	2.780948
RPS8 /// SI	7901046	-0.64454	6.125789	-5.80698	1.57E-05	0.123468	2.77755
SGCB	8100318	0.743322	7.158506	5.687808	2.02E-05	0.123468	2.577282
#NV	7893757	-1.07467	3.889639	-5.61691	2.35E-05	0.123468	2.457018
RFX5	7919971	0.492969	6.086326	5.576398	2.56E-05	0.123468	2.387929
DPP3	7941621	0.495435	6.85981	5.56966	2.60E-05	0.123468	2.376412
IL32	7992828	1.434413	7.73016	5.447995	3.36E-05	0.130579	2.167195
AGK	8136614	0.400572	6.410806	5.309883	4.52E-05	0.130579	1.926865
SNORD41	8034512	-0.64852	11.06296	-5.28441	4.78E-05	0.130579	1.88222
UBQLNL	7946082	-0.70423	4.089539	-5.28125	4.81E-05	0.130579	1.876673
TNRC6C	8010188	-0.47106	6.486099	-5.27119	4.92E-05	0.130579	1.859012
NUSAP1	7982889	0.42734	4.937344	5.24974	5.15E-05	0.130579	1.821293
RAP2A	7969693	0.536908	6.644343	5.184426	5.93E-05	0.130579	1.706033
SNORD32E	8117746	-0.55496	5.137442	-5.13493	6.60E-05	0.130579	1.618268
PIGR	7923929	0.519416	7.663289	5.10365	7.07E-05	0.130579	1.562623
#NV	7894078	0.585226	5.488189	5.072849	7.56E-05	0.130579	1.507693
#NV	8170955	0.455524	4.97543	5.011698	8.64E-05	0.130579	1.398245
ZNF69	8025968	-0.46164	6.79015	-5.00693	8.73E-05	0.130579	1.389683
#NV	7892680	-0.59244	8.356215	-4.99958	8.87E-05	0.130579	1.376499
#NV	7894980	-0.53441	6.412599	-4.9987	8.89E-05	0.130579	1.374921
SNORD116	7981994	-0.64248	7.598905	-4.98834	9.09E-05	0.130579	1.356303
RPL13A ///	8030360	-0.46692	10.57052	-4.98149	9.23E-05	0.130579	1.343987
TP53I3	8050702	0.78967	5.6318	4.972374	9.41E-05	0.130579	1.327591
#NV	7895660	0.763786	3.734052	4.94354	0.0001	0.133522	1.275652
GNA12	8137865	0.469257	6.700239	4.889422	0.000113	0.144561	1.177875
C5orf24	8108163	0.343593	8.744946	4.857651	0.000121	0.149268	1.120294
ULBP2	8122720	-0.33088	2.595687	-4.80453	0.000136	0.15597	1.023733
#NV	8012518	-0.30863	3.673918	-4.79445	0.000139	0.15597	1.005383
#NV	7960359	-0.44613	9.166536	-4.78982	0.000141	0.15597	0.996932
WDR45L	8019523	0.315849	8.195043	4.724257	0.000162	0.174428	0.87717
VPS33A	7967240	0.487316	5.758354	4.694556	0.000173	0.179498	0.822748
RET	7927120	0.597856	4.313304	4.670644	0.000183	0.179498	0.778858
ARRDC4	7986350	0.717193	6.646736	4.651926	0.000191	0.179498	0.744458
LINC00575	8101359	-0.40321	2.854601	-4.64167	0.000195	0.179498	0.725591
PDE7A	8151074	0.288314	5.028451	4.620813	0.000204	0.179498	0.687192
#NV	8084122	-0.43077	4.482891	-4.61564	0.000207	0.179498	0.677657
PDIA6	8050278	0.418483	9.661318	4.611256	0.000209	0.179498	0.66958
#NV	7894838	0.53184	6.764126	4.607582	0.00021	0.179498	0.662808
SNORD116	7981976	-0.61309	10.43758	-4.58194	0.000223	0.183282	0.615496
MIR1292 /	8060503	-0.49847	10.86583	-4.55121	0.000238	0.183282	0.558701
GALNTL4	7946641	0.530248	5.299748	4.545485	0.000241	0.183282	0.548116
AKR1A1	7901110	0.298752	9.687642	4.536798	0.000246	0.183282	0.53204
NTAN1	7999598	0.64795	7.254673	4.52811	0.000251	0.183282	0.515953
VAMP8	8043197	0.324326	9.406543	4.522432	0.000254	0.183282	0.505437
TMEM154	8103226	1.691003	6.311823	4.507309	0.000263	0.183282	0.477409
SNORD46	7901048	-0.54681	9.013704	-4.50636	0.000263	0.183282	0.475659
SNORD116	7981970	-0.64644	5.180899	-4.47943	0.000279	0.183282	0.425692
SNORD116	7981960	-0.4527	7.261537	-4.47781	0.000281	0.183282	0.422684
#NV	7895169	-0.84525	5.479708	-4.46664	0.000288	0.183282	0.401931
DUS2L	7996725	0.389062	6.089287	4.462832	0.00029	0.183282	0.394853
#NV	8059712	-0.85837	8.599734	-4.44999	0.000298	0.183282	0.370972
MPZL2	7952046	0.445144	7.816198	4.44732	0.0003	0.183282	0.366016
GPT	8148902	-0.49737	8.216095	-4.4365	0.000308	0.183282	0.345887
#NV	7895782	-0.47333	7.294467	-4.41698	0.000321	0.183282	0.309543
RPL13A ///	8030362	-0.38226	11.53386	-4.41084	0.000326	0.183282	0.298106
GJB3	7899932	-0.31673	3.468453	-4.39753	0.000335	0.183282	0.273302
#NV	7990564	-1.04052	5.372436	-4.39622	0.000336	0.183282	0.270865
MTCH2	7947934	0.352661	9.72621	4.384992	0.000345	0.183282	0.249927
#NV	7893452	-0.96868	3.687011	-4.38053	0.000348	0.183282	0.24161
TMEM19	7957167	0.463826	6.520245	4.379268	0.000349	0.183282	0.23925
#NV	8005630	-0.46105	3.431711	-4.36605	0.00036	0.183282	0.21458
#NV	8152819	-0.57581	4.161926	-4.35353	0.00037	0.183282	0.191205
TSPAN17	8110224	0.323761	6.632778	4.343235	0.000379	0.183282	0.171965
#NV	7894476	-0.82567	5.237518	-4.33306	0.000387	0.183282	0.152941
#NV	7894322	-0.968	5.270751	-4.33181	0.000388	0.183282	0.150605
B4GALT6	8022747	0.486376	5.026308	4.324253	0.000395	0.183282	0.136478
NRSA2	7908597	-0.24325	8.843344	-4.31154	0.000406	0.183282	0.112692
SLC2A13	7962327	0.44039	6.189933	4.306757	0.000411	0.183282	0.103743
SCARNA5	8049297	-0.73037	8.216163	-4.30398	0.000413	0.183282	0.098542
HSPA8 ///	7952339	-0.59101	9.307381	-4.30354	0.000414	0.183282	0.097712
KRT222 ///	8015049	0.35538	3.496287	4.292874	0.000424	0.183282	0.07775
PYGB	8061447	0.386933	6.291286	4.280836	0.000435	0.183282	0.055202
GREM2	7925452	-0.4552	6.988636	-4.27801	0.000438	0.183282	0.049907
NAPEPLD	8141872	-0.6026	7.512032	-4.278	0.000438	0.183282	0.049886
INHBC	7956423	0.467765	9.464047	4.276292	0.00044	0.183282	0.046688
NOMO1 //	7993371	0.362428	9.720163	4.273397	0.000443	0.183282	0.041262
NOMO1 //	7993511	0.362428	9.720163	4.273397	0.000443	0.183282	0.041262
NOMO1 //	7999791	0.362428	9.720163	4.273397	0.000443	0.183282	0.041262
SLC27A2	7983650	0.571538	10.54731	4.271382	0.000445	0.183282	0.037484
ME1	8127854	1.016731	6.481465	4.270157	0.000446	0.183282	0.03519
OR52H1	7946087	-0.73018	4.806707	-4.26115	0.000455	0.184307	0.018305
PPP4R1	8022251	0.35761	6.650342	4.246437	0.00047	0.184307	-0.00929
MTUS1	8149500	-0.31468	7.424612	-4.24639	0.00047	0.184307	-0.00939
TRGV9	8139107	0.557671	3.695482	4.24612	0.00047	0.184307	-0.00989
GLB1	8086028	0.296344	8.122102	4.231149	0.000487	0.186809	-0.03798
GPI	8027621	0.445895	9.629675	4.229701	0.000488	0.186809	-0.0407
DAO	7958425	0.431492	9.513948	4.214581	0.000505	0.191045	-0.06909
#NV	8153320	-0.35284	4.889629	-4.19313	0.00053	0.194212	-0.1094
RPN1	8090490	0.342561	9.202456	4.191983	0.000531	0.194212	-0.11156
RNU4-7P	8130181	-0.46227	3.438394	-4.18851	0.000535	0.194212	-0.11809
MIR4800 /	8098995	0.319752	6.534054	4.18363	0.000541	0.194212	-0.12726
#NV	7893150	-0.4237	6.072817	-4.18256	0.000542	0.194212	-0.12927
VRK2	8042086	0.336975	6.386224	4.162805	0.000567	0.197601	-0.16643
TTC7B	7980720	0.588751	7.331794	4.155798	0.000576	0.197601	-0.17962
#NV	8096331	-0.37904	5.401794	-4.15443	0.000578	0.197601	-0.18219
#NV	7934297	-1.28045	4.366591	-4.14553	0.000589	0.197601	-0.19894
#NV	7900336	-0.31066	7.082027	-4.14134	0.000595	0.197601	-0.20683
FAT1	8104079	0.945922	6.900047	4.136979	0.000601	0.197601	-0.21505
#NV	7893849	0.774387	6.577002	4.135466	0.000603	0.197601	-0.2179
FBXO16 //,	8149986	-0.38667	7.014136	-4.1302	0.00061	0.197601	-0.22782
#NV	7896284	-1.08255	2.508744	-4.12961	0.000611	0.197601	-0.22893
#NV	8049071	-0.39535	3.463656	-4.12873	0.000612	0.197601	-0.23059
RNU4-2	7967028	-1.20852	8.687894	-4.1113	0.000636	0.197601	-0.26343
PPIL1	8126058	0.386655	5.537191	4.106064	0.000644	0.197601	-0.27329
C22orf28	8075585	0.340581	8.266556	4.105508	0.000645	0.197601	-0.27434
#NV	7895265	-0.47467	2.176171	-4.10255	0.000649	0.197601	-0.27992
#NV	7894082	0.650765	2.729652	4.099558	0.000653	0.197601	-0.28556
PDIA4	8143684	0.390538	9.788474	4.093022	0.000663	0.197601	-0.29788
HYOU1	7952145	0.547426	7.155851	4.092762	0.000663	0.197601	-0.29837
LANCL1	8058614	0.289592	7.337116	4.091056	0.000666	0.197601	-0.30159
#NV	7894930	0.893458	3.643689	4.084241	0.000676	0.197601	-0.31444
NUP93	7995843	0.42949	6.250248	4.083916	0.000677	0.197601	-0.31505
RBMX /// S	8175432	-0.69388	4.952711	-4.0822	0.000679	0.197601	-0.31828
MIR1304 /	7951038	-0.4532	6.851167	-4.07592	0.000689	0.197601	-0.33013
#NV	7928815	-0.33413	3.258196	-4.07263	0.000694	0.197601	-0.33635
ZNF174	7992897	0.3303	5.291092	4.072432	0.000694	0.197601	-0.33671
MGAT2	7974207	0.453763	5.412207	4.066805	0.000703	0.197693	-0.34733
MUTED-TX	8123802	0.348476	8.050581	4.057157	0.000719	0.197693	-0.36554
DAPK1	8156199	-0.39404	9.274811	-4.04692	0.000735	0.197693	-0.38485
IKBKAP	8163023	0.266865	8.056995	4.044129	0.00074	0.197693	-0.39013
GPR148	8045216	-0.34312	3.75864	-4.04332	0.000741	0.197693	-0.39165
AMFR	8001477	0.318106	9.446631	4.042037	0.000743	0.197693	-0.39408
PHLPP2	8002571	0.497919	6.160444	4.039618	0.000747	0.197693	-0.39864
ATP8B1	8023497	0.449521	6.939234	4.039465	0.000748	0.197693	-0.39893
CDK18	7909104	-0.50623	6.64099	-4.02767	0.000768	0.197693	-0.42121
SNORD105	8025584	-0.569	5.369664	-4.02437	0.000773	0.197693	-0.42745

Obese type2 diabetic group versus non-obese group							
Name	probe_ID	logFC	AveExpr	t	P.Value	FDR	B
PRKCE	8041763	1.326419	6.86951	4.354631	0.000369	0.095471	0.266886
ACLY	8015460	0.525385	7.015875	3.23275	0.004544	0.19962	-1.94936
NR5A2	7908597	-0.39549	8.843344	-7.00991	1.39E-06	0.029933	5.039808
GAS6	7970329	0.854495	6.48088	6.564718	3.34E-06	0.029933	4.317044
NUDT9P1	7934993	-0.52452	4.010846	-6.51337	3.70E-06	0.029933	4.231486
IL32	7992828	1.673065	7.73016	6.354412	5.10E-06	0.029933	3.963782
CDKN1A	8119088	1.037604	5.614176	6.224791	6.63E-06	0.029933	3.742311
#NV	8096077	-0.61113	7.248785	-6.13967	7.89E-06	0.029933	3.595344
FAM134B	8111136	-0.97088	6.763045	-6.13	8.05E-06	0.029933	3.578562
#NV	7931168	-0.63198	10.1272	-6.0739	9.04E-06	0.029933	3.480946
ALPK2	8023528	2.007309	5.646167	6.065706	9.19E-06	0.029933	3.466647
TNRC6C	8010188	-0.53906	6.486099	-6.03204	9.85E-06	0.029933	3.407781
KYNU	8045539	-0.51685	8.846854	-6.01595	1.02E-05	0.029933	3.379562
CRELD2	8073949	0.570553	6.114595	5.904059	1.28E-05	0.029933	3.182265
CDNF	7932177	-0.61859	6.64075	-5.89561	1.31E-05	0.029933	3.167281
RET	7927120	0.75329	4.313304	5.884939	1.34E-05	0.029933	3.148345
C4orf37	8101816	-0.33939	4.580864	-5.88082	1.35E-05	0.029933	3.141034
H2AFY2	7928107	0.937605	5.157024	5.814229	1.55E-05	0.030963	3.022397
AJUBA	7977854	0.930244	6.251157	5.804743	1.58E-05	0.030963	3.005439
#NV	7894078	0.664782	5.488189	5.76246	1.73E-05	0.031058	2.929678
PPM1K	8101701	-0.94763	5.58706	-5.73873	1.82E-05	0.031058	2.887039
PLD1	8092134	-0.49978	8.549163	-5.7259	1.87E-05	0.031058	2.863945
C5orf24	8108163	0.401212	8.744946	5.672255	2.09E-05	0.03229	2.767115
NAPEPLD	8141872	-0.79743	7.512032	-5.66114	2.14E-05	0.03229	2.747
L3MBTL3	8122013	-0.76956	6.489783	-5.63155	2.28E-05	0.03229	2.693346
CLDN12	8134091	-0.33202	9.09801	-5.60865	2.39E-05	0.03229	2.651735
SMPDL3A	8121794	-0.57539	7.344832	-5.58683	2.50E-05	0.03229	2.612004
KMO	7910950	-0.87183	8.568422	-5.58334	2.52E-05	0.03229	2.605649
RBMS1	8056201	-0.85566	7.197228	-5.54549	2.73E-05	0.033495	2.536532
GYS2	7961673	-0.34685	10.46994	-5.53122	2.82E-05	0.033495	2.510427
GNA12	8137865	0.52385	6.700239	5.458248	3.29E-05	0.037341	2.376438
RBMS1P1	7964757	-0.77343	6.33267	-5.44791	3.36E-05	0.037341	2.357387
MIR4800 /	8098995	0.410388	6.534054	5.369522	3.98E-05	0.042059	2.212467
ATG2B	7981192	-0.36767	7.922724	-5.36226	4.04E-05	0.042059	2.198993
NUDT13	7928342	-0.70277	5.310278	-5.33219	4.31E-05	0.042722	2.143138
C12orf49	7966738	0.526776	6.36028	5.326771	4.36E-05	0.042722	2.133058
HNMT	8045499	-0.38059	8.786716	-5.30108	4.61E-05	0.043861	2.085208
INHBE	7956426	1.387783	9.06172	5.273093	4.90E-05	0.045294	2.032983
FAT1	8104079	1.198675	6.900047	5.242392	5.23E-05	0.045728	1.975567
ULBP2	8122720	-0.36039	2.595687	-5.233	5.34E-05	0.045728	1.957983
FERMT2	7979204	-0.37013	8.785457	-5.23122	5.36E-05	0.045728	1.954639
HYOU1	7952145	0.698185	7.155851	5.219896	5.49E-05	0.045728	1.933412
DAPK1	8156199	-0.49342	9.274811	-5.0676	7.65E-05	0.062091	1.646248
SEPSECS	8099696	-0.41977	8.807067	-5.04569	8.02E-05	0.062196	1.604692
SERPINE1	8135069	1.69581	7.350442	5.044851	8.03E-05	0.062196	1.603102
NR2F6	8035249	0.353545	8.071004	5.025507	8.38E-05	0.062196	1.566357
#NV	8170955	0.456654	4.97543	5.02413	8.41E-05	0.062196	1.563741
PDGFA	8137670	0.788163	5.5341	5.00205	8.82E-05	0.062592	1.521737
SLC16A13	8004266	1.151149	8.506601	4.997289	8.91E-05	0.062592	1.512673
PREB	8051012	0.423675	7.467153	4.991674	9.02E-05	0.062592	1.501979
KRT8	7963567	0.611965	9.732278	4.972373	9.41E-05	0.063957	1.46519
TP53I3	8050702	0.78737	5.6318	4.957893	9.71E-05	0.064696	1.437559
NKRF	8174684	-0.30224	5.562047	-4.94469	1.00E-04	0.065287	1.412345
UBQLNL	7946082	-0.65015	4.089539	-4.87565	0.000116	0.073033	1.28016
EYS	8127396	0.909818	2.941046	4.873659	0.000117	0.073033	1.276334
PSD3	8149555	-0.64792	8.84969	-4.86074	0.00012	0.073033	1.251536
ABCA8	8017885	-0.57086	8.734687	-4.8537	0.000122	0.073033	1.23801
CTH	7902290	-0.75189	8.715336	-4.84235	0.000125	0.073033	1.216192
#NV	8097809	-0.64051	4.643435	-4.8363	0.000127	0.073033	1.204564
HBB	7946033	1.717022	8.304631	4.834028	0.000127	0.073033	1.200197
ARHGAP29	7917850	-0.39585	7.79776	-4.82724	0.000129	0.073033	1.187147
HPS5	7946988	0.900179	6.768116	4.803929	0.000136	0.075598	1.142257
#NV	8149627	-0.2909	2.047911	-4.79585	0.000139	0.075694	1.126686
SLC16A12	7934936	-1.10762	4.256379	-4.77278	0.000146	0.0762	1.082181
AHCY	8065738	-0.39761	9.178486	-4.76351	0.000149	0.0762	1.064297
#NV	8156969	-0.72062	4.358179	-4.7525	0.000153	0.0762	1.043027
FAM221A	8131881	-0.45364	5.740421	-4.73789	0.000158	0.0762	1.014784
RBMS1	8056206	-0.73195	7.090963	-4.73108	0.00016	0.0762	1.001621
SNORD116	7981960	-0.47738	7.261537	-4.72188	0.000163	0.0762	0.983817
MIR34A	7912250	0.746136	5.68999	4.721662	0.000163	0.0762	0.983392
MET	8135601	-0.60134	8.935059	-4.71602	0.000165	0.0762	0.972467
MTMR10	7987048	-0.33846	8.831583	-4.71587	0.000165	0.0762	0.972177
MBTD1	8016789	-0.3493	6.996747	-4.71358	0.000166	0.0762	0.967748
#NV	7896098	-0.72648	5.023862	-4.71185	0.000167	0.0762	0.964399
AASS	8142554	-0.90496	9.233137	-4.70908	0.000168	0.0762	0.959035
ASS1	8158671	-0.54195	11.78321	-4.70528	0.000169	0.0762	0.951676
HSD17B11	8101648	-0.79451	9.57788	-4.6933	0.000174	0.076359	0.928454
#NV	8007990	-0.6206	7.541219	-4.69228	0.000174	0.076359	0.926475
SLC4A2	8137352	0.405683	6.883308	4.678229	0.00018	0.077426	0.899237
C11orf1	7943779	-0.39984	6.3745	-4.67426	0.000181	0.077426	0.891531
PSMG3	8137798	0.35761	6.440387	4.658582	0.000188	0.079145	0.861107
HBA1 /// H	7991762	1.510196	9.143064	4.642215	0.000195	0.08004	0.829315
HBA1 /// H	7991766	1.510196	9.143064	4.642215	0.000195	0.08004	0.829315
ENPP3	8122071	-0.78062	6.649874	-4.63398	0.000198	0.080519	0.813309
#NV	7967658	-0.55543	5.376206	-4.61896	0.000205	0.082242	0.784096
PRAP1 ///	7931571	0.502919	7.59654	4.611869	0.000208	0.08255	0.7703
#NV	7893800	-0.45719	8.332877	-4.59545	0.000216	0.083621	0.73833
#NV	7895751	-0.45719	8.332877	-4.59545	0.000216	0.083621	0.73833
FAM129B	8164217	0.559294	5.890549	4.582009	0.000223	0.085162	0.712149
KLF12	7972003	-0.44826	8.378716	-4.57324	0.000227	0.085849	0.695052
GRAMD1C	8081758	-0.49514	8.32513	-4.54074	0.000244	0.091238	0.631644
IGSF9	7921492	1.088572	6.448576	4.527137	0.000251	0.091435	0.60508
RNS5110	8046018	-0.72741	5.79378	-4.52713	0.000251	0.091435	0.605062
#NV	7983922	-0.87006	7.974671	-4.52287	0.000254	0.091435	0.596748
KANSL1L	8058570	-0.50559	6.496253	-4.51999	0.000255	0.091435	0.59111
ZCCHC6	8162147	-0.65009	8.771084	-4.51052	0.000261	0.092388	0.572598
#NV	7955419	-0.51824	6.308547	-4.49378	0.000271	0.094342	0.539869
#NV	7934297	-1.38522	4.366591	-4.48475	0.000276	0.094342	0.522192
MSN	8167965	0.673988	8.704564	4.483846	0.000277	0.094342	0.520425
#NV	7893757	-0.8576	3.889639	-4.48238	0.000278	0.094342	0.517556
ADAMTSL5	8032249	0.385673	4.681297	4.468669	0.000286	0.095471	0.490712
SLC16A4	7918426	-1.21242	6.331581	-4.466	0.000288	0.095471	0.48549
#NV	8114006	-0.44128	7.142986	-4.46195	0.000291	0.095471	0.477553
#NV	7957536	-0.76239	5.81491	-4.45097	0.000298	0.095471	0.45604
PDE7B	8122222	-0.63615	6.721057	-4.44566	0.000301	0.095471	0.445619
MFNG	8075924	0.328711	5.636324	4.445534	0.000301	0.095471	0.445382
#NV	7983924	-0.8965	5.612225	-4.44348	0.000303	0.095471	0.441362
#NV	7895252	-0.43717	6.76124	-4.43864	0.000306	0.095471	0.43187
GPC1	8049670	0.504578	5.880173	4.432887	0.00031	0.095471	0.420584
ARRDC4	7986350	0.681725	6.646736	4.421872	0.000318	0.095471	0.398978
LAMA5	8067409	0.676927	6.368012	4.419213	0.00032	0.095471	0.39376
LGALS1	8072876	0.441486	9.538258	4.412285	0.000325	0.095471	0.380165
MIR32	8163107	-0.75324	5.675018	-4.41143	0.000325	0.095471	0.378485
HMBOX1	8145636	-0.2648	7.545211	-4.40778	0.000328	0.095471	0.371315
CDH23	7928218	-1.58924	6.981322	-4.4053	0.00033	0.095471	0.366446
CA14	7905131	-0.88772	5.277867	-4.4011	0.000333	0.095471	0.358211
#NV	7893165	-0.7063	5.918788	-4.39807	0.000335	0.095471	0.352257
#NV	7893263	-0.58326	5.106148	-4.39629	0.000336	0.095471	0.348766
#NV	8180267	0.547658	5.750718	4.38796	0.000343	0.095471	0.332398
TFPI	8057599	-0.46881	9.479522	-4.38781	0.000343	0.095471	0.332108
UBR2	8119529	-0.25807	8.621884	-4.38607	0.000344	0.095471	0.328676
#NV	7908610	-0.44097	7.219183	-4.38269	0.000347	0.095471	0.32204
MTUS1	8149500	-0.32342	7.424612	-4.36436	0.000361	0.095471	0.286012
TMCC2	7909088	-0.27996	3.167546	-4.35568	0.000368	0.095471	0.268941
TTC9	7975412	0.587946	5.1551	4.355138	0.000369	0.095471	0.267882
FPGT-TNNI	7902317	-0.2717	2.698395	-4.35441	0.000369	0.095471	0.266446
WBP1L	7930162	-0.41293	7.625875	-4.35412	0.00037	0.095471	0.265889
TFE3	8172520	0.39213	7.107494	4.354037	0.00037	0.095471	0.265717

Obese non-diabetic group versus Obese type2 diabetic group							
Name	probe_ID	logFC	AveExpr	t	P.Value	FDR	B
SNORA55	7915227	-1.12042	6.174885	-6.4721	4.02E-06	0.13382	3.464961
SNHG12 //	7914212	-0.84869	7.777199	-5.87655	1.36E-05	0.168211	2.584545
SNORD14E	7952335	-1.19041	6.572392	-5.82489	1.52E-05	0.168211	2.505182
#NV	7908610	0.557171	7.219183	5.537525	2.78E-05	0.204247	2.055104
BBS2	8001507	0.553204	6.616028	5.450203	3.35E-05	0.204247	1.915531
DUX4L4 //,	8176570	-0.86526	3.318763	-5.40595	3.68E-05	0.204247	1.844305
#NV	8023862	-0.46834	4.626697	-5.31307	4.49E-05	0.209089	1.693776
#NV	7894322	-1.1757	5.270751	-5.26127	5.02E-05	0.209089	1.609208
#NV	7894719	-0.80989	4.669857	-5.16526	6.18E-05	0.223374	1.451335
RPS8 /// SI	7901046	-0.56914	6.125789	-5.1277	6.71E-05	0.223374	1.389172
CLDN12	8134091	0.300003	9.09801	5.067851	7.64E-05	0.231302	1.289681
RPL13 /// S	7997940	-0.53526	8.178815	-4.93743	0.000102	0.254446	1.071013
#NV	7895841	-0.57451	7.561394	-4.93251	0.000103	0.254446	1.06271
#NV	8139887	-0.46279	4.629469	-4.91388	0.000107	0.254446	1.031257
FAM134B	8111136	0.771795	6.763045	4.873004	0.000117	0.255925	0.962079
CCDC9	8029894	-0.41915	5.530042	-4.85042	0.000123	0.255925	0.923754
SNHG12 //	7914214	-0.68707	5.572051	-4.7737	0.000146	0.274092	0.793037
RNS5491	8068510	-0.33384	4.634801	-4.76579	0.000148	0.274092	0.77951
SNORA42	7920873	-1.5089	10.33362	-4.72697	0.000161	0.282141	0.713036
BBS4	7984686	0.343089	6.431662	4.704959	0.000169	0.282141	0.675252
TRMT1L	7922870	0.29041	7.

MSN	8167965	0.604048	8.704564	4.018557	0.000784	0.197693	-0.43842
#NV	7893327	0.587043	2.258655	4.017465	0.000785	0.197693	-0.44048
SIGLEC12	8038852	-0.31179	3.988818	-4.01359	0.000792	0.197693	-0.4478
TCTA	8079746	0.380017	7.489008	4.013268	0.000793	0.197693	-0.44841
#NV	7893838	-0.43833	10.49834	-4.01153	0.000796	0.197693	-0.4517
ZBTB33	8169683	0.470959	7.845789	4.00753	0.000803	0.197693	-0.45925
RPL13A ///	8030366	-0.81586	8.782847	-4.00712	0.000804	0.197693	-0.46003
#NV	8136059	-0.31475	2.545016	-4.00381	0.00081	0.197693	-0.46628
#NV	8149627	-0.24268	2.047911	-4.00079	0.000815	0.197693	-0.47199
#NV	7893702	0.772845	2.076673	3.995739	0.000825	0.197693	-0.48153
#NV	7893263	-0.52998	5.106148	-3.99467	0.000827	0.197693	-0.48356
ANXA6	8115234	0.512979	10.52119	3.990855	0.000834	0.197693	-0.49076
LPAL2	8130598	-0.42007	9.128438	-3.98876	0.000838	0.197693	-0.49473
FAM9B	8171271	-0.60129	3.508536	-3.98755	0.00084	0.197693	-0.49701
#NV	7896050	0.327801	10.95674	3.983264	0.000848	0.197693	-0.50511
#NV	7895857	-0.53699	7.83354	-3.98235	0.00085	0.197693	-0.50684
LOC100501	7982020	-0.77803	3.019329	-3.97969	0.000855	0.197693	-0.51187
FAM98A	8051413	0.360918	7.573228	3.97068	0.000872	0.199926	-0.5289
SNORD63	8114468	-0.55417	5.371115	-3.96854	0.000877	0.199926	-0.53295
GATSL3	8075322	-0.37697	5.439917	-3.96418	0.000885	0.200519	-0.5412
#NV	8180386	0.317752	9.308023	3.959834	0.000894	0.201117	-0.54942
RALGPS1	8157949	0.561224	5.195621	3.952741	0.000908	0.202973	-0.56283
#NV	7960434	-0.28178	2.700687	-3.94926	0.000915	0.2032	-0.56941
SNORD116	7981996	-0.50116	10.61273	-3.94387	0.000927	0.204311	-0.5796
BAMBI	7926875	-0.51788	6.377384	-3.93568	0.000944	0.205389	-0.5951
#NV	7917726	-0.33918	2.82836	-3.93538	0.000944	0.205389	-0.59567
SNORD115	7982070	-0.90207	5.035176	-3.93213	0.000951	0.205389	-0.60182
KIAA0100	8013696	0.220127	8.084027	3.929885	0.000956	0.205389	-0.60607
PDHA1	8166335	0.382477	8.343463	3.919794	0.000978	0.207285	-0.62516
PPIB	7989619	0.280539	10.60964	3.916162	0.000986	0.207285	-0.63204
TWSG1	8020090	0.315298	5.843973	3.913049	0.000993	0.207285	-0.63793
TMBIM1	8058927	0.363605	9.914981	3.91185	0.000996	0.207285	-0.6402
LOC100501	7981955	-0.48003	6.979061	-3.91165	0.000996	0.207285	-0.64058
NUDT9P1	7934993	-0.31378	4.010846	-3.89647	0.001031	0.208929	-0.6693
TUBG1	8007302	0.376749	8.206375	3.894663	0.001035	0.208929	-0.67273
#NV	8019517	-0.33893	3.082118	-3.89308	0.001038	0.208929	-0.67573
SNORD116	7981982	-0.33429	11.22942	-3.8831	0.001062	0.208929	-0.69463
SNORD116	7981986	-0.33429	11.22942	-3.8831	0.001062	0.208929	-0.69463
FBXO2	7912473	0.607956	5.840583	3.882774	0.001063	0.208929	-0.69524
PDGFA	8137670	0.611397	5.5341	3.880208	0.001069	0.208929	-0.7001
#NV	8041170	-0.51128	8.059372	-3.87694	0.001077	0.208929	-0.70628
ZDHHC2	8144758	0.596234	6.616174	3.871273	0.001091	0.208929	-0.71702
#NV	7892677	-0.36508	8.961351	-3.871	0.001091	0.208929	-0.71753
#NV	7894872	-0.36508	8.961351	-3.871	0.001091	0.208929	-0.71753
LRP4	7947744	-0.43699	4.945244	-3.87043	0.001093	0.208929	-0.71861
DIO3OS	7981326	-0.67236	5.360552	-3.86921	0.001096	0.208929	-0.72092
#NV	7893800	-0.38465	8.332877	-3.86635	0.001103	0.208929	-0.72634
#NV	7895751	-0.38465	8.332877	-3.86635	0.001103	0.208929	-0.72634
ANKRD36B	7922121	0.454854	4.297106	3.865443	0.001105	0.208929	-0.72806
#NV	8180387	0.312837	9.374158	3.863155	0.001111	0.208929	-0.73239
#NV	8180389	0.29822	9.309014	3.855338	0.00113	0.210565	-0.74719
#NV	7894183	0.99012	4.52317	3.850523	0.001143	0.210565	-0.75631
RND1	7962884	-0.77687	6.709055	-3.85002	0.001144	0.210565	-0.75727
#NV	8180388	0.306589	9.297491	3.845893	0.001155	0.210565	-0.76508
PPP1R2	8092959	0.336147	7.099488	3.844488	0.001158	0.210565	-0.76774
CEP78	8156026	0.569045	5.346632	3.843406	0.001161	0.210565	-0.76979
MANEAL	7900183	0.415939	5.813396	3.842404	0.001164	0.210565	-0.77169
#NV	8114006	-0.37935	7.142986	-3.83581	0.001181	0.211413	-0.78418
TTC36	7944271	-0.36289	7.939875	-3.83326	0.001188	0.211413	-0.78902
AASS	8142554	-0.73651	9.233137	-3.83253	0.00119	0.211413	-0.79039
#NV	7895090	0.417021	8.131744	3.823435	0.001214	0.211413	-0.80762
INSR	8033362	-0.26987	8.463744	-3.82226	0.001217	0.211413	-0.80986
RRM1	7937915	0.326144	6.883209	3.822101	0.001218	0.211413	-0.81015
HBB	7946033	1.356981	8.304631	3.820385	0.001223	0.211413	-0.8134
#NV	7980304	-0.42468	3.657455	-3.8169	0.001232	0.211413	-0.82
VAC14	8002421	0.345632	6.987907	3.816385	0.001234	0.211413	-0.82098
SNORD60	7998722	-0.69106	6.692967	-3.81463	0.001238	0.211413	-0.82431
#NV	7895792	0.673288	4.073402	3.813956	0.00124	0.211413	-0.82558
OR4C16	7939926	-0.36606	2.465458	-3.81123	0.001248	0.211413	-0.83074
#NV	8154981	0.309024	7.032803	3.810205	0.001251	0.211413	-0.83269
FPGS	8158123	-0.30858	7.047735	-3.80747	0.001259	0.211642	-0.83787
CDKN1A	8119088	0.63414	5.614176	3.804328	0.001267	0.212067	-0.84382
ATP12A	7968062	-0.2961	2.691402	-3.79649	0.00129	0.214754	-0.85868
SNORD116	7981978	-0.37914	11.73151	-3.78878	0.001312	0.216119	-0.87329
#NV	7894550	-0.71995	5.808783	-3.78673	0.001318	0.216119	-0.87716
MID2	8169249	0.393682	6.638612	3.781297	0.001335	0.216119	-0.88746
#NV	8144701	-0.65874	4.966932	-3.78096	0.001336	0.216119	-0.8881
NSMAF	8150928	0.370818	6.712796	3.774089	0.001356	0.216119	-0.90112
#NV	8016504	-0.37785	3.098448	-3.77372	0.001358	0.216119	-0.90182
MYO18A	8013860	-0.41854	7.939363	-3.77278	0.00136	0.216119	-0.90359
#NV	7893334	-0.52083	8.344782	-3.77128	0.001365	0.216119	-0.90644
#NV	7894309	-0.48609	7.51479	-3.76996	0.001369	0.216119	-0.90894
PGAM1	7958152	0.31786	8.849032	3.7686	0.001373	0.216119	-0.91152
ACOT2	7975602	0.632408	8.522223	3.767929	0.001375	0.216119	-0.91279
RBM18	8163948	0.322665	6.072573	3.762842	0.001391	0.216119	-0.92243
LDLRAP1	7899023	0.353409	6.879978	3.762073	0.001394	0.216119	-0.92388
TCF7L2	7930537	-0.35684	7.751336	-3.76061	0.001398	0.216119	-0.92666
GPR88	7903355	-0.92312	5.987051	-3.75893	0.001403	0.216119	-0.92983
VPS29	7966343	0.486778	5.818092	3.758162	0.001406	0.216119	-0.93129
SNORD116	7981988	-0.49494	10.76185	-3.7552	0.001415	0.216119	-0.9369
#NV	7892905	-0.42842	3.00959	-3.75379	0.00142	0.216119	-0.93958
DIP2B	7955376	-0.2897	8.08486	-3.75323	0.001421	0.216119	-0.94065
#NV	7896069	0.67044	8.356068	3.748486	0.001437	0.216349	-0.94963
RABGGTB	7902398	-0.41025	9.932336	-3.74705	0.001441	0.216349	-0.95234
#NV	7893789	-0.67479	8.623513	-3.74669	0.001442	0.216349	-0.95303
#NV	7896079	0.653104	4.222918	3.741411	0.00146	0.217945	-0.96304
LOC440337	7993108	-0.33653	3.044142	-3.73879	0.001468	0.218251	-0.968
MAMLD1	8170420	-0.41703	5.919304	-3.73184	0.001491	0.220697	-0.98117
#NV	7933931	-0.48329	6.955516	-3.72266	0.001522	0.221643	-0.99856
MIR1304 /	7951032	-0.70992	7.586365	-3.722	0.001525	0.221643	-0.99981
RBBP9	8065230	0.566903	7.278156	3.718126	0.001538	0.221643	-1.00716
GLYCTK	8080212	-0.4418	8.902409	-3.71727	0.001541	0.221643	-1.00878
ALPK2	8023528	1.229498	5.646167	3.71531	0.001548	0.221643	-1.01249
C8orf82	8153868	-0.25621	6.017021	-3.71421	0.001551	0.221643	-1.01457
PGAM1	7929624	0.308244	8.773781	3.71373	0.001553	0.221643	-1.01549
SMCR8	8005441	0.272303	6.129257	3.709568	0.001568	0.221643	-1.02337
PGAM1	7965480	0.313953	8.911039	3.709328	0.001569	0.221643	-1.02383
SLC25A17	8076260	0.301291	6.83309	3.70531	0.001583	0.221643	-1.03144
#NV	7892925	-0.46681	8.47434	-3.70377	0.001588	0.221643	-1.03436
COPB1	7946703	0.347828	8.152867	3.702944	0.001591	0.221643	-1.03592
DDX23	7962869	0.245303	8.280908	3.702118	0.001594	0.221643	-1.03749
SNORD146	7952335	-0.75547	6.572392	-3.69666	0.001614	0.221643	-1.04783
CYP4F22	8026424	0.793742	6.576951	3.693318	0.001626	0.221643	-1.05416
ZDHHC24	7949645	0.254942	6.384527	3.690943	0.001635	0.221643	-1.05866
TBCB	8028162	0.290193	7.516943	3.687833	0.001646	0.221643	-1.06456
TAS1R2	7912968	-0.24152	3.323108	-3.6849	0.001657	0.221643	-1.07011
#NV	7895855	-0.58067	5.814548	-3.68003	0.001675	0.221643	-1.07935
#NV	7895401	0.595786	3.931232	3.67828	0.001682	0.221643	-1.08265
CSTB	8070701	0.4107	7.923635	3.678206	0.001682	0.221643	-1.0828
DDAH1	7917347	0.572991	9.643008	3.676538	0.001688	0.221643	-1.08595
#NV	7894008	-1.02941	5.434613	-3.67396	0.001698	0.221643	-1.09084
#NV	7896366	-0.39496	11.40566	-3.67333	0.0017	0.221643	-1.09204
#NV	8158684	-0.89592	10.8217	-3.66888	0.001718	0.221643	-1.10046
#NV	7894055	0.589298	7.499612	3.663381	0.001739	0.221643	-1.11088
PPIP5K1	7988124	0.371016	6.631014	3.663027	0.00174	0.221643	-1.11155
#NV	7960700	-0.29447	2.863027	-3.66301	0.00174	0.221643	-1.11158
YIF1A	7949577	0.30766	7.842476	3.662998	0.00174	0.221643	-1.11161
PAR4 /// S	7982052	-0.87436	3.891318	-3.662	0.001744	0.221643	-1.1135
#NV	8115677	-0.20896	1.997033	-3.65806	0.00176	0.221643	-1.12097
VNN1	8129618	0.429551	10.48587	3.655707	0.001769	0.221643	-1.12542
#NV	7894213	-0.36627	8.650845	-3.65463	0.001773	0.221643	-1.12745
#NV	7896333	-0.36627	8.650845	-3.65463	0.001773	0.221643	-1.12745

#NV	8133110	-0.33035	6.191567	-4.35099	0.000372	0.095471	0.259724
#NV	7958015	-0.61944	5.302723	-4.34994	0.000373	0.095471	0.257657
#NV	8014664	-0.54833	6.78313	-4.34687	0.000376	0.095471	0.251628
#NV	8019649	-0.54833	6.78313	-4.34687	0.000376	0.095471	0.251628
FAM110B	8146533	-0.38364	5.773252	-4.33357	0.000387	0.096976	0.225457
LOC40094	8050227	0.856076	3.955988	4.333085	0.000387	0.096976	0.224494
EPDR1	8132369	0.570504	5.476251	4.327116	0.000393	0.097544	0.212746
#NV	8083933	-0.56142	6.463481	-4.32008	0.000399	0.09798	0.198899
AKR1A1	7901110	0.284377	9.687642	4.318491	0.0004	0.09798	0.195764
SNORD12C	8063345	0.391726	4.593273	4.313325	0.000405	0.098394	0.185591
ARFIP2	7946201	0.28403	7.622995	4.307243	0.00041	0.099018	0.173611
PACSIN3	7947801	-0.48422	6.512889	-4.28743	0.000429	0.100866	0.134577
#NV	7895099	-2.24211	4.777332	-4.28447	0.000432	0.100866	0.128739
SLC19A2	7922162	-0.63043	7.400909	-4.28447	0.000432	0.100866	0.128737
#NV	8119580	-0.64594	3.97217	-4.28223	0.000434	0.100866	0.124331
GOLM1	8162117	1.333075	6.357459	4.282113	0.000434	0.100866	0.12409
MKL1	8076241	0.283013	6.015729	4.279938	0.000436	0.100866	0.119803
APOL3	8075695	1.050209	6.134571	4.274435	0.000442	0.10141	0.108954
RNS5491	8068510	0.299	4.634801	4.268435	0.000448	0.101939	0.097121
ALDH6A1	7980096	-0.59098	7.756984	-4.2659	0.00045	0.101939	0.092116
#NV	7893720	-0.48041	7.373885	-4.26157	0.000455	0.101939	0.083585
MT1X	7995838	-0.39544	11.77958	-4.25994	0.000456	0.101939	0.080374
ATG2B	7981217	-0.35125	7.901307	-4.2518	0.000465	0.103121	0.064315
HEY2	8121850	-0.54476	6.147121	-4.24608	0.000471	0.103301	0.053018
PYGB	8061447	0.383704	6.291286	4.245104	0.000472	0.103301	0.051095
KLF11	8040211	0.491151	7.103212	4.238577	0.000479	0.104136	0.038213
FLII	8013191	0.285404	7.530041	4.23238	0.000485	0.104589	0.025982
TMEM154	8103226	1.587159	6.311823	4.230518	0.000487	0.104589	0.022304
BLMH	8014008	-0.50027	6.123542	-4.2232	0.000495	0.104589	0.007857
#NV	8097116	-0.69832	5.824057	-4.22278	0.000496	0.104589	0.007028
FRMD4B	8088745	-0.38784	8.333177	-4.2159	0.000503	0.104589	-0.00656
HTRA1	7931097	0.455806	7.856321	4.212116	0.000508	0.104589	-0.01403
DR1	7903079	0.315836	7.542983	4.207205	0.000513	0.104589	-0.02373
RFX5	7919971	0.371793	6.086326	4.205676	0.000515	0.104589	-0.02675
#NV	7916775	-0.77114	5.60255	-4.20553	0.000515	0.104589	-0.02704
DYNC1H1	7976876	0.260536	8.514497	4.203617	0.000517	0.104589	-0.03082
#NV	8180246	-0.61457	7.890692	-4.19926	0.000523	0.104589	-0.03942
C18orf1	8020308	0.343009	6.69498	4.194195	0.000528	0.104589	-0.04944
EPHB1	8082846	-0.79536	4.351744	-4.19264	0.00053	0.104589	-0.05252
PAIP2B	8052940	-0.37325	8.159554	-4.19009	0.000533	0.104589	-0.05755
SLC39A7	8118613	0.560676	7.582963	4.189577	0.000534	0.104589	-0.05856
SLC39A7	8178225	0.560676	7.582963	4.189577	0.000534	0.104589	-0.05856
SLC39A7	8179525	0.560676	7.582963	4.189577	0.000534	0.104589	-0.05856
RDH16	7964292	0.558119	9.603887	4.182966	0.000542	0.105171	-0.07163
C8orf44	8146711	-0.45199	6.050118	-4.18188	0.000543	0.105171	-0.07378
#NV	8172195	-1.06294	2.807894	-4.17116	0.000556	0.106148	-0.09496
#NV	8070255	-0.69826	2.791511	-4.16916	0.000559	0.106148	-0.09891
ARHGEF16	7897154	0.377282	4.305752	4.16858	0.00056	0.106148	-0.10007
IFT81	7958620	-0.53005	4.720561	-4.16554	0.000564	0.106148	-0.10607
C9orf72	8160531	-0.48723	6.170818	-4.16496	0.000564	0.106148	-0.10723
MED13	8017312	-0.3158	9.3633	-4.15087	0.000582	0.107867	-0.1351
#NV	7893248	0.328356	7.367329	4.14888	0.000585	0.107867	-0.13903
#NV	8023862	0.365641	4.626697	4.148026	0.000586	0.107867	-0.14072
TES	8135576	0.514776	6.60296	4.144555	0.000591	0.107867	-0.14758
#NV	7896307	0.67781	2.943674	4.144085	0.000591	0.107867	-0.14851
FAT4	8097288	-0.38904	7.424706	-4.14207	0.000594	0.107867	-0.15249
SIPA1L3	8028286	0.271899	6.296535	4.140483	0.000596	0.107867	-0.15564
ZNF577	8055016	-0.53227	6.64466	-4.1265	0.000615	0.110429	-0.18331
#NV	8038904	-0.38463	6.60382	-4.12409	0.000618	0.110429	-0.18808
FBXL4	7895123	0.449229	7.671169	4.122795	0.00062	0.110429	-0.19064
#NV	8128356	-0.3679	7.636708	-4.11403	0.000632	0.112021	-0.20798
SLC7A2	7901858	-0.42318	5.654573	-4.10736	0.000642	0.113108	-0.22119
#NV	7893538	-0.59577	5.228563	-4.09395	0.000662	0.115155	-0.24774
AEN	8144786	-0.51625	10.78393	-4.09247	0.000664	0.115155	-0.25068
MANF	7985767	0.592	5.134165	4.09234	0.000664	0.115155	-0.25093
AGPAT2	8080084	0.576069	6.787033	4.08706	0.000672	0.115923	-0.26139
ABCA7	8165258	0.580774	7.616359	4.077951	0.000686	0.116787	-0.27943
CPS1	8024120	0.401093	4.916308	4.077439	0.000687	0.116787	-0.28044
LCORL	8048026	-0.26999	12.05622	-4.07652	0.000688	0.116787	-0.28226
AGL	8099581	-0.31649	6.072208	-4.07338	0.000693	0.116787	-0.28847
PTCH1	7937508	0.709659	9.140524	4.071822	0.000695	0.116787	-0.29157
LINC00575	7903239	-0.42033	8.631201	-4.06671	0.000703	0.116787	-0.3017
JMJD1C	7933877	-0.39585	8.717622	-4.0285	0.000766	0.119338	-0.37742
PTCH1	8101359	-0.3499	2.854601	-4.02793	0.000767	0.119338	-0.37853
ACOT2	8162533	-0.57915	6.309522	-4.02757	0.000768	0.119338	-0.37925
#NV	8154510	-0.43531	2.628013	-4.02641	0.00077	0.119338	-0.38155
ACOT2	7975602	0.675709	8.522223	4.025917	0.000771	0.119338	-0.38253
ABCA6	8017964	-0.3251	10.07986	-4.02393	0.000774	0.119338	-0.38647
#NV	7893654	-0.67546	6.671865	-4.01926	0.000782	0.119779	-0.39572
KDM8	7994269	0.719829	8.289948	4.01818	0.000784	0.119779	-0.39787
MRAS	8082965	0.443809	5.479242	4.016	0.000788	0.119816	-0.40219
TTC12	7943919	-0.29309	6.230007	-4.00888	0.000801	0.121194	-0.41632
FAM53B	7936884	0.337861	5.631897	4.002444	0.000812	0.12175	-0.42907
FMO5	7919314	-0.45201	10.68341	-4.00138	0.000814	0.12175	-0.43118
PPARGC1A	8099633	-1.04155	7.931443	-4.0008	0.000815	0.12175	-0.43232
LGSN	8127380	-0.65047	5.249966	-3.99692	0.000823	0.122267	-0.44002
LOC100129	8017344	-0.54992	6.559996	-3.99288	0.00083	0.122797	-0.44803
C17orf62	7895110	0.278467	11.04092	3.991034	0.000833	0.122797	-0.45169
#NV	7896331	-0.35524	8.209787	-3.98193	0.000851	0.124779	-0.46974
DNAJC12	7933933	-0.60352	7.214296	-3.97628	0.000862	0.125026	-0.48095
FAM108B1	8161727	-0.34323	6.100054	-3.97269	0.000869	0.125026	-0.48808
#NV	7920025	-0.40228	4.252094	-3.97228	0.000869	0.125026	-0.48888
#NV	8144699	-0.70528	7.166358	-3.9716	0.000871	0.125026	-0.49024
C17orf62	8019507	0.305484	6.205964	3.96929	0.000875	0.125026	-0.49482
LRRC59	8016708	0.471498	8.355017	3.968371	0.000877	0.125026	-0.49664
PLAUR	8037374	0.482269	4.647436	3.964329	0.000885	0.125026	-0.50466
#NV	7895158	-0.7094	3.240234	-3.96343	0.000887	0.125026	-0.50643
HPRT1	8169984	-0.59117	6.720444	-3.96324	0.000887	0.125026	-0.50681
LRFN3	8028112	0.359352	5.010255	3.961846	0.00089	0.125026	-0.50958
#NV	8180216	0.36805	6.395909	3.958171	0.000897	0.125124	-0.51687
MYO9A	7990092	-0.28994	6.30138	-3.95775	0.000898	0.125124	-0.5177
FOXP1	8088776	-0.34246	7.835085	-3.9544	0.000905	0.125543	-0.52435
ELP2	8020930	-0.29306	7.733364	-3.95153	0.000911	0.125831	-0.53005
#NV	7893253	-0.64124	4.560382	-3.94913	0.000916	0.125987	-0.5348
#NV	7896650	-0.67682	8.719915	-3.94379	0.000927	0.126983	-0.5454
WDR19	8094638	-0.35749	6.851046	-3.94142	0.000932	0.127137	-0.5501
KIAA1217	7926679	-0.35576	7.664048	-3.93744	0.00094	0.127158	-0.558
FAM9B	8171271	-0.59353	3.508536	-3.93609	0.000943	0.127158	-0.56067
RNF152	8023598	-0.931	7.584319	-3.9359	0.000943	0.127158	-0.56105
KLF16	8032365	0.313127	5.869034	3.931616	0.000952	0.127406	-0.56955
ABHD8	8035271	0.308458	5.88733	3.931444	0.000953	0.127406	-0.56989
ENTPD7	7929750	0.64407	6.54974	3.925056	0.000967	0.128729	-0.58257
TMEM45B	7945169	1.363032	7.933365	3.916255	0.000986	0.129046	-0.60003
#NV	7892995	0.393075	2.165289	3.914937	0.000989	0.129046	-0.60264
ABCA2	8165345	0.43504	7.570815	3.914252	0.00099	0.129046	-0.60401
NOL3	7996448	0.390158	5.952501	3.913751	0.000991	0.129046	-0.605
PDPR	7997025	-0.45302	7.881329	-3.91061	0.000998	0.129046	-0.61123
AGPAT5	8144378	-0.65297	6.632463	-3.90953	0.001001	0.129046	-0.61337
#NV	8021540	-0.30022	2.592014	-3.90565	0.00101	0.129046	-0.62108
C11orf54	7943162	-0.45801	10.04705	-3.9055	0.00101	0.129046	-0.62136
BSG	8023955	0.415068	9.373057	3.905286	0.00101	0.129046	-0.6218

RNGTT	8128052	0.33341	6.392963	3.814609	0.001239	0.316412	-0.89452
#NV	8144699	0.677331	7.166358	3.814222	0.00124	0.316412	-0.89521
CHIC2	8100382	0.235927	8.003967	3.810311	0.001251	0.316412	-0.90223
SNORA49	7960052	-0.63115	7.555965	-3.80622	0.001262	0.316412	-0.90956
CDK18	7909104	-0.47793	6.64099	-3.80253	0.001273	0.316412	-0.91618
UBR3	8046213	0.249058	8.210763	3.798275	0.001285	0.316412	-0.92382
MIR30B	8153065	0.423153	2.698938	3.795217	0.001294	0.316412	-0.92931
RBM18	8163948	0.324997	6.072573	3.790039	0.001309	0.316412	-0.9386
SETD9	8105456	0.369529	5.483889	3.789936	0.001309	0.316412	-0.93878
HDGFRP2	8024864	-0.27997	6.067792	-3.78826	0.001314	0.316412	-0.94179
RFC3	7968563	0.328544	6.043501	3.780237	0.001338	0.316412	-0.95618
#NV	8102728	0.402644	5.576339	3.770151	0.001368	0.316412	-0.97428
#NV	8014664	0.475462	6.78313	3.769247	0.001371	0.316412	-0.97591
#NV	8019649	0.475462	6.78313	3.769247	0.001371	0.316412	-0.97591
ZNF618	8157381	-0.37016	4.410687	-3.7684	0.001374	0.316412	-0.97742
RNU4-7P	8130181	-0.4158	3.438394	-3.76744	0.001377	0.316412	-0.97915
EGFL7	8159354	-0.32186	5.713925	-3.76403	0.001387	0.316412	-0.98528
ACAD8	7945283	0.284091	7.674979	3.762283	0.001393	0.316412	-0.98841
#NV	8047503	-0.29102	2.939445	-3.76099	0.001397	0.316412	-0.99073
HNMT	8045499	0.269434	8.786716	3.752827	0.001423	0.318444	-1.00538
MAP4K3	8051707	0.245612	7.469065	3.746374	0.001443	0.318444	-1.01697
FAM185A	8140461	0.382178	7.217166	3.744937	0.001448	0.318444	-1.01954
ALG10 ///	7954777	0.258362	6.938194	3.743695	0.001452	0.318444	-1.02177
C1D	8052698	0.507766	6.475387	3.737183	0.001474	0.318444	-1.03347
LRPPRC	8051882	0.281425	8.297828	3.735562	0.001479	0.318444	-1.03638
PEBP4	8149725	0.649556	4.490849	3.730403	0.001496	0.318444	-1.04564
SH2B1	7994445	-0.31562	5.435951	-3.72942	0.001499	0.318444	-1.04741
LOC150197	8071355	-0.4459	3.246776	-3.7277	0.001505	0.318444	-1.05049
ACAP2	8092933	0.271382	7.126249	3.727472	0.001506	0.318444	-1.0509
C20orf72	8061129	0.309328	6.536539	3.724787	0.001515	0.318444	-1.05572
JMY	8106516	0.281197	6.354398	3.723166	0.001521	0.318444	-1.05863
#NV	7895579	-0.21907	9.770432	-3.70865	0.001571	0.

MTMR10	7987048	-0.26193	8.831583	-3.64957	0.001794	0.221643	-1.13705
SLC16A12	7934936	-0.84692	4.256379	-3.64941	0.001794	0.221643	-1.13734
#NV	7958015	-0.51963	5.302723	-3.64903	0.001796	0.221643	-1.13807
#NV	8006028	-0.60522	3.950711	-3.64807	0.0018	0.221643	-1.13988
DLD	8135464	0.401835	8.124891	3.646509	0.001806	0.221643	-1.14284
C1orf122	7900192	0.364531	5.182256	3.642133	0.001824	0.221643	-1.15113
LOC10050	8010078	-0.41157	6.962791	-3.64209	0.001824	0.221643	-1.15121
ISM1	8061013	0.983541	6.284994	3.640849	0.001829	0.221643	-1.15356
UGGT1	8045090	0.364393	8.443343	3.64077	0.001829	0.221643	-1.15371
SLC17A5	8127549	0.385483	7.442738	3.640005	0.001832	0.221643	-1.15516
TSTA3	8153474	0.411763	7.285439	3.639832	0.001833	0.221643	-1.15549
H2AFY2	7928107	0.58676	5.157024	3.638586	0.001838	0.221643	-1.15785
ELOVL2	8123920	0.792387	8.808599	3.637169	0.001844	0.221643	-1.16053
C1QL4	7963061	-0.33056	3.233133	-3.63711	0.001844	0.221643	-1.16065
#NV	7981523	-0.43664	3.839133	-3.63624	0.001848	0.221643	-1.1623
RHOXF1	8174755	-0.22082	3.094343	-3.63565	0.00185	0.221643	-1.1634
IQCJ-SCHIF	8083677	0.530597	6.170171	3.632387	0.001864	0.221643	-1.16959
#NV	8062842	-0.36927	3.832061	-3.63231	0.001864	0.221643	-1.16973
PDCL	8163964	0.33476	5.352408	3.631959	0.001866	0.221643	-1.1704
VTA1	8122348	0.297564	7.917415	3.629213	0.001877	0.221643	-1.1756
SRPK1	8125941	0.308458	7.066191	3.628949	0.001878	0.221643	-1.1761
SEL1L	7980547	0.370454	9.110985	3.62834	0.001881	0.221643	-1.17725
HCAR3	7967322	-0.53805	2.710666	-3.62798	0.001882	0.221643	-1.17793
ATOH7	7933978	-0.55065	4.643289	-3.62765	0.001884	0.221643	-1.17856
MCU	7928318	0.28969	6.458649	3.623083	0.001903	0.222651	-1.18721
#NV	8055486	-0.61573	7.331346	-3.62248	0.001906	0.222651	-1.18834
KLHL5	8094625	0.401125	7.422726	3.616225	0.001933	0.224632	-1.20019
STAT6	7964360	-0.28963	8.631733	-3.61499	0.001938	0.224632	-1.20254
RAE1	8063566	0.289189	6.226038	3.613856	0.001943	0.224632	-1.20468
#NV	8161693	-0.49026	4.622439	-3.61088	0.001956	0.2247	-1.21032
#NV	7892539	0.932286	4.395939	3.610631	0.001957	0.2247	-1.21078
DCAF6	7907104	-0.24029	9.451202	-3.60849	0.001966	0.225002	-1.21483
#NV	8007917	-0.44705	3.940784	-3.60656	0.001975	0.225207	-1.2185
#NV	7918876	-0.43061	4.004029	-3.60089	0.002	0.226005	-1.22923
#NV	7896446	-0.64996	6.316601	-3.60062	0.002001	0.226005	-1.22974
RFC3	7968563	0.312915	6.043501	3.600413	0.002002	0.226005	-1.23013
SULF2	8066822	0.747764	8.183016	3.597498	0.002015	0.226718	-1.23565
#NV	7894761	0.4674	8.090232	3.595946	0.002022	0.226741	-1.23858
ZNF577	8038904	-0.3352	6.60382	-3.59402	0.002031	0.226956	-1.24223
LOC10063	7922351	-0.51696	4.780733	-3.58665	0.002065	0.229296	-1.25618
ATP6V1B2	8144931	0.234061	8.884514	3.586453	0.002066	0.229296	-1.25655
#NV	8096025	-0.32879	3.933422	-3.58083	0.002092	0.229377	-1.2672
APOC2 ///	8029547	-0.38834	6.808804	-3.58056	0.002093	0.229377	-1.2677
TST	8075857	0.298025	11.06846	3.58001	0.002096	0.229377	-1.26875
ZNF232	8011817	0.260165	4.254055	3.57914	0.0021	0.229377	-1.2704
SYT7	7948588	0.924832	6.446904	3.577721	0.002107	0.229377	-1.27308
CCT7	8042720	0.239073	8.639224	3.576586	0.002112	0.229377	-1.27523
RNS5164	8096459	-0.51422	2.083604	-3.57599	0.002115	0.229377	-1.27635
CHI3L1	7923547	2.106419	6.831742	3.568488	0.002151	0.231017	-1.29055
ATG4A	8169272	0.353538	6.082153	3.567346	0.002156	0.231017	-1.29271
RPL13A ///	8030364	-0.44761	6.845314	-3.56556	0.002165	0.231017	-1.29609
PLOD1	7897803	0.281974	8.478456	3.565468	0.002165	0.231017	-1.29627
GPR21	8157727	-0.35287	6.278878	-3.56393	0.002173	0.231017	-1.29918
NACC1	8026155	0.300287	6.768993	3.563871	0.002173	0.231017	-1.29929
RBMS1P1	7964757	-0.5058	6.33267	-3.56274	0.002179	0.231017	-1.30143
ZNF643	7900438	0.398736	3.884759	3.56128	0.002186	0.231037	-1.30419
BHLHA9	8003633	-0.33382	4.289037	-3.5565	0.002209	0.23211	-1.31324
MIR200A	7896861	-0.30434	3.011834	-3.55212	0.002231	0.23211	-1.32153
BRCA1	8015769	0.461686	4.440791	3.551505	0.002234	0.23211	-1.32268
CNTN3	8088866	-0.44125	6.62596	-3.55139	0.002235	0.23211	-1.3229
CTNNA3	7933904	-0.57469	5.722362	-3.55032	0.00224	0.23211	-1.32493
PDPK1 ///	7998825	0.253856	9.227292	3.549228	0.002245	0.23211	-1.32699
SLITRK2	8170307	-0.44117	3.674932	-3.54399	0.002272	0.23211	-1.33689
DUX4L4 //,	8176570	-0.56691	3.318763	-3.54191	0.002282	0.23211	-1.34083
#NV	8127542	-0.28998	4.723514	-3.53782	0.002303	0.23211	-1.34856
#NV	8069508	0.654387	4.22454	3.536309	0.002311	0.23211	-1.35143
#NV	8072007	-0.35406	4.872987	-3.53543	0.002316	0.23211	-1.35309
DERL1	8152628	0.360995	9.142939	3.533644	0.002325	0.23211	-1.35647
#NV	8085784	-0.24467	2.528109	-3.53302	0.002328	0.23211	-1.35764
SLC9A6	8170097	0.408031	6.548858	3.531027	0.002339	0.23211	-1.36141
ACER3	7942679	0.533428	5.39075	3.529315	0.002348	0.23211	-1.36465
TRIM40	8177750	-0.31971	3.755761	-3.52925	0.002348	0.23211	-1.36478
TRIM40	8179060	-0.31971	3.755761	-3.52925	0.002348	0.23211	-1.36478
#NV	7892952	-0.50023	6.198061	-3.52914	0.002349	0.23211	-1.36499
DESI1	8076365	0.307575	8.997126	3.529027	0.002349	0.23211	-1.3652
#NV	8053427	-0.73199	3.638847	-3.52792	0.002355	0.23211	-1.3673
GINS2	8003204	0.716095	5.461144	3.524876	0.002371	0.23211	-1.37304
ACAP2	8092933	0.256622	7.126249	3.52475	0.002372	0.23211	-1.37328
SNHG15 //	8139456	-0.64229	5.69731	-3.52368	0.002378	0.23211	-1.37531
INHBE	7956426	0.927139	9.06172	3.522807	0.002382	0.23211	-1.37696
GAS6	7970329	0.458408	6.48088	3.521751	0.002388	0.23211	-1.37895
MTOR	7912412	0.283356	8.130458	3.521126	0.002391	0.23211	-1.38013
#NV	7895674	-0.29775	9.912873	-3.52028	0.002396	0.23211	-1.38173
#NV	7893922	-0.47885	7.50106	-3.52017	0.002396	0.23211	-1.38195
KRT8	7963567	0.433129	9.732278	3.519287	0.002401	0.23211	-1.38361
TRPT1	7949046	-0.23595	6.016403	-3.51854	0.002405	0.23211	-1.38501
#NV	8071817	-0.30271	2.667434	-3.51548	0.002422	0.232694	-1.39081
TMEM9B	7946439	0.39677	7.444973	3.514652	0.002426	0.232694	-1.39237
ATL3	7948997	0.418591	7.084604	3.513391	0.002433	0.232694	-1.39476
FKBP1A-SD	8064418	0.460779	5.705099	3.512266	0.002439	0.232694	-1.39688
#NV	8101607	-0.34237	2.617732	-3.51016	0.00245	0.233126	-1.40087
LRRC16A	8117243	0.375038	6.5591	3.506652	0.00247	0.233428	-1.40749
#NV	7909888	-0.44338	3.177013	-3.50352	0.002487	0.233428	-1.41342
DTL	7909568	0.619778	3.773744	3.501659	0.002497	0.233428	-1.41693
#NV	7896415	-0.58465	5.226029	-3.50061	0.002503	0.233428	-1.4189
MLPH	8049487	-0.40234	6.591003	-3.50022	0.002506	0.233428	-1.41965
AAGAB	7989953	0.305993	5.384089	3.499572	0.002509	0.233428	-1.42087
#NV	7894525	-0.61134	5.697887	-3.49951	0.00251	0.233428	-1.42099
#NV	7892728	-0.44775	3.417467	-3.49622	0.002528	0.233428	-1.4272
#NV	7894793	0.610034	2.732144	3.495884	0.00253	0.233428	-1.42784
DPH3	8085660	0.303904	6.383122	3.495794	0.00253	0.233428	-1.42801
#NV	7896381	-0.42376	8.441142	-3.49573	0.002531	0.233428	-1.42813
SLC6A16	8038326	-0.66118	7.21491	-3.49308	0.002546	0.233782	-1.43313
#NV	7894490	-0.47715	5.806789	-3.48997	0.002564	0.233782	-1.43902
#NV	7894975	-0.47715	5.806789	-3.48997	0.002564	0.233782	-1.43902
#NV	7893891	0.437769	2.007449	3.489844	0.002564	0.233782	-1.43925
HSP90B1 /	7958130	0.247326	10.97724	3.488899	0.00257	0.233782	-1.44104
CORO1C	7966135	0.237634	8.491175	3.485325	0.00259	0.234539	-1.44779
SNORA55	7915227	-0.60297	6.174885	-3.48306	0.002603	0.234539	-1.45207
#NV	7895220	-0.46651	9.399783	-3.48205	0.002609	0.234539	-1.45397
PANX2	8073992	-0.48277	4.952961	-3.48068	0.002617	0.234539	-1.45657
SMPD2	8121418	0.321681	5.3586	3.480253	0.00262	0.234539	-1.45737
TTC40	7937112	-0.27977	3.071979	-3.48017	0.00262	0.234539	-1.45752
DR1	7903079	0.261124	7.542983	3.478393	0.002631	0.234747	-1.46088
SNORA42	7920873	-1.11002	10.33362	-3.47738	0.002637	0.234747	-1.4628
BPESC1	8083025	-0.24656	3.630871	-3.47503	0.002651	0.234765	-1.46723
TSPYL1	8129099	0.256396	8.859631	3.472787	0.002664	0.234765	-1.47147
KDELC1	7972682	0.561063	5.358771	3.47143	0.002672	0.234765	-1.47403
CCDC9	8029894	-0.2999	5.530042	-3.47052	0.002677	0.234765	-1.47576
#NV	8131612	-0.85727	4.429621	-3.47047	0.002678	0.234765	-1.47585
ATXN7L1	8142104	-0.23845	6.16426	-3.47022	0.002679	0.234765	-1.47632
CNGA3	8043782	-0.27888	2.794546	-3.46739	0.002696	0.235634	-1.48167
GNPTAB	7965812	0.327892	6.646503	3.461493	0.002732	0.237132	-1.4928
FGF21	8030105	0.623043	4.418886	3.461395	0.002733	0.237132	-1.49298
SLC7A2	8144786	-0.4366	10.78393	-3.46104	0.002735	0.237132	-1.49366
#NV	8150862	-0.56179	4.302674	-3.45621	0.002764	0.239076	-1.50276
TRIM40	8117840	-0.33323	3.948549	-3.45352	0.002781	0.239898	-1.50785
RAB6A ///	8055261	0.315537	8.115391	3.447268	0.00282	0.242378	-1.51965
#NV	7893130	-0.47977	10.51035	-3.44347	0.002844	0.242378	-1.52682
#NV	8180390	0.333372	6.47678	3.442922	0.002848	0.242378	-1.52785
SLC16A13	8004266	0.792948	8.506601	3.44229	0.002852	0.242378	-1.52904
#NV	7893030	1.042476	4.051914	3.440933	0.00286	0.242378	-1.5316

PIBF1	7969390	-0.31231	6.445221	-3.90257	0.001017	0.129046	-0.62719
AMDHD1	7957654	-0.98885	8.798245	-3.90228	0.001017	0.129046	-0.62775
AADAT	8103706	-0.39506	9.799298	-3.90183	0.001018	0.129046	-0.62865
CPE3	7935011	-0.42832	6.882543	-3.89939	0.001024	0.129046	-0.6335
SLC25A20	8087224	0.518462	8.59766	3.898514	0.001026	0.129046	-0.63523
CSTB	8070701	0.435236	7.923635	3.897947	0.001027	0.129046	-0.63636
#NV	8180255	0.721151	6.245055	3.894603	0.001035	0.129046	-0.64299
#NV	8180321	0.721151	6.245055	3.894603	0.001035	0.129046	-0.64299
GPR89A //	7904930	-0.38731	7.537882	-3.8916	0.001042	0.129046	-0.64894
SULF2	8066822	0.80851	8.183016	3.889747	0.001046	0.129046	-0.65263
#NV	7944147	0.330032	3.773168	3.889682	0.001046	0.129046	-0.65276
#NV	8047159	-0.62871	6.626363	-3.88457	0.001058	0.129762	-0.66291
#NV	7892705	-0.5738	7.339349	-3.88393	0.00106	0.129762	-0.66418
ART4	7961507	-0.40621	8.332305	-3.87927	0.001071	0.130104	-0.67342
C10orf62	7929674	-0.83433	5.896426	-3.87796	0.001074	0.130104	-0.67602
FOLH1 ///	7948058	-0.4582	8.645299	-3.87631	0.001078	0.130104	-0.6793
SGCB	8100318	0.506436	7.158506	3.875191	0.001081	0.130104	-0.68151
EIF3E	8152323	-0.33621	7.591783	-3.87464	0.001082	0.130104	-0.6826
KIAA1804	7910600	-0.40678	5.538647	-3.87139	0.00109	0.130586	-0.68905
EHD4	7987772	0.465487	5.913824	3.868732	0.001097	0.130897	-0.69433
#NV	7893530	0.383535	10.21835	3.865387	0.001105	0.131413	-0.70097
LMNB2	8032491	0.264487	5.547836	3.856758	0.001127	0.133507	-0.71809
C11orf71	8110882	-0.73208	4.724979	-3.85207	0.001139	0.13417	-0.7274
MVP	7951781	-0.35431	6.797607	-3.85098	0.001141	0.13417	-0.72956
CYP26A1	7994659	0.459814	5.772679	3.84982	0.001144	0.13417	-0.73186
#NV	7929322	-1.60585	5.643954	-3.84401	0.001159	0.134695	-0.7434
#NV	7893549	-0.73197	5.930135	-3.8429	0.001162	0.134695	-0.74559
C10orf62	7983926	-0.82108	6.09462	-3.84207	0.001164	0.134695	-0.74724
#NV	8180207	-0.24789	6.941042	-3.84185	0.001165	0.134695	-0.74768
METTL21C	7969955	-0.82517	4.64179	-3.83666	0.001179	0.135801	-0.75797
#NV	8169000	-0.50846	4.851486	-3.82924	0.001198	0.137508	-0.77269
VTRNA1-1	8108627	1.138131	6.001697	3.82803	0.001202	0.137508	-0.7751
LOC10013	7933261	-0.53573	4.607331	-3.82332	0.001215	0.138021	-0.78445
LOC10013	7933572	-0.53573	4.607331	-3.82332	0.001215	0.138021	-0.78445
CASP4	7951372	0.253166	7.244018	3.820993	0.001221	0.138272	-0.78907
ACOT1	7975598	0.842541	6.921353	3.817049	0.001232	0.138397	-0.79689
ZNF69	8025968	-0.3516	6.79015	-3.81342	0.001242	0.138397	-0.80408
C11orf83	7940669	0.296892	4.223516	3.813328	0.001242	0.138397	-0.80428
ALDH5A1	8117207	-0.25409	8.89434	-3.81031	0.001251	0.138397	-0.81027
P4HA1	7934278	-1.34533	6.409704	-3.80849	0.001256	0.138397	-0.81388
HAL	7965606	-0.8899	9.015643	-3.80727	0.001259	0.138397	-0.8163
FKBP1A-SD	8064418	0.499432	5.705099	3.806895	0.00126	0.138397	-0.81704
#NV	7895857	-0.51316	7.83354	-3.80558	0.001264	0.138397	-0.81965
CYTH2	8030049	0.238436	7.925855	3.803474	0.00127	0.138397	-0.82383
ALG10 ///	7954789	-0.26827	7.005036	-3.8001	0.00128	0.138397	-0.83052
NHLRC2	7930614	-0.26328	8.249386	-3.79921	0.001282	0.138397	-0.83229
#NV	8131612	-0.9384	4.429621	-3.79892	0.001283	0.138397	-0.83287
#NV	7960359	-0.35368	9.166536	-3.79733	0.001287	0.138397	-0.83602
PDIA4	8143684	0.362208	9.788474	3.796112	0.001291	0.138397	-0.83844
AP5B1	7949490	0.351567	5.451726	3.795383	0.001293	0.138397	-0.83988
PTGFRN	7904293	0.382051	6.121558	3.794587	0.001295	0.138397	-0.84146
RAB32	8122554	0.348746	5.622613	3.793453	0.001299	0.138397	-0.84371
MAN2A1	8107234	-0.25742	8.990768	-3.79344	0.001299	0.138397	-0.84373
FAM162A	8082066	-0.41741	7.257997	-3.79269	0.001301	0.138397	-0.84522
ATP2B1	7965359	-0.31617	7.184229	-3.79032	0.001308	0.138563	-0.84993
PLCG1	8062623	0.328325	7.028981	3.789319	0.001311	0.138563	-0.85192
IGFBP1	8132694	-2.79915	8.084699	-3.78712	0.001317	0.13881	-0.85629
#NV	8005655	-0.71333	5.670158	-3.78546	0.001322	0.138886	-0.85957
#NV	7944021	-0.25494	2.25831	-3.78392	0.001327	0.138928	-0.86262
C7orf10	8132439	-0.39053	7.662766	-3.78039	0.001337	0.139283	-0.86962
PDSS1	7926807	0.597188	6.394943	3.778435	0.001343	0.139283	-0.87351
#NV	7896522	-0.55633	7.811846	-3.77758	0.001346	0.139283	-0.87521
SH3RF1	8103630	-0.24253	6.868521	-3.77722	0.001347	0.139283	-0.87592
ATAD3A	7896952	0.391725	6.235607	3.771831	0.001363	0.14027	-0.88661
WWP2	7996976	0.258084	6.416709	3.770219	0.001368	0.14027	-0.88981
TESK2	7915718	-0.28333	7.172171	-3.76886	0.001372	0.14027	-0.89251
LPCAT1	8110841	0.339133	6.066691	3.768572	0.001373	0.14027	-0.89308
#NV	7892732	1.670782	3.590724	3.764612	0.001386	0.141089	-0.90093
#NV	8164967	0.343521	7.738813	3.758708	0.001404	0.142535	-0.91264
ASS1P11	8138487	-0.7402	5.568373	-3.75422	0.001418	0.142911	-0.92154
LGALS3BP	8018975	0.730724	8.320692	3.75386	0.001419	0.142911	-0.92226
TSPAN17	8110224	0.279799	6.632778	3.753476	0.001421	0.142911	-0.92302
TRGV9	8139107	0.492767	3.695482	3.751944	0.001426	0.142971	-0.92606
INPP1	8047069	-0.45617	5.997534	-3.74274	0.001455	0.145256	-0.94432
42255	8114050	0.278781	6.796986	3.742201	0.001457	0.145256	-0.94539
NANOGP1	7953689	-0.5148	3.22162	-3.73822	0.00147	0.145597	-0.95328
SNHG12 //	7914212	0.53987	7.777199	3.738212	0.00147	0.145597	-0.9533
FAM98A	8051413	0.339693	7.573228	3.737171	0.001474	0.145597	-0.95536
NACC1	8026155	0.314239	6.768993	3.729464	0.001499	0.147651	-0.97065
BAMBI	7926875	-0.49046	6.377384	-3.72728	0.001507	0.147651	-0.97498
TMEM133	7943369	-0.3746	7.23253	-3.72698	0.001508	0.147651	-0.97558
IQCJ-SCHIF	8083677	0.544133	6.170171	3.725054	0.001514	0.147855	-0.97939
MTCH2	7947934	0.299459	9.72621	3.723479	0.00152	0.147944	-0.98252
ENOSF1	8021966	-0.30518	8.602496	-3.72122	0.001527	0.148156	-0.987
AP4M1	8134712	0.246295	5.050223	3.720243	0.001531	0.148156	-0.98893
#NV	7895047	-0.34354	8.999204	-3.71864	0.001536	0.148259	-0.99211
#NV	8149248	-0.75457	7.226504	-3.71489	0.001549	0.148896	-0.99954
#NV	7933931	-0.48218	6.955516	-3.71415	0.001552	0.148896	-1.00102
TBL1XR1	8092201	-0.32937	7.912442	-3.71221	0.001558	0.149117	-1.00487
ORC2	8058161	-0.3473	6.739526	-3.70849	0.001572	0.149731	-1.01224
SETDB2	7969114	-0.38971	6.143921	-3.70782	0.001574	0.149731	-1.01356
GLS2	7964183	-0.64032	9.451252	-3.70391	0.001588	0.150471	-1.02131
APOF	7964142	-0.58732	9.379358	-3.70221	0.001594	0.150471	-1.02468
TOMM70A	8089128	-0.18997	7.553333	-3.70182	0.001595	0.150471	-1.02546
ALG10 ///	7954777	-0.25535	6.938194	-3.70008	0.001601	0.150494	-1.02892
LDLRAP1	7899023	0.347506	6.879978	3.69923	0.001605	0.150494	-1.0306
#NV	7907788	-0.66679	5.556366	-3.69615	0.001616	0.151112	-1.0367
OR52H1	7946087	-0.63301	4.806707	-3.6941	0.001623	0.151383	-1.04077
PELI2	7974533	-0.49097	5.437822	-3.69258	0.001629	0.151475	-1.04377
#NV	7917974	-0.4943	3.030622	-3.68759	0.001647	0.152753	-1.05367
#NV	7980350	-0.2507	2.393616	-3.68454	0.001658	0.153021	-1.05972
TADA1	7922008	-0.32846	7.577885	-3.68416	0.00166	0.153021	-1.06047
#NV	7895724	-0.44005	7.739664	-3.68223	0.001667	0.153021	-1.06429
UBQLN3	7946078	-0.38515	3.428466	-3.68109	0.001671	0.153021	-1.06655
NFATC3	7996744	-0.24936	8.25136	-3.68064	0.001673	0.153021	-1.06745
HELZ	8017776	-0.21726	9.009915	-3.67813	0.001682	0.153209	-1.07242
C19orf80	8025850	0.781132	6.870346	3.677652	0.001684	0.153209	-1.07337
TRAF6	7947540	-0.32292	7.232725	-3.67643	0.001689	0.153211	-1.0758
ZSWIM5	7915682	-0.43604	4.733553	-3.67159	0.001707	0.154462	-1.08539
PAR4 /// S	7982052	-0.87534	3.891318	-3.6661	0.001728	0.155949	-1.09625
PPP2R4	8158523	0.255374	6.762566	3.66282	0.001741	0.156677	-1.10276
LRRC8E	8025347	0.342959	4.545602	3.657291	0.001763	0.158203	-1.11371
#NV	7895511	-0.70212	6.007773	-3.65444	0.001774	0.158655	-1.11937
VAMP8	8043197	0.261994	9.406543	3.653266	0.001779	0.158655	-1.12169
OMD	8171921	-0.34446	5.981337	-3.65024	0.001791	0.158655	-1.12768
FUZ	8038443	-0.33114	5.587725	-3.64998	0.001792	0.158655	-1.12821
FBXO30	8130032	0.34491	7.151905	3.648423	0.001798	0.158655	-1.13128
ABCG2	8101675	-0.532	7.029523	-3.64809	0.001799	0.158655	-1.13194
TXLNA	7899703	0.434134	7.640591	3.646782	0.001805	0.158655	-1.13453
#NV	7971373	0.503254	6.850063	3.646503	0.001806	0.158655	-1.13509
#NV	7989218	-0.61404	7.548276	-3.64471	0.001813	0.158875	-1.13864
RPS6P6	8101357	-0.46065	4.987303	-3.64171	0.001825	0.159526	-1.14458
#NV	7894013	-0.8582	4.483801	-3.6388	0.001837	0.160063	-1.15034
RALGPS1	8157949	0.516356	5.195621	3.636734	0.001846	0.160063	-1.15443
PAPD4	8106534	-0.27647	8.271645	-3.6362	0.001848	0.160063	-1.15549
WDR45L	8019523	0.243045	8.195043	3.635303	0.001852	0.160063	-1.15727
SRPK1	8125941	0.308921	7.066191	3.634393	0.001856	0.160063	-1.15907
RPS6P6	7939102	-0.30661	6.746701	-3.63235	0.001864	0.160383	-1.16312
PVRL3	8081548	-0.27427	7.651559	-3.62766	0.001884	0.16166	-1.17241
SNORA31	7971386	0.589835	4.666009	3.621751	0.001909	0.163393	-1.1841
#NV	8141358	-0.75433	5.456394	-3.62032	0.001915	0.16348	-1.18693
BCL3	8029465	0.397225	7.107508	3.619223	0.00192	0.16348	-1.18911

ULK1	7959957	-0.40484	7.078957	-3.44419	0.00284	0.351451	-1.55953
#NV	8065196	-0.41058	4.374004	-3.43704	0.002885	0.351451	-1.57235
GABRE ///	8175666	-0.93078	6.186229	-3.43461	0.002901	0.351451	-1.57671
#NV	8128245	-0.52352	2.529468	-3.42749	0.002947	0.351451	-1.58948
KIAA0196	8152782	0.221855	7.399615	3.426775	0.002952	0.351451	-1.59076
RN5S119	8048075	-0.5111	4.855349	-3.42494	0.002964	0.351451	-1.59405
#NV	7894047	-0.77374	2.754309	-3.42012	0.002996	0.351451	-1.60269
MBIP	7978666	0.322341	7.370797	3.417987	0.00301	0.351451	-1.60651
NOSIP	8038395	-0.2943	6.489343	-3.41799	0.003011	0.351451	-1.60652
ALG10 ///	7954789	0.241229	7.005036	3.417057	0.003017	0.351451	-1.60818
LAMA5	8067409	-0.5234	6.368012	-3.41694	0.003018	0.351451	-1.60839
SNORD13P	8131263	-0.49026	5.32506	-3.41654	0.00302	0.351451	-1.60911
STXBP4	8008566	0.322044	5.377095	3.41646	0.003021	0.351451	-1.60925
#NV	7894406	-0.34621	10.44998	-3.41515	0.00303	0.351451	-1.61161
PPP1R14B	7949060	-0.24015	7.511319	-3.41489	0.003031	0.351451	-1.61206
MMP17	7959946	-0.23353	3.728324	-3.41414	0.003036	0.351451	-1.6134
RNL5	7934885	0.349683	7.109066	3.413451	0.003041	0.351451	-1.61464
TBC1D10B	8000856	-0.26503	4.821847	-3.4128	0.003046	0.351451	-1.6158
PHF6	8169969	0.289415	5.963007	3.41233	0.003049	0.351451	-1.61665
F

MT1IP	7995834	-0.36792	6.470458	-3.44013	0.002865	0.242378	-1.5331	#NV	8150214	-0.40152	5.642976	-3.61674	0.00193	0.163974	-1.19403	#NV	8165696	-0.6388	11.20708	-3.25586	0.004317	0.36437	-1.8964
PACSIN3	7947801	-0.38849	6.512889	-3.43976	0.002868	0.242378	-1.53381	#NV	8083445	-0.42875	7.245242	-3.61459	0.00194	0.164076	-1.19828	ANO6	7954997	0.27833	9.119777	3.253724	0.004338	0.36437	-1.9002
TPPP2	7973142	-0.65046	6.037695	-3.4387	0.002875	0.242378	-1.53582	RN5S505	8167786	-0.38382	2.836675	-3.6121	0.001951	0.164076	-1.20321	BRD1	8076836	-0.31477	5.791921	-3.2535	0.00434	0.36437	-1.9006
GM2A	8109344	0.325607	8.135033	3.438035	0.002879	0.242378	-1.53707	#NV	7929664	-0.45208	7.481821	-3.61076	0.001956	0.164076	-1.20585	MXRA5	8171172	0.528711	6.023649	3.253104	0.004344	0.36437	-1.90131
#NV	7895123	0.374552	7.671169	3.437449	0.002883	0.242378	-1.53817	RAP2A	7969693	0.373867	6.644343	3.610086	0.001959	0.164076	-1.2072	SNORD43	8076223	-0.94739	6.058736	-3.25306	0.004344	0.36437	-1.9014
MT1P2	7925413	-0.35582	6.335336	-3.434	0.002905	0.242494	-1.54467	#NV	7907964	-0.42186	3.459817	-3.60971	0.001961	0.164076	-1.20794	ACP6	7919326	0.504296	7.254308	3.250073	0.004373	0.365865	-1.90671
#NV	7983987	-0.36803	4.800754	-3.43393	0.002905	0.242494	-1.54481	MAP4K3	8051707	-0.23658	7.469065	-3.60856	0.001966	0.164076	-1.21022	ARFIP2	7946201	-0.21382	7.622995	-3.24254	0.004447	0.370312	-1.92015
SEMA4G	7929882	-0.22412	8.701569	-3.43385	0.002906	0.242494	-1.54496	GM2A	8109344	0.341604	8.135033	3.606946	0.001973	0.164076	-1.21341	SNX16	8151572	0.34982	3.778752	3.241234	0.00446	0.370312	-1.92247
AK3	8159945	0.266449	9.584354	3.432071	0.002917	0.242715	-1.54832	ZNF383	8028227	-0.41869	6.494063	-3.60674	0.001974	0.164076	-1.21382	ANGEL2	7924190	0.211729	6.575069	3.239893	0.004473	0.370312	-1.92485
#NV	7892948	-0.35774	9.25522	-3.4312	0.002923	0.242715	-1.54996	#NV	8036989	-0.45593	7.326768	-3.60633	0.001976	0.164076	-1.21464	RN5S443	8016213	-0.67982	3.911382	-3.23913	0.004481	0.370312	-1.92622
#NV	7930915	-0.44049	3.921971	-3.4298	0.002932	0.242872	-1.55261	CENPV	8013015	-0.46685	7.116961	-3.60116	0.001999	0.165572	-1.22486	SNORD13 /	8145793	-0.30595	12.29964	-3.23899	0.004482	0.370312	-1.92647
NQO1	8002303	0.406208	4.035906	3.424708	0.002966	0.243668	-1.5622	YKT6	8132580	0.414465	7.036864	3.599885	0.002005	0.165634	-1.22739	CREBRF	8110032	0.295276	7.532701	3.236022	0.004511	0.371468	-1.93175
OMP	7942715	-0.37907	5.310045	-3.42442	0.002968	0.243668	-1.56275	#NV	8097062	-0.37102	6.387812	-3.59599	0.002022	0.166198	-1.23509	STXBP3	7903541	0.249672	6.918873	3.232899	0.004543	0.371468	-1.93731
PDHB	8088384	0.280664	7.481004	3.424027	0.00297	0.243668	-1.56349	OR3A1	8011337	-0.29486	2.824096	-3.59493	0.002027	0.166198	-1.23719	#NV	8097062	0.333511	6.387812	3.23245	0.004547	0.371468	-1.93811
RFK	8161857	0.448859	6.858016	3.423891	0.002971	0.243668	-1.56374	PPP4R1	8022251	0.302672	6.650342	3.594079	0.002031	0.166198	-1.23888	KLF16	8032365	-0.25736	5.869034	-3.23136	0.004558	0.371468	-1.94005
#NV	8031867	-0.76407	7.067451	-3.4216	0.002986	0.244117	-1.56807	EYS	8127391	-0.36142	4.181775	-3.59121	0.002044	0.166198	-1.24455	HPS5	7946988	-0.60541	6.768116	-3.23088	0.004563	0.371468	-1.94091
#NV	7892633	-0.5588	7.300479	-3.42023	0.002995	0.244117	-1.57065	#NV	7911349	-0.52632	4.243503	-3.58972	0.002051	0.166198	-1.24749	PCMTD1	8150714	0.303935	8.389789	3.230701	0.004565	0.371468	-1.94123
HPGD	8103769	0.739707	9.611057	3.419765	0.002999	0.244117	-1.57152	SEC13	8085300	0.245698	7.539606	3.589083	0.002054	0.166198	-1.24876	HOXC9	7955865	-0.22844	2.566488	-3.22727	0.0046	0.371468	-1.94733
COQ6	7975661	0.289523	6.269914	3.418533	0.003007	0.244192	-1.57385	GRAMD3	8107673	-0.40984	7.494671	-3.58444	0.002075	0.166198	-1.25794	NEK7	7908543	0.399327	7.803073	3.225738	0.004615	0.371468	-1.95007
GCDH	8026090	-0.62442	8.668184	-3.41728	0.003015	0.24428	-1.57621	RICTOR	8111698	-0.31222	7.699955	-3.58423	0.002076	0.166198	-1.25836	WDR74	7948894	-0.52487	9.573884	-3.22509	0.004622	0.371468	-1.95122
NIN	7979044	0.352013	5.910172	3.411861	0.003052	0.245781	-1.58643	HERC5	8096361	-0.6641	5.276742	-3.5835	0.00208	0.166198	-1.2598	LCORL	8099581	0.250576	6.072208	3.225058	0.004622	0.371468	-1.95128
IPO9	7908732	0.216746	7.968774	3.41173	0.003053	0.245781	-1.58667	#NV	7894385	0.408646	7.667171	3.583144	0.002081	0.166198	-1.26051	#NV	7892693	-0.56036	5.78182	-3.22471	0.004626	0.371468	-1.9519
#NV	7895846	0.591743	8.983312	3.41127	0.003056	0.245781	-1.58754	NDFIP2	7969544	-0.31997	7.332021	-3.5822	0.002086	0.166198	-1.26238	LAG3	7953418	-0.37672	5.010562	-3.22433	0.00463	0.371468	-1.95257
BID	8074261	0.358877	7.231549	3.409149	0.00307	0.245991	-1.59154	#NV	8086181	-0.54519	4.289664	-3.58152	0.002089	0.166198	-1.26373	PPP1R9B /	8016628	-0.32511	5.566182	-3.22092	0.004665	0.373381	-1.95864
#NV	8040415	-0.38849	4.049148	-3.40872	0.003073	0.245991	-1.59234	IIH	8059067	-0.24465	4.182923	-3.58126	0.00209	0.166198	-1.26423	FAM72A //	8039928	0.363831	3.103197	3.217938	0.004696	0.374422	-1.96396
#NV	7943193	0.243891	3.950779	3.406152	0.003091	0.246813	-1.59719	VPS18	7982845	0.347456	5.906933	3.581172	0.00209	0.166198	-1.26441	ZFP161	8022110	0.210209	7.142049	3.217498	0.0047	0.374422	-1.96474
IL13RA2	8174598	0.612809	4.602951	3.403306	0.003111	0.247674	-1.60255	SNORA70F	8056359	-0.37624	6.131067	-3.58051	0.002094	0.166198	-1.26573	#NV	7894146	-0.42678	6.515099	-3.2122	0.004756	0.376495	-1.97417
ARF1 /// N	7910229	0.249694	10.01941	3.39987	0.003135	0.247674	-1.60902	FBXO4	8105111	-0.46197	5.545258	-3.57753	0.002108	0.166198	-1.27162	#NV	7893849	0.601439	6.577002	3.211872	0.004759	0.376495	-1.97475
ASS1	8158671	-0.39157	11.78321	-3.39966	0.003136	0.247674	-1.60942	ALDH6A1	7980098	-0.35573	10.8461	-3.57722	0.002109	0.166198	-1.27223	CREG1	7922051	0.395532	9.899679	3.211771	0.00476	0.376495	-1.97493
SNORD50A	8127987	-0.47737	7.062494	-3.39864	0.003143	0.247674	-1.61134	#NV	7972932	0.941066	3.855519	3.575935	0.002115	0.166198	-1.27477	PIAS4	8024740	-0.21975	5.867337	-3.20916	0.004788	0.377408	-1.97958
HGFAC	8093792	-0.24078	9.025604	-3.39602	0.003162	0.247674	-1.61627	COBLL1	8056343	-0.24241	9.247917	-3.57571	0.002116	0.166198	-1.27522	NOXO1	7998668	-0.25275	4.036634	-3.20849	0.004795	0.377408	-1.98077
#NV	7893392	0.725191	4.230254	3.392084	0.003189	0.247674	-1.62369	#NV	8166925	-0.36456	9.157846	-3.57535	0.002118	0.166198	-1.27592	NUP155	8111629	0.268449	7.28151	3.207431	0.004806	0.377408	-1.98265
#NV	8162249	0.231521	2.575361	3.390284	0.003202	0.247674	-1.62708	#NV	7895941	0.883601	5.543909	3.575213	0.002119	0.166198	-1.2762	PKD1	7998700	-0.29376	5.649377	-3.20594	0.004822	0.377408	-1.9853
SNORD114	7976816	-0.83239	7.326892	-3.38957	0.003207	0.247674	-1.62843	HN1	8018305	0.374404	5.599623	3.57463	0.002121	0.166198	-1.27735	TMX1	7974303	0.430586	7.606057	3.201975	0.004865	0.377408	-1.99236
OXER1	8051793	-0.62227	8.629266	-3.38882	0.003213	0.247674	-1.62983	AGRN	7896822	0.348024	6.243405	3.573359	0.002127	0.16628	-1.27986	SLC7A5	8003298	-0.38107	5.34422	-3.20156	0.004869	0.377408	-1.99309
SNORD42A	8005955	-0.32547	6.039702	-3.38838	0.003216	0.247674	-1.63066	#NV	7893144	-0.84372	2.662865	-3.56974	0.002145	0.167241	-1.28703	XPNPEP3	8073311	0.213565	7.474209	3.201286	0.004872	0.377408	-1.99358
CCDC99	8109830	0.416144	5.296944	3.388333	0.003216	0.247674	-1.63076	KIAA0825	8113097	-0.49869	5.676302	-3.56422	0.002171	0.16838	-1.29793	ANKS1B	7965686	-1.00187	3.689516	-3.20039	0.004882	0.377408	-1.99518
ANO10	8086467	0.395329	6.857385	3.388075	0.003218	0.247674	-1.63124	CCT6B	8014172	-0.38067	4.867404	-3.5634	0.002175	0.16838	-1.29956	STAG2	8169750	0.263829	7.4392	3.19938	0.004893	0.377408	-1.99697
#NV	8136612	-0.36274	2.480863	-3.38785	0.00322	0.247674	-1.63167	ABR	8010983	0.530553	5.768546	3.563123	0.002177	0.16838	-1.30011	SEC61A2	7926189	0.35043	6.569813	3.198875	0.004898	0.377408	-1.99787
CISD2	8096663	0.389438	7.556091	3.387494	0.003222	0.247674	-1.63234	WNT11	7950534	0.783535	5.098973	3.56254	0.00218	0.16838	-1.30126	#NV	8171491	-0.37061	4.255857	-3.19691	0.004919	0.377408	-2.00137
EMC1	7913110	0.285339	7.589327	3.38639	0.00323	0.247674	-1.63442	TRIAP1	7967056	0.320829	6.124604	3.560503	0.002189	0.168752	-1.30529	SLC37A4 /	7952132	0.294438	9.378301	3.194613	0.004944	0.377408	-2.00545
#NV	8126627	-0.26029	2.333629	-3.3861	0.003232	0.247674	-1.63497	#NV	7893122	0.614852	6.2204	3.556387	0.00221	0.168752	-1.31342	RN5S454	8021043	-1.93684	7.274088	-3.1943	0.004948	0.377408	-2.00601
#NV	7993017	-0.40715	4.55434	-3.38409	0.003247	0.247674	-1.63875	#NV	7961602	-0.32953	4.11457	-3.55481	0.002218	0.168752	-1.31654	MAP3K2	8054997	0.301116	8.04723	3.193906	0.004952	0.377408	-2.00671
#NV	7894719	-0.5305	4.669857	-3.38339	0.003252	0.247674	-1.64006	ELF2	8102817	-0.23927	6.90702	-3.55404	0.002221	0.168752	-1.31807	HCFC2	7958158	0.196516	6.646656	3.193764	0.004954	0.377408	-2.00696
#NV	7893504	0.238449	9.51176	3.380401	0.003274	0.247674	-1.6457	LRP6	7961339	-0.28023	9.401559	-3.55217	0.002231	0.168752	-1.32177	FOXD4 ///	8044634	-0.22023	4.155393	-3.19301	0.004962	0.377408	-2.0083
DPF1	8036460	-0.29793	3.155923	-3.3802	0.003275	0.247674	-1.64608	C3orf62 //	8087374	0.372982	5.546666	3.550884	0.002237	0.168752	-1.3243	LRRC40	7916910	0.331751	6.957444	3.192777	0.004965	0.377408	-2.00872
PI4K2A	7929677	0.43502	6.27656	3.379653	0.003279	0.247674	-1.6471	#NV	8008991	-0.60309	3.363013	-3.55086	0.002237	0.168752	-1.32434	JDP2	7975787	-0.35426	5.796504	-3.18776	0.00502	0.3785	-2.01764
MST4	8169949	0.280431	5.910528	3.379123	0.003283	0.247674	-1.6481	#NV	8135929	-0.32814	6.745813	-3.549	0.002247	0.168752	-1.32803	EIF1AX	8171747	0.263526	7.697523	3.187665	0.005021	0.3785	-2.0178
NSUN6	7932433	-0.47825	8.774249	-3.3791	0.003283	0.247674	-1.64815	LZTFL1	8086555	-0.26652	5.794286	-3.5477	0.002253	0.168752	-1.3306	PNN	7974066	-0.28493	8.298073	-3.18749	0.005023	0.3785	-2.01811
PDXDC2P	8002322	-0.35952	9.88427	-3.37845	0.003288	0.247674	-1.64937	ANKAR	8047006	-0.29168	5.584973	-3.5476	0.002254	0.168752	-1.33079	#NV	7967620	-0.39451	10.44163	-3.18652	0.005034	0.3785	-2.01984
B4GALT7	8110399	0.204729	6.7791	3.378224	0.003289	0.247674	-1.6498	KCND3	7918558	-0.49023	7.090312	-3.54749	0.002254	0.168752	-1.33101	BNIP2	7989323	0.233335	7.531529	3.184703	0.005054	0.3785	-2.02307
#NV	7919594	-0.29318	2.294092	-3.37675	0.0033	0.247674	-1.65257	ATF5	8030557	0.650132	10.59896	3.545169	0.002266	0.168752	-1.3356	NR2F6	8035249	-0.224	8.071004	-3.18411	0.005061	0.3785	-2.02412
#NV	7893517	0.427174	6.246273	3.376432	0.003303	0.247674	-1.65317	#NV	8136612	-0.37953	2.480863	-3.54462	0.002269	0.168752	-1.33668	#NV	8150214	0.353445	5.642976	3.183733	0.005065	0.3785	-2.02479
SNORD115	7982082	-0.5728	2.627738	-3.37525	0.003311	0.24777	-1.6554	#NV	8072344	-0.58677	10.06874	-3.54421	0.002271	0.168752	-1.33748	TSHZ1	8021768	0.19222	6.285143	3.179637	0.005111	0.3785	-2.03207
VPS45	7905099	0.228748	7.695363	3.368957	0.003358	0.249859	-1.66724	CDC42SE1	7919888	0.274486	6.726123	3.543913	0.002272	0.168752	-1.33808	ABAT	7993126	0.230385	10.58837	3.175736	0.005155	0.3785	-2.039
#NV	7894808	0.217947	10.75254	3.368696	0.00336	0.249859	-1.66773	ZBTB33	8169683	0.416473	7.845789	3.543885	0.002272	0.168752	-1.33814	#NV	8097809	0.420583	6.643435	3.17568	0.005156	0.3785	-2.0391
XK	8166723	0.546095	4.42145	3.368461	0.003362	0.249859	-1.66817	#NV	7987403	-0.69508	4.397281	-3.54374	0.002273	0.168752	-1.33843	ZBTB12	8125201	-0.24246	4.141536	-3.17173	0.005201	0.3785	-2.04612
#NV	8122740	-0.35878	4.804758	-3.36528	0.003386	0.250385	-1.67417	#NV	7916225	-0.37881	4.380693	-3.54269	0.002279	0.168752	-1.34049	ZBTB12	8178683	-0.24246	4.141536	-3.17173	0.005201	0.3785	-2.04612
#NV	7893798	0.615752	3.228531	3.365193	0.003386	0.250385	-1.67433	#NV	7893973	0.279424	9.262963	3.542277	0.002281	0.168752	-1.34131	C17orf62	8019507	-0.24406	6.205964	-3.17121	0.005207	0.3785	-2.04703
RPS12	8122136	-0.453	7.653688	-3.36444	0.003392	0.250385	-1.67573	ACTR1A	7936028	0.305738	7.581143	3.540362	0.00229	0.1691	-1.3451	NANOGP1	7953689	0.43662	3.22162	3.170541	0.005215	0.3785	-2.04823
C15orf59	7990269	-0.27814	4.083336	-3.36352	0.003399	0.250385	-1.67747	CUEDC1	8016878	0.294056	5.259166	3.533676	0.002325	0.170451	-1.35831	ZNF324	8031956	-0.32917	5.18244	-3.16993	0.005222	0.3785	-2.04932
SNORD116	7982006	-0.53469	5.237531	-3.3625	0.003407	0.250402	-1.67939	#NV	7909888	-0.44718	3.177013	-3.53359	0.002325	0.170451	-1.35848	CRIPT	8041813	0.239174	7.395507	3.169377	0.005228	0.3785	-2.05029
#NV	8170237	-0.29596	4.123083	-3.35966	0.003428	0.250433	-1.68473	CCNG1	8109697	-0.394	9.809682	-3.53254	0.002331	0.170451	-1.36056	#NV	7895784	-0.44342	6.465308	-3.169	0.005232	0.3785	-2.05096
#NV	7894861	-0.67996	6.316741	-3.35778	0.003443	0.250433	-1.68827	WWC1	8109773	0.463462	5.813341	3.530204	0.002343	0.170451	-1.36517	DUSP9	8170695	-0.27699	4.255105	-3.16773	0.005247	0.3785	-2.05321
#NV	8054354	-0.44291	4.145904	-3.35596	0.003457	0.250433	-1.69169	EIF5	7977058	-0.2736	9.526085	-3.53004	0.002344	0.170451	-1.36549	#NV	8150864	-0.32852	4.822074	-3.16769	0.005247	0.3785	-2.05329
TMEM64	8151747	0.253298	7.794111	3.355249	0.003462	0.250433	-1.69304	CKS1BP6	8166630	-0.89821	6.620693	-3.52853	0.002352	0.170451	-1.36847	#NV	8180393	0.248551	6.960491	3.165227	0.005276	0.3785	-2.05766
ABHD1	8040815	0.464247	6.472339	3.354516	0.003468	0.250433	-1.69441	KBTBD3	7951429	-0.241	3.731451	-3.52787	0.002355	0.170451	-1.36979	#NV	7894577	0.467658	6.661841	3.164765	0.005281	0.3785	-2.05848
GBAP1	7920687	0.380711	4.792447	3.352434	0.003484	0.250433	-1.69833	#NV	7896375	0.26667	10.99597	3.525859	0.002366	0.170451	-1.37375	APCDD1L	8067270	-0.25596	4.644905	-3.1626	0.005307	0.3785	-2.06233
#NV	7977474	-0.21977	2.623026	-3.35236	0.003484	0.250433	-1.69847	#NV	8133036	-0.38169	2.704872	-3.52578	0.002366	0.170451	-1.37391	SLC6A3	8110821	-0.32574	4.202529	-3.16247	0.005308	0.3785	-2.06256
GPR162	7953442	-0.44982	4.786119	-3.35226	0.003485	0.250433	-1.69865	PYY	8015890	-0.36879	4.069382	-3.5253	0.002369	0.170451	-1.37486	BCR	8071691	-0.22984	7.36003	-3.16062	0.00533	0.3785	-2.06584
XRRA1	7950447	0.811088	6.304346	3.351965	0.003488	0.250433	-1.69921	METTL7A	7955441	-0.31593	9.951212	-3.52453	0.002373	0.170451	-1.37638	TRAF7	7992529	-0.2483	7.001472	-3.15978	0.00534	0.3785	-2.06733
IRS1	8059470	-0.31997	7.282921	-3.35181	0.003489	0.250433	-1.69951	#NV	7896677	0.470932	6.683804	3.524183	0.002375	0.170451	-1.37706	SRPK2	8142036	0.239741	6.583344	3.157975	0.005361	0.3785	-2.07054
RBMS1	8056206	-0.51845	7.090963	-3.35107	0.003494	0.250433	-1.70089	RB1CC1	8150757	-0.26683	6.704529	-3.52365	0.002378	0.170451	-1.37812	#NV	7896439	-0.56404	5.401167	-3.15786	0.005363	0.3785	-2.07074
FOXP1	8088776	-0.29018	7.835085	-3.3507	0.003497	0.250433	-1.70159	SNAP23	7983111	-0.30585	7.95584	-3.52267	0.002383	0.170451	-1.38004	LMAN1	8023561	0.23198	10.37474	3.155805	0.005387	0.3785	-2.07439
DTD1	8061211	0.295259	5.906581	3.348858	0.003512	0.250565	-1.70506	LMBRD1	8127425	-0.26631	8.121355	-3.52165	0.002388	0.170451	-1.38207	CNOT3	8031122	-0.24116	6.791672	-3.15391	0.005409	0.3785	-2.07774
#NV	7895979	-0.45259	2.727646	-3.34784	0.00352	0.250565	-1.70698	#NV	7892605	-0.46966	7.075888	-3.52122	0.002391	0.170451	-1.38292	PACS2	7977344	-0.28243	6.298055	-3.15087	0.005446	0.3785	-2.08314
MED27	8164698	0.42276	4.578223	3.346644	0.003529	0.250565	-1.70922	#NV	8113232	-1.10412	4.954168	-3.51882	0.002404	0.170539	-1.38766	#NV	8169634	-0.78375	9.733561	-3.15003	0.005456	0.3785	-2.08463
SLC35A2	8172460	0.296285	5.784373	3.345948	0.003535	0.250565	-1.71053	#NV	7893254	-0.73532	5.084615	-3.51802	0.002408	0.170539	-1.38924	STS	8165866	0.384322	6.492231	3.149878	0.005458	0.3785	-2.0849
ENPP4	8120061	0.363348	5.216305	3.345655	0.003537	0.250565	-1.71108	SNORD63	8114468	-0.49124	5.371115	-3.51782	0.002409	0.170539	-1.38962	HSPA8 ///	7952339	-0.43255	9.307381	-3.14967	0.00546	0.3785	-2.08528
SERPINA13	7976506	-0.33211	3.47899	-3.34273	0.00356	0.250864	-1.71658	SNORD115	7982068	-0.61678	2.726533	-3.51718	0.002412	0.170539	-1.3909	#NV	7989216	0.916539	4.417912	3.149652	0.005461	0.3785	-2.0853
GCAT	8072931	-0.58185	5.820632	-3.34271	0.00356	0.250864	-1.71662	#NV	7928815	-0.28843	3.258196	-3.51554	0.002421	0.170802	-1.39414	PRRC2A	8178011	-0.24083	6.943722	-3.14839	0.005476	0.3785	-2.08754
ATP9A	8067055	0.37697	6.601767	3.341683	0.003568	0.250864	-1.71855	PGP	7998759	0.305887	6.183389	3.512147	0.00244	0.171453	-1.40083	DIRC2	8082120	0.248487	7.569064	3.146271	0.005501	0.3785	-2.0913
APOL5	8072721	-0.60573	3.639183	-3.3398	0.003583	0.250864	-1.7221	TSHZ1	8021768	-0.21231	6.285143	-3.51194	0.002441	0.171453	-1.40123	TRNAF16P	7919598	-0.29691	4.819835	-3.14065	0.00557	0.3785	-2.10126
PPP2R1A	8030881	0.252076	8.289702	3.33889	0.00359	0.250864	-1.7238	#NV	8031906	-0.27877	3.243694	-3.50986	0.002452	0.171744	-1.40535	BHLHE23	8067585	-0.23821	4.408638	-3.13945	0.005585	0.3785	-2.1034
SPSB3	7998590	-0.22987	6.891739	-3.3383	0.003595	0.250864	-1.72491	MORC3	8068460	-0.35161	7.375335	-3.5089	0.002457	0.171744	-1.40723	#NV	7965478	-0.41999	4.656046	-3.13935	0.005586	0.3785	-2.10357
#NV	8156110	-0.25722	3.143025	-3.33818	0.003596	0.250864	-1.72513	SNORD116	7982006	-0.55754	5.237531	-3.50621	0.002472	0.171744	-1.41254	#NV	7954787	-0.35426	4.613998	-3.13841	0.005598	0.3785	-2.10524
RIC8A	7937275	0.213731	7.227877	3.337504	0.003602	0.250864	-1.72641	ABHD6	8080762	0.411472	8.839826	3.505222	0.002478	0.171744	-1.4145	#NV	7893195	0.649546	3.236148	3.136936	0.005616	0.3785	-2.10785
RPPH1	7977507	-0.348	9.838973	-3.33561	0.003617	0.250864	-1.72997	#NV	7896138	-0.46221	7.629104	-3.50463	0.002481	0.171744	-1.41566	IER5L	8164554	-0.27338	5.195133	-3.13662	0.00562	0.3785	-2.10842
C1orf131	7925033	-0.31187	5.038486	-3.33467	0.003624	0.250864	-1.73174	#NV	8121390	-0.59102	3.356538	-3.50404	0.002484	0.171744	-1.41684	PMPCB	8135235	0.268228	8.743567	3.136568	0.00562	0.3785	-2.1085
CELF3	7920027	-0.20412	4.373505	-3.33443	0.003626	0.250864	-1.73218	LOC100506	7981945	-0.44079	3.845904	-3.50089	0.002502	0.171744	-1.42305	RIC3	7946340	0.552487	4.732801	3.136514	0.005621	0.3785	-2.1086
PJA1	8173340	0.276243	4.284232	3.333784	0.003631	0.250864	-1.7334	GALNTL4	7946641	0.408385	5.299748	3.500834	0.002502	0.171744	-1.42316	#NV	7895868	-0.49294	5.57053	-3.13578	0.00563	0.3785	-2.10991
#NV	7893613	-0.45086	8.148293	-3.33203	0.003646	0.251117	-1.7367	RNPEPL1	8049689	0.304682	7.395781	3.500409	0.002504	0.171744	-1.424	METTL5	8056716	0.245567	6.260358	3.134463	0.005647	0.3785	-2.11223
KBTBD11	8144317	-0.41141	4.619788	-3.32966	0.003665	0.251117	-1.74114	#NV	7894490	-0.47823	5.806789	-3.49784	0.002519	0.171744	-1.42907	#NV	7922418	-0.42446	9.843163	-3.13303	0.005664	0.3785	-2.11477
RN5S139	8082406	-0.30727	3.866428	-3.32806	0.003678	0.251117	-1.74415	#NV	7894975	-0.47823	5.806789	-3.49784	0.002519	0.171744	-1.42907	HIATL1	8156538	0.309746	6.890444	3.132859	0.005667	0.3785	-2.11508
PGD	7897620	0.444553	9.012348	3.327976	0.003679	0.251117	-1.74431	#NV	7895855	-0.55173	5.814548	-3.49659	0.002526	0.171744	-1.43153	SPPL2A	7988753	0.282019	9.386558	3.132652	0.005669	0.3785	-2.11544
OBP2A	8159259	-0.3398	4.66581	-3.32631	0.003692	0.251117	-1.74744	METTL2A	8009008	-0.41459	5.926925	-3.49475	0.002536	0.171744	-1.43518	#NV	7919267	-0.39453	4.412468	-3.12901	0.005715	0.3785	-2.1219
#NV	7895277	0.346165	9.092583	3.324491	0.003707	0.251117	-1.75086	DIP2B	7955376	-0.2697	8.08486	-3.49404	0.00254	0.171744	-1.43656	#NV	7919347	-0.39453	4.412468	-3.12901	0.005715	0.3785	-2.1219
#NV	7893870	0.530044	5.552863	3.324416	0.003708	0.251117

SNORD114	7976826	-0.64816	4.507751	-3.2846	0.004051	0.255766	-1.82574	#NV	7896641	-0.78886	2.662344	-3.45385	0.002779	0.176188	-1.51583	NQO1	8002303	0.367904	4.035906	3.101764	0.006068	0.3785	-2.17014
ATG2B	7981192	-0.22514	7.922724	-3.28349	0.004061	0.255766	-1.82782	CYBASC3	7948565	0.275544	6.385857	3.453336	0.002782	0.176188	-1.51683	RNU2-1 ///	8019631	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
FBXO48	8052742	0.293651	4.759255	3.282786	0.004067	0.255766	-1.82915	PRODH	8074335	-0.8306	5.244114	-3.45214	0.00279	0.176188	-1.5192	RNU2-1 ///	8019633	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
NUDT13	7928342	-0.43263	5.310278	-3.28249	0.00407	0.255766	-1.82971	GPANK1	8124998	-0.23881	5.450545	-3.4516	0.002793	0.176188	-1.52026	RNU2-1 ///	8019635	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
#NV	8173611	-0.23692	2.657289	-3.27974	0.004095	0.255766	-1.83487	#NV	8103725	-2.0943	4.330768	-3.45146	0.002794	0.176188	-1.52054	RNU2-1 ///	8019637	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
SCO1	8012823	0.27618	7.335223	3.278128	0.004109	0.255766	-1.83788	ATAD3B	7896961	0.294421	6.10186	3.450096	0.002802	0.17639	-1.52322	RNU2-1 ///	8019639	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
TRAM1	8151281	0.275249	8.854021	3.277903	0.004111	0.255766	-1.83831	FBXO2	7912473	0.539928	5.840583	3.448308	0.002814	0.176496	-1.52674	RNU2-1 ///	8019641	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
RPL12	8164210	-0.25132	4.697202	-3.2777	0.004113	0.255766	-1.83869	TMEM161	8113023	-0.28869	8.331024	-3.44749	0.002819	0.176496	-1.52836	RNU2-1 ///	8019703	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
#NV	7896430	0.528821	8.003327	3.273084	0.004156	0.255766	-1.84734	SLC35C1	7939590	0.762783	7.048292	3.446847	0.002823	0.176496	-1.52962	RNU2-1 ///	8019705	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
#NV	7892738	0.418369	7.378378	3.272614	0.00416	0.255766	-1.84822	LOC100506	7982020	-0.67378	3.019329	-3.44645	0.002825	0.176496	-1.5304	RNU2-1 ///	8019707	-0.34309	11.77976	-3.10161	0.00607	0.3785	-2.1704
#NV	7894597	0.418369	7.378378	3.272614	0.00416	0.255766	-1.84822	#NV	8154215	-0.38271	2.333292	-3.44319	0.002846	0.177144	-1.53682	TRMT10A	8101916	0.325381	5.160075	3.099613	0.006097	0.379457	-2.17394
FAM20B	7907680	0.200151	7.042304	3.271789	0.004168	0.255766	-1.84977	PPIL1	8126058	0.324229	5.537191	3.443133	0.002846	0.177144	-1.53694	#NV	7892838	0.327818	8.025629	3.09825	0.006115	0.379887	-2.17635
#NV	7896160	-0.462	8.58675	-3.27117	0.004173	0.255766	-1.85092	KLHL29	8040490	0.383568	4.018772	3.440487	0.002863	0.177835	-1.54215	RAD21	8152477	0.172257	7.198372	3.095744	0.006149	0.380987	-2.18078
SLC23A2	8064808	-0.56278	9.263202	-3.27073	0.004177	0.255766	-1.85175	RAB6A ///	8045136	0.255023	6.943707	3.439182	0.002871	0.177835	-1.54472	LOC10013	8061483	-0.43031	5.413104	-3.09492	0.00616	0.380987	-2.18224
CHURC1-FI	7975121	0.319161	6.858682	3.270566	0.004179	0.255766	-1.85206	#NV	8154227	-0.39244	7.351796	-3.43888	0.002873	0.177835	-1.54531	CNOT7	8149475	0.278817	8.505684	3.093641	0.006178	0.380987	-2.1845
ELOVL5	8127145	0.398788	10.17493	3.268523	0.004198	0.255766	-1.85589	C12orf69	7961503	-0.46823	3.840841	-3.43753	0.002882	0.17804	-1.54796	C5orf51	8105104	0.281705	7.414146	3.092614	0.006192	0.380987	-2.18632
ERGIC1	8109999	0.330104	9.577765	3.268377	0.004199	0.255766	-1.85616	#NV	7896030	0.450429	8.095373	3.435735	0.002894	0.17831	-1.55151	HBS1L	8129706	0.196855	7.713277	3.092327	0.006195	0.380987	-2.18683
#NV	7892966	0.455607	8.438201	3.267675	0.004206	0.255766	-1.85748	ZCCHC14	8003263	-0.28296	7.600107	-3.4352	0.002897	0.17831	-1.55257	NUMBL	8036923	-0.22987	5.830355	-3.09187	0.006202	0.380987	-2.18763
SNORD116	7981958	-0.40405	9.099429	-3.267	0.004212	0.255766	-1.85874	C11orf65	7951521	-0.33802	4.224925	-3.43173	0.00292	0.179214	-1.55938	STX10	8034631	-0.21151	7.27887	-3.08611	0.006281	0.382283	-2.19782
SNORD116	7981962	-0.40405	9.099429	-3.267	0.004212	0.255766	-1.85874	C8orf40	8146225	-0.26365	8.498281	-3.43017	0.00293	0.179214	-1.56246	LYPLA1	8150830	0.287263	8.468474	3.08608	0.006281	0.382283	-2.19787
ESYT1	7956166	0.329644	8.193894	3.266901	0.004213	0.255766	-1.85893	ZMAT3	8092230	0.680974	6.37762	3.429805	0.002932	0.179214	-1.56318	KCND1	8172493	-0.31346	4.454913	-3.08508	0.006295	0.382283	-2.19963
#NV	7894687	0.330118	10.62243	3.266004	0.004221	0.255766	-1.86061	RGS9	8009277	0.346242	3.931818	3.429609	0.002933	0.179214	-1.56357	PLS1	8083146	0.340159	6.729487	3.082795	0.006327	0.382283	-2.20367
#NV	8152096	0.268645	9.062238	3.264647	0.004234	0.255766	-1.86315	#NV	8065990	-0.48446	4.333503	-3.42865	0.00294	0.179214	-1.56545	FEM1B	7984470	0.24641	6.929203	3.082484	0.006331	0.382283	-2.20422
SLC39A9	7975344	0.229442	8.744013	3.264332	0.004237	0.255766	-1.86374	FURIN	7986092	0.36241	9.083367	3.427984	0.002944	0.179214	-1.56677	TESK2	7915718	0.231681	7.172171	3.081802	0.00634	0.382283	-2.20543
SLC9B2	8102050	0.387443	8.614676	3.264182	0.004239	0.255766	-1.86402	SPATS2	7955217	0.33842	6.063449	3.425229	0.002962	0.17999	-1.57219	#NV	7893612	0.590636	2.98377	3.081515	0.006344	0.382283	-2.20593
C9orf64	8162039	0.363282	6.677803	3.263623	0.004244	0.255766	-1.86507	ADHFE1	8146687	-0.37983	9.86092	-3.42298	0.002977	0.180564	-1.57661	#NV	7896344	0.590636	2.98377	3.081515	0.006344	0.382283	-2.20593
FIG4	8121429	0.299228	6.536402	3.263436	0.004246	0.255766	-1.86542	PFN1	8011759	0.243767	10.14698	3.421585	0.002986	0.180593	-1.57936	HMGA1 //,	8118794	-0.24567	5.000893	-3.08119	0.006349	0.382283	-2.2065
#NV	7895135	0.53879	3.399873	3.263134	0.004248	0.255766	-1.86599	RABAC1	8037071	0.260783	7.381457	3.419479	0.003	0.180593	-1.58351	TUBE1	8128977	0.359465	6.767606	3.08023	0.006362	0.382283	-2.2082
MRAS	8082965	0.360571	5.479242	3.262783	0.004252	0.255766	-1.86664	RNU4-4P	8092185	-0.45115	3.775397	-3.41826	0.003009	0.180593	-1.58591	OR52I1	7937948	-0.24567	3.214076	-3.07977	0.006369	0.382283	-2.20902
FANCI	7985829	0.355142	4.413213	3.262351	0.004256	0.255766	-1.86745	#NV	8064857	-0.26991	8.039014	-3.41735	0.003015	0.180593	-1.5877	ALPP	8049123	-0.59951	3.480532	-3.07962	0.006371	0.382283	-2.20928
PSD3	8149555	-0.43479	8.84969	-3.26184	0.004261	0.255766	-1.86841	KIAA0513	7997662	0.34851	5.002613	3.416686	0.003019	0.180593	-1.589	#NV	7949019	0.320684	2.203796	3.079546	0.006372	0.382283	-2.20941
PTPN11	7958846	0.291309	8.370372	3.259441	0.004283	0.255766	-1.87291	#NV	7894476	-0.65103	5.237518	-3.41659	0.00302	0.180593	-1.58919	HSD11B1	7909446	0.277345	9.885112	3.075308	0.006432	0.385165	-2.2169
TFB1M	8130438	0.336894	6.632352	3.258204	0.004295	0.255766	-1.87522	KDM8	8000411	0.69117	5.543255	3.415025	0.00303	0.180593	-1.59227	APIP	7947490	-0.5006	4.534644	-3.07295	0.006465	0.386467	-2.22106
CDH26	8063761	-0.3238	3.701782	-3.25367	0.004338	0.255766	-1.88372	#NV	8128695	-0.23568	3.43726	-3.41485	0.003032	0.180593	-1.59263	UPF3A	7970370	-0.33841	6.32411	-3.0705	0.0065	0.387101	-2.22538
#NV	7986348	-0.33099	3.716279	-3.2535	0.00434	0.255766	-1.88403	#NV	8163000	-0.75772	6.715748	-3.41368	0.00304	0.180593	-1.59492	EEF1B2 ///	8047780	-0.81359	6.321314	-3.07017	0.006505	0.387101	-2.22597
SPTLC3	8060997	0.521905	8.478188	3.252781	0.004347	0.255766	-1.88538	APIP	7947490	0.555981	4.534644	3.412912	0.003045	0.180593	-1.59643	SCARNA6	8049299	-0.58049	7.170644	-3.06976	0.00651	0.387101	-2.22669
FBXO8	8103755	0.288246	8.017035	3.2517	0.004357	0.255766	-1.8874	#NV	7895405	0.316077	8.514197	3.41283	0.003045	0.180593	-1.59659	CNGA3	8043782	-0.24662	2.794546	-3.06622	0.006561	0.388499	-2.23294
BTRC	7929958	0.212251	6.812881	3.250274	0.004371	0.255766	-1.89007	PLLP	8001547	-0.71413	6.509745	-3.41246	0.003048	0.180593	-1.59732	FOXD4L2 /,	8161533	-0.24386	4.155832	-3.06615	0.006562	0.388499	-2.23306
MXRA5	8171172	0.528214	6.023649	3.250047	0.004373	0.255766	-1.8905	PIGN	8023605	-0.26786	6.527029	-3.41242	0.003048	0.180593	-1.5974	ZNF232	8011817	0.222841	4.254055	3.065672	0.006569	0.388499	-2.23391
CREB3	8155096	0.384289	6.848816	3.248185	0.004392	0.255766	-1.89398	#NV	7893664	0.318064	7.857374	3.411457	0.003055	0.180659	-1.59929	RNU2-1 ///	8019709	-0.34615	11.7336	-3.06439	0.006588	0.388499	-2.23617
#NV	7892955	-0.40084	8.276285	-3.24694	0.004404	0.255766	-1.89632	SCAMP1 //	8106479	-0.324	7.149089	-3.40887	0.003072	0.181166	-1.60439	#NV	7916775	0.561724	5.60255	3.06344	0.006601	0.388499	-2.23785
NKD1	7995525	-0.34926	5.595049	-3.24599	0.004413	0.255766	-1.89809	#NV	8103374	-0.34022	5.439529	-3.40861	0.003074	0.181166	-1.6049	C16orf80	8001658	0.29367	8.000634	3.063266	0.006604	0.388499	-2.23815
ZNF32	7933186	0.313965	5.886941	3.245617	0.004417	0.255766	-1.89879	#NV	7896481	-0.4258	8.453667	-3.40632	0.00309	0.181543	-1.60941	TMEM17	8052585	0.314347	4.151656	3.061907	0.006624	0.388973	-2.24055
ERAL1	8005994	0.296106	8.018051	3.245414	0.004419	0.255766	-1.89917	SLC27A4	8158224	0.356365	6.58562	3.405829	0.003093	0.181543	-1.61036	SNORD41	8034512	-0.37542	11.06296	-3.05909	0.006665	0.390692	-2.24552
KPNA2	8009417	0.685626	6.519137	3.24472	0.004425	0.255766	-1.90047	NMRK1	8161839	-0.48006	6.560298	-3.4053	0.003097	0.181543	-1.6114	CAPZA2	8135625	0.264474	7.435833	3.055612	0.006716	0.391605	-2.25166
FAM218A	8098167	-0.38381	3.104768	-3.24453	0.004427	0.255766	-1.90082	MARS	7956443	0.364888	7.324305	3.403796	0.003107	0.181814	-1.61436	KIAA0182	7997680	-0.31698	7.398038	-3.0548	0.006728	0.391605	-2.25309
HBA1 /// H	7991762	1.055426	9.143064	3.244289	0.00443	0.255766	-1.90128	ARF4	8088339	0.451408	9.316313	3.399065	0.00314	0.181814	-1.62366	#NV	8096077	0.303971	7.248785	3.05381	0.006742	0.391605	-2.25484
HBA1 /// H	7991766	1.055426	9.143064	3.244289	0.00443	0.255766	-1.90128	METAP1	8096556	-0.24105	8.117234	-3.3983	0.003146	0.181814	-1.62517	FOXD4L2 /,	8155661	-0.25323	4.540928	-3.05359	0.006746	0.391605	-2.25523
RBMS1	8056201	-0.50055	7.197228	-3.24405	0.004432	0.255766	-1.90172	SERINC1	8129317	-0.23482	9.877516	-3.39817	0.003146	0.181814	-1.62542	#NV	8133038	-0.45352	4.842986	-3.05159	0.006775	0.391605	-2.25875
KIAA2013	7999596	0.302659	8.101858	3.243941	0.004433	0.255766	-1.90193	MEIS2	7987385	-0.37109	6.327301	-3.39727	0.003153	0.181814	-1.6272	#NV	8133219	-0.29287	6.680596	-3.05151	0.006776	0.391605	-2.25889
SNORD13F	8076415	-0.6249	3.167876	-3.24378	0.004435	0.255766	-1.90223	NSUN6	7932433	-0.48079	8.774249	-3.39699	0.003155	0.181814	-1.62774	SRD5A3	8095139	0.355377	6.766799	3.049932	0.0068	0.391605	-2.26167
#NV	7892672	0.929083	4.712521	3.243456	0.004438	0.255766	-1.90284	RBL2	7995631	-0.34887	8.769675	-3.39597	0.003162	0.181814	-1.62975	OSBPL9	7901385	0.294719	9.139989	3.049727	0.006803	0.391605	-2.26204
CDH1	7996837	0.310571	9.661157	3.242968	0.004443	0.255766	-1.90375	#NV	8069508	0.628292	4.22454	3.395293	0.003167	0.181814	-1.63108	MLLT1	8033118	-0.31518	6.780507	-3.04534	0.006869	0.391605	-2.26976
ABCA8	8017885	-0.38125	8.734687	-3.24153	0.004457	0.255766	-1.90644	BHMT	8106504	-0.34957	11.62708	-3.39517	0.003168	0.181814	-1.63132	GAS6	7970329	-0.39609	6.48088	-3.04297	0.006905	0.391605	-2.27395
DNAJC10	8046759	0.35705	6.973048	3.241158	0.00446	0.255766	-1.90714	#NV	7894577	-0.50164	6.661841	-3.39473	0.003171	0.181814	-1.63219	SNORD53	8041168	-0.60468	8.724432	-3.04239	0.006913	0.391605	-2.27497
DSG2	8020779	0.38745	6.669836	3.241137	0.004461	0.255766	-1.90718	VSNL1	8040430	-0.66506	9.054273	-3.39469	0.003171	0.181814	-1.63228	ZNF787	8039569	-0.22487	5.552238	-3.04154	0.006926	0.391605	-2.27646
CYBASC3	7948565	0.258522	6.385857	3.239999	0.004472	0.255766	-1.90931	SGSM3	8073259	0.258793	5.580109	3.394452	0.003173	0.181814	-1.63273	C11orf55 /	7947528	0.252072	4.175994	3.040485	0.006942	0.391605	-2.27832
VCP	8160914	0.331874	9.196253	3.239959	0.004472	0.255766	-1.90938	#NV	8066459	-0.40797	3.465311	-3.39374	0.003178	0.181814	-1.63413	SYTL1	7899323	-0.25654	4.230756	-3.03992	0.006951	0.391605	-2.27932
P4HB	8019250	0.247063	11.66119	3.238636	0.004485	0.255766	-1.91186	#NV	7892677	-0.31993	8.961351	-3.3923	0.003188	0.181814	-1.63696	ADK	7928471	0.289399	8.780449	3.039241	0.006961	0.391605	-2.28052
FLJ42280 /	8141127	0.481628	4.819697	3.238032	0.004491	0.255766	-1.91299	#NV	7894872	-0.31993	8.961351	-3.3923	0.003188	0.181814	-1.63696	SEMA7A	7990345	-0.29209	3.698792	-3.03866	0.00697	0.391605	-2.28154
#NV	7896657	0.390688	10.01242	3.237888	0.004493	0.255766	-1.91326	MIR9-1	7921012	-0.19774	2.311933	-3.39217	0.003189	0.181814	-1.63722	SCO1	8012823	0.255999	7.335223	3.038596	0.006971	0.391605	-2.28165
DNAJB11	8084634	0.40969	7.303156	3.237816	0.004494	0.255766	-1.91339	#NV	8043502	-1.02285	4.972143	-3.39129	0.003195	0.18186	-1.63896	FIG4	8121429	0.27859	6.536402	3.038358	0.006975	0.391605	-2.28207
PEBP4	8149725	0.562803	4.490849	3.232183	0.00455	0.258101	-1.92393	GLYAT	7948344	-0.207	10.79139	-3.38999	0.003204	0.182076	-1.64151	#NV	7922266	-0.26024	3.656246	-3.03812	0.006978	0.391605	-2.28249
ATRX	8176276	0.330008	6.116809	3.230666	0.004565	0.258101	-1.92677	KIAA0825	8113103	-0.4257	6.466686	-3.38458	0.003243	0.183164	-1.65213	#NV	7894592	-0.27041	5.990023	-3.03699	0.006996	0.391605	-2.28449
#NV	7896142	0.268495	11.17338	3.229936	0.004573	0.258101	-1.92813	MLXIP	7959361	0.343612	7.990979	3.384471	0.003244	0.183164	-1.65235	MSI2	8008682	-0.21347	6.171259	-3.03399	0.007042	0.391605	-2.28977
SLC16A11	8012006	0.457188	5.137021	3.229511	0.004577	0.258101	-1.92893	FKBP7	8057045	-0.39495	5.440093	-3.38421	0.003246	0.183164	-1.65287	RN5S174	8098721	-0.26382	4.066222	-3.0335	0.007049	0.391605	-2.29063
PGAM1 ///	8173729	0.249246	8.592535	3.229107	0.004581	0.258101	-1.92968	GPR88	7903355	-0.83095	5.987051	-3.38363	0.00325	0.183164	-1.65401	#NV	7893244	-0.4946	8.044796	-3.03322	0.007054	0.391605	-2.29112
PGAM1 ///	8176282	0.249246	8.592535	3.229107	0.004581	0.258101	-1.92968	#NV	7894008	-0.94801	5.434613	-3.38345	0.003251	0.183164	-1.65435	NEUROG3	7934083	-0.36229	3.481784	-3.03318	0.007054	0.391605	-2.2912
MIR1304 /	7951034	-0.49565	8.779056	-3.22609	0.004612	0.258732	-1.93533	GPT	8148902	-0.37908	8.216095	-3.38135	0.003267	0.183164	-1.65848	STK32C	7937089	-0.24004	4.339462	-3.0325	0.007065	0.391605	-2.29239
MBTPS1	8003089	0.185552	8.793324	3.225487	0.004618	0.258732	-1.93645	SPATA7	7976084	-0.26562	5.704874	-3.38095	0.00327	0.183164	-1.65926	DDX52	8014574	0.283092	6.779457	3.030664	0.007093	0.391605	-2.29562
#NV	7894202	1.152798	4.041485	3.22502	0.004623	0.258732	-1.93733	#NV	7961420	-0.35231	2.68584	-3.37949	0.00328	0.183164	-1.66215	MCMDC2	8146738	0.3264	3.792424	3.029886	0.007105	0.391605	-2.29699
#NV	8031906	-0.25614	3.243694	-3.22496	0.004623	0.258732	-1.93745	FBXO8	8103755	0.299541	8.017035	3.379124	0.003283	0.183164	-1.66286	C4orf29	8097373	0.210839	7.410509	3.029489	0.007112	0.391605	-2.29769
SEZ6	8013833	-0.21281	3.072067	-3.22263	0.004647	0.259207	-1.9418	AHR	8131614	-0.55474	9.161654	-3.37904	0.003284	0.183164	-1.66302	OR6K2	7921420	-0.34483	2.887369	-3.02935	0.007114	0.391605	-2.29794
ANKRD18A	8161270	1.000599	4.533287	3.222612	0.004647	0.259207	-1.94183	ABAT	7993126	-0.24508	10.58837	-3.37833	0.003289	0.183164	-1.66443	POLR3F	8061171	0.262143	5.331353	3.028395	0.007129	0.391605	-2.29962
SNORD116	7981949	-0.40459	9.107871	-3.21906	0.004684	0.260492	-1.94847	PLCH2	7897089	0.281354	5.497971	3.377847	0.003292	0.183164	-1.66536	RNU1-11P	8116952	-0.79684	8.094578	-3.02825	0.007131	0.391605	-2.29987
L3MBTL3	8122013	-0.43968	6.489783	-3.21756	0.0047	0.260492	-1.95128	MYO16	7969995	-0.29165	4.595822	-3.37746	0.003295	0.183164	-1.66612	ABCB7	8173629	0.275294	7.627284	3.026547	0.007158	0.391605	-2.30287
#NV	7893570	-1.27096	3.655849	-3.21654	0.00471	0.260492	-1.95318	#NV	7893014	-0.99118	5.768281	-3.37599	0.003306	0.18335	-1.66902	TMEM106	8131539	0.266378	8.260252	3.025451	0.007175	0.391605	-2.3048
CHEK1	7945014	0.3771	3.644882	3.215462	0.004722	0.260492	-1.95519	RPS6KA4	7941039	0.221907	5.279667	3.375511	0.003309	0.18335	-1.66995	GSTM2 ///	7898375	-0.66278	12.76521	-3.02482	0.007185	0.391605	-2.30591
THAP4	8060274	-0.20081	6.873961	-3.21446	0.004732	0.260492	-1.95707	FANCL	8052382	-0.34005	6.971468	-3.37378	0.003322	0.183752	-1.67335	GSTM2 ///	7898411	-0.66278	12.76521	-3.02482	0.007185	0.391605	-2.30591
THAP4	8077250	-0.20081	6.873961	-3.21446	0.004732	0.260492	-1.95707	SLC25A47	7976755	0.759361	8.914823	3.372185	0.003334	0.183917	-1.67649	GSTM2 ///	7912800	-0.66278	12.76521	-3.02482	0.007185	0.391605	-2.30591
#NV	7929664	-0.4024	7.481821	-3.21397	0.004737	0.260492	-1.95799	ANKS1B	7965686	1.055466	3.689516	3.371593	0.003338	0.183917	-1.67765	GSTM2 ///	7912850	-0.66278	12.76521	-3.02482	0.007185	0.391605	-2.30591
IMPAD1	8150908	0.294113	6.968648	3.213727	0.00474	0.260492	-1.95844	#NV	7929256	-0.80495	5.524121	-3.37115	0.003342	0.183917	-1.67853	GSTM2 ///	7919576	-0.66278	12.76521	-3.02482	0.007185	0.391605	-2.30591
CPT2	7901549	0.407902	7.768224	3.213617	0.004741	0.260492	-1.95864	SCN8A	7955502	-0.3285	6.865818	-3.37038	0.003347	0.183926	-1.68003	HMGN5	8173812	0.25713	4.664188	3.024728	0.007186	0.391605	-2.30607
GANAB	7948744	0.200639	9.554833	3.212271	0.004755	0.260839	-1.96116	MBTPS2	8166382	-0.26359	7.039987	-3.36696	0.003373	0.184733	-1.68674	SNORD30	7948900	-0.34168	6.002005	-3.0212	0.007242	0.391605	-2.31228
JMY	8106516	0.242544	6.354398	3.211388	0.004764	0.260919	-1.96281	#NV	7902074	-0.52071	8.809007	-3.36694	0.003373	0.184733	-1.68679	#NV	7896646	-0.48878	7.303786	-3.02116	0.007243	0.391605	-2.31236
SPPL2A	7988753	0.288899	9.386558	3.209069	0.004789	0.261671	-1.96714	TACO1	8009176	0.296864	7.353521	3.366135	0.003379	0.184759	-1.68837	#NV	7892916	-0.23553	4.667249	-3.02043	0.007254	0.391605	-2.31364
SGK1	8129677	0.795798	5.760378	3.208603	0.004794	0.261671	-1.96801	#NV	7893517	0.425521	6.246273	3.363366	0.0034	0.184937	-1.6938	#NV	7892733	-1.10179	3.763998	-3.01924	0.007273	0.391605	-2.31573
SNORD115	7982056	-0.74191	4.455555	-3.2065	0.004816	0.262461	-1.97194	#NV	8053427	-0.69777	3.638847	-3.363	0.003403	0.184937	-1.69453	DYNC2H1	7943498	0.264733	2.880872	3.01912	0.007275	0.391605	-2.31594
ECHDC3	7926152	0.666838	8.210635	3.205397	0.004828	0.262672	-1.974	C4orf29	8097373	-0.23404	7.410509	-3.36287	0.003404	0.184937	-1.69477	#NV	7893799	0.482808	2.273959	3.018885	0.007279	0.391605	-2.31635
LINC00338	8010137	-0.40738	5.537922	-3.20387	0.004844	0.263131	-1.97685	SLCO2B1	7942569	-0.27513	10.2152	-3.36276	0.003405	0.184937	-1.69499	#NV	8111796	0.223841	8.410089	3.018788	0.00728	0.391605	-2.31652
#NV	8159957	-0.29182	3.843346	-3.2029	0.004855	0.263162	-1.97867	#NV	8101657	-0.47867	4.815527	-3.36193	0.003411	0.184979	-1.69663	ZNF692	7925773	-0.38738	6.79527	-3.01864	0.007283	0.391605	-2.31678
CTNS	8003824	0.372882	6.411246	3.202262	0.004862	0.263162	-1.97985	IRS1	8059470	-0.32048	7.282921	-3.35717	0.003447	0.186643	-1.70596	CACNA1F	8172580	-0.17842	3.146581	-3.01843	0.007286	0.391605	-2.31715
#NV	7893042	-0.46155	7.540633	-3.20161	0.004869	0.263162	-1.98107	#NV	7896599	0.308772	9.009603	3.35534	0.003461	0.187102	-1.70956	GDPD3	8000799	-0.33013	5.027165	-3.01833	0.007288	0.391605	-2.31733
RAB6A ///	8045136	0.237351	6.943707	3.200862	0.004877	0.26317	-1.98247	#NV	7926565	-0.20774	7.527675	-3.35087	0.003496	0.188648	-1.71832	C6orf225	8121547	0.304018	5.165437	3.016948	0.00731	0.391605	-2.31976
#NV	8167772	0.387772	2.946112	3.199807	0.004888	0.263358	-1.98444	STX5	7948864	0.293148	7.069446	3.349764	0.003505	0.188648	-1.7205	FAM75A1 ,	8156253	0.401328	2.772839	3.016556	0.007316	0.391605	-2.32045
GYS1	8038261	-0.27671	6.560436	-3.19722	0.004916	0.264439	-1.98926	TUBE1	8128977	-0.39088	6.767606	-3.34946	0.003507	0.188648	-1.7211	#NV	8156024	-0.29119	2.677357	-3.01652	0.007317	0.391605	-2.32051
LMO7	7969438	-0.23759	7.750996	-3.19487	0.004942	0.265392	-1.99366	SNORA

MAPK13	8119016	-0.33202	4.959889	-3.15241	0.005428	0.275304	-2.07282
ATP6V0D1	8002041	0.431088	8.410249	3.151593	0.005437	0.275304	-2.07434
GAS5 /// S	7922402	-0.41481	7.12261	-3.15126	0.005441	0.275304	-2.07495
SNORD116	7981998	-0.46689	6.320563	-3.15005	0.005456	0.275304	-2.07721
#NV	7896440	0.551463	3.873601	3.149952	0.005457	0.275304	-2.07739
#NV	7894722	-0.34176	7.896626	-3.14846	0.005475	0.275749	-2.08016
KPNA2	8019737	0.647791	6.277191	3.145526	0.005511	0.275749	-2.08563
SATB2	8058091	0.468456	6.549697	3.144566	0.005522	0.275749	-2.08742
CCDC96	8099242	-0.21715	3.117424	-3.14444	0.005524	0.275749	-2.08765
TMED2	7959597	0.305155	11.09629	3.144138	0.005527	0.275749	-2.08821
#NV	7894337	0.759623	4.607823	3.142586	0.005546	0.275749	-2.0911
USP5	7953483	0.269403	6.676857	3.142258	0.00555	0.275749	-2.09171
CTSD	7945666	0.24228	10.81515	3.140609	0.005571	0.275749	-2.09478
#NV	8180310	0.292511	7.239724	3.140489	0.005572	0.275749	-2.095
SNX29 ///	7994576	-0.4117	7.681582	-3.13939	0.005586	0.275749	-2.09705
#NV	7894778	0.680617	3.343797	3.138772	0.005593	0.275749	-2.0982
#NV	7895669	-0.50721	6.710496	-3.13826	0.005599	0.275749	-2.09915
MOB1B	8095566	0.299663	6.127361	3.138034	0.005602	0.275749	-2.09957
#NV	8056792	-0.68565	5.656849	-3.13801	0.005603	0.275749	-2.09961
#NV	7977734	0.267467	5.329044	3.138013	0.005603	0.275749	-2.09961
#NV	7895030	0.834372	4.010266	3.136856	0.005617	0.275749	-2.10176
#NV	7895097	0.834372	4.010266	3.136856	0.005617	0.275749	-2.10176
SACM1L	8079346	0.215836	7.940958	3.136717	0.005619	0.275749	-2.10202
ZBTB7A	8032755	-0.29924	6.651311	-3.13635	0.005623	0.275749	-2.1027
PPME1	7942503	0.274097	6.80072	3.13467	0.005644	0.276364	-2.10582
ESRRB	7975876	-0.22811	3.197919	-3.13363	0.005657	0.276593	-2.10776
GPC1	8049670	0.356543	5.880173	3.132354	0.005673	0.276597	-2.11013
LOC100506	7981992	-0.5794	4.494669	-3.13229	0.005674	0.276597	-2.11025
B9D1	8013331	0.235689	5.067793	3.130201	0.0057	0.277468	-2.11414
ZNRF3	8072160	-0.22662	6.854416	-3.1254	0.00576	0.27898	-2.12306
BCAT1	7961829	0.33268	3.18897	3.124528	0.005772	0.27898	-2.12468
#NV	7892816	-0.47219	7.820938	-3.12378	0.005781	0.27898	-2.12608
#NV	7896445	-0.42671	7.320236	-3.12304	0.00579	0.27898	-2.12744
TRANK1	8086125	-0.23579	6.96834	-3.12245	0.005798	0.27898	-2.12854
NR3C2	8103094	-0.2941	6.805903	-3.12243	0.005798	0.27898	-2.12858
NR1I3	7921840	-0.29433	9.534539	-3.12142	0.005811	0.27898	-2.13045
LGSN	8127380	-0.50799	5.249966	-3.12141	0.005811	0.27898	-2.13047
PDE7B	8122222	-0.44658	6.721057	-3.12089	0.005818	0.27898	-2.13144
LOC146880	8017671	-0.24968	6.432811	-3.12085	0.005818	0.27898	-2.13151
SNX29P1 /	7993825	-0.40201	7.565819	-3.12041	0.005824	0.27898	-2.13234
GAPDH	7953385	0.300356	11.78162	3.119533	0.005835	0.27898	-2.13396
#NV	8122174	-0.35508	5.540845	-3.11918	0.00584	0.27898	-2.13462
#NV	7895794	-0.37485	6.05455	-3.11789	0.005857	0.27898	-2.13702
ANAPC13	8090866	0.341846	6.61226	3.117398	0.005863	0.27898	-2.13793
HMGN2P1	8133900	0.210329	3.349435	3.117237	0.005865	0.27898	-2.13823
ZDHHC11	8110721	-0.42871	4.68942	-3.11501	0.005894	0.279111	-2.14236
ZC2HC1C	7975772	0.251593	4.507995	3.114952	0.005895	0.279111	-2.14247
B4GALNT4	7937341	-0.23803	3.904848	-3.11476	0.005897	0.279111	-2.14283
RAB42P1	7976158	-0.48213	5.088278	-3.11341	0.005915	0.279111	-2.14533
SLC6A17	7903854	-0.32474	2.887361	-3.11332	0.005916	0.279111	-2.1455
SLC25A20	8087224	0.414016	8.59766	3.113147	0.005918	0.279111	-2.14582
#NV	7920025	-0.31518	4.252094	-3.11215	0.005931	0.279328	-2.14767
PDIA3 /// I	7904881	0.278126	9.775006	3.111028	0.005946	0.279624	-2.14976
#NV	7892954	0.52823	8.465997	3.110024	0.005959	0.279847	-2.15162
NF2	8072242	0.331263	6.247384	3.10896	0.005973	0.280108	-2.1536
USO1	8095773	0.300192	9.059366	3.107505	0.005992	0.280566	-2.1563
SH3PXD2A	7936115	-0.51315	5.949986	-3.10694	0.005999	0.280566	-2.15735
RHOQ /// I	8045289	0.358861	7.180952	3.104535	0.006031	0.280959	-2.16181
SCNN1A	7960529	-0.31796	5.255104	-3.103	0.006052	0.280959	-2.16467
#NV	7894346	-0.36935	7.421908	-3.10279	0.006054	0.280959	-2.16505
#NV	7948397	-0.50425	4.258113	-3.10277	0.006055	0.280959	-2.1651
#NV	7896243	-0.36505	9.24837	-3.10217	0.006063	0.280959	-2.1662
PRKAA2	7901720	0.695429	5.929938	3.101248	0.006075	0.280959	-2.16791
PTGFRN	7904293	0.312227	6.121558	3.10108	0.006077	0.280959	-2.16822
TOE1	7901091	0.284245	6.537657	3.100731	0.006082	0.280959	-2.16887
#NV	8060835	0.201417	2.259615	3.100595	0.006084	0.280959	-2.16912
#NV	7896481	-0.3871	8.453667	-3.09668	0.006136	0.282712	-2.17638
#NV	8159846	0.228765	2.787804	3.096508	0.006139	0.282712	-2.17671
E2F8	7947110	0.297848	2.863657	3.094687	0.006163	0.282816	-2.18008
SNRNP27	8042495	0.303646	6.815668	3.094545	0.006165	0.282816	-2.18035
SAA2-SAA4	7946977	0.334896	10.86592	3.094368	0.006168	0.282816	-2.18067
SNHG1 ///	7948902	-0.2842	8.512975	-3.09368	0.006177	0.282816	-2.18195
ELOVL1	7915504	0.347964	7.799821	3.093207	0.006183	0.282816	-2.18283
ACSS3	7957386	0.424487	8.993029	3.089269	0.006237	0.284725	-2.19013
#NV	7924443	-0.251	3.826138	-3.0889	0.006242	0.284725	-2.19081
PLD6	8013068	-0.38088	5.310161	-3.08816	0.006252	0.284753	-2.19218
#NV	7893704	-0.63234	4.700999	-3.08699	0.006269	0.284753	-2.19435
#NV	7895240	-0.63234	4.700999	-3.08699	0.006269	0.284753	-2.19435
#NV	8096077	-0.30716	7.248785	-3.08586	0.006284	0.28507	-2.19644
PP13004	8132302	0.340468	2.880276	3.084803	0.006299	0.285145	-2.19841
ACTN4	8028524	0.198093	10.37834	3.083695	0.006314	0.285145	-2.20046
OLFM2	8033818	1.618309	8.642522	3.083434	0.006318	0.285145	-2.20095
ELL	8035477	-0.26047	5.719612	-3.08299	0.006324	0.285145	-2.20177
UHMK1	7906852	0.245857	7.849179	3.082508	0.006331	0.285145	-2.20266
#NV	7895941	0.761664	5.543909	3.081831	0.00634	0.285145	-2.20391
#NV	7902474	-0.44057	4.780723	-3.08143	0.006346	0.285145	-2.20467
LANCL2	8132897	0.3276	7.547357	3.080681	0.006356	0.285227	-2.20605
SPANXN5	8172800	-0.21517	2.762863	-3.08001	0.006365	0.285264	-2.20729
#NV	8101210	-0.28177	4.745451	-3.07847	0.006387	0.28563	-2.21014
ALDH18A1	7935230	0.579935	6.741766	3.078047	0.006393	0.28563	-2.21093
STT3B	8078360	0.204272	9.540885	3.076493	0.006415	0.28563	-2.2138
BBS4	7984686	0.224319	6.431662	3.076197	0.006419	0.28563	-2.21435
NF1	8006239	0.250628	8.506744	3.075865	0.006424	0.28563	-2.21497
#NV	8162998	-0.36815	3.321057	-3.07577	0.006425	0.28563	-2.21515
CD36	8133876	0.576292	7.885276	3.071759	0.006482	0.287221	-2.22257
LOC646214	7986603	0.365655	3.868381	3.071429	0.006487	0.287221	-2.22318
#NV	7959010	-0.39027	3.783518	-3.07051	0.0065	0.287221	-2.22489
DNAJC3	7969651	0.351712	7.827487	3.070384	0.006501	0.287221	-2.22512
#NV	7944021	-0.20686	2.25831	-3.07021	0.006504	0.287221	-2.22544
SNHG12 //	7914214	-0.44129	5.572051	-3.06604	0.006564	0.289152	-2.23316
MDGA1	8126102	-0.50261	4.397383	-3.06494	0.00658	0.289152	-2.2352
ALDOC	8013660	0.650618	8.730451	3.064546	0.006585	0.289152	-2.23592
TSPAN33	8136067	0.28877	7.501506	3.063524	0.0066	0.289152	-2.23781
#NV	8146468	-0.25967	2.438734	-3.06283	0.00661	0.289152	-2.23909
ANKRD45	7922382	-0.2018	2.245378	-3.06202	0.006622	0.289152	-2.2406
IFI27L1	7976436	0.275967	4.959416	3.06109	0.006636	0.289152	-2.24232
EBPL	7971615	-0.29219	10.03099	-3.06105	0.006636	0.289152	-2.24239
C10orf62	7929674	-0.65853	5.896426	-3.06082	0.006639	0.289152	-2.24282
PZP	7960984	1.60436	7.435919	3.060049	0.006651	0.289152	-2.24424
GPR89A //	7919251	-0.29948	7.512804	-3.06004	0.006651	0.289152	-2.24426
#NV	7904967	-0.35282	5.74298	-3.05996	0.006652	0.289152	-2.2444
RAD51AP1	7953218	0.317581	3.127734	3.058508	0.006673	0.289605	-2.2471
TEF	8073422	-0.31187	6.13659	-3.05788	0.006682	0.289605	-2.24825
#NV	8051773	-0.46912	5.623563	-3.05715	0.006693	0.289605	-2.24961
C9orf89	8156404	-0.20581	5.953064	-3.05663	0.006701	0.289605	-2.25056
EIF4E3	8088803	0.345334	6.285541	3.056103	0.006709	0.289605	-2.25154
FLJ33360	8110882	-0.58073	4.724979	-3.05569	0.006715	0.289605	-2.2523
ITGAM	7995096	0.312412	5.161658	3.05274	0.006758	0.290836	-2.25776
#NV	7894925	1.202183	3.570174	3.051315	0.006779	0.290836	-2.26039
PNPO	8008064	0.304967	9.485908	3.050256	0.006795	0.290836	-2.26235
#NV	7895026	-0.3621	7.710897	-3.0502	0.006796	0.290836	-2.26245
PP14571	8060101	-0.29076	3.45524	-3.0491	0.006812	0.290836	-2.26449
#NV	8096002	-0.34008	2.981007	-3.04903	0.006813	0.290836	-2.26462
PSMC4	8028756	0.398005	8.218446	3.04861	0.00682	0.290836	-2.2654
LAS1L	8173269	0.181223	6.993901	3.048348	0.006824	0.290836	-2.26588
TSNARE1	8153304	-0.21806	5.310221	-3.04803	0.006828	0.290836	-2.26647
C12orf49	7966738	0.301356	6.36028	3.047322	0.006839	0.290836	-2.26778
#NV	8160086	-0.25801	2.871433	-3.0469	0.006845	0.290836	-2.26855
#NV	8055204	-0.27859	2.950722	-3.0461	0.006857	0.290836	-2.27003
LMNB2	8032491	0.208874	5.547836	3.045804	0.006862	0.290836	-2.27058
#NV	7898607	-0.32345	3.99567	-3.0455	0.006866	0.290836	-2.27115
SNORA7B	8090565	-0.48021	8.37084	-3.04487	0.006876	0.290836	-2.2723

TTTY8 /// T	8177048	-0.26214	3.014861	-3.31213	0.003811	0.192201	-1.79427
CEBPG	8027566	0.276367	6.694736	3.310776	0.003822	0.192201	-1.79691
RNS5129	8078603	-0.45965	5.825695	-3.31009	0.003828	0.192201	-1.79825
TOM1L1	8008547	-0.30764	9.60584	-3.30919	0.003836	0.192201	-1.80002
STK3	8151967	-0.28514	7.536797	-3.30864	0.00384	0.192201	-1.8011
#NV	7895044	-0.78013	6.071428	-3.30851	0.003841	0.192201	-1.80135
TDRD3	7969341	-0.23101	6.419877	-3.30698	0.003854	0.192201	-1.80436
PIGV	7899244	-0.22634	8.366967	-3.3068	0.003856	0.192201	-1.8047
YWHAH	8072577	0.305852	7.111973	3.305391	0.003868	0.192201	-1.80746
BTF3P10	8122732	-0.24764	3.903648	-3.30521	0.00387	0.192201	-1.80781
#NV	7894299	-0.52572	6.556218	-3.30507	0.003871	0.192201	-1.80809
SNORD3A,	8005547	1.206449	8.463336	3.304559	0.003875	0.192201	-1.80909
SNORD3A,	8005553	1.206449	8.463336	3.304559	0.003875	0.192201	-1.80909
SNORD3A,	8013323	1.206449	8.463336	3.304559	0.003875	0.192201	-1.80909
SNORD3A,	8013325	1.206449	8.463336	3.304559	0.003875	0.192201	-1.80909
SNORD3A,	8013329	1.206449	8.463336	3.304559	0.003875	0.192201	-1.80909
F13B	7923073	-0.30367	9.891021	-3.30412	0.003879	0.192201	-1.80995
LOC150622	8040073	-0.50453	3.488377	-3.30149	0.003902	0.193037	-1.81509
FAM87A	7896756	-0.28066	3.501088	-3.29954	0.003919	0.193199	-1.81891
#NV	8159846	0.243759	2.787804	3.299467	0.003919	0.193199	-1.81905
CYP4F22	8026424	0.709022	6.576951	3.299111	0.003922	0.193199	-1.81975
#NV	7894432	-0.55714	6.874345	-3.29709	0.00394	0.193396	-1.8237
RNU5A-4P	7970945	0.19098	2.518858	3.296344	0.003947	0.193396	-1.82516
BACH1 ///	8068105	-0.27356	6.657053	-3.29605	0.003949	0.193396	-1.82574
NUDT4 ///	7919193	-0.57216	9.505572	-3.29429	0.003965	0.193396	-1.82919
GJA9 /// G	7915178	0.261234	2.556859	3.294156	0.003966	0.193396	-1.82944
TSPAN3	7990620	0.432382	7.828036	3.293832	0.003969	0.193396	-1.83008
#NV	7990564	-0.77942	5.372436	-3.2931	0.003975	0.193396	-1.83151
IPO5	7969703	-0.27654	8.440543	-3.29242	0.003981	0.193396	-1.83284
LSG1	8092905	0.251318	7.311427	3.291947	0.003985	0.193396	-1.83376
IRF7	7945462	0.426913	5.704007	3.291217	0.003992	0.193396	-1.83519
#NV	7892771	-0.37465	8.293798	-3.29017	0.004001	0.193396	-1.83724
CPNE8	7962250	-0.3156	7.242641	-3.28942	0.004008	0.193396	-1.8387
#NV	8099922	-0.59839	3.02086	-3.2881	0.004019	0.193396	-1.84128
INPP4A	8043791	0.266779	6.622767	3.287813	0.004022	0.193396	-1.84185
#NV	7892982	1.676236	4.009746	3.286931	0.00403	0.193396	-1.84358
#NV	7892555	-0.3142	6.879703	-3.28599	0.004038	0.193396	-1.84542
MIR30B	8153065	-0.36636	2.698938	-3.28583	0.00404	0.193396	-1.84572
KPNA2	8009417	0.694218	6.519137	3.285385	0.004044	0.193396	-1.8466
SEMA5A	8110932	-0.35431	7.538587	-3.28449	0.004052	0.193396	-1.84835
ZC3H6	8044450	-0.44411	6.883932	-3.28342	0.004061	0.193396	-1.85043
FGD4	7954729	-0.40225	8.201001	-3.2827	0.004068	0.193396	-1.85185
LINC00478	8067932	-0.34617	6.448521	-3.28233	0.004071	0.193396	-1.85256
SYT12	7941749	0.342867	3.984837	3.282123	0.004073	0.193396	-1.85297
#NV	7892838	-0.34727	8.025629	-3.28209	0.004073	0.193396	-1.85304
SNORD7	8006540	0.410218	3.807099	3.281778	0.004076	0.193396	-1.85365
#NV	8014861	-0.34264	2.761284	-3.28127	0.004081	0.193396	-1.85464
ITCH	8061986	-0.19257	8.992632	-3.28101	0.004083	0.193396	-1.85515
CLCN7	7998510	0.28279	6.754246	3.280146	0.004091	0.193493	-1.85684
C1orf95	7910142	0.213047	3.703662	3.27842	0.004107	0.193858	-1.86021
LPHN2	7902565	-0.30034	8.710238	-3.27802	0.00411	0.193858	-1.861
MYO1C	8011027	0.308924	7.621864	3.276176	0.004127	0.194083	-1.8646
RND1	7962884	-0.66102	6.709055	-3.27592	0.00413	0.194083	-1.86511
DNAH14	7910030	-0.35893	4.928663	-3.27558	0.004133	0.194083	-1.86576
#NV	7894930	0.716153	3.643689	3.273728	0.00415	0.194388	-1.86938
RNS5176	8104392	0.320489	2.611193	3.272892	0.004157	0.194388	-1.87102
#NV	8031680	-0.25128	1.959375	-3.27253	0.004161	0.194388	-1.87173
#NV	7960434	-0.23349	2.700687	-3.27234	0.004162	0.194388	-1.8721
SCARNA9L	8171758	-0.31266	3.568061	-3.2712	0.004173	0.194602	-1.87431
FAM83G	8013312	0.581107	5.108798	3.270503	0.004179	0.194602	-1.87569
RARB	8078286	-0.50254	5.386296	-3.26945	0.004189	0.194602	-1.87774
HSD3B7	7995007	0.32723	7.327184	3.269323	0.00419	0.194602	-1.87799
CABIN1	8071823	0.310902	6.597438	3.268253	0.0042	0.194793	-1.88008
RARS2	8128013	-0.24518	7.424255	-3.26677	0.004214	0.195161	-1.88297
MID1IP1	8166797	0.557325	6.758337	3.265841	0.004223	0.195294	-1.88479
THTPA	7973427	0.264877	6.464725	3.264861	0.004232	0.195447	-1.88671
#NV	7973873	-0.39039	4.379141	-3.26334	0.004246	0.195834	-1.88967
MIR205	7909422	-0.34889	3.151959	-3.26263	0.004253	0.195875	-1.89107
UBP1	8086057	0.242024	8.0647	3.261977	0.004259	0.195886	-1.89234
LPAL2	8130598	-0.34311	9.128438	-3.25797	0.004297	0.196709	-1.90015
COL5A3	8033825	0.397099	4.773696	3.257784	0.004299	0.196709	-1.90053
PDXDC2P	8002322	-0.34667	9.88427	-3.25777	0.004299	0.196709	-1.90055
SLC17A1	8124337	-0.41611	8.444473	-3.2576	0.004301	0.196709	-1.90088
#NV	7896353	-0.67592	2.894068	-3.25481	0.004328	0.197658	-1.90633
SLC16A11	8012006	0.460625	5.137021	3.253792	0.004337	0.197742	-1.90832
KRIT1	8140878	-0.17982	7.927214	-3.25299	0.004345	0.197742	-1.90989
GPR162	7953442	-0.43647	4.786119	-3.25277	0.004347	0.197742	-1.91032
CHPF	8059244	0.301952	6.514777	3.251527	0.004359	0.197831	-1.91274
G6PC	8007429	-0.67506	10.98642	-3.25042	0.00437	0.197831	-1.91489
#NV	7895276	0.22627	12.119	3.249512	0.004379	0.197831	-1.91667
TREM2	8126279	0.546415	4.005504	3.246906	0.004404	0.197831	-1.92176
#NV	7895094	-0.65399	6.952706	-3.24682	0.004405	0.197831	-1.92192
LASP1	8006820	0.329489	8.598236	3.246785	0.004405	0.197831	-1.92199
AAGAB	7989953	0.28385	5.384089	3.246329	0.00441	0.197831	-1.92288
ATP9A	8067055	0.366131	6.601767	3.245602	0.004417	0.197831	-1.9243
#NV	7896018	-0.64937	6.277334	-3.24557	0.004417	0.197831	-1.92437
KRT18	7955637	0.4353	8.336145	3.245364	0.004419	0.197831	-1.92477
LOC147727	8034097	-0.34334	5.192547	-3.24432	0.004429	0.197831	-1.92681
PDXK	8068919	0.360675	6.581362	3.244183	0.004431	0.197831	-1.92707
#NV	8146468	-0.27503	2.438734	-3.24393	0.004433	0.197831	-1.92756
KIAA0100	8013696	0.18169	8.084027	3.243672	0.004436	0.197831	-1.92807
TTC7B	7980720	0.459478	7.331794	3.243302	0.004439	0.197831	-1.92879
RNU11	7899502	0.585753	6.293086	3.242808	0.004444	0.197831	-1.92975
SDE2	7924686	0.261027	6.068893	3.240569	0.004466	0.198549	-1.93412
RNS5238	8142444	0.194218	2.135659	3.239575	0.004476	0.198722	-1.93606
GPX2	7979658	1.440453	9.136181	3.23874	0.004484	0.198823	-1.93768
#NV	7893381	-0.64816	2.771249	-3.23814	0.00449	0.198823	-1.93885
GRTP1	7972890	-0.31455	8.375193	-3.23512	0.004521	0.19962	-1.94475
MFSD8	8102730	-0.24294	7.645932	-3.23427	0.004529	0.19962	-1.9464
GPR52	7907531	-0.251	6.519381	-3.23418	0.00453	0.19962	-1.94657
DLG2	7950764	-0.41696	4.750972	-3.23393	0.004532	0.19962	-1.94707
YIF1A	7949577	0.271564	7.842476	3.233231	0.004539	0.19962	-1.94843
TBC1D10C	7941879	0.391099	4.940424	3.231999	0.004552	0.199689	-1.95083
DMRTA1	8154656	-0.36652	6.16259	-3.23024	0.00457	0.19971	-1.95427
PRRG1	8166705	-0.34427	6.227029	-3.22968	0.004575	0.19971	-1.95535
DNAJC19	8092314	-0.48832	6.28068	-3.22911	0.004581	0.19971	-1.95645
#NV	7893951	-0.82213	4.618223	-3.22897	0.004582	0.19971	-1.95673
#NV	7895299	0.288064	10.47345	3.228906	0.004583	0.19971	-1.95686
#NV	7894877	-0.59018	6.116928	-3.22793	0.004593	0.19971	-1.95877
IFT88	7967933	-0.37419	6.189677	-3.22757	0.004597	0.19971	-1.95947
HS3ST3B1	8005097	-0.3434	7.790115	-3.22701	0.004602	0.19971	-1.96055
#NV	7989144	-0.60321	4.048071	-3.22663	0.004606	0.19971	-1.9613
DPP6	8137485	-0.24933	3.225464	-3.22471	0.004626	0.200091	-1.96504
#NV	7894337	0.779446	4.607823	3.224592	0.004627	0.200091	-1.96526
CCDC38	7965589	-0.42117	3.586431	-3.22238	0.00465	0.200559	-1.96958
#NV	8133187	-0.38514	2.854617	-3.22213	0.004652	0.200559	-1.97005
NFYC	7900468	-0.24187	7.992293	-3.22178	0.004656	0.200559	-1.97074
DIO3OS	7981326	-0.55963	5.360552	-3.22046	0.00467	0.2006	-1.97332
GDPD5	7950501	0.337175	5.53717	3.22026	0.004672	0.2006	-1.9737
SNORA71C	8066260	0.347902	7.489241	3.219937	0.004675	0.2006	-1.97433
PRRG2	8030393	0.359917	4.024413	3.218526	0.00469	0.200969	-1.97708
AXIN1	8055486	-0.54678	7.331346	-3.21682	0.004707	0.201471	-1.98041
ABCB4	7998211	0.30033	5.402821	3.216022	0.004716	0.201567	-1.98196
FOPNL	7999718	-0.27561	6.939164	-3.2145	0.004732	0.201806	-1.98492
MAN2A2	7896040	-0.40618	6.95361	-3.21407	0.004736	0.201806	-1.98577
TMEM214	8040753	0.299196	8.158409	3.21342	0.004743	0.201806	-1.98702
ZNF174	7992897	0.260609	5.291092	3.213171	0.004746	0.201806	-1.98751
SLC2A10	8063177	0.519406	7.78173	3.212425	0.004753	0.201882	-1.98896
ABCB4	8140752	0.48603	9.691714	3.211135	0.004767	0.202171	-1.99147
MAN2A2	7986132	0.323508	8.585543	3.2105	0.004774	0.202171	-1.99271
EIF4A1 ///	8004508	0.362035	6.987881	3.210023	0.004779	0.202171	-1.99364
#NV	8088634	-0.37115	5.298716	-3.20948	0.004785	0.202171	-1.9947

#NV	7893924	-0.967	5.540027	-2.98495	0.007839	0.396569	-2.37597
LYPD4	8037061	-0.21387	2.967338	-2.98489	0.00784	0.396569	-2.37607
SYCP3	7965800	0.298687	3.872242	2.983946	0.007857	0.396569	-2.37774
RNU6ATAC	8112176	-0.5494	5.958171	-2.9827	0.007878	0.396569	-2.37993
CETN3	8113050	0.395746	4.171742	2.982314	0.007885	0.396569	-2.3806
#NV	7972932	-0.78459	3.855519	-2.98134	0.007901	0.396569	-2.3823
SNORA31	7971386	-0.48544	4.666009	-2.98073	0.007912	0.396569	-2.38339
SNORD32B	8117746	-0.32199	5.137442	-2.97925	0.007938	0.396569	-2.38598
SLC30A6	8041257	0.297067	8.02071	2.978469	0.007951	0.396569	-2.38734
LYRM2 ///	7999752	0.440306	7.816881	2.977946	0.00796	0.396569	-2.38826
ADAMTSL5	8032249	-0.257	4.681297	-2.97781	0.007963	0.396569	-2.3885
SNORD62A	8158862	-0.27956	4.481515	-2.97751	0.007968	0.396569	-2.38902
SNORD62A	8158864	-0.27956	4.481515	-2.97751	0.007968	0.396569	-2.38902
AGR3	8138392	0.223055	2.169035	2.976309	0.007989	0.397017	-2.39113
AMZ2	8009432	0.224204	7.669503	2.972462	0.008056	0.39951	-2.39788
THAP4	8060274	-0.18563	6.873961	-2.97139	0.008075	0.39951	-2.39975
THAP4	8077250	-0.18563	6.873961	-2.97139	0.008075	0.39951	-2.39975
PPP1R14C	8122734	-0.17573	3.625604	-2.96838	0.008128	0.400344	-2.40503
#NV	8048116	-0.34267	6.142786	-2.96778	0.008139	0.400344	-2.40608
C2orf

BCAP31	8175835	0.204295	8.073378	3.044408	0.006883	0.290836	-2.27316
TES	8135576	0.37804	6.60296	3.043671	0.006894	0.290938	-2.27452
LARP6	7990080	0.274289	5.375903	3.041564	0.006926	0.291579	-2.27842
DSCR3	8070269	0.315049	8.298268	3.041236	0.006931	0.291579	-2.27902
#NV	7893939	-0.47007	7.612077	-3.04094	0.006935	0.291579	-2.27958
TAF4B	8020702	-0.29705	2.752218	-3.0397	0.006954	0.291666	-2.28186
#NV	8139887	-0.28627	4.629469	-3.03965	0.006955	0.291666	-2.28195
TSSK3	7899790	-0.30149	4.159686	-3.0374	0.006989	0.292634	-2.28611
CRELD2	8073949	0.293487	6.114595	3.036989	0.006996	0.292634	-2.28686
SMARCAL1	8048175	0.18982	6.764521	3.035875	0.007013	0.29276	-2.28892
LINC00478	8067932	-0.32016	6.448521	-3.03565	0.007016	0.29276	-2.28934
PNO1	8042381	0.223837	4.969889	3.034769	0.00703	0.292811	-2.29097
RHBG	7906163	-1.15708	6.503403	-3.03443	0.007035	0.292811	-2.2916
FAM129B	8164217	0.370197	5.890549	3.032836	0.00706	0.293466	-2.29453
MIR205	7909422	-0.32424	3.151959	-3.03218	0.00707	0.293499	-2.29574
PSMD10	8174379	0.35652	7.543031	3.031648	0.007078	0.293499	-2.29673
MEIS2	7987385	-0.33102	6.327301	-3.03041	0.007097	0.293733	-2.299
COPS4	8096098	0.247112	6.350656	3.030147	0.007101	0.293733	-2.2995
ING5	8049906	-0.29913	5.727603	-3.02871	0.007124	0.294297	-2.30216
#NV	8140127	-0.24568	2.487985	-3.0264	0.00716	0.295421	-2.30641
CALR	8026106	0.292623	10.69075	3.025509	0.007174	0.295631	-2.30805
#NV	7894464	-0.46711	7.283079	-3.02412	0.007196	0.296165	-2.31062
KIF5B	7932911	0.234201	8.177614	3.020818	0.007248	0.297209	-2.31671
SNORD116	7982000	-0.5458	6.805184	-3.01987	0.007263	0.297209	-2.31846
PC	7949719	-0.30421	8.649778	-3.01923	0.007273	0.297209	-2.31963
#NV	8010285	-0.24146	4.055192	-3.01921	0.007274	0.297209	-2.31968
OTOP2	8009705	-0.27697	3.634727	-3.01905	0.007276	0.297209	-2.31996
#NV	7894725	0.249149	10.28339	3.018591	0.007283	0.297209	-2.32081
#NV	7893258	0.748988	7.158325	3.018579	0.007284	0.297209	-2.32084
PRR25	7992121	0.24733	3.458513	3.017264	0.007305	0.297701	-2.32326
SARDH	8164940	-0.30519	8.888085	-3.0163	0.00732	0.29783	-2.32504
#NV	7896686	-0.52291	3.313556	-3.01496	0.007342	0.29783	-2.3275
BLMH	8014008	-0.35712	6.123542	-3.01474	0.007345	0.29783	-2.32792
SNORD115	7982054	-0.3523	2.944708	-3.01415	0.007355	0.29783	-2.329
MAGI1	8088602	-0.22614	8.323196	-3.01346	0.007366	0.29783	-2.33027
#NV	7937508	0.525188	9.140524	3.013381	0.007367	0.29783	-2.33042
TMEM74	8152335	0.369259	3.71563	3.013168	0.00737	0.29783	-2.33081
#NV	7961602	-0.27919	4.11457	-3.01173	0.007394	0.29812	-2.33346
ZNF804A	8046815	0.254672	2.899832	3.011588	0.007396	0.29812	-2.33372
ABCG2	8101675	-0.43906	7.029523	-3.01079	0.007409	0.29812	-2.33519
#NV	8180286	0.30292	6.827515	3.010299	0.007417	0.29812	-2.3361
#NV	8154979	-0.38114	3.970477	-3.00996	0.007422	0.29812	-2.33673
#NV	8168727	-0.38364	4.941866	-3.00875	0.007442	0.298268	-2.33896
STIL	7915926	0.327639	4.035508	3.006938	0.007472	0.298268	-2.34229
#NV	7899251	-0.35822	3.592046	-3.00583	0.00749	0.298268	-2.34433
#NV	7892960	-0.41826	8.399444	-3.00578	0.007491	0.298268	-2.34443
P4HA1	7934278	-1.06095	6.409704	-3.00345	0.007529	0.298268	-2.34872
#NV	8057561	0.34154	3.75091	3.003383	0.00753	0.298268	-2.34884
ERO1L	7979179	0.341826	8.210079	3.003354	0.00753	0.298268	-2.34889
PHOX2A	7950136	-0.21844	3.307279	-3.00278	0.00754	0.298268	-2.34995
ATG13	7939676	0.269298	7.255028	3.001727	0.007557	0.298268	-2.35189
#NV	8006319	-0.51326	3.934372	-3.00111	0.007567	0.298268	-2.35303
#NV	7893437	0.56171	2.630102	3.000664	0.007575	0.298268	-2.35385
#NV	7893769	0.391675	6.471673	3.000219	0.007582	0.298268	-2.35466
SOCS7	8006768	-0.21805	5.297257	-3.0001	0.007584	0.298268	-2.35488
FAM206A	8157144	0.534542	6.296512	2.999112	0.007601	0.298268	-2.3567
PDIA3 /// I	7983274	0.282946	9.744511	2.997689	0.007624	0.298268	-2.35932
TSPAN11	7954653	0.382755	3.965714	2.997547	0.007627	0.298268	-2.35958
#NV	8133623	-0.32266	6.819962	-2.99735	0.00763	0.298268	-2.35994
#NV	8139975	-0.32266	6.819962	-2.99735	0.00763	0.298268	-2.35994
#NV	7895016	0.570313	8.797014	2.996167	0.00765	0.298268	-2.36212
SLC2A10	8063177	0.484304	7.78173	2.99533	0.007664	0.298268	-2.36366
SRPR	7952557	0.22827	10.11578	2.994732	0.007674	0.298268	-2.36476
#NV	8172086	-0.48743	5.281598	-2.99436	0.00768	0.298268	-2.36545
GPR89A //	7904930	-0.29794	7.537882	-2.99364	0.007692	0.298268	-2.36677
HEPACAM	7944911	-0.42593	3.556192	-2.9934	0.007696	0.298268	-2.36721
CLPB	7950142	0.333711	6.712096	2.993056	0.007702	0.298268	-2.36785
SCARNA10	7953383	-0.50741	8.093806	-2.99233	0.007714	0.298268	-2.36918
#NV	7966299	-0.51623	5.244008	-2.99131	0.007731	0.298268	-2.37105
ISCA1	8112331	0.433921	7.607662	2.991027	0.007736	0.298268	-2.37158
#NV	7892613	-0.39791	7.877745	-2.99051	0.007745	0.298268	-2.37253
GNB1	7911619	0.180812	10.09068	2.990475	0.007745	0.298268	-2.3726
TYMS	8019842	0.447345	5.729568	2.99041	0.007746	0.298268	-2.37272
FAM124A	7969192	-0.19951	3.750264	-2.98928	0.007766	0.298268	-2.3748
RPSA /// SI	8078918	-0.75741	6.100201	-2.98897	0.007771	0.298268	-2.37536
HCFC2	7958158	0.183891	6.646656	2.988583	0.007777	0.298268	-2.37608
#NV	8147564	-0.23244	2.70763	-2.98844	0.00778	0.298268	-2.37634
#NV	7894628	-0.46962	4.022041	-2.98796	0.007788	0.298268	-2.37722
KIF21A	7962274	0.213224	6.951391	2.987361	0.007798	0.298268	-2.37832
#NV	7922266	-0.25586	3.656246	-2.98696	0.007805	0.298268	-2.37907
#NV	8110461	-0.298	4.094522	-2.98679	0.007808	0.298268	-2.37937
#NV	7895440	-0.28993	9.685641	-2.98592	0.007823	0.298268	-2.38098
#NV	7895804	-0.51267	2.329117	-2.98546	0.007831	0.298268	-2.38183
LOC613261	8065084	-0.22874	3.123811	-2.98478	0.007842	0.298268	-2.38308
#NV	8146425	-0.28493	2.680085	-2.98448	0.007847	0.298268	-2.38362
#NV	8129069	0.52258	3.254458	2.984384	0.007849	0.298268	-2.3838
CDRT1 ///	8012931	-0.40328	4.192791	-2.98432	0.00785	0.298268	-2.38392
OR7E154P	8144496	-0.19601	4.736782	-2.98409	0.007854	0.298268	-2.38434
#NV	8089293	-0.32711	4.73461	-2.98358	0.007863	0.298268	-2.38528
UBE2H	8142886	0.199179	7.684572	2.983465	0.007865	0.298268	-2.38549
SNX33	7985016	-0.29851	7.02407	-2.98346	0.007865	0.298268	-2.38549
DKFZp686I	7939120	0.254102	7.743738	2.982767	0.007877	0.298381	-2.38677
PSMD2	8084423	0.278925	7.353764	2.981412	0.0079	0.298715	-2.38926
METTL4	8022009	0.305676	5.734791	2.981161	0.007905	0.298715	-2.38972
#NV	8069559	-0.16418	2.052381	-2.98019	0.007921	0.298715	-2.3915
YWHAH	8072577	0.27576	7.111973	2.980176	0.007922	0.298715	-2.39153
MLF1IP	8103932	0.494891	3.923723	2.979655	0.007931	0.298717	-2.39249
#NV	8091554	-0.50583	5.712586	-2.97902	0.007942	0.298793	-2.39366
SNORD115	7982068	-0.52226	2.726533	-2.97815	0.007957	0.29902	-2.39525
PREP	8128572	0.27308	5.825646	2.975997	0.007994	0.29923	-2.39921
PREB	8051012	0.252591	7.467153	2.975987	0.007994	0.29923	-2.39923
ZMYM3	8173457	-0.24728	7.006502	-2.97539	0.008005	0.29923	-2.40033
IKZF2	8058670	0.333121	4.904123	2.975247	0.008007	0.29923	-2.40059
GRIK3	7914974	-0.30862	3.454996	-2.97495	0.008013	0.29923	-2.40114
#NV	7892830	0.301689	10.32486	2.974742	0.008016	0.29923	-2.40152
EZH2	8143663	0.329745	5.055838	2.972176	0.008061	0.300403	-2.40623
PPP3CA	8101971	0.21035	7.664908	2.971038	0.008081	0.300403	-2.40832
POU3F3	8044109	-0.24524	4.040132	-2.97101	0.008082	0.300403	-2.40838
ASUN	7961964	0.209544	6.212789	2.970024	0.008099	0.300403	-2.41018
#NV	7995417	-0.28822	5.272265	-2.96975	0.008104	0.300403	-2.41069
#NV	7892763	-0.4961	6.933899	-2.96908	0.008116	0.300403	-2.41191
ABCE1	8097647	0.285486	6.286828	2.968305	0.00813	0.300403	-2.41334
RSU1	7932311	0.289184	8.001235	2.968278	0.00813	0.300403	-2.41339
TRNAE37P	8172711	-0.23094	2.35856	-2.96789	0.008137	0.300403	-2.4141
ACAD8	7945283	0.224072	7.674979	2.967441	0.008145	0.300403	-2.41493
#NV	8038343	-0.48337	6.476754	-2.96733	0.008147	0.300403	-2.41513
WWP2	7996976	0.202849	6.416709	2.963316	0.008218	0.3016	-2.4225
PLA2G12B	7934271	0.291919	8.09671	2.963094	0.008222	0.3016	-2.4229
#NV	8157103	-0.20517	2.845782	-2.96308	0.008223	0.3016	-2.42292
HDAC8	8173531	0.234094	7.241734	2.962731	0.008229	0.3016	-2.42357
MT1G	8001531	-0.24707	12.52928	-2.96263	0.008231	0.3016	-2.42375
ACTB /// L	8137979	0.23059	11.87195	2.962474	0.008234	0.3016	-2.42404
SNORD117	8124940	-0.2786	6.290723	-2.96141	0.008253	0.301655	-2.42599
MDH2	8133690	0.259023	10.1096	2.961382	0.008253	0.301655	-2.42605
ANKRD39	8053998	0.210341	7.003428	2.959356	0.00829	0.302059	-2.42976
PLEKHG4B	8104141	-0.17667	3.172446	-2.9593	0.008291	0.302059	-2.42987
#NV	8153835	-0.37587	5.363684	-2.95815	0.008312	0.302059	-2.43197
C11orf54	7943162	-0.34672	10.04705	-2.95656	0.00834	0.302059	-2.43489
OR4E2	7973296	-0.24178	2.55022	-2.9548	0.008373	0.302059	-2.43812
LYPD4	8037061	-0.2117	2.967338	-2.95454	0.008377	0.302059	-2.4386
SNORD115	7982046	-0.7371	5.479809	-2.95449	0.008378	0.302059	-2.43868
RN5S24	7967874	-0.20919	2.589575	-2.95448	0.008378	0.302059	-2.43871

#NV	8068214	-0.30732	2.925711	-3.20831	0.004797	0.20231	-1.99697
#NV	8013013	-0.3545	4.264162	-3.20797	0.004801	0.20231	-1.99763
NR3C2	8103094	-0.3021	6.805903	-3.20735	0.004807	0.20231	-1.99884
CCBL2	7917482	-0.34702	7.454054	-3.20688	0.004812	0.20231	-1.99976
SCARNA8	8160295	0.54645	4.997418	3.206068	0.004821	0.202417	-2.00133
EXTL3	8145624	0.250235	6.528482	3.20514	0.004831	0.202578	-2.00314
CA2	8147132	-0.28035	9.497634	-3.2041	0.004842	0.202787	-2.00516
ABCB11	8056583	-0.51	9.053634	-3.20281	0.004856	0.203112	-2.00767
TMTC1	7962058	-0.67304	5.676305	-3.2013	0.004872	0.203537	-2.01061
MFSD2A	7900365	1.198806	8.95738	3.198082	0.004907	0.204733	-2.01687
#NV	7895362	-0.53423	7.156963	-3.19664	0.004922	0.205129	-2.01967
#NV	7895714	-0.29146	10.34487	-3.196	0.004929	0.205164	-2.02092
ALG13	8169419	-0.30609	6.002038	-3.19183	0.004975	0.206807	-2.02904
ZNF585A	8036373	-0.35031	4.987811	-3.19125	0.004981	0.206811	-2.03015
MYO1B	8047127	-0.25503	10.09777	-3.18944	0.005001	0.207383	-2.03368
CDC6	8007071	0.685365	3.299927	3.188427	0.005013	0.207421	-2.03565
#NV	7902474	-0.45584	4.780723	-3.18823	0.005015	0.207421	-2.03603
#NV	7894039	-0.44583	6.254087	-3.18716	0.005027	0.207656	-2.03811
KIAA0564	7971246	-0.22812	8.941494	-3.18614	0.005038	0.207765	-2.04009
HEATR5B	8051464	-0.20625	7.868867	-3.1858	0.005042	0.207765	-2.04076
#NV	7896499	0.736532	5.242094	3.184862	0.005052	0.207765	-2.04257
CAMK2D	8102415	-0.27909	7.721468	-3.18435	0.005058	0.207765	-2.04357
#NV	8022247	0.232506	2.542032	3.184123	0.00506	0.207765	-2.04401
PPP1R14B	7949060	0.223871	7.511319	3.183355	0.005069	0.207861	-2.0455
FLJ13197	8099817	-0.49156	5.681908	-3.18276	0.005076	0.207879	-2.04666
C8orf46	8146703	-0.70543	6.663361	-3.18151	0.00509	0.207992	-2.04908
PIK3R2	8026954	0.404123	6.327187	3.181402	0.005091	0.207992	-2.0493
PDZD4	8175860	0.322229	3.529775	3.179582	0.005111	0.20833	-2.05283
#NV	7988410	-0.52592	4.037165	-3.17956	0.005112	0.20833	-2.05288
BBS2	8001507	-0.32259	6.616028	-3.17819	0.005127	0.208706	-2.05555
CES3	7996361	0.363123	8.286936	3.174822	0.005165	0.209826	-2.06208
POM121L9	8071877	0.359833	4.885839	3.174403	0.00517	0.209826	-2.06289
BCAT1	7961829	0.337959	3.18897	3.174105	0.005174	0.209826	-2.06347
RBM14	7941707	0.243256	6.986593	3.173337	0.005182	0.209927	-2.06496
MFN1	8084045	-0.21952	6.8485	-3.17038	0.005216	0.211048	-2.07071
#NV	7895908	1.001205	5.309846	3.168992	0.005232	0.211436	-2.0734
UPF1	8027074	0.207289	7.746149	3.168388	0.005239	0.211462	-2.07457
C4orf36 //,	8101616	-0.25212	3.257811	-3.16779	0.005246	0.211483	-2.07573
EGFR	8132860	-0.27413	8.705534	-3.16716	0.005254	0.211521	-2.07695
MYADML	8051422	0.225357	3.676816	3.165587	0.005272	0.212003	-2.08001
MCEE	8052934	-0.25874	6.021363	-3.16088	0.005327	0.212972	-2.08915
ZEB1	7926916	-0.30634	7.087143	-3.16073	0.005329	0.212972	-2.08944
CNOT6L	8101228	-0.28569	6.375201	-3.15983	0.005339	0.212972	-2.09118
PIGL	8005157	-0.28306	6.91097	-3.1596	0.005342	0.212972	-2.09162
#NV	8153835	-0.40144	5.363684	-3.15937	0.005345	0.212972	-2.09207
#NV	7893769	0.412452	6.471673	3.159371	0.005345	0.212972	-2.09207
CCND1	7942123	0.647451	8.049324	3.158709	0.005353	0.212972	-2.09336
GPR126	8122365	-0.30521	9.336868	-3.15793	0.005362	0.212972	-2.09487
#NV	7894475	-0.35758	7.98731	-3.15737	0.005368	0.212972	-2.09595
RN5S432	8003087	-0.44228	5.365948	-3.15722	0.00537	0.212972	-2.09624
SESTD1	8057394	-0.418	6.569705	-3.15666	0.005377	0.212972	-2.09733
SLC10A5	8151559	-0.50354	10.16512	-3.15497	0.005397	0.212972	-2.1006
#NV	7892765	-0.36582	7.886213	-3.15482	0.005399	0.212972	-2.1009
GTPBP8	8081676	-0.30447	5.969436	-3.15456	0.005402	0.212972	-2.1014
#NV	7894046	-0.58232	5.862522	-3.15454	0.005402	0.212972	-2.10144
CEPT1	7903908	-0.2308	8.556064	-3.15453	0.005402	0.212972	-2.10146
SEC61A2	7926189	-0.34543	6.569813	-3.15321	0.005418	0.212972	-2.10403
#NV	7894309	-0.40651	7.51479	-3.15276	0.005423	0.212972	-2.10488
#NV	8131441	-0.55949	4.045672	-3.15208	0.005431	0.212972	-2.10622
#NV	8067963	-0.54965	6.112385	-3.15191	0.005433	0.212972	-2.10654
ZBTB34	8157945	0.2881	5.929831	3.151862	0.005434	0.212972	-2.10663
CPSF6	7957008	-0.24289	7.380739	-3.1511	0.005443	0.212972	-2.1081
TEAD1	7938544	-0.33776	7.895404	-3.15057	0.00545	0.212972	-2.10914
#NV	7895116	-1.01514	5.371773	-3.15055	0.00545	0.212972	-2.10918
ALDH7A1	8113773	-0.2659	9.15152	-3.14971	0.00546	0.212972	-2.11081
AZGP1	8141374	-0.17211	11.8592	-3.1493	0.005465	0.212972	-2.11159
COL4A6	8174389	-0.176	2.96328	-3.14898	0.005469	0.212972	-2.11222
ZNF643	7900438	0.352504	3.884759	3.14836	0.005476	0.213014	-2.11342
#NV	8134429	-0.48968	7.458448	-3.14651	0.005499	0.213636	-2.11701
LOC100133	7991047	-0.32139	7.439476	-3.14321	0.005539	0.214869	-2.1234
ACMSD	8045368	-0.4775	8.738847	-3.14284	0.005543	0.214869	-2.12412
MUT	8126860	-0.26532	10.11272	-3.14215	0.005552	0.214948	-2.12546
ITGB1BP1	8050176	0.305813	6.112205	3.14093	0.005567	0.215275	-2.12782
MAT1A	7934755	-0.28181	11.54537	-3.13924	0.005587	0.215588	-2.1311
SLC3A2	7940717	-0.28452	8.028686	-3.13922	0.005588	0.215588	-2.13113
RN5S50	7917002	-0.60438	2.069475	-3.13788	0.005604	0.215977	-2.13374
UBASH3B	7944722	0.237978	4.300702	3.135622	0.005632	0.216308	-2.1381
UBR3	8046213	-0.2056	8.210763	-3.13545	0.005634	0.216308	-2.13843
FABP5 ///	7948420	0.470206	4.821726	3.135152	0.005638	0.216308	-2.13901
FAM19A2	7964631	-0.2884	3.46236	-3.13413	0.005651	0.216308	-2.14099
#NV	7995336	0.343059	5.119336	3.133446	0.005659	0.216308	-2.14232
#NV	8132992	0.351426	5.26709	3.132372	0.005673	0.216308	-2.1444
PAF1	8036720	0.258355	6.950704	3.131622	0.005682	0.216308	-2.14585
#NV	8129069	0.548126	3.254458	3.130278	0.005699	0.216308	-2.14845
SNORA10	7998664	0.746235	7.097855	3.129958	0.005703	0.216308	-2.14907
SNORA10	8041204	0.746235	7.097855	3.129958	0.005703	0.216308	-2.14907
BNIP2	7989323	-0.2293	7.531529	-3.1296	0.005707	0.216308	-2.14977
FAM227B	7988625	-0.32196	3.657798	-3.12866	0.005719	0.216308	-2.15158
C20orf20	8063949	0.274037	6.066444	3.128569	0.00572	0.216308	-2.15176
MT1IP	7995834	-0.3346	6.470458	-3.12856	0.00572	0.216308	-2.15177
RHOD	7941761	0.331068	7.966046	3.12823	0.005725	0.216308	-2.15242
ZFP14	8036304	-0.36085	4.552282	-3.12741	0.005735	0.216308	-2.15401
CFLAR	8047401	-0.28489	8.059827	-3.12691	0.005741	0.216308	-2.15496
#NV	7932304	-0.34167	1.858631	-3.1264	0.005748	0.216308	-2.15595
ZNF507	8027439	-0.26739	6.789153	-3.12631	0.005749	0.216308	-2.15613
MASTL	7926821	-0.32392	6.347725	-3.1258	0.005755	0.216308	-2.15712
ABCF2	8143905	0.27264	5.145456	3.125659	0.005757	0.216308	-2.15739
ADCY10	7922058	-0.70212	5.581022	-3.12547	0.00576	0.216308	-2.15775
STK11	8024204	0.2464	6.282088	3.12526	0.005762	0.216308	-2.15816
MMP15	7996185	0.337665	6.629335	3.124383	0.005773	0.216441	-2.15986
PPIE	7900354	-0.27074	6.233007	-3.12353	0.005784	0.216441	-2.1615
#NV	7892928	-0.28814	9.369852	-3.12345	0.005785	0.216441	-2.16167
RNF125	8020806	-0.49183	7.408915	-3.12223	0.005801	0.216536	-2.16402
NUP153	8124059	-0.21868	7.973872	-3.12179	0.005806	0.216536	-2.16488
#NV	7987066	-0.5088	6.999513	-3.12113	0.005815	0.216536	-2.16615
NANOG	7953675	-0.40217	5.333552	-3.12012	0.005828	0.216536	-2.1681
#NV	7894965	-0.60456	5.827922	-3.1185	0.005849	0.216536	-2.17125
KDELR3	8073015	0.830116	5.712231	3.117492	0.005862	0.216536	-2.17319
#NV	7893540	-0.2664	10.45922	-3.1174	0.005863	0.216536	-2.17338
SPAG9	8016745	-0.26703	8.702078	-3.11677	0.005871	0.216536	-2.1746
ZBTB44	7952739	-0.23342	8.354195	-3.11623	0.005878	0.216536	-2.17563
HIST2H2A(	7905088	-0.26197	7.136812	-3.11599	0.005881	0.216536	-2.1761
AIG1	8122396	-0.24073	9.299773	-3.11579	0.005884	0.216536	-2.17649
ATL2	8051589	-0.25991	7.494093	-3.11559	0.005886	0.216536	-2.17686
NAT9	8018209	0.33714	5.835748	3.115508	0.005887	0.216536	-2.17703
TNFRSF12A	7992789	0.521824	5.181793	3.115329	0.00589	0.216536	-2.17737
CALR	8026106	0.30124	10.69075	3.114608	0.005899	0.216536	-2.17877
SIRT5	8116956	-0.27466	7.412665	-3.11384	0.005909	0.216536	-2.18025
AKAP6	7973850	-0.35931	6.389069	-3.11278	0.005923	0.216536	-2.18231
GABRE ///	8175683	0.688924	3.192684	3.112345	0.005928	0.216536	-2.18314
#NV	8063240	0.299815	2.924156	3.112228	0.00593	0.216536	-2.18337
PRAMEF10	7898020	0.614506	3.727076	3.11148	0.00594	0.216536	-2.18482
PRAMEF10	7898034	0.614506	3.727076	3.11148	0.00594	0.216536	-2.18482
ABCA10	8009474	-0.23786	2.06419	-3.11066	0.005951	0.216536	-2.18641
PHLPP2	8002571	0.383348	6.160444	3.110098	0.005958	0.216536	-2.18749
SCN8A	7955533	-0.36871	5.795802	-3.10995	0.00596	0.216536	-2.18778
TRANK1	8086125	-0.23482	6.96834	-3.10968	0.005963	0.216536	-2.18829
#NV	7895328	0.27892	10.11631	3.108846	0.005974	0.216536	-2.18991
#NV	8093683	-0.31641	3.800667	-3.10795	0.005986	0.216536	-2.19165
N4BP2L2	7970907	-0.24327	9.046875	-3.10748	0.005992	0.216536	-2.19255
#NV	7896284	-0.81446	2.508744	-3.10693	0.006	0.216536	-2.1936

KBTBD11	8144317	-0.35643	4.619788	-2.88467	0.009752	0.410206	-2.5512
HERC5	8096361	0.534549	5.276742	2.884457	0.009756	0.410206	-2.55157
SLC30A3	8051050	-0.24671	4.002094	-2.88409	0.009764	0.410206	-2.55221
SLC35F5	8054771	0.190972	8.512474	2.883598	0.009774	0.410206	-2.55307
#NV	7892771	0.328349	8.293798	2.883537	0.009776	0.410206	-2.55317
GLCCI1	8131496	0.225889	7.042415	2.883248	0.009782	0.410206	-2.55368
TXNDC15	8108166	0.19576	6.750108	2.88247	0.009798	0.410382	-2.55503
#NV	8014749	-0.24288	6.251268	-2.88122	0.009825	0.410391	-2.5572
TSNAX ///	7910550	0.309312	6.327712	2.880871	0.009832	0.410391	-2.55781
ZP3	8133728	0.307109	3.636218	2.87947	0.009862	0.410391	-2.56025
CLEC1A	7961111	0.290238	3.166267	2.879246	0.009867	0.410391	-2.56064
MRPS33	8143433	0.345424	5.924479	2.878847	0.009876	0.410391	-2.56133
OR3A1	8011337	0.23604	2.824096	2.877786	0.009898	0.410391	-2.56317
SLC10A3	8176109	-0.28227	4.79957	-2.87759	0.009903	0.410391	-2.56352
MTTP	8096580	0.225257	10.22455	2.876544	0.009925	0.410391	-2.56533
ZNF219	7977646	-0.22074	5.109145	-2.87652	0.009926	0.410391	-2.56538
WASL	8142671	0.174948	8.296281	2.87573	0.009943	0.410391	-2.56675
#NV	7896458	-0.27047	11.14697	-2.87551	0.009947	0.410391	-2.56713
CDSN	8178442	-0.22292	4.067193	-2.87498	0.009959	0.410391	-2.56806
OR52E2	7946019	-0.20306	2.717515	-2.87495	0.009959	0.410391	-2.5681
PPP1R2	8092959	0.251327	7.099488	2.874406	0.009971	0.410391	-2.56905

YJEFN3	8027213	-0.2684	5.755457	-2.95433	0.008381	0.302059	-2.43898
#NV	7895362	-0.49364	7.156963	-2.95373	0.008392	0.302059	-2.44007
CMTM8	8078397	-0.28423	6.877245	-2.9536	0.008395	0.302059	-2.44033
ALG1	7993071	0.255953	7.002875	2.953524	0.008396	0.302059	-2.44046
CASP14	8026398	-0.23622	2.804139	-2.95336	0.008399	0.302059	-2.44075
PNPLA8	8142307	0.305584	6.530992	2.952822	0.008409	0.302059	-2.44175
HGD	8089851	-0.36239	11.26647	-2.95215	0.008421	0.302059	-2.44297
HGD	8093278	-0.36239	11.26647	-2.95215	0.008421	0.302059	-2.44297
LOC100506	7982084	-0.77853	7.778157	-2.95196	0.008425	0.302059	-2.44333
SIGMAR1	8160857	0.289066	9.028893	2.951793	0.008428	0.302059	-2.44363
ANAPC15	7950128	0.32106	6.837543	2.950267	0.008456	0.30274	-2.44643
SEC61A1	8082408	0.369119	9.851948	2.948073	0.008496	0.302776	-2.45045
LYRM2 ///	7999752	0.435795	7.816881	2.947434	0.008508	0.302776	-2.45162
DPYSL2	8145470	0.401392	7.958623	2.947246	0.008511	0.302776	-2.45197
CAMK2G	7934477	0.212471	7.633156	2.946843	0.008519	0.302776	-2.4527
#NV	7919160	0.397915	4.002433	2.946794	0.00852	0.302776	-2.45279
#NV	7919166	0.397915	4.002433	2.946794	0.00852	0.302776	-2.45279
#NV	7957536	-0.50474	5.81491	-2.94677	0.00852	0.302776	-2.45284
FBXO30	8130032	0.278422	7.151905	2.945118	0.008551	0.303544	-2.45587
#NV	7893514	-0.77113	5.215833	-2.94359	0.008579	0.303578	-2.45866
MAGEA4	8170531	-0.25569	2.187296	-2.9435	0.008581	0.303578	-2.45883
#NV	8109303	0.27456	2.384237	2.94283	0.008594	0.303578	-2.46006
#NV	7893253	-0.47782	4.560382	-2.94271	0.008596	0.303578	-2.46029
YWHAB	8062880	0.255716	8.731886	2.942626	0.008598	0.303578	-2.46043
HARS	8114628	0.255789	7.437574	2.940739	0.008633	0.303979	-2.46389
#NV	7893127	-0.97133	3.684063	-2.94057	0.008636	0.303979	-2.46419
CMAS	7954407	0.380451	7.329814	2.940561	0.008636	0.303979	-2.46421
#NV	7960898	-0.23984	5.024254	-2.9393	0.00866	0.304311	-2.46652
TRH	8082574	-0.21692	3.97469	-2.93909	0.008664	0.304311	-2.46691
AMPD3	7938396	0.374947	4.334543	2.936041	0.008722	0.306015	-2.47249
RIOK2	8113286	0.364581	5.832547	2.935107	0.008739	0.306315	-2.4742
#NV	7894680	-0.37898	6.867401	-2.934	0.008761	0.306422	-2.47622
#NV	7895839	0.768812	3.620343	2.93398	0.008761	0.306422	-2.47626
ECT2	8083941	0.30801	3.413455	2.933346	0.008773	0.306523	-2.47742
EXT2	7939524	0.234262	8.168396	2.932658	0.008786	0.30666	-2.47868
SIRT7	8019296	-0.26053	5.346043	-2.93182	0.008802	0.3069	-2.48022
SNX16	8151572	0.316114	3.778752	2.928941	0.008858	0.308271	-2.48548
#NV	7947127	-0.28018	2.70009	-2.92881	0.00886	0.308271	-2.48572
STK17A	8132503	0.344908	5.9214	2.927858	0.008878	0.308587	-2.48746
ANKH	8111101	0.227209	8.299628	2.925872	0.008917	0.3096	-2.4911
IP6K2	8087201	0.245284	7.070275	2.925302	0.008928	0.309661	-2.49214
HAND1	8115391	-0.23227	2.871245	-2.92467	0.00894	0.309761	-2.49328
RRP1B	8068902	0.285244	6.578573	2.923363	0.008966	0.310323	-2.49568
S100A16	7920291	0.289573	7.926678	2.922732	0.008978	0.310427	-2.49684
SNORD116	7981964	-0.32615	9.896313	-2.92091	0.009014	0.310945	-2.50017
PTPRU	7899562	0.462184	6.300673	2.920408	0.009023	0.310945	-2.50109
MYL3	8086689	-0.3181	3.902738	-2.9196	0.009039	0.310945	-2.50257
RNPEP	7908779	0.290682	7.953021	2.919434	0.009043	0.310945	-2.50286
PEX3	8122409	0.306834	6.789429	2.919259	0.009046	0.310945	-2.50319
#NV	7928489	-0.3928	8.569571	-2.91904	0.00905	0.310945	-2.50358
C8orf17	8148463	-0.29182	2.810498	-2.91854	0.00906	0.310945	-2.50451
SLC27A4	8158224	0.305314	6.58562	2.91793	0.009072	0.310945	-2.50561
PRSS8	8001007	0.600937	5.983997	2.917232	0.009086	0.310945	-2.50689
ZNF141	8093336	-0.19867	7.486013	-2.91699	0.009091	0.310945	-2.50734
#NV	8176566	-0.3514	10.27739	-2.91622	0.009106	0.310945	-2.50875
SWSAP1	8025888	-0.19432	5.179986	-2.91586	0.009113	0.310945	-2.5094
CHD1L	7904883	0.391279	6.484175	2.915797	0.009114	0.310945	-2.50951
HIST1H3A	8124531	0.442369	6.145969	2.915172	0.009127	0.311049	-2.51065
C19orf53	8026193	0.193828	8.312879	2.913452	0.009161	0.311581	-2.5138
#NV	7895143	-0.53766	5.896012	-2.91345	0.009161	0.311581	-2.51381
#NV	7894745	-0.52277	2.45211	-2.91282	0.009174	0.311677	-2.51495
#NV	8143984	-0.28408	3.428084	-2.91166	0.009197	0.311677	-2.51707
ZWILCH	7984330	0.301709	5.800686	2.910901	0.009212	0.311677	-2.51845
ABCB4	8140752	0.440577	9.691714	2.910837	0.009213	0.311677	-2.51857
SETDB2	7969114	-0.30594	6.143921	-2.91083	0.009213	0.311677	-2.51858
KIF11	7929258	0.264627	3.107165	2.909909	0.009232	0.311677	-2.52027
GLG1	8002729	0.175052	9.008862	2.909823	0.009234	0.311677	-2.52042
#NV	8172195	-0.74116	2.807894	-2.90844	0.009261	0.311677	-2.52294
#NV	7943191	0.317387	2.699462	2.908179	0.009267	0.311677	-2.52343
#NV	7893122	0.502744	6.2204	2.907942	0.009271	0.311677	-2.52386
FAM92B	8003193	-0.21544	4.409615	-2.9077	0.009276	0.311677	-2.52431
RELT	7942439	-0.25078	4.711066	-2.9067	0.009296	0.311789	-2.52613
SRD5A3	8095139	0.338677	6.766799	2.906603	0.009298	0.311789	-2.5263
#NV	7893140	-0.45623	9.818822	-2.90573	0.009316	0.311803	-2.52789
CTH	7902290	-0.45117	8.715336	-2.90566	0.009317	0.311803	-2.52803
ARMCX3	8168875	0.369574	5.384419	2.903969	0.009352	0.311875	-2.53111
CANX	8110522	0.196542	11.2521	2.903018	0.009371	0.311875	-2.53284
#NV	7894495	-0.45129	5.438057	-2.90243	0.009383	0.311875	-2.53393
#NV	8130565	-0.33678	7.749154	-2.90206	0.009391	0.311875	-2.53459
MRPS11	7985757	0.322868	8.640028	2.901983	0.009392	0.311875	-2.53473
MSI1	7967039	-0.22891	3.826797	-2.90196	0.009393	0.311875	-2.53478
SLC46A3	7970793	0.34739	9.269362	2.901875	0.009394	0.311875	-2.53493
ASNA1	8026024	0.23337	7.766489	2.901671	0.009398	0.311875	-2.5353
FURIN	7986092	0.306739	9.083367	2.901403	0.009404	0.311875	-2.53579
LYRM2	8128133	0.278922	6.466735	2.900733	0.009418	0.312019	-2.53701
OR51A9P	7945989	-0.30144	2.864427	-2.89914	0.00945	0.312487	-2.53992
#NV	8112611	-0.24851	2.859159	-2.89913	0.009451	0.312487	-2.53994
MUL1	7913242	0.395011	5.333505	2.898031	0.009473	0.312742	-2.54194
NAA30	7974576	0.237715	6.463645	2.897836	0.009477	0.312742	-2.5423
RNU4-10P	7969424	-0.21688	2.181471	-2.89634	0.009508	0.31319	-2.54503
#NV	7895934	-0.27959	7.694657	-2.89626	0.009509	0.31319	-2.54516
#NV	7894718	-0.4833	3.954245	-2.89335	0.00957	0.314477	-2.55047
#NV	7893212	-0.50887	5.251789	-2.89263	0.009585	0.314477	-2.5518
OR13C4	8162929	-0.63213	3.879374	-2.89164	0.009605	0.314477	-2.5536
SNAPIN	7905598	0.265463	6.872577	2.891516	0.009608	0.314477	-2.55382
#NV	7896589	0.584836	2.412332	2.891287	0.009613	0.314477	-2.55424
RAB5A	8078214	0.287727	7.855019	2.89125	0.009613	0.314477	-2.55431
EXOG	8078818	0.296359	4.381174	2.891053	0.009618	0.314477	-2.55467
#NV	7896044	0.262714	10.41966	2.890742	0.009624	0.314477	-2.55523
FLJ36840	8144228	-0.42818	9.331996	-2.88939	0.009652	0.314716	-2.5577
FAM53B	7936884	0.243898	5.631897	2.889323	0.009654	0.314716	-2.55782
ZNF512B	8067773	-0.26717	6.061276	-2.88832	0.009675	0.314716	-2.55965
C2orf57	8049079	-0.21929	3.06434	-2.88812	0.009679	0.314716	-2.56001
LIG3	8006479	0.21311	6.586922	2.887373	0.009695	0.314716	-2.56137
NFATC3	7996744	-0.19561	8.25136	-2.88726	0.009697	0.314716	-2.56158
DYNC2H1	7943498	0.253123	2.880872	2.886712	0.009709	0.314716	-2.56257
#NV	7894007	-0.35012	9.790364	-2.88582	0.009727	0.314716	-2.5642
#NV	7896282	-0.35012	9.790364	-2.88582	0.009727	0.314716	-2.5642
#NV	7892582	-0.49668	2.562391	-2.88562	0.009732	0.314716	-2.56456
#NV	7893806	0.630588	4.685291	2.884634	0.009752	0.314716	-2.56636
#NV	7982152	-0.34465	4.530812	-2.8841	0.009764	0.314716	-2.56733
#NV	7986661	-0.34465	4.530812	-2.8841	0.009764	0.314716	-2.56733
#NV	7986943	-0.34465	4.530812	-2.8841	0.009764	0.314716	-2.56733
#NV	8094499	-0.44694	4.843109	-2.88335	0.00978	0.314792	-2.5687
FAIM	8083000	0.390101	3.341682	2.883002	0.009787	0.314792	-2.56933
CNDP2	8021727	0.251546	8.988741	2.882653	0.009794	0.314792	-2.56997
#NV	7892860	0.49088	2.974389	2.881414	0.009821	0.315163	-2.57222
TSPAN3	7990620	0.378219	7.828036	2.88122	0.009825	0.315163	-2.57258
RAN	7959882	0.269107	6.343609	2.880249	0.009846	0.315523	-2.57435
FATE1	8170513	-0.27116	2.954607	-2.87832	0.009887	0.316538	-2.57785
PPP2R4	8158523	0.200613	6.762566	2.877382	0.009907	0.316544	-2.57956
#NV	8034871	-0.43624	5.696409	-2.87721	0.009911	0.316544	-2.57987
LRRC59	8016708	0.341827	8.355017	2.876987	0.009915	0.316544	-2.58028
#NV	8163424	-0.4229	5.74387	-2.87586	0.00994	0.317012	-2.58233
FAM118B	7945058	0.329262	6.571296	2.874823	0.009962	0.317423	-2.58422
RGS14	8110327	-0.22885	6.341352	-2.87434	0.009972	0.317451	-2.5851
GRB7	8006940	-0.4159	5.710032	-2.87369	0.009987	0.317595	-2.58628

ZCCHC8	7967287	-0.25138	6.962385	-3.10611	0.00601	0.216536	-2.19519
BAZ2B	8056060	-0.27611	7.572145	-3.10611	0.00601	0.216536	-2.1952
STX4	7995017	0.248874	7.160396	3.105966	0.006012	0.216536	-2.19547
FNIP1	8113914	-0.21522	7.699603	-3.10545	0.006019	0.216536	-2.19647
MOGAT3	8141676	0.768303	6.861926	3.105305	0.006021	0.216536	-2.19675
#NV	7895440	-0.30152	9.685641	-3.10524	0.006022	0.216536	-2.19688
GCN1L1	7966938	0.214235	7.483828	3.10329	0.006048	0.216958	-2.20064
#NV	7904693	-0.40739	7.095903	-3.10289	0.006053	0.216958	-2.20141
#NV	7892782	-0.31428	10.56344	-3.10288	0.006053	0.216958	-2.20143
#NV	8156339	-0.28856	2.678131	-3.10107	0.006077	0.217474	-2.20494
#NV	7894282	0.171672	10.50796	3.100102	0.00609	0.217474	-2.2068
#NV	8145685	-0.68109	5.673704	-3.09986	0.006094	0.217474	-2.20728
NANOG	7987365	-0.38988	5.408491	-3.09943	0.006099	0.217474	-2.2081
TBC1D22B	8119169	0.226757	6.079057	3.099365	0.0061	0.217474	-2.20822
FAM59A	8022803	-0.33917	6.676395	-3.09887	0.006107	0.217477	-2.20918
TTC40	7937112	-0.24897	3.071979	-3.09712	0.00613	0.218083	-2.21256
#NV	7892615	0.668639	4.648823	3.094673	0.006164	0.21878	-2.21728
FABP5 ///	8147049	0.45551	4.702001	3.094142	0.006171	0.21878	-2.21831
DSG1	8020724	-0.55945	7.367165	-3.09332	0.006182	0.21878	-2.21989
#NV	7893570	-1.22218	3.655849	-3.09308	0.006185	0.21878	-2.22035
CENPC1	8100603	-0.30749	7.388889	-3.0928	0.006189	0.21878	-2.22089
#NV	7892898	-0.54023	5.566705	-3.09262	0.006191	0.21878	-2.22125
ODF2	8158269	0.248124	6.52066	3.092282	0.006196	0.21878	-2.2219
FAM160A1	8097801	-0.54243	6.684559	-3.09146	0.006207	0.218828	-2.22348
VIPR2	8144213	-0.56076	3.356046	-3.09094	0.006214	0.218828	-2.22449
#NV	7895917	-0.41714	8.445625	-3.09018	0.006225	0.218828	-2.22595
ZNF347	8039054	-0.35151	4.678369	-3.09005	0.006226	0.218828	-2.2262
CYP2C19	7929478	-1.10367	10.15104	-3.08875	0.006244	0.218828	-2.22872
#NV	7892879	0.571824	2.809583	3.088601	0.006246	0.218828	-2.229
MYD88	8078729	0.283731	7.589438	3.088368	0.00625	0.218828	-2.22945
PHF7	8080306	-0.27427	5.651098	-3.08834	0.00625	0.218828	-2.22951
#NV	8014749	0.259973	6.251268	3.083939	0.006311	0.220304	-2.238
#NV	8020352	0.414091	2.987098	3.083304	0.00632	0.220304	-2.23922
GATSL3	8075322	-0.29318	5.439917	-3.08307	0.006323	0.220304	-2.23968
RBM14-RB	7941709	0.242605	7.579698	3.082976	0.006324	0.220304	-2.23986
PAN3	7968274	-0.25231	7.856845	-3.08265	0.006329	0.220304	-2.24049
#NV	7952225	0.254565	2.503027	3.082421	0.006332	0.220304	-2.24093
#NV	7893949	-0.39162	8.669278	-3.08015	0.006364	0.221176	-2.24531
BHLHE40	8077441	0.458876	8.201148	3.079344	0.006375	0.221304	-2.24686
GPR89A //	7904853	-0.35501	7.058676	-3.07894	0.006381	0.221304	-2.24765
OCLM	7908347	-0.52496	5.933311	-3.0784	0.006388	0.221335	-2.24868
MT1P2	7925413	-0.31891	6.335336	-3.07772	0.006398	0.221435	-2.24999
#NV	8096331	-0.28065	5.401794	-3.07604	0.006421	0.22202	-2.25323
SPSB1	7897449	0.566254	5.363221	3.075454	0.00643	0.22202	-2.25436
SMARCA1	8174985	-0.21522	8.937246	-3.07483	0.006438	0.22202	-2.25556
#NV	7893705	-0.55665	7.411078	-3.07463	0.006441	0.22202	-2.25595
#NV	7892903	-0.63179	6.364589	-3.07234	0.006474	0.222644	-2.26037
#NV	7895178	-0.34309	6.61515	-3.07158	0.006484	0.222644	-2.26183
SLCO4A1	8063923	0.367973	3.809293	3.070777	0.006496	0.222644	-2.26337
#NV	7895576	-0.78061	6.233863	-3.07057	0.006499	0.222644	-2.26378
CAMK1D	7926223	0.410176	7.271769	3.069733	0.006511	0.222644	-2.26538
#NV	7907462	-0.238	2.760083	-3.06874	0.006525	0.222644	-2.26731
MYOT	8108256	-0.41326	3.604505	-3.06729	0.006546	0.222644	-2.2701
MSI2	8008682	0.2158	6.171259	3.067175	0.006547	0.222644	-2.27031
RBBP6	7994161	-0.20666	7.714326	-3.06693	0.006551	0.222644	-2.27078
#NV	7896294	0.647248	5.012014	3.066914	0.006551	0.222644	-2.27082
SPRYD3	7963577	0.30545	5.952943	3.066406	0.006559	0.222644	-2.27179
CDH15	7997880	0.947715	4.010485	3.06546	0.006572	0.222644	-2.27362
#NV	7895919	-0.49965	8.591146	-3.06477	0.006582	0.222644	-2.27495
TBC1D23	8081256	-0.22044	7.570864	-3.06466	0.006584	0.222644	-2.27515
SPP1	8096301	1.037331	6.763019	3.064418	0.006587	0.222644	-2.27562
#NV	7894428	0.306579	7.292115	3.063641	0.006598	0.222644	-2.27712
#NV	7893838	-0.33467	10.49834	-3.06278	0.006611	0.222644	-2.27878
BAAT	8162870	-0.33887	11.68716	-3.06243	0.006616	0.222644	-2.27945
MIR17HG ,	7969576	-0.35303	4.930316	-3.06208	0.006621	0.222644	-2.28012
ANKS4B	7993815	-0.26179	7.375469	-3.06156	0.006629	0.222644	-2.28113
KTN1	7974483	-0.19973	7.80791	-3.06016	0.006649	0.222644	-2.28382
#NV	7893220	-0.45596	7.8246	-3.05992	0.006653	0.222644	-2.28428
NT5C2	7936064	-0.2221	7.890414	-3.05906	0.006665	0.222644	-2.28594
NR1I3	7921840	-0.28844	9.534539	-3.05897	0.006667	0.222644	-2.28612
ZNF701	8030950	-0.50506	4.098223	-3.05833	0.006676	0.222644	-2.28734
C6orf48 //	8118322	0.425271	5.684627	3.058227	0.006677	0.222644	-2.28754
ALMS1P	8042761	-0.43869	5.767113	-3.0582	0.006678	0.222644	-2.28759
#NV	8156024	0.295171	2.677357	3.05778	0.006684	0.222644	-2.2884
#NV	8152819	-0.40442	4.161926	-3.05776	0.006684	0.222644	-2.28844
#NV	8145134	-0.42208	5.843339	-3.05742	0.006689	0.222644	-2.2891
ADCY6	7962842	0.327264	6.717172	3.056629	0.006701	0.222644	-2.29062
TMBIM1	8058927	0.284072	9.914981	3.056188	0.006707	0.222644	-2.29147
ZBTB7C	8023212	-0.24966	4.769101	-3.05611	0.006708	0.222644	-2.29162
#NV	7892613	-0.4066	7.877745	-3.05579	0.006713	0.222644	-2.29223
#NV	8104650	-0.28831	2.371015	-3.05574	0.006714	0.222644	-2.29234
KCTD5	7992685	0.288245	6.039442	3.055732	0.006714	0.222644	-2.29234
CD300E	8018189	0.241406	4.165635	3.055607	0.006716	0.222644	-2.29259
CD52	7899160	0.619845	6.165411	3.055424	0.006719	0.222644	-2.29294
#NV	7892816	-0.46184	7.820938	-3.05532	0.00672	0.222644	-2.29313
#NV	8083320	-0.334	2.355104	-3.05378	0.006743	0.223178	-2.29611
ANGEL2	7924190	-0.19951	6.575069	-3.05296	0.006755	0.22329	-2.29768
THEM4	7920114	-0.2862	7.122946	-3.05264	0.00676	0.22329	-2.29829
CCBP2	8079117	-0.46791	6.601235	-3.05138	0.006778	0.223687	-2.30071
DPH5	7903389	-0.32821	5.462619	-3.04962	0.006805	0.224333	-2.30411
SDF2L1	8071559	0.412887	5.655453	3.04755	0.006836	0.225129	-2.30808
#NV	7894352	-0.8909	5.186781	-3.04615	0.006857	0.2256	-2.31079
#NV	7895209	-0.42163	7.450477	-3.04483	0.006877	0.225709	-2.31332
BTBD8	7902965	-0.59041	4.424185	-3.04476	0.006878	0.225709	-2.31346
#NV	7892681	0.580354	5.86443	3.044185	0.006886	0.225709	-2.31456
LINC00461	8113037	-0.15073	1.869676	-3.04413	0.006887	0.225709	-2.31467
B4GALNT2	8008172	0.277278	3.165723	3.043127	0.006902	0.225903	-2.31659
FBXO38	8109062	-0.25912	7.7357	-3.04284	0.006907	0.225903	-2.31715
FRRS1	7917954	-0.28968	9.523327	-3.03937	0.006959	0.227405	-2.32381
DNAI1	8154892	-0.19945	3.386546	-3.03829	0.006976	0.227577	-2.32589
#NV	8133189	-0.21229	2.876041	-3.03705	0.006995	0.227577	-2.32827
DRAP1	7941460	0.23218	7.842976	3.036512	0.007003	0.227577	-2.3293
SLC22A7	8119782	0.366928	10.69375	3.036346	0.007006	0.227577	-2.32962
#NV	7892717	0.436868	4.088921	3.036119	0.007009	0.227577	-2.33006
#NV	7894353	-0.64316	3.433787	-3.03588	0.007013	0.227577	-2.33053
DBT	7918008	-0.3394	8.553105	-3.03551	0.007018	0.227577	-2.33123
GLTPD2	8003948	0.270428	6.419413	3.035455	0.007019	0.227577	-2.33133
#NV	7893816	0.407324	9.528342	3.034383	0.007036	0.227685	-2.33339
TAF13	7918284	0.335368	5.652431	3.034299	0.007037	0.227685	-2.33355
PLEKHA5	7954245	-0.20637	7.681683	-3.03323	0.007054	0.227685	-2.3356
OR13C4	8162929	-0.66306	3.879374	-3.03316	0.007055	0.227685	-2.33574
ZBTB2	8130185	-0.31022	5.530726	-3.03248	0.007065	0.227685	-2.33705
DCAF6	7907104	-0.20191	9.451202	-3.03216	0.00707	0.227685	-2.33766
LARGE	8075637	-0.30676	7.690622	-3.03214	0.00707	0.227685	-2.3377
FABP4	8151532	1.057801	5.152042	3.030961	0.007089	0.227963	-2.33996
#NV	7893140	-0.47583	9.818822	-3.03054	0.007095	0.227963	-2.34078
PRF1	7934161	0.540085	5.142982	3.02994	0.007105	0.227963	-2.34193
#NV	7892531	0.490744	5.513448	3.029819	0.007107	0.227963	-2.34216
SNORD15A	7942592	0.431778	6.031489	3.02891	0.007121	0.228185	-2.3439
RNS565	7907049	0.417682	3.1056	3.028495	0.007127	0.228185	-2.3447
SERTAD3	8036908	0.494415	4.324	3.027328	0.007145	0.22855	-2.34694
FBXW5	8165319	0.251322	8.414978	3.025513	0.007174	0.22924	-2.35042
#NV	7894624	-0.4603	6.126476	-3.02336	0.007208	0.230101	-2.35455
USP51	8173174	-0.26159	4.016111	-3.02286	0.007216	0.230133	-2.35551
#NV	7934154	-0.45707	5.383326	-3.02098	0.007245	0.230466	-2.35911
#NV	8131335	-0.2698	2.196459	-3.02072	0.00725	0.230466	-2.35963
PRSS8	8001007	0.622249	5.983997	3.020695	0.00725	0.230466	-2.35967
NUP43	8130129	-0.20195	7.626831	-3.01988	0.007263	0.230466	-2.36123
OR13C3	8162931	-0.72991	4.779331	-3.01978	0.007264	0.230466	-2.36143
C1orf122	7900192	0.302157	5.182256	3.018932	0.007278	0.230466	-2.36305
42257	8054467	-0.22649	6.913773	-3.01885	0.007279	0.230466	-2.36321
NET1	7925954	-0.24943	8.046858	-3.01788	0.007295	0.230466	-2.36508

UNC119B	7959212	0.271538	5.853134	3.017763	0.007297	0.230466	-2.3653
ANXA5	8102619	0.440955	8.602816	3.017684	0.007298	0.230466	-2.36545
FLJ45079	8018818	-0.19834	2.652971	-3.01741	0.007302	0.230466	-2.36596
#NV	8161737	-0.41852	5.533029	-3.01681	0.007312	0.230553	-2.36713
RN7SKP1	7971075	0.223446	2.095273	3.01572	0.007329	0.230792	-2.36921
#NV	7939374	-0.27255	7.378743	-3.01479	0.007344	0.230792	-2.371
#NV	8091885	-0.20406	2.180667	-3.01439	0.007351	0.230792	-2.37177
POLG	7991258	0.185785	6.155726	3.014324	0.007352	0.230792	-2.37189
PION	8140478	-0.33051	8.163154	-3.01418	0.007354	0.230792	-2.37217
#NV	7895332	-0.70258	4.538412	-3.01178	0.007393	0.231771	-2.37676
#NV	7994570	-0.56296	5.000217	-3.01138	0.007399	0.231771	-2.37753
#NV	7896240	0.344506	8.223079	3.008551	0.007445	0.232529	-2.38296
#NV	7894830	0.457978	6.198987	3.00816	0.007452	0.232529	-2.38371
#NV	8180390	0.291174	6.47678	3.007125	0.007468	0.232529	-2.38569
#NV	7933929	-0.50924	3.076398	-3.00705	0.00747	0.232529	-2.38584
ZMYND12	7915425	-0.3323	5.449726	-3.00674	0.007475	0.232529	-2.38643
RAP2B	8083457	0.309155	6.187474	3.00653	0.007478	0.232529	-2.38683
PLGLA ///	8044149	-0.19427	8.861755	-3.00646	0.007479	0.232529	-2.38696
DNMT1	8033912	0.332735	6.150795	3.005696	0.007492	0.232529	-2.38843
#NV	7894570	-1.27523	3.582526	-3.00555	0.007494	0.232529	-2.3887
HMCN1	7908204	0.596872	6.992084	3.005469	0.007496	0.232529	-2.38886
RRS1	8146685	0.241013	5.206216	3.004029	0.007519	0.232529	-2.39162
ZNF141	8093336	-0.20456	7.486013	-3.00334	0.007531	0.232529	-2.39295
ARHGAP5	7973840	-0.1981	7.515647	-3.00284	0.007539	0.232529	-2.3939
TAOK2	7994692	0.176734	6.968891	3.002821	0.007539	0.232529	-2.39394
SLCO1A2	7961626	-1.0064	5.43882	-3.0019	0.007554	0.232529	-2.39569
XAGE-4	8173176	0.41287	3.749163	3.00189	0.007554	0.232529	-2.39572
GABRE ///	8175666	0.813462	6.186229	3.001709	0.007557	0.232529	-2.39607
PRAMEF10	7912561	0.611151	3.728909	3.001538	0.00756	0.232529	-2.39639
#NV	7893922	-0.40827	7.50106	-3.00135	0.007563	0.232529	-2.39675
MTOR	7912412	0.241495	8.130458	3.000942	0.00757	0.232529	-2.39753
KPNA2	8019737	0.617831	6.277191	3.000047	0.007585	0.232529	-2.39925
DSG3	8020762	0.208135	2.495803	2.999458	0.007595	0.232529	-2.40038
MTMR4	8017019	-0.22548	9.430489	-2.9993	0.007597	0.232529	-2.40067
FEM1A	8024898	0.47294	4.523553	2.99913	0.0076	0.232529	-2.401
SNORD115	7982070	-0.68782	5.035176	-2.99821	0.007615	0.232529	-2.40276
#NV	8180206	-0.20473	6.152655	-2.99597	0.007653	0.232529	-2.40705
EFCAB4B	7960381	-0.39822	5.697534	-2.99542	0.007662	0.232529	-2.40811
#NV	7894731	-0.45875	5.50091	-2.99498	0.007669	0.232529	-2.40895
#NV	7894935	-0.45875	5.50091	-2.99498	0.007669	0.232529	-2.40895
#NV	7894918	-1.13749	3.296845	-2.99482	0.007672	0.232529	-2.40925
#NV	7896214	-1.13749	3.296845	-2.99482	0.007672	0.232529	-2.40925
KCND1	8172493	0.304287	4.454913	2.994804	0.007672	0.232529	-2.40929
#NV	8106816	-0.45288	4.81318	-2.99466	0.007675	0.232529	-2.40956
#NV	8019910	0.223319	2.772244	2.994353	0.00768	0.232529	-2.41015
C6orf25	8179313	0.234193	4.341404	2.993644	0.007692	0.232529	-2.41151
TRAF7	7992529	0.235243	7.001472	2.993617	0.007692	0.232529	-2.41156
POLR3B	7958275	-0.25203	6.763283	-2.99358	0.007693	0.232529	-2.41163
LRRC58	8089830	-0.21969	7.340514	-2.99311	0.007701	0.232529	-2.41253
FOXP2	8135544	-0.35369	6.138001	-2.99303	0.007702	0.232529	-2.41269
#NV	8115677	-0.17097	1.997033	-2.993	0.007703	0.232529	-2.41274
FKBP1B	8040530	0.391574	5.974593	2.992541	0.00771	0.23255	-2.41362
HSF4	7996430	0.387515	6.144565	2.990736	0.007741	0.233258	-2.41707
SNORA55	7915227	0.51745	6.174885	2.989041	0.00777	0.233912	-2.42031
#NV	7996805	-0.58733	4.021186	-2.98861	0.007777	0.233919	-2.42113
ZCCHC11	7916185	-0.20944	7.388787	-2.98735	0.007798	0.234352	-2.42354
SNORD115	7982060	-0.35235	2.314553	-2.98677	0.007808	0.234439	-2.42466
NADK	7911600	0.333842	7.345943	2.986293	0.007816	0.234473	-2.42557
LOC10065	8007976	-0.22174	8.420021	-2.98354	0.007864	0.235677	-2.43085
CBR4	8103622	-0.35242	7.791335	-2.98288	0.007875	0.235801	-2.43209
GNB2	8134890	0.199344	7.65133	2.981068	0.007906	0.236314	-2.43556
PARK2	8130645	-0.33065	5.709999	-2.98071	0.007912	0.236314	-2.43624
ZNF808	8030946	-0.38931	7.617566	-2.98065	0.007913	0.236314	-2.43635
CCT3	7920984	0.258736	8.212432	2.980077	0.007923	0.2364	-2.43746
METTL20	7954701	-0.37336	5.634403	-2.9788	0.007945	0.236846	-2.43989
SNORA57	7940667	0.701546	7.113458	2.977346	0.007971	0.237388	-2.44268
#NV	8078497	-0.32684	3.559217	-2.97515	0.008009	0.238132	-2.44687
UBXN7	8093112	-0.21736	7.901647	-2.97509	0.00801	0.238132	-2.44698
TSSK3	7899790	-0.29505	4.159686	-2.97248	0.008056	0.239097	-2.45197
RN7SKP8	7972442	-0.26166	3.604323	-2.97226	0.00806	0.239097	-2.4524
PTPN4	8044849	-0.22254	6.009865	-2.97192	0.008066	0.239097	-2.45304
RPL10 ///	8170863	0.251577	9.14646	2.970668	0.008088	0.239097	-2.45543
#NV	7893491	-0.33949	9.205566	-2.97059	0.008089	0.239097	-2.45558
FAM185A	8140461	-0.30315	7.217166	-2.97052	0.00809	0.239097	-2.45572
LRRC40	7916910	-0.30848	6.957444	-2.96877	0.008121	0.239097	-2.45906
HIST1H4A	7961483	0.324184	4.865743	2.968734	0.008122	0.239097	-2.45913
NAP1L2	8173600	0.218913	2.844046	2.968559	0.008125	0.239097	-2.45946
SFXN2	7930148	-0.35586	7.99519	-2.96813	0.008133	0.239097	-2.46029
#NV	8056823	0.245862	2.38667	2.967769	0.008139	0.239097	-2.46097
FOXN3	7980680	-0.26707	8.655795	-2.96773	0.00814	0.239097	-2.46105
WASL	8142671	-0.18054	8.296281	-2.96759	0.008142	0.239097	-2.4613
#NV	8078384	-0.18553	1.896241	-2.96733	0.008147	0.239097	-2.46181
CDH26	8063761	-0.29528	3.701782	-2.96713	0.00815	0.239097	-2.46218
SLC26A6	8087119	0.32062	5.460669	2.966742	0.008157	0.239097	-2.46293
#NV	7895946	-0.50904	7.921987	-2.96615	0.008168	0.239196	-2.46406
DNAJB11	8084634	0.375172	7.303156	2.965014	0.008188	0.239404	-2.46623
PI4K2A	7929677	0.38164	6.27656	2.964945	0.008189	0.239404	-2.46636
ATPBD4	7987369	-0.31537	6.574893	-2.96419	0.008203	0.239586	-2.4678
#NV	7894828	-0.39505	1.946143	-2.96334	0.008218	0.239703	-2.46941
#NV	7895538	-0.54485	6.970315	-2.9631	0.008222	0.239703	-2.46987
SNORD115	7982088	-0.64573	2.378537	-2.96277	0.008228	0.239703	-2.47052
#NV	7893726	-0.38708	5.876254	-2.96212	0.00824	0.239788	-2.47175
CYP2A13	8028973	-0.37882	11.32222	-2.96147	0.008252	0.239788	-2.47298
WEE1	7938348	-0.22523	6.215707	-2.9614	0.008253	0.239788	-2.47312
NEK8	8005959	0.248009	4.662067	2.959735	0.008283	0.240183	-2.4763
PHC3	8092035	-0.22408	9.176166	-2.95948	0.008288	0.240183	-2.47679
PCBP1	8042515	0.243942	8.701592	2.959447	0.008288	0.240183	-2.47685
GAPDHP27	7919049	-0.30346	3.821864	-2.95809	0.008313	0.240391	-2.47944
ZNF254	8027368	-0.36974	7.018581	-2.95775	0.008319	0.240391	-2.4801
ACTB /// L	8137979	0.230186	11.87195	2.957288	0.008327	0.240391	-2.48097
ENPP1	8122099	-0.24109	10.23621	-2.9569	0.008334	0.240391	-2.48171
#NV	7894960	-0.42093	8.598866	-2.95676	0.008337	0.240391	-2.48197
NLRP14	7938195	-0.4215	3.91463	-2.95648	0.008342	0.240391	-2.48251
#NV	8058693	0.24631	2.480082	2.955877	0.008353	0.240391	-2.48366
HTR5A	8137517	0.237726	3.536764	2.955866	0.008353	0.240391	-2.48368
ESRRB	7975876	-0.21498	3.197919	-2.95325	0.008401	0.24062	-2.48866
TTLL8 /// T	8076882	0.182343	3.414379	2.953238	0.008401	0.24062	-2.48869
#NV	7924551	-0.28454	6.69429	-2.95307	0.008404	0.24062	-2.48901
#NV	7925523	-0.28454	6.69429	-2.95307	0.008404	0.24062	-2.48901
#NV	8132690	-0.28454	6.69429	-2.95307	0.008404	0.24062	-2.48901
KLKB1	8098654	-0.1803	11.15619	-2.95274	0.00841	0.24062	-2.48964
ZFHX4	8147000	-0.30066	7.894217	-2.95242	0.008416	0.24062	-2.49025
TOR1AIP2	7922637	-0.25763	8.749988	-2.95223	0.00842	0.24062	-2.49061
BOP1	8153664	0.224467	5.875129	2.950276	0.008455	0.24062	-2.49434
TRIM16 //,	8005475	-0.26304	6.669353	-2.95009	0.008459	0.24062	-2.49469
#NV	7895084	0.398042	8.067585	2.950013	0.00846	0.24062	-2.49484
ZC2HC1C	7975772	0.238226	4.507995	2.949464	0.00847	0.24062	-2.49589
LRIG3	7964602	-0.29302	7.373761	-2.94933	0.008473	0.24062	-2.49614
CCDC144A	8013479	-0.55623	5.851612	-2.94874	0.008484	0.24062	-2.49727
ABCF1	8117929	0.271885	7.379436	2.948736	0.008484	0.24062	-2.49727
ABCF1	8177797	0.271885	7.379436	2.948736	0.008484	0.24062	-2.49727
ABCF1	8179112	0.271885	7.379436	2.948736	0.008484	0.24062	-2.49727
FAM50A	8170906	0.229289	7.246598	2.947948	0.008498	0.240829	-2.49877
PDIA6	8050278	0.267431	9.661318	2.946811	0.00852	0.241221	-2.50094
SFT2D3 ///	8055060	-0.25994	8.129226	-2.94473	0.008558	0.242109	-2.5049
#NV	8085784	-0.20383	2.528109	-2.94324	0.008586	0.242652	-2.50774
#NV	7895846	0.510482	8.983312	2.942821	0.008594	0.242652	-2.50854
LOC10050	8084215	0.646383	5.281896	2.942537	0.008599	0.242652	-2.50908
#NV	7895430	0.465013	3.364373	2.941635	0.008616	0.242844	-2.5108
ORC3	8121043	-0.27442	7.235293	-2.94139	0.008621	0.242844	-2.51126
RAB13	7963986	-0.22911	7.146948	-2.94062	0.008635	0.242844	-2.51273
CHST9	8022666	0.897644	6.354968	2.940616	0.008635	0.242844	-2.51274

SCN2A	8046020	-0.2749	3.106751	-2.94023	0.008643	0.242844	-2.51347
OSGEPL1	8057689	-0.28987	5.867877	-2.93822	0.00868	0.243411	-2.5173
FAM59B	8040632	0.225455	4.233627	2.937642	0.008691	0.243411	-2.5184
SH3D19	8103166	-0.21009	8.057231	-2.93757	0.008693	0.243411	-2.51855
#NV	7893123	-0.47516	6.978402	-2.93695	0.008705	0.243411	-2.51972
EGFL7	8159354	0.251081	5.713925	2.936301	0.008717	0.243411	-2.52095
#NV	7901852	-0.38066	4.977944	-2.9363	0.008717	0.243411	-2.52096
#NV	7895990	-0.62808	5.208603	-2.93583	0.008726	0.243411	-2.52185
TNAP	7971159	-0.3247	3.000595	-2.93562	0.00873	0.243411	-2.52226
VKORC1	8000998	0.482209	10.52004	2.935332	0.008735	0.243411	-2.5228
LOC100501	8056426	-0.38092	6.547488	-2.9353	0.008736	0.243411	-2.52286
#NV	8070755	-0.26868	2.553565	-2.93485	0.008744	0.243445	-2.52371
ARF1 /// M	7910229	0.215399	10.01941	2.93291	0.008781	0.244202	-2.52741
MYO9B	8026638	0.249351	7.325513	2.932209	0.008795	0.244202	-2.52874
EIF2AK3	8053668	0.351567	6.457683	2.931659	0.008805	0.244202	-2.52979
DCUN1D1	8092321	-0.3324	8.28249	-2.93112	0.008816	0.244202	-2.5308
#NV	7942912	-0.45417	5.924706	-2.93083	0.008821	0.244202	-2.53137
SND1	8135876	0.292915	8.846291	2.930052	0.008836	0.244202	-2.53284
#NV	7917050	-0.46008	6.908174	-2.92963	0.008844	0.244202	-2.53364
FBXL14	7960280	-0.29843	5.311185	-2.92963	0.008844	0.244202	-2.53365
C7orf49 //,	8143065	0.298132	6.760068	2.928792	0.00886	0.244202	-2.53524
PIK3C2G	7954208	-0.30056	8.528425	-2.92841	0.008868	0.244202	-2.53597
KAT8	7995055	0.145857	6.663424	2.928384	0.008868	0.244202	-2.53602
#NV	8068733	0.245901	2.246958	2.928333	0.008869	0.244202	-2.53611
SPTSSA	7978553	0.600858	5.626497	2.927672	0.008882	0.244202	-2.53737
#NV	7894613	-0.3602	10.2024	-2.92745	0.008886	0.244202	-2.53779
PLEKHO2	7984217	0.252693	5.938278	2.927242	0.00889	0.244202	-2.53819
WIPI1	8017850	0.381355	7.612754	2.926884	0.008897	0.244202	-2.53887
PXDC1	8123678	0.466264	8.799164	2.926563	0.008903	0.244202	-2.53948
PTPRK	8129418	-0.19244	8.365974	-2.92656	0.008904	0.244202	-2.53948
MLLT4	8123407	-0.20937	8.249173	-2.92578	0.008919	0.244229	-2.54097
CARD11	8137874	0.249322	4.480979	2.925495	0.008924	0.244229	-2.54151
#NV	7896251	0.794494	4.759009	2.925376	0.008927	0.244229	-2.54173
GPC5	7969596	-0.50951	5.075856	-2.92378	0.008958	0.24475	-2.54476
KCTD15	8027584	0.382804	5.863564	2.923641	0.00896	0.24475	-2.54503
#NV	8090934	-0.27974	5.520329	-2.92212	0.00899	0.245358	-2.54792
#NV	7982292	-0.20058	2.259445	-2.9202	0.009028	0.246186	-2.55158
RFC5	7959052	-0.26089	7.010704	-2.9179	0.009073	0.246404	-2.55593
#NV	7982533	-0.22201	2.603546	-2.91781	0.009075	0.246404	-2.55612
FPGS	8158123	-0.23646	7.047735	-2.91753	0.00908	0.246404	-2.55664
RSL24D1P3	8021374	-0.28442	2.88504	-2.91711	0.009088	0.246404	-2.55745
#NV	8097947	-0.22511	2.718974	-2.91692	0.009092	0.246404	-2.55781
#NV	8123340	-0.24103	3.806681	-2.91599	0.009111	0.246404	-2.55956
RANGAP1	8076307	0.269766	7.04126	2.915409	0.009122	0.246404	-2.56067
#NV	7894178	0.679315	4.293788	2.915362	0.009123	0.246404	-2.56076
#NV	7896145	0.679315	4.293788	2.915362	0.009123	0.246404	-2.56076
SNORD115	7982040	-0.51853	3.376602	-2.91513	0.009128	0.246404	-2.5612
SNORD115	7982042	-0.51853	3.376602	-2.91513	0.009128	0.246404	-2.5612
SNORD115	7982044	-0.51853	3.376602	-2.91513	0.009128	0.246404	-2.5612
ST3GAL2	8002370	0.301401	6.528438	2.914616	0.009138	0.246404	-2.56218
SLC9A3R1	8009685	0.233109	8.952812	2.913494	0.00916	0.246404	-2.56431
#NV	8111913	-0.28926	4.00573	-2.91332	0.009164	0.246404	-2.56465
#NV	7895004	-0.33434	8.365555	-2.91288	0.009172	0.246404	-2.56547
FBXO17 //,	8036676	0.390568	8.221484	2.912431	0.009181	0.246404	-2.56633
#NV	7896418	-0.61884	6.327449	-2.91242	0.009182	0.246404	-2.56635
DAPK3	8032718	0.299943	5.446162	2.912363	0.009183	0.246404	-2.56646
C15orf52	7987511	0.236434	4.47539	2.910965	0.009211	0.246404	-2.56911
RPS6KA1	7899192	0.377526	6.28841	2.910828	0.009213	0.246404	-2.56937
PDPK1 ///	7998825	0.208181	9.227292	2.910635	0.009217	0.246404	-2.56974
PNN	7974066	0.260139	8.298073	2.910206	0.009226	0.246404	-2.57055
ST3GAL1	8153021	-0.24662	9.15566	-2.91016	0.009227	0.246404	-2.57064
DMRTB1	7901557	0.223996	3.986622	2.909849	0.009233	0.246404	-2.57123
LOC100133	7958724	-0.25623	3.525926	-2.90956	0.009239	0.246404	-2.57178
STK32C	7937089	0.230283	4.339462	2.909289	0.009244	0.246404	-2.57229
IRGQ	8037352	0.234018	4.206897	2.909176	0.009247	0.246404	-2.57251
AP1G2	7978066	0.453397	6.512624	2.908989	0.00925	0.246404	-2.57286
#NV	7892501	-0.72928	2.861198	-2.90816	0.009267	0.24665	-2.57443
#NV	8130470	0.274729	5.230008	2.907245	0.009285	0.246654	-2.57617
#NV	7896574	-0.56053	6.217453	-2.90724	0.009286	0.246654	-2.57619
ARHGAP5-	7978538	-0.36983	4.849341	-2.90698	0.009291	0.246654	-2.57667
BMP2K	8096004	-0.21876	6.962776	-2.90636	0.009303	0.246654	-2.57786
KLHDC1	7974214	-0.30971	7.053742	-2.90632	0.009304	0.246654	-2.57793
CTBP1	8098880	0.1717	8.402547	2.905531	0.00932	0.246803	-2.57942
GORASP1	8086317	0.185604	5.689932	2.905121	0.009328	0.246803	-2.5802
MBNL3	8175177	-0.2983	9.160786	-2.90471	0.009337	0.246803	-2.58099
#NV	7892734	-0.56287	5.449261	-2.90439	0.009343	0.246803	-2.58159
LYPLAL1	7909801	-0.30943	5.95147	-2.90407	0.00935	0.246803	-2.5822
PHF3	8120441	-0.21424	8.279413	-2.90385	0.009354	0.246803	-2.58262
WT1-AS	7939131	-0.41861	3.09269	-2.90308	0.00937	0.246896	-2.58407
#NV	8097305	-0.35971	5.366995	-2.90256	0.00938	0.246896	-2.58507
RALGAPA1	7978653	-0.28385	7.816801	-2.90216	0.009389	0.246896	-2.58582
#NV	7923179	-0.39387	3.893991	-2.90194	0.009393	0.246896	-2.58624
NR4A2	8055952	-0.38473	4.462699	-2.90185	0.009395	0.246896	-2.5864
PSEN2	7910146	0.317893	5.859383	2.901	0.009412	0.247158	-2.58802
#NV	8113346	0.533522	3.395499	2.900364	0.009425	0.247305	-2.58922
KIAA2026	8160011	-0.29197	9.03745	-2.89987	0.009435	0.247374	-2.59016
MANEAL	7900183	0.313592	5.813396	2.89693	0.009496	0.248763	-2.59573
#NV	7893610	-0.56576	3.92529	-2.89481	0.00954	0.249285	-2.59976
#NV	7893298	-0.56341	9.711731	-2.89475	0.009541	0.249285	-2.59987
NT5E	8120967	-0.42023	7.818171	-2.89458	0.009544	0.249285	-2.60019
#NV	8163714	-0.27034	8.374792	-2.89451	0.009546	0.249285	-2.60032
#NV	7916851	-0.22696	3.165461	-2.89416	0.009553	0.249285	-2.60099
#NV	7892968	0.324097	7.267824	2.893597	0.009565	0.24932	-2.60205
#NV	7894094	0.543512	5.32246	2.893152	0.009574	0.24932	-2.60289
#NV	8167893	-0.35004	4.103263	-2.8927	0.009583	0.24932	-2.60375
PABPC3	7968128	-0.15955	4.435676	-2.89265	0.009584	0.24932	-2.60385
E2F4	7996455	0.22265	6.747396	2.890946	0.00962	0.249744	-2.60707
NOMO1 //	7993371	0.245138	9.720163	2.890428	0.009631	0.249744	-2.60805
NOMO1 //	7993511	0.245138	9.720163	2.890428	0.009631	0.249744	-2.60805
NOMO1 //	7999791	0.245138	9.720163	2.890428	0.009631	0.249744	-2.60805
GZMA	8105340	0.4657	4.539075	2.889725	0.009645	0.24993	-2.60938
#NV	8038343	-0.47057	6.476754	-2.8888	0.009665	0.250176	-2.61114
#NV	7895604	0.446017	8.063978	2.888419	0.009673	0.250176	-2.61186
#NV	7895302	-0.77771	5.851282	-2.8882	0.009677	0.250176	-2.61228
RHOQ /// I	8045289	0.333717	7.180952	2.887016	0.009702	0.250482	-2.61451
#NV	8071817	-0.24857	2.667434	-2.88668	0.009709	0.250482	-2.61515
FASTK	8143863	0.286545	6.138808	2.886401	0.009715	0.250482	-2.61568
#NV	7896107	-0.44419	7.346207	-2.88604	0.009723	0.250482	-2.61637
USP53	8097098	-0.26376	7.464312	-2.88548	0.009735	0.250482	-2.61742
FICD	7958410	0.675188	5.695471	2.885097	0.009743	0.250482	-2.61815
PAH	7965884	-0.18347	12.26052	-2.8849	0.009747	0.250482	-2.61852
SWSAP1	8025888	-0.19225	5.179986	-2.88478	0.009749	0.250482	-2.61875
ZNF334	8066745	-0.53223	5.198506	-2.8831	0.009785	0.250918	-2.62193
#NV	8154221	-0.29953	2.254082	-2.88297	0.009788	0.250918	-2.62217
C19orf10	8032863	0.264961	7.632907	2.882772	0.009792	0.250918	-2.62255
CNKSR2	8166355	-0.43884	5.257172	-2.88224	0.009803	0.250918	-2.62356
SNORA45	7938293	0.396704	5.738318	2.882039	0.009807	0.250918	-2.62394
SNORA70B	8052524	-0.30844	4.396393	-2.88083	0.009833	0.250918	-2.62622
#NV	7896247	0.438738	10.36099	2.880406	0.009842	0.250918	-2.62703
GPR148	8045216	-0.24443	3.75864	-2.88033	0.009844	0.250918	-2.62717
TXNDC16	7979158	-0.33971	4.43798	-2.87997	0.009852	0.250918	-2.62786
GPD1	7955348	0.441134	8.977955	2.879676	0.009858	0.250918	-2.62841
DPYSL2	8145470	0.392077	7.958623	2.878847	0.009876	0.250918	-2.62998
#NV	8111796	-0.21346	8.410089	-2.87874	0.009878	0.250918	-2.63017
#NV	7896440	0.503916	3.873601	2.878364	0.009886	0.250918	-2.63089
KRTAP10-1	8069153	-0.26755	4.723035	-2.87814	0.009891	0.250918	-2.63132
CRTC2	7920382	-0.25215	7.067329	-2.87785	0.009897	0.250918	-2.63186
EGLN2 ///	8028940	0.251568	5.201122	2.877833	0.009897	0.250918	-2.63189
IKZF5	7936826	-0.3534	7.032284	-2.87774	0.009899	0.250918	-2.63208
MOCS1	8126214	-0.29647	6.781254	-2.87761	0.009902	0.250918	-2.63231
GSDMC	8152828	0.199868	2.422786	2.876453	0.009927	0.251359	-2.6345
HSD3BP4	7904429	-0.46923	3.584163	-2.87566	0.009944	0.25152	-2.636

STK17A	8132503	0.338735	5.9214	2.875456	0.009948	0.25152	-2.63639	
NPM1P8	8166659	-0.25148	2.127608	-2.87357	0.009989	0.252361	-2.63996	

Table_S4 List of genes that with altered DNA methylation and gene expression in obese non-diabetic or obese type 2 diabetic group

Obese non-diabetic group versus non-obese group							
Probe ID	Gene name	Changes in Expression (logFC)	Changes in Methylation	Exp_up&me_up	Exp_up&me_down	Exp_down&me_up	Exp_down&me_down
cg16854489	AASS	-0.73651457	-0.034291429	no	no	no	yes
cg17738782	AASS	-0.73651457	-0.058011429	no	no	no	yes
cg18961788	DIO3OS	-0.67236144S	-0.062865714	no	no	no	yes
cg18287066	GREM2	-0.455202508	-0.125975714	no	no	no	yes
cg02786378	SLC7A2	-0.436598967	-0.065004286	no	no	no	yes
cg24827071	MLPH	-0.402315261	-0.057264286	no	no	no	yes
cg14286712	DAPK1	-0.394042163	-0.084521429	no	no	no	yes
cg05389989	TRIM40	-0.319709481	-0.043432857	no	no	no	yes
cg07408232	TRIM40	-0.319709481	-0.074052857	no	no	no	yes
cg13961318	TRIM40	-0.319709481	-0.033581429	no	no	no	yes
cg26091747	TRIM40	-0.319709481	-0.063021429	no	no	no	yes
cg21151355	GJB3	-0.31673336	-0.159708571	no	no	no	yes
cg00121389	MTUS1	-0.314677971	-0.17207	no	no	no	yes
cg02776177	CCDC9	-0.299903444	-0.043511429	no	no	no	yes
cg11780053	INSR	-0.269874513	-0.025034286	no	no	no	yes
cg03835229	HGFAC	-0.240775148	-0.042424286	no	no	no	yes
cg04677405	HGFAC	-0.240775148	-0.042305714	no	no	no	yes
cg12421814	HGFAC	-0.240775148	-0.034198571	no	no	no	yes
cg22661239	ATXN7L1	-0.239450919	-0.031056286	no	no	no	yes
cg11586034	VPS45	0.22874806	-0.049202857	no	yes	no	no
cg08314499	CORO1C	0.23763362	-0.096152857	no	yes	no	no
cg15772261	CCT7	0.230072547	-0.076974286	no	yes	no	no
cg10552698	PDHB	0.280664625	-0.064645286	no	yes	no	no
cg05217329	PGAM1	0.31785957	-0.084812857	no	yes	no	no
cg11940177	PGAM1	0.31785957	-0.09258	no	yes	no	no
cg01019246	AMFR	0.31810561	-0.030077143	no	yes	no	no
cg27230554	PPP1R2	0.336147094	-0.061411429	no	yes	no	no
cg11190278	NIN	0.352012761	-0.056702857	no	yes	no	no
cg09003002	ANO10	0.395329052	-0.032977143	no	yes	no	no
cg03334660	KLHL5	0.401124979	-0.033625714	no	yes	no	no
cg18550212	ATL3	0.418590703	-0.120181429	no	yes	no	no
cg02641941	SLC2A13	0.440389755	-0.101664286	no	yes	no	no
cg08933276	GNA12	0.46925735	-0.042478571	no	yes	no	no
cg13083679	B4GALT6	0.486375614	-0.044152857	no	yes	no	no
cg07349899	GALNT14	0.530247767	-0.042725714	no	yes	no	no
cg02208432	ACER3	0.533428096	-0.086911429	no	yes	no	no
cg19283298	RAP2A	0.536907809	-0.098154286	no	yes	no	no
cg18808054	DDAH1	0.572991402	-0.045588571	no	yes	no	no
cg13788829	RET	0.597856416	-0.054328571	no	yes	no	no
cg19095000	FBXO2	0.607955869	-0.045874286	no	yes	no	no
cg25276694	FBXO2	0.607955869	0.04408	yes	no	no	no
cg21410120	PDGFA	0.61139682	-0.035387143	no	yes	no	no
cg13395854	SYT7	0.924831656	-0.048285714	no	yes	no	no
cg21917844	SYT7	0.924831656	-0.065451429	no	yes	no	no
cg25396645	FAT1	0.945922204	-0.024594286	no	yes	no	no
cg25123881	FAT1	0.945922204	-0.042257143	no	yes	no	no

Obese type2 diabetic group versus non-obese group							
Probe ID	Gene name	Changes in Expression (logFC)	Changes in Methylation	Exp_up&me_up	Exp_up&me_down	Exp_down&me_up	Exp_down&me_down
cg17738782	AASS	-0.90496469	-0.031291786	no	no	no	yes
cg22040158	KCND3	-0.490231354	-0.035212321	no	no	no	yes
cg05128832	JMJD1C	-0.395854618	0.126708107	no	no	yes	no
cg04171487	FAT4	-0.389038406	-0.027271071	no	no	no	yes
cg11830605	FAM110B	-0.383637025	-0.023997321	no	no	no	yes
cg21122466	FBN1A	-0.367895005	-0.029000536	no	no	no	yes
cg10359332	AKAP6	-0.359313805	-0.029321429	no	no	no	yes
cg17356750	FOXP2	-0.353691936	-0.037176607	no	no	no	yes
cg15584946	ZNF147	-0.351508722	-0.075091964	no	no	no	yes
cg13810683	TET1	-0.338624079	-0.019392857	no	no	no	yes
cg17972572	EIF3E	-0.336210941	-0.020346071	no	no	no	yes
cg08288330	FUZ	-0.331140772	-0.036591786	no	no	no	yes
cg00121389	MTUS1	-0.323420254	-0.046108393	no	no	no	yes
cg06234253	PIBF1	-0.312314973	-0.022024107	no	no	no	yes
cg09363891	PK3C2G	-0.300561128	-0.038815179	no	no	no	yes
cg04116217	EGFR	-0.274127202	-0.016368571	no	no	no	yes
cg20062492	EGFR	-0.274127202	-0.026255357	no	no	no	yes
cg09913449	C6orf40	-0.263645002	-0.015580071	no	no	no	yes
cg23746577	ZBTB7C	-0.249657642	-0.02113	no	no	no	yes
cg00902815	LMO7	-0.247283264	-0.023512857	no	no	no	yes
cg19881914	LMO7	-0.247283264	0.071110357	no	no	yes	no
cg26460954	LMO7	-0.247283264	-0.031122143	no	no	no	yes
cg21234032	AIG1	-0.240726417	-0.024371786	no	no	no	yes
cg11219400	TRANK1	-0.234821257	-0.022248518	no	no	no	yes
cg14220170	TRANK1	-0.234821257	-0.057096786	no	no	no	yes
cg02255510	HEATR5B	-0.206254611	-0.040966429	no	no	no	yes
cg18637383	HEATR5B	-0.206254611	-0.0377	no	no	no	yes
cg19237600	AZGP1	-0.172107536	-0.023006071	no	no	no	yes
cg08948841	CTBP1	0.171609862	-0.115214107	no	yes	no	no
cg26479374	CTBP1	0.171609862	-0.160493214	no	yes	no	no
cg08788712	MS12	0.21579998	-0.034657143	no	yes	no	no
cg27170947	FAM59B	0.225454732	0.025316107	yes	no	no	no
cg17267681	STK32C	0.230283417	-0.039379821	no	yes	no	no
cg03463948	UBASH3B	0.237977555	0.019329464	yes	no	no	no
cg07847891	USP1	0.242024475	-0.026748214	no	yes	no	no
cg14524579	STK11	0.246399808	-0.023714643	no	yes	no	no
cg12928081	DYNC1H1	0.260535706	0.014916607	yes	no	no	no
cg09527731	42255	0.27878139	-0.021375536	no	yes	no	no
cg01486818	PLCH2	0.281354051	-0.04188875	no	yes	no	no
cg18023674	PLCH2	0.281354051	-0.067702143	no	yes	no	no
cg10261751	CLCN7	0.282789884	-0.026007679	no	yes	no	no
cg06688399	FUI	0.285403539	-0.027298554	no	yes	no	no
cg03966955	ICTD5	0.288244538	-0.018750179	no	yes	no	no
cg20591408	RNPEPL1	0.304682319	-0.031498036	no	yes	no	no
cg00160059	ADCY6	0.327264393	-0.02470125	no	yes	no	no
cg24092939	ADCY6	0.327264393	-0.05374125	no	yes	no	no
cg05517218	MMP15	0.337665036	-0.033069464	no	yes	no	no
cg05521581	MMP15	0.337665036	-0.0417075	no	yes	no	no
cg11576486	LPCAT1	0.339133443	-0.035810357	no	yes	no	no
cg23779708	AGRN	0.348023629	-0.031413571	no	yes	no	no
cg20663852	ATP9A	0.366130982	-0.06926125	no	yes	no	no
cg13275679	HN1	0.374403811	-0.040636429	no	yes	no	no
cg15055596	ARHGEF16	0.377282041	-0.038314286	no	yes	no	no
cg15900221	ARHGEF16	0.377282041	-0.025528393	no	yes	no	no
cg08034986	RPS6KA1	0.377526333	-0.050262679	no	yes	no	no
cg05633196	WIPI1	0.381354759	-0.046432141	no	yes	no	no
cg04566826	ECTD15	0.382803615	-0.030929286	no	yes	no	no
cg21235754	KLHL29	0.383568003	-0.027314643	no	yes	no	no
cg12419482	P2RY2	0.509557788	-0.025180536	no	yes	no	no
cg05633070	ABR	0.5305534	-0.056346964	no	yes	no	no
cg14236443	ABR	0.5305534	-0.054076786	no	yes	no	no
cg17126533	MPV17L2	0.539570528	0.014807482	yes	no	no	no
cg25276694	FBXO2	0.539928261	0.026282679	yes	no	no	no
cg23364656	PIBF1	0.540085165	-0.032785357	no	yes	no	no
cg00890054	SPSB1	0.566254236	-0.052271607	no	yes	no	no
cg06941197	SPSB1	0.566254236	-0.015162857	no	yes	no	no
cg00248856	CCND1	0.64745072	-0.029243393	no	yes	no	no
cg20955839	SULT1C2	0.647541448	-0.060961429	no	yes	no	no
cg17066254	SLC35C1	0.762783896	-0.021081071	no	yes	no	no
cg23373850	WNT11	0.783534932	-0.055720714	no	yes	no	no
cg21410120	PDGFA	0.788161228	-0.02035375	no	yes	no	no
cg08203192	PRKCE	1.32641914	-0.028576071	no	yes	no	no
cg08809251	TMEM45B	1.363032065	-0.037582857	no	yes	no	no

Table S5 Target genes of the top 3 active and inactive transcription factors in non-obese liver

filtered target genes of AACACUG in non-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_T	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	ND-non
chr8_+_17354562	0.446	SLC7A2	SLC7A2	8144786	-0.4366	0.002735	0.237132	cg02786378	N/A	Body;Body;5'UTR	SLC7A2	-6.50E-02
chr9_+_90112754	0.456	DAPK1	DAPK1	8156199	-0.39404	0.000735	0.197693	cg14286732	N/A	Body	DAPK1	-8.45E-02

filtered target genes of AAGGCAC in non-obese liver

Promoter	**Score**	**Gene Symbol**	**Name**	**probe_ID**	**logFC**	**PValue**	**FDR**	**Probe ID**	**RELATION_T**	**UCSC_REFGENE_GROUP**	**UCSC_REFGENE_NAME**	**ND-non**
chr9_-_130331350	1.183	FAM129B	FAM129B	8164217	0.370197	0.00706	0.293466	cg14409919	N/A	Body;Body	FAM129B	-2.53E-02
chr6_-_134496006	2.152	SGK1	SGK1	8129677	0.795798	0.004794	0.261671	cg21078322	N/A	3'UTR;3'UTR;3'UTR;3'UTR	SGK1	-9.01E-02

filtered target genes of IKZF2 in non-obese liver

Promoter	**Score**	**Gene Symbol**	**Name**	**probe_ID**	**logFC**	**PValue**	**FDR**	**Probe ID**	**RELATION_T**	**UCSC_REFGENE_GROUP**	**UCSC_REFGENE_NAME**	**ND-non**
chr8_-_18541441	1.7	PSD3	PSD3	8149555	-0.43479	0.004261	0.255766	cg12082271	N/A	Body;Body	PSD3	-5.96E-02

filtered target genes of RBPJ in non-obese liver

Promoter	**Score**	**Gene Symbol**	**Name**	**probe_ID**	**logFC**	**PValue**	**FDR**	**Probe ID**	**RELATION_T**	**UCSC_REFGENE_GROUP**	**UCSC_REFGENE_NAME**	**ND-non**
chr8_-_18541441	0.638	PSD3	PSD3	8149555	-0.43479	0.004261	0.255766	cg12082271	N/A	Body;Body	PSD3	-5.96E-02
chr10_-_105437908	0.522	SH3PXD2A	SH3PXD2A	7936115	-0.51315	0.005999	0.280566	cg12569119	N/A	Body	SH3PXD2A	-5.34E-02
chr10_-_105437908	0.522	SH3PXD2A	SH3PXD2A	7936115	-0.51315	0.005999	0.280566	cg20241299	Island	Body	SH3PXD2A	-3.45E-02

Promoter	**Score**	**Gene Symbol**	**Name**	**probe_ID**	**logFC**	**PValue**	**FDR**	**Probe ID**	**RELATION_T**	**UCSC_REFGENE_GROUP**	**UCSC_REFGENE_NAME**	**T2D-non**
chr6_+_143382030	0.968	AIG1	AIG1	8122396	-0.24073	0.005884	0.216536	cg21234032	N/A	Body	AIG1	-2.44E-02

filtered target genes of UUGGUCC in non-obese liver

Promoter	**Score**	**Gene Symbol**	**Name**	**probe_ID**	**logFC**	**PValue**	**FDR**	**Probe ID**	**RELATION_T**	**UCSC_REFGENE_GROUP**	**UCSC_REFGENE_NAME**	**ND-non**
chr6_-_134496006	1.448	SGK1	SGK1	8129677	0.795798	0.004794	0.261671	cg21078322	N/A	3'UTR;3'UTR;3'UTR;3'UTR	SGK1	-9.01E-02

Promoter	**Score**	**Gene Symbol**	**Name**	**probe_ID**	**logFC**	**PValue**	**FDR**	**Probe ID**	**RELATION_T**	**UCSC_REFGENE_GROUP**	**UCSC_REFGENE_NAME**	**T2D-non**
chr12_-_49177876	0.555	ADCY6	ADCY6	7962842	0.327264	0.006701	0.222644	cg00160359	S_Shore	5'UTR;TSS1500	ADCY6	-0.0247
chr19_+_34287662	0.568	KCTD15	KCTD15	8027584	0.382804	0.00896	0.24475	cg04566826	S_Shore	5'UTR;5'UTR;5'UTR	KCTD15	-3.09E-02
chr16_+_58059281	0.89	MMP15	MMP15	7996185	0.337665	0.005773	0.216441	cg05517218	S_Shore	3'UTR	MMP15	-3.31E-02
chr16_+_58059281	0.89	MMP15	MMP15	7996185	0.337665	0.005773	0.216441	cg05521581	N_Shore	Body	MMP15	-4.17E-02
chr12_-_49177876	0.555	ADCY6	ADCY6	7962842	0.327264	0.006701	0.222644	cg24092939	N_Shore	5'UTR	ADCY6	-0.05374

filtered target genes of TP53 in non-obese liver

Position	Score	Gene Name	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_T	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	T2D-non
chr11_+_45826640	1.584	SLC35C1	SLC35C1	7939590	0.762783	0.002823	0.176496	cg17066254	N_Shore	TSS1500;TSS1500	SLC35C1	-2.11E-02

Table S6 Target genes of the top 3 active and inactive transcription factors in ND-obese liver

filtered target genes of HMX1 in ND-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_	UCSC_REFGENE_GROUP	UCSC_REFGENE_	ND-non
chr9_-_1303	0.58	FAM129B	FAM129B	8164217	0.370197	0.00706	0.293466	cg1440991	N/A	Body;Body	FAM129B	-0.02526
chr9_-_1303	0.327	FAM129B	FAM129B	8164217	0.370197	0.00706	0.293466	cg1440991	N/A	Body;Body	FAM129B	-0.02526

filtered target genes of MAFB in ND-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_	UCSC_REFGENE_GROUP	UCSC_REFGENE_	ND-non
chr12_-_404	0.794	SLC2A13	SLC2A13	7962327	0.44039	0.000411	0.183282	cg0264194	N/A	Body	SLC2A13	-0.10166
chr7_-_2883	0.544	GNA12	GNA12	8137865	0.469257	0.000113	0.144561	cg0893327	N/A	3'UTR	GNA12	-0.04248
chr11_-_613	1.256	SYT7	SYT7	7948588	0.924832	0.002107	0.229377	cg1339585	N/A	Body	SYT7	-0.04829
chr13_+_980	0.711	RAP2A	RAP2A	7969693	0.536908	5.93E-05	0.130579	cg1928329	S_Shelf	Body	RAP2A	-0.09815
chr13_+_980	0.799	RAP2A	RAP2A	7969693	0.536908	5.93E-05	0.130579	cg1928329	S_Shelf	Body	RAP2A	-0.09815
chr11_-_613	1.256	SYT7	SYT7	7948588	0.924832	0.002107	0.229377	cg2391784	N/A	Body	SYT7	-0.06545
chr3_-_1952	0.49	PPP1R2	PPP1R2	8092959	0.336147	0.001158	0.210565	cg2723053	N_Shelf	Body	PPP1R2	-0.06141

filtered target genes of NKX2-3_NKX2-5 in ND-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_	UCSC_REFGENE_GROUP	UCSC_REFGENE_	ND-non
chr8_-_1757	0.762	MTUS1	MTUS1	8149500	-0.31468	0.00047	0.184307	cg0012138	N/A	Body;TSS200;Body;Body;Bod	MTUS1	-0.17207
chr3_-_7117	0.286	FOXP1	FOXP1	8088776	-0.29018	0.003497	0.250433	cg0097075	N/A	Body	FOXP1	-0.06017
chr3_-_7117	0.297	FOXP1	FOXP1	8088776	-0.29018	0.003497	0.250433	cg0097075	N/A	Body	FOXP1	-0.06017
chr3_-_7117	0.286	FOXP1	FOXP1	8088776	-0.29018	0.003497	0.250433	cg0736885	N/A	5'UTR;5'UTR	FOXP1	-0.09083
chr3_-_7117	0.297	FOXP1	FOXP1	8088776	-0.29018	0.003497	0.250433	cg0736885	N/A	5'UTR;5'UTR	FOXP1	-0.09083
chr10_-_105	0.297	SH3PXD2A	SH3PXD2A	7936115	-0.51315	0.005999	0.280566	cg1256911	N/A	Body	SH3PXD2A	-0.05335
chr3_-_7117	0.286	FOXP1	FOXP1	8088776	-0.29018	0.003497	0.250433	cg1547288	N/A	Body	FOXP1	-0.03368
chr3_-_7117	0.297	FOXP1	FOXP1	8088776	-0.29018	0.003497	0.250433	cg1547288	N/A	Body	FOXP1	-0.03368
chr6_+_1361	0.676	PDE7B	PDE7B	8122222	-0.44658	0.005818	0.27898	cg1714850	N/A	Body	PDE7B	-0.04140
chr17_+_378	0.258	GRB7	GRB7	8006940	-0.4159	0.009987	0.317595	cg1735571	N/A	TSS1500;TSS1500	GRB7	0.07341
chr10_-_105	0.297	SH3PXD2A	SH3PXD2A	7936115	-0.51315	0.005999	0.280566	cg2024129	Island	Body	SH3PXD2A	-0.03453
chr17_+_378	0.258	GRB7	GRB7	8006940	-0.4159	0.009987	0.317595	cg2567621	N/A	Body;Body	GRB7	-0.03880

filtered target genes of PAX2 in ND-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_	UCSC_REFGENE_GROUP	UCSC_REFGENE_	ND-non
chr6_-_5321	1.121	ELOVL5	ELOVL5	8127145	0.398788	0.004198	0.255766	cg1174835	N/A	5'UTR	ELOVL5	-0.07295
chr6_-_5321	0.753	ELOVL5	ELOVL5	8127145	0.398788	0.004198	0.255766	cg1174835	N/A	5'UTR	ELOVL5	-0.07295
chr6_-_5321	0.983	ELOVL5	ELOVL5	8127145	0.398788	0.004198	0.255766	cg1174835	N/A	5'UTR	ELOVL5	-0.07295
chr17_-_269	0.937	ALDOC	ALDOC	8013660	0.650618	0.006585	0.289152	cg1569223	N/A	TSS200	ALDOC	0.02484
chr17_-_269	0.938	ALDOC	ALDOC	8013660	0.650618	0.006585	0.289152	cg1569223	N/A	TSS200	ALDOC	0.02484
chr6_-_1344	1.182	SGK1	SGK1	8129677	0.795798	0.004794	0.261671	cg2107832	N/A	3'UTR;3'UTR;3'UTR;3'UTR	SGK1	-0.09014

filtered target genes of UUUUUGC in ND-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_	UCSC_REFGENE_GROUP	UCSC_REFGENE_	ND-non
chr7_-_1217	1.337	AASS	AASS	8142554	-0.73651	0.00119	0.211413	cg1168548	N/A	Body	AASS	-0.03429
chr7_-_1217	1.337	AASS	AASS	8142554	-0.73651	0.00119	0.211413	cg1173878	N/A	Body	AASS	-0.05801

filtered target genes of ZNF423 in ND-obese liver

No results found

Table S7 Target genes of the top 3 active and inactive transcription factors in T2D-obese liver

filtered target genes of ACAGUAU in T2D-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_ISL	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	T2D-non
chr4_+_126237566	0.53	FAT4	FAT4	8097288	-0.38904	0.000594	0.107867	cg04171487	N/A	Body	FAT4	-2.73E-02

filtered target genes of CUUUGGU in T2D-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_ISL	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	T2D-non
chr7_-_121784236	0.542	AASS	AASS	8142554	-0.90496	0.000168	0.0762	cg11738782	N/A	Body	AASS	-3.13E-02
chr7_+_114055048	0.439	FOXP2	FOXP2	8135544	-0.35369	0.007702	0.232529	cg17356750	N/A	Body;Body;Body	FOXP2	-3.72E-02

filtered target genes of AGCUGCC in T2D-obese liver

Position	Score	GeneName	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_ISL	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	T2D-non
chr12_-_49177876	0.381	ADCY6	ADCY6	7962842	0.327264	0.006701	0.222644	cg00160359	S_Shore	5'UTR;TSS1500	ADCY6	-0.0247
chr12_-_49177876	0.381	ADCY6	ADCY6	7962842	0.327264	0.006701	0.222644	cg24092939	N_Shore	5'UTR	ADCY6	-0.05374

filtered target genes of PATZ1 in T2D-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_ISL	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	T2D-non
chr12_-_49182718	1.228	ADCY6	ADCY6	7962842	0.327264	0.006701	0.222644	cg00160359	S_Shore	5'UTR;TSS1500	ADCY6	-0.0247
chr11_+_69455837	0.831	CCND1	CCND1	7942123	0.647451	0.005353	0.212972	cg00248856	S_Shelf	Body	CCND1	-2.92E-02
chr11_+_69455938	0.85	CCND1	CCND1	7942123	0.647451	0.005353	0.212972	cg00248856	S_Shelf	Body	CCND1	-2.92E-02
chr1_+_9352931	0.904	SPSB1	SPSB1	7897449	0.566254	0.00643	0.22202	cg00890054	N/A	5'UTR	SPSB1	-5.23E-02
chr1_+_9352955	0.974	SPSB1	SPSB1	7897449	0.566254	0.00643	0.22202	cg00890054	N/A	5'UTR	SPSB1	-5.23E-02
chr17_-_1083008	0.901	ABR	ABR	8010983	0.530553	0.002177	0.16838	cg05633070	Island	Body;Body;Body	ABR	-5.63E-02
chr1_+_9352931	0.904	SPSB1	SPSB1	7897449	0.566254	0.00643	0.22202	cg06943197	N_Shore	5'UTR	SPSB1	-1.52E-02
chr1_+_9352955	0.974	SPSB1	SPSB1	7897449	0.566254	0.00643	0.22202	cg06943197	N_Shore	5'UTR	SPSB1	-1.52E-02
chr2_+_45878912	1.746	PRKCE	PRKCE	8041763	1.326419	0.000369	0.095471	cg08203192	S_Shore	Body	PRKCE	-2.86E-02
chr11_+_129685732	0.955	TMEM45B	TMEM45B	7945169	1.363032	0.000986	0.129046	cg08809251	N/A	Body	TMEM45B	-3.76E-02
chr5_-_1523908	0.913	LPCAT1	LPCAT1	8110841	0.339133	0.001373	0.14027	cg11576486	N/A	Body	LPCAT1	-3.58E-02
chr17_-_1083008	0.901	ABR	ABR	8010983	0.530553	0.002177	0.16838	cg14236443	N/A	Body;Body;Body	ABR	-5.41E-02
chr1_+_955609	1.203	AGRN	AGRN	7896822	0.348024	0.002127	0.16628	cg22379708	N_Shore	Body	AGRN	-3.14E-02
chr1_+_955468	1.067	AGRN	AGRN	7896822	0.348024	0.002127	0.16628	cg22379708	N_Shore	Body	AGRN	-3.14E-02
chr12_-_49182718	1.228	ADCY6	ADCY6	7962842	0.327264	0.006701	0.222644	cg24092939	N_Shore	5'UTR	ADCY6	-0.05374
chr1_-_11714738	1.377	FBXO2	FBXO2	7912473	0.539928	0.002814	0.176496	cg25276694	Island	Body	FBXO2	2.93E-02
chr1_-_11714471	1.341	FBXO2	FBXO2	7912473	0.539928	0.002814	0.176496	cg25276694	Island	Body	FBXO2	2.93E-02
chr1_-_11714396	0.955	FBXO2	FBXO2	7912473	0.539928	0.002814	0.176496	cg25276694	Island	Body	FBXO2	2.93E-02

filtered target genes of PRRX1 in T2D-obese liver

Promoter	Score	Gene Symbol	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_ISL	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	T2D-non
chr14_+_32798478	1.587	AKAP6	AKAP6	7973850	-0.35931	0.005923	0.216536	cg10359332	N/A	5'UTR	AKAP6	-2.93E-02
chr7_+_114066554	3.421	FOXP2	FOXP2	8135544	-0.35369	0.007702	0.232529	cg17356750	N/A	Body;Body;Body	FOXP2	-3.72E-02

filtered target genes of TP53 in T2D-obese liver

Position	Score	Gene Name	Name	probe_ID	logFC	PValue	FDR	Probe ID	RELATION_TO_UCSC_CPG_ISL/	UCSC_REFGENE_GROUP	UCSC_REFGENE_NAME	T2D-non
chr11_+_45826640	1.584	SLC35C1	SLC35C1	7939590	0.762783	0.002823	0.176496	cg17066254	N_Shore	TSS1500;TSS1500	SLC35C1	-2.11E-02

Table S8 Hypomethylation of glycolytic and lipogenic genes.

		Obese *versus* Non-Obese		Type 2 diabetic *versus* Non-Obese	
gene name	**total # probes**	**hypomethylated**	**hypermethylated**	**hypomethylated**	**hypermethylated**
GCK	25	14	2	9	0
PFKL	31	11	2	6	1
ACACA	48	20	0	10	1
ACLY	22	2	1	1	1
FASN	55	14	2	7	1
PRKCE	61	26	2	12	1
ATF6	25	5	2	5	1

CpG-methylation measured using an Illumina Infinium 450k Bead Chip. Column entitled *total # probes* describes total number of probes per gene measured by the Bead Chip. Remaining columns describe number of probes per gene hypo- or hypermethylated. Hypomethylation was assumed when $\text{M-value}_{\text{obese}}$ - $\text{M-value}_{\text{non-obese}} \leq 0.25$. Hypermethylation was assumed when $\text{M-value}_{\text{obese}}$ - $\text{M-value}_{\text{non-obese}} \geq 0.25$. This table is related to Figure 4.

Table S9 Correlation between ATF-motif methylation and clinical parameters

		Correlations				
Parameter		**FASN_ATF**	**PRKCE_ATF**	**PFKL_ATF**	**ACLY_ATF**	**ACACA_ATF**
Age	*r*	-.032	-.072	-.042	.167	-.112
	P-value	.868	.722	.827	.378	.587
Height	*r*	.199	-.154	-.131	.038	-.204
	P-value	.259	.399	.461	.829	.272
Weight	*r*	-.215	-.273	**-.597****	-.032	**-.487****
	P-value	.223	.130	**.000**	.855	**.005**
BMI	*r*	-.311	-.259	**-.619****	-.050	**-.459****
	P-value	.073	.152	**.000**	.777	**.009**
Waist	*r*	-.201	-.234	**-.641****	-.054	**-.411***
	P-value	.296	.240	**.000**	.778	**.037**
HDL	*r*	.034	.312	.089	.199	.224
	P-value	.873	.158	.679	.339	.329
LDL	*r*	.095	.241	.087	.013	.103
	P-value	.667	.280	.692	.952	.656
Cholesterol	*r*	.300	.209	.069	-.005	.081
	P-value	.154	.351	.748	.980	.727
Triglycerides	*r*	**-.408***	**-.443***	-.225	-.085	-.340
	P-value	**.048**	**.039**	.290	.686	.132
HbA_{1c}	*r*	**-.557****	-.306	-.236	.062	-.413
	P-value	**.005**	.166	.268	.767	.063
Glucose	*r*	**-.640****	-.110	-.239	.009	**-.516***
	P-value	**.000**	.609	.240	.966	**.012**
Insulin	*r*	-.217	**-.554****	**-.588****	-.140	**-.648****
	P-value	.277	**.004**	**.001**	.477	**.001**
HOMA-IR	*r*	-.377	**-.520***	**-.588****	-.103	**-.713****
	P-value	.076	**.016**	**.003**	.631	**.000**

Pearson correlation coefficients (*r*) between ATF-motif methylation and clinical parameters studied. Significant relationships are highlighted in bold font. **P<0.01 (2-tailed). *P<0.05 (2-tailed). This table is related to Figure 4.

Table S10 Comparison of MBD4 Chip ENCODE data with DNA methylation (Infinium 450k) in liver from T2D-obese and non-diabetic obese men

Comparison of MBD4 Chip ENCODE data with DNA methylation (Infinium 450k) in liver from non-diabetic obese versus non-obese men

Chromosome	MBD4_ENCFF002CKQ_Start	MBD4_ENCFF002CKQ_End	MBD4_ENCFF002CKC	ND-non_Start	ND-non_End	ND-non_450K_Name	ND-non_GeneName	ND-non M-value
chr14	102701517	102702081	ENCODE_MBD4_3331	102702045	102702095	cg02022488	RAGE	-0.757933929
chr8	132915493	132916057	ENCODE_MBD4_4004	132915715	132915765	cg07665487	EFR3A	-0.743278571
chr11	82611614	82612178	ENCODE_MBD4_4451	82612022	82612072	cg03602013	C11orf82	-0.6579375
chr6	44225252	44225816	ENCODE_MBD4_4523	44225648	44225698	cg11699666	SLC35B2	-0.639560714
chr11	64007783	64008347	ENCODE_MBD4_5883	64007813	64007863	cg12423493	FKBP2	-0.633054821
chr2	21231099	21231663	ENCODE_MBD4_1497	21231605	21231655	cg05961176	APOB	-0.60185
chr6	26594815	26595379	ENCODE_MBD4_4570	26595280	26595330	cg26478107	N/A	-0.581525714
chr3	128399898	128400462	ENCODE_MBD4_3807	128400220	128400270	cg02610898	N/A	-0.508798214
chr10	81965285	81965849	ENCODE_MBD4_2795	81965490	81965540	cg15186042	ANXA11	-0.494023214
chr7	138818153	138818717	ENCODE_MBD4_3217	138818388	138818438	cg04662241	TTC26	-0.457928571
chr15	38746039	38746603	ENCODE_MBD4_4281	38746242	38746292	cg05843574	FAM98B	-0.413928571
chr6	155816112	155816676	ENCODE_MBD4_3505	155816164	155816214	cg16095551	N/A	-0.409040714
chr4	84376928	84377492	ENCODE_MBD4_2219	84377292	84377342	cg22541143	HELQ	-0.391464286
chr5	33440514	33441078	ENCODE_MBD4_3994	33440737	33440787	cg06484562	TARS	-0.360903571
chr16	67260774	67261338	ENCODE_MBD4_4470	67260827	67260877	cg22834154	LRRC29	-0.3544125
chr11	119039023	119039587	ENCODE_MBD4_3009	119039171	119039221	cg05169666	NLRX1	-0.351985714
chr7	94286670	94287234	ENCODE_MBD4_3186	94286669	94286719	cg20041873	SGCE	-0.341902929
chr9	136218911	136219475	ENCODE_MBD4_4536	136219331	136219381	cg13454524	SURF1	-0.336157143
chr6	52860000	52860564	ENCODE_MBD4_274	52860082	52860132	cg25760338	GSTA4	-0.3346875
chr7	94286670	94287234	ENCODE_MBD4_3186	94286793	94286843	cg05509218	SGCE	-0.306770563
chr13	103497959	103498523	ENCODE_MBD4_1912	103497941	103497991	cg20374041	ERCC5	-0.297808929
chr2	192542647	192543211	ENCODE_MBD4_5580	192542877	192542927	cg19839149	OBFC2A	-0.2941875
chr6	126307900	126308464	ENCODE_MBD4_4709	126307897	126307947	cg12199684	TRMT11	0.276058929
chr3	142297403	142297967	ENCODE_MBD4_3793	142297747	142297797	cg00969988	ATR	0.280758929
chr2	95830964	95831528	ENCODE_MBD4_5716	95831296	95831346	cg17995403	ZNF2	0.296353571
chr12	32111664	32112228	ENCODE_MBD4_4600	32112207	32112257	cg17281556	C12orf35	0.298735714
chr14	24616079	24616643	ENCODE_MBD4_5374	24616618	24616668	cg12590010	PSME2	0.3497875
chr5	112196496	112197060	ENCODE_MBD4_5465	112197007	112197057	cg10484990	SRP19	0.357289286
chr17	80476681	80477245	ENCODE_MBD4_3518	80477010	80477060	cg01137065	FOXK2	0.373189286
chr4	103940479	103941043	ENCODE_MBD4_4781	103941039	103941089	cg06618713	NHEDC1	0.397458929
chr6	148663144	148663708	ENCODE_MBD4_3962	148663626	148663676	cg01452444	SASH1	0.421192857
chr12	81471064	81471628	ENCODE_MBD4_5519	81471419	81471469	cg00354572	ACSS3	0.438119643
chr12	81471366	81471930	ENCODE_MBD4_5286	81471419	81471469	cg00354572	ACSS3	0.438119643
chr10	5726157	5726721	ENCODE_MBD4_1067	5726466	5726516	cg20676401	C10orf18	0.450503571
chr10	116286163	116286727	ENCODE_MBD4_1373	116286605	116286655	cg01449818	ABLIM1	0.471242857
chr3	57541526	57542090	ENCODE_MBD4_315	57541798	57541848	cg07317755	PDE12	0.542855357

Comparison of MBD4 Chip ENCODE data with DNA methylation (Infinium 450k) in liver from T2-diabetic obese versus non-obese men

Chromosome	MBD4_ENCFF002CKQ_Start	MBD4_ENCFF002CKQ_End	MBD4_ENCFF002CKC	T2D-non_Start	T2D-non_End	T2D-non_450K_Name	T2D-non_GeneName	T2D-non M-value
chr7	11012820	11013384	ENCODE_MBD4_5736	11013340	11013390	cg07287563	PHF14	-0.670432143
chr5	74162556	74163120	ENCODE_MBD4_3826	74162851	74162901	cg06460691	FAM169A	-0.532806143
chr6	27447138	27447702	ENCODE_MBD4_2385	27447492	27447542	cg27226147	N/A	1.126012857
chr6	87864882	87865446	ENCODE_MBD4_5775	87865314	87865364	cg03098356	ZNF292	-0.40785
chr6	143771597	143772161	ENCODE_MBD4_3452	143771552	143771602	cg08452146	ADAT2	0.408916071
chr10	75935830	75936394	ENCODE_MBD4_4126	75936028	75936078	cg16088251	ADK	-0.7512625
chr10	121484607	121485171	ENCODE_MBD4_2681	121485064	121485114	cg19004007	INPP5F	-0.832216071
chr11	16759866	16760430	ENCODE_MBD4_3195	16760230	16760280	cg25556987	C11orf58	-0.4267625
chr4	103940479	103941043	ENCODE_MBD4_4781	103941039	103941089	cg06618713	NHEDC1	0.439883929
chr12	57482027	57482591	ENCODE_MBD4_1448	57482528	57482578	cg06200494	NAB2	-0.254073214
chr1	235814038	235814602	ENCODE_MBD4_2381	235814009	235814059	cg17816394	GNG4	0.646419643
chr2	15701265	15701829	ENCODE_MBD4_1116	15701450	15701500	cg04222876	NBAS	0.309708929
chr2	20646601	20647165	ENCODE_MBD4_3548	20646743	20646793	cg19594691	RHOB	0.378032143
chr14	24630104	24630668	ENCODE_MBD4_1466	24630380	24630430	cg11065693	IRF9	0.276928571
chr14	24630368	24630932	ENCODE_MBD4_4676	24630380	24630430	cg11065693	IRF9	0.276928571
chr15	38746039	38746603	ENCODE_MBD4_4281	38746242	38746292	cg05843574	FAM98B	-0.649541071
chr17	79476223	79476787	ENCODE_MBD4_1256	79476521	79476571	cg22098511	N/A	-0.4889
chr17	79476223	79476787	ENCODE_MBD4_1256	79476186	79476236	cg02500691	N/A	-0.535840375
chr17	80225376	80225940	ENCODE_MBD4_3142	80225377	80225427	cg04428071	CSNK1D	0.323494286

Comparison of MBD4 Chip ENCODE data with DNA methylation (Infinium 450k) in liver from ND-obese versus T2D-obese men

Chromosome	MBD4_ENCFF002CKQ_Start	MBD4_ENCFF002CKQ_End	MBD4_ENCFF002CKC	ND-T2D_Start	ND-T2D_End	ND-T2D_450K_Name	ND-T2D_GeneName	ND-T2D M-value
chr7	138818153	138818717	ENCODE_MBD4_3217	138818388	138818438	cg04662241	TTC26	-0.40085
chr3	57541526	57542090	ENCODE_MBD4_315	57541798	57541848	cg07317755	PDE12	0.5383
chr11	65769412	65769976	ENCODE_MBD4_4568	65769428	65769478	cg09783858	EIF1AD	0.3677125
chr11	75946401	75946965	ENCODE_MBD4_1896	75946452	75946502	cg08868379	N/A	-1.48969125
chr12	32111664	32112228	ENCODE_MBD4_4600	32112207	32112257	cg17281556	C12orf35	0.4857125
chr12	57482027	57482591	ENCODE_MBD4_1448	57482528	57482578	cg06200494	NAB2	0.326125
chr1	93810820	93811384	ENCODE_MBD4_5279	93810826	93810876	cg02421543	DR1	-0.521225
chr20	3800427	3800991	ENCODE_MBD4_3616	3800838	3800888	cg10780647	C20orf29	0.250975
chr20	3800626	3801190	ENCODE_MBD4_4910	3800838	3800888	cg10780647	C20orf29	0.250975
chr20	35724220	35724784	ENCODE_MBD4_4211	35724590	35724640	cg16239906	RBL1	0.4400375
chr16	29984483	29985047	ENCODE_MBD4_1148	29984665	29984715	cg10316764	TAOK2	-0.473952625
chr17	80476681	80477245	ENCODE_MBD4_3518	80477010	80477060	cg01137065	FOXK2	0.5166375

Table S11 Primer sequences for bisulfite PCR pyrosequencing and Luciferase Assays

Gene	Forward Primer	Reverse Primer	Sequencing Primer
GCK_ATF	GTTATATGGAGGAGATGTAGAATGT	[Btn]ACACCAAAACCACCCAAAACCTAAATTATA	AATGTGGAGTTGGT
PFKL_ATF	GGGTTTTAGGGAGTAGTTGTATTT	[Btn]CCTCCCTTTCTACCCTAACAAT	TGAGTTTGGAGGAGG
ACLY_ATF	TTTGTAGTTGGTAGGGTAGATAGA	[Btn]AACATCAAAACCAAAATTACACAATCACT	TTGGTAGGGTAGATAGATTA
ACACA_ATF	AAGGTAGTAGTGAATGGAGATTGTATTA	[Btn]ACCCCACCTCCATATATTTTCTCTA	ATTGTATTGGAGTGGTAT
FASN_ATF	GGAGTTTTGGAAGGTTGAGA	[Btn]CCCTTCCTCATATAACCAATTCC	TTTGGAAGGTTGAGATTT
PRKCE_ATF	AGATTGGTATATAGAGTATTATGATGTAGG	[Btn]ATTATAAAATACACTAAACCCACAACA	GTATATAGAGTATTATGATGTAGGA
PFKL_Luci	TTAATGCATCAGAGGGTCGAGAGGCAGA	TTAGGATCCTCGGTCTCCCTGCTGAAGG	
ACACA_Luci	TTAATGCATTGGCCTGCGTCACAAATCAA	TTAGGATCCCGCACTTCTAATTAAGCCAACTGA	
FASN_Luci	TTAATGCATCAGGACAAGGCCCAAGGTAG	TTAGGATCCACCACGTCAGCCACTGTG	
PRKCE_Luci	TTAATGCATATATTCCCCGGAGAGCAATTATTC	TTAGGATCCCACTAAACCCACAGCAAAATAGCC	

Primer sequences are in 5’ to 3’ orientation. Primers for pyrosequencing of the common ATF motif (Primer name_ATF) were generated using the PyroMark Assay Design Software (Qiagen) and are designed to bind to human bisulfite-treated DNA. Primers to amplify human genomic DNA for the Luciferase-Assay (primer name_Luci) were generated using Primer3. This table is related to the information provided in Experimental Procedures.