

Supplementary Table 17. *cis*-eQTM analysis between gene patterns and cpG patterns . Columns are: 'gene': gene name; 'cpG': CpG site name; 'gene_chr': chromosome number of gene; 'gene_s1': gene position s1; 'gene_s2': gene position s2; 'cpG_chr': chromosome number of CpG; 'dist': genomic distance between gene and CpG; 'statistic': t-statistic; 'beta': effect size; 'pvalue': raw p-value; 'fdr': false discovery rate; 'gene_pattern': gene pattern; 'cpG_pattern': CpG pattern.

		gene											
gene	cpG	_chr	gene_s1	gene_s2	cpG_c	cpG_pos	dist	statistic	beta	pvalue	fdr	gene_patter	cpG_pattern
ZNF684	cg2101111C	1	40997233	41013841	1	40157436	839797	-151.50	-3.7	4.36E-05	0.049	patternV	PatternI
TRIM39	cg2389735C	6	30294256	30311506	6	30688013	376507	88.90	48.2	1.27E-04	0.058	patternA	PatternI
BLOC1S3	cg0725157C	19	45682003	45685059	19	45349316	332687	76.43	10.7	1.71E-04	0.058	patternA	PatternI
GSDMD	cg0071393C	8	144635377	144645232	8	144660590	15358	67.17	120.2	2.22E-04	0.058	patternA	PatternI
FKBPL	cg06414921	6	32096484	32098068	6	31276504	819980	58.95	69.6	2.88E-04	0.058	patternA	PatternI
PEF1	cg24691844	1	32095463	32110497	1	32254595	144098	57.01	85.6	3.08E-04	0.058	patternA	PatternI
SCYL1	cg1049847C	11	65292548	65306175	11	66035147	728972	46.73	163.0	4.58E-04	0.070	patternA	PatternI
GNA15	cg05228284	19	3136191	3163767	19	2720847	415344	43.57	14.5	5.26E-04	0.070	patternA	PatternI
STK11	cg0749225C	19	1189406	1228428	19	1748825	520397	36.54	57.2	7.48E-04	0.070	patternA	PatternI
HMG20B	cg2679758C	19	3572775	3579086	19	3585609	6523	35.60	201.8	7.88E-04	0.070	patternA	PatternI
NFKBIL1	cg1957900C	6	31514647	31526606	6	30782272	732375	34.37	38.3	8.46E-04	0.070	patternA	PatternIV
GALK1	cg0586567C	17	73747675	73761792	17	73452251	295424	30.71	45.7	1.06E-03	0.070	patternA	PatternI
RAB3A	cg1252692C	19	18307594	18314884	19	17439208	868386	30.20	8.1	1.09E-03	0.070	patternA	PatternI
STARD3	cg0630716C	17	37793318	37819737	17	38296698	476961	29.24	39.4	1.17E-03	0.070	patternA	PatternI
SULT1A1	cg0610079C	16	28616903	28634946	16	28875018	240072	28.35	73.4	1.24E-03	0.070	patternA	PatternI
MYPOP	cg1830447C	19	46393278	46405862	19	45844176	549102	28.21	18.3	1.25E-03	0.070	patternA	PatternI
PRELID1	cg02460251	5	176730775	176733960	5	176107427	623348	28.10	2059.3	1.26E-03	0.070	patternA	PatternI
PEF1	cg2519294C	1	32095463	32110497	1	32479490	368993	25.66	69.9	1.52E-03	0.070	patternA	PatternI
RXRB	cg14560317	6	33161365	33168630	6	32940489	220876	24.78	375.3	1.62E-03	0.070	patternA	PatternI
SGTA	cg2679758C	19	2754712	2783369	19	3585609	802240	22.79	54.7	1.92E-03	0.070	patternA	PatternI
UBE2M	cg2545817C	19	59067079	59070327	19	59025570	41509	22.45	559.0	1.98E-03	0.070	patternA	PatternI
ARID3B	cg2676925C	15	74833518	74890472	15	75165338	274866	21.76	15.9	2.10E-03	0.070	patternA	PatternIII
MYPOP	cg2483607C	19	46393278	46405862	19	46498091	92229	21.45	16.8	2.17E-03	0.070	patternA	PatternI
AGPAT2	cg14095044	9	139567595	139581875	9	140314220	732345	21.18	176.0	2.22E-03	0.070	patternA	PatternIII
CD59	cg1589265C	11	33719807	33757991	11	33757569	422	20.95	38.4	2.27E-03	0.070	patternA	PatternI
RXRB	cg0609904C	6	33161365	33168630	6	32164151	997214	20.89	349.1	2.28E-03	0.070	patternA	PatternI

RAB3A	cg16572859	19	18307594	18314884	19	18263815	43779	20.18	12.5	2.45E-03	0.070	patternA	PatternI
BRMS1	cg10498476	11	66104804	66112596	11	66035147	69657	19.84	103.7	2.53E-03	0.070	patternA	PatternI
TBC1D10B	cg16947339	16	30368423	30381585	16	30546198	164613	19.70	261.3	2.57E-03	0.070	patternA	PatternI
KLF16	cg05228284	19	1852399	1863567	19	2720847	857280	19.68	89.9	2.57E-03	0.070	patternA	PatternI
COPE	cg11610754	19	19010323	19030206	19	18722595	287728	19.67	232.4	2.58E-03	0.070	patternA	PatternI
LRP3	cg21518056	19	33668509	33698694	19	33183187	485322	19.38	17.8	2.65E-03	0.070	patternA	PatternI
RNF5	cg14560317	6	32146131	32151930	6	32940489	788559	19.32	384.5	2.67E-03	0.070	patternA	PatternI
RXRB	cg22065976	6	33161365	33168630	6	33589061	420431	19.27	296.5	2.68E-03	0.070	patternA	PatternI
GRAMD1A	cg08333703	19	35485688	35517375	19	35225315	260373	19.14	155.3	2.72E-03	0.070	patternA	PatternI
FHOD1	cg24654547	16	67263290	67281561	16	68057165	775604	18.80	61.8	2.82E-03	0.070	patternA	PatternI
RAB3A	cg11610754	19	18307594	18314884	19	18722595	407711	18.77	15.7	2.83E-03	0.070	patternA	PatternI
SNAI3	cg18665648	16	88744090	88752901	16	87799740	944350	18.64	49.6	2.86E-03	0.070	patternA	PatternI
GALK1	cg04510639	17	73747675	73761792	17	74722764	960972	18.57	30.8	2.89E-03	0.070	patternA	PatternI
ZNF684	cg15728256	1	40997233	41013841	1	40254184	743049	-18.45	-2.8	2.92E-03	0.070	patternV	PatternIII
BCL3	cg18075720	19	45250962	45263301	19	45349207	85906	18.43	379.4	2.93E-03	0.070	patternA	PatternI
SIRT6	cg13357752	19	4174106	4182601	19	4639397	456796	18.16	49.9	3.02E-03	0.070	patternA	PatternI
CCS	cg04321378	11	66360292	66373490	11	65819389	540903	18.15	10.6	3.02E-03	0.070	patternA	PatternI
VPS37C	cg05179487	11	60897728	60929089	11	61129696	200607	18.15	41.4	3.02E-03	0.070	patternA	PatternI
GP3M3	cg06099048	6	32158543	32163300	6	32164151	851	18.01	5652.4	3.07E-03	0.070	patternA	PatternI
TPM2	cg20741293	9	35681989	35691017	9	34958139	723850	17.66	13.2	3.19E-03	0.070	patternA	PatternIII
NFKBIL1	cg12478978	6	31514647	31526606	6	30710766	803881	-17.55	-63.9	3.23E-03	0.070	patternA	PatternIII
ZNF684	cg19320564	1	40997233	41013841	1	40157253	839980	-17.31	-2.0	3.32E-03	0.070	patternV	PatternI
SH3GL1	cg26797585	19	4360367	4400544	19	3585609	774758	16.81	46.5	3.52E-03	0.070	patternA	PatternI
GALE	cg09896346	1	24122089	24127271	1	23751195	370894	16.71	34.8	3.56E-03	0.070	patternA	PatternI
FLOT1	cg01365762	6	30695486	30710510	6	30457827	237659	16.63	880.8	3.60E-03	0.070	patternA	PatternI
SCYL1	cg23430644	11	65292548	65306175	11	65383542	77367	16.57	220.0	3.62E-03	0.070	patternA	PatternI
SNAI3	cg16567770	16	88744090	88752901	16	89283922	531021	16.54	71.3	3.64E-03	0.070	patternA	PatternI
ZNF524	cg11781339	19	56111388	56114504	19	56092040	19348	16.43	149.2	3.68E-03	0.070	patternA	PatternI
MRPL28	cg07664667	16	417384	420527	16	778351	357824	16.37	251.9	3.71E-03	0.070	patternA	PatternI
RNASEK	cg20347916	17	6915736	6917851	17	7621118	703267	16.23	3475.9	3.77E-03	0.070	patternA	PatternI
GNA15	cg26797585	19	3136191	3163767	19	3585609	421842	16.22	35.1	3.78E-03	0.070	patternA	PatternI
FXR2	cg02705837	17	7494548	7518189	17	7554666	36477	16.22	21.4	3.78E-03	0.070	patternA	PatternI

SAFB	cg13357752	19	5623046	5668489	19	4639397	983649	15.85	34.2	3.95E-03	0.070	patternA	PatternI
WNK2	cg26786723	9	95947198	96082854	9	96792955	710101	15.73	0.6	4.02E-03	0.070	patternA	PatternI
S1PR4	cg05228284	19	3172344	3180329	19	2720847	451497	15.64	771.7	4.06E-03	0.070	patternA	PatternI
TBC1D10B	cg27609508	16	30368423	30381585	16	30905407	523822	15.52	150.3	4.12E-03	0.070	patternA	PatternI
SULT1A1	cg02215815	16	28616903	28634946	16	28962783	327837	15.48	38.6	4.15E-03	0.070	patternA	PatternI
SLC27A1	cg16572859	19	17579578	17616977	19	18263815	646838	15.39	10.0	4.20E-03	0.070	patternA	PatternI
FLOT1	cg06414921	6	30695486	30710510	6	31276504	565994	15.36	465.9	4.21E-03	0.070	patternA	PatternI
MLLT1	cg21575584	19	6212966	6279959	19	5690316	522650	15.09	65.9	4.36E-03	0.070	patternA	PatternI
ARID5A	cg10816249	2	97202480	97218375	2	96782111	420369	15.02	224.2	4.40E-03	0.070	patternA	PatternI
TBKBP1	cg21816532	17	45771447	45789416	17	46680006	890590	14.99	99.4	4.42E-03	0.070	patternA	PatternI
FKBPL	cg27196273	6	32096484	32098068	6	32632992	534924	14.87	49.4	4.49E-03	0.070	patternA	PatternI
BLOC1S3	cg18075720	19	45682003	45685059	19	45349207	332796	14.63	11.8	4.64E-03	0.070	patternA	PatternI
HCAR2	cg21131339	12	123185840	123187890	12	123848917	661027	14.61	1209.7	4.65E-03	0.070	patternA	PatternI
ZBTB45	cg21994576	19	59024897	59050278	19	58739778	285119	14.40	9.4	4.79E-03	0.070	patternA	PatternIV
RXRB	cg04263436	6	33161365	33168630	6	33245467	76837	14.32	392.1	4.84E-03	0.070	patternA	PatternI
HMG20B	cg05228284	19	3572775	3579086	19	2720847	851928	13.92	82.8	5.12E-03	0.070	patternA	PatternI
BRMS1	cg15082918	11	66104804	66112596	11	66104153	651	13.75	157.8	5.25E-03	0.070	patternA	PatternI
PHF23	cg02705837	17	7138347	7143041	17	7554666	411625	13.71	241.9	5.28E-03	0.070	patternA	PatternI
ARID5A	cg17609600	2	97202480	97218375	2	97535892	317517	13.65	183.3	5.33E-03	0.070	patternA	PatternI
B3GALT4	cg23011817	6	33244917	33252609	6	33422290	169681	13.64	97.9	5.33E-03	0.070	patternA	PatternI
SKIL	cg07139301	3	170075466	170114623	3	170746207	631584	-13.62	-10.7	5.34E-03	0.070	patternV	PatternIV
ZBTB45	cg25458175	19	59024897	59050278	19	59025570	673	13.54	15.5	5.41E-03	0.070	patternA	PatternI
LRSAM1	cg13568343	9	130213765	130265780	9	129676623	537142	13.49	13.2	5.45E-03	0.070	patternA	PatternI
SIRT6	cg14710040	19	4174106	4182601	19	3985464	188642	13.45	31.0	5.48E-03	0.070	patternA	PatternI
GSS	cg24253482	20	33516236	33543620	20	33064396	451840	-13.45	-31.0	5.48E-03	0.070	patternA	PatternIII
SIRT6	cg26797585	19	4174106	4182601	19	3585609	588497	13.38	105.4	5.54E-03	0.070	patternA	PatternI
B3GALT4	cg01170201	6	33244917	33252609	6	32820976	423941	13.33	134.9	5.58E-03	0.070	patternA	PatternI
FFAR2	cg05815685	19	35934809	35942669	19	36036576	93907	13.33	1048.0	5.58E-03	0.070	patternA	PatternI
SULT1A1	cg08495403	16	28616903	28634946	16	28222985	393918	13.30	39.8	5.61E-03	0.070	patternA	PatternI
SPNS2	cg09904774	17	4402133	4442330	17	3539754	862379	13.27	3.2	5.64E-03	0.070	patternA	PatternI
SPNS2	cg20866375	17	4402133	4442330	17	3572559	829574	13.21	2.8	5.68E-03	0.070	patternA	PatternI
ZBTB45	cg01268824	19	59024897	59050278	19	58220818	804079	13.14	5.9	5.74E-03	0.070	patternA	PatternI

RNF5	cg01170201	6	32146131	32151930	6	32820976	669046	13.13	411.9	5.75E-03	0.070	patternA	PatternI
RXRB	cg06618123	6	33161365	33168630	6	33377795	209165	13.12	304.9	5.76E-03	0.070	patternA	PatternI
ZNF219	cg18415585	14	21558205	21572881	14	21100888	457317	13.02	7.8	5.85E-03	0.070	patternA	PatternI
DAXX	cg04263436	6	33286335	33297046	6	33245467	40868	13.00	591.3	5.87E-03	0.070	patternA	PatternI
USF1	cg00329300	1	161009041	161015767	1	161008462	579	12.86	296.0	6.00E-03	0.070	patternA	PatternI
BLOC1S3	cg23048660	19	45682003	45685059	19	45004795	677208	12.85	14.6	6.00E-03	0.070	patternA	PatternI
SPNS2	cg17199681	17	4402133	4442330	17	3540328	861805	12.72	3.8	6.12E-03	0.070	patternA	PatternI
MVD	cg18665648	16	88718343	88729569	16	87799740	918603	12.64	20.0	6.20E-03	0.070	patternA	PatternI
DAXX	cg14560317	6	33286335	33297046	6	32940489	345846	12.54	563.9	6.30E-03	0.070	patternA	PatternI
CCS	cg23430644	11	66360292	66373490	11	65383542	976750	12.52	36.7	6.32E-03	0.070	patternA	PatternI
ZBTB45	cg02344833	19	59024897	59050278	19	58545285	479612	12.48	12.3	6.36E-03	0.070	patternA	PatternI
MYPOP	cg09120986	19	46393278	46405862	19	47249219	843357	12.32	29.5	6.52E-03	0.070	patternA	PatternI
TRIOBP	cg05293930	22	38093011	38172563	22	39151089	978526	12.29	37.9	6.56E-03	0.070	patternA	PatternI
ZC3H3	cg00713939	8	144519825	144623623	8	144660590	36967	12.23	8.0	6.62E-03	0.070	patternA	PatternI
FKBPL	cg00124488	6	32096484	32098068	6	31509762	586722	12.07	48.9	6.80E-03	0.070	patternA	PatternI
RXRB	cg11348335	6	33161365	33168630	6	32939525	221840	12.04	168.6	6.83E-03	0.070	patternA	PatternI
TSG101	cg06671842	11	18489883	18548779	11	18813477	264698	12.02	10.4	6.85E-03	0.070	patternA	PatternI
KRT23	cg13092355	17	39078948	39093886	17	39992602	898716	12.00	152.9	6.87E-03	0.070	patternA	PatternI
NR2F6	cg12526923	19	17342692	17356749	19	17439208	82459	11.93	8.7	6.95E-03	0.070	patternA	PatternI
PANX2	cg11875773	22	50609160	50618723	22	50468633	140527	11.82	200.1	7.08E-03	0.070	patternA	PatternI
SPNS2	cg14640386	17	4402133	4442330	17	5185735	743405	11.79	2.0	7.12E-03	0.070	patternA	PatternI
PPP4C	cg16947339	16	30087299	30096698	16	30546198	449500	11.75	653.0	7.16E-03	0.070	patternA	PatternI
SCYL1	cg04321378	11	65292548	65306175	11	65819389	513214	11.74	63.2	7.17E-03	0.070	patternA	PatternI
PEF1	cg22123309	1	32095463	32110497	1	31191561	903902	11.71	42.8	7.22E-03	0.070	patternA	PatternI
AGPAT2	cg14788802	9	139567595	139581875	9	140446233	864358	11.67	80.5	7.26E-03	0.070	patternA	PatternI
PRCC	cg03055346	1	156720402	156770607	1	156830080	59473	11.62	21.0	7.33E-03	0.070	patternA	PatternI
PRR14	cg16947339	16	30662038	30667761	16	30546198	115840	11.56	518.3	7.40E-03	0.070	patternA	PatternI
KLF16	cg16238993	19	1852399	1863567	19	1132372	720027	11.49	194.2	7.49E-03	0.070	patternA	PatternI
DVL2	cg02705837	17	7128660	7137864	17	7554666	416802	11.44	114.2	7.55E-03	0.070	patternA	PatternI
SGTA	cg05228284	19	2754712	2783369	19	2720847	33865	11.42	22.4	7.59E-03	0.070	patternA	PatternI
KCNQ1	cg07333715	11	2465914	2870339	11	2292691	173223	11.42	3.8	7.59E-03	0.070	patternA	PatternI
TADA3	cg10683958	3	9821544	9834695	3	9885602	50907	11.33	268.5	7.70E-03	0.070	patternA	PatternI

BLOC1S3	cg24836072	19	45682003	45685059	19	46498091	813032	11.16	12.2	7.94E-03	0.070	patternA	PatternI
RBAK	cg01275887	7	5085452	5109119	7	4747216	338236	-11.12	-42.5	7.98E-03	0.070	patternV	PatternII
SLC25A1	cg19940065	22	19163095	19166343	22	19701734	535391	11.12	280.0	7.99E-03	0.070	patternA	PatternI
SPRYD3	cg21845580	12	53458388	53473204	12	53472882	322	11.10	68.4	8.02E-03	0.070	patternA	PatternI
BBC3	cg09120986	19	47724081	47736023	19	47249219	474862	10.95	133.5	8.24E-03	0.070	patternA	PatternI
FKBPL	cg06099048	6	32096484	32098068	6	32164151	66083	10.93	98.8	8.26E-03	0.070	patternA	PatternI
PRR14	cg27609508	16	30662038	30667761	16	30905407	237646	10.93	298.2	8.27E-03	0.070	patternA	PatternI
BLOC1S3	cg18304472	19	45682003	45685059	19	45844176	159117	10.89	13.2	8.32E-03	0.070	patternA	PatternI
SGTA	cg16260977	19	2754712	2783369	19	3761708	978339	10.86	43.6	8.37E-03	0.070	patternA	PatternI
TBC1D10B	cg15853475	16	30368423	30381585	16	29757565	610858	10.82	242.7	8.44E-03	0.070	patternA	PatternI
PANX2	cg02486929	22	50609160	50618723	22	50609012	148	10.77	107.2	8.51E-03	0.070	patternA	PatternI
SCYL1	cg19626726	11	65292548	65306175	11	65668074	361899	10.76	119.2	8.53E-03	0.070	patternA	PatternI
MYO7B	cg00906167	2	128293378	128395304	2	128615801	220497	10.68	4.7	8.65E-03	0.070	patternA	PatternI
MVD	cg16567770	16	88718343	88729569	16	89283922	554353	10.67	28.7	8.67E-03	0.070	patternA	PatternI
MYO7B	cg09131629	2	128293378	128395304	2	128433309	38005	10.67	6.4	8.67E-03	0.070	patternA	PatternI
RAB43	cg08867370	3	128806412	128841644	3	129034220	192576	10.64	23.8	8.72E-03	0.070	patternA	PatternI
GRAMD1A	cg05815685	19	35485688	35517375	19	36036576	519201	10.62	129.9	8.76E-03	0.070	patternA	PatternI
B3GALT4	cg04263436	6	33244917	33252609	6	33245467	550	10.58	131.2	8.81E-03	0.070	patternA	PatternI
DDA1	cg12526923	19	17420327	17434110	19	17439208	5098	10.56	31.5	8.85E-03	0.070	patternA	PatternI
FFAR2	cg08333703	19	35934809	35942669	19	35225315	709494	10.55	1240.9	8.86E-03	0.070	patternA	PatternI
COPE	cg16572859	19	19010323	19030206	19	18263815	746508	10.54	184.3	8.88E-03	0.070	patternA	PatternI
ZNF787	cg11781339	19	56598732	56632649	19	56092040	506692	10.50	27.5	8.96E-03	0.070	patternA	PatternI
S1PR4	cg26797585	19	3172344	3180329	19	3585609	405280	10.33	1862.2	9.24E-03	0.071	patternA	PatternI
UBE2M	cg01268824	19	59067079	59070327	19	58220818	846261	10.30	210.4	9.29E-03	0.071	patternA	PatternI
RXRB	cg01170201	6	33161365	33168630	6	32820976	340389	10.28	400.1	9.34E-03	0.071	patternA	PatternI
BRMS1	cg23430644	11	66104804	66112596	11	65383542	721262	10.27	139.4	9.34E-03	0.071	patternA	PatternI
ZNF775	cg11490987	7	150065879	150109558	7	149535717	530162	10.23	66.7	9.43E-03	0.071	patternA	PatternI
PPP4C	cg27609508	16	30087299	30096698	16	30905407	808709	10.10	375.1	9.65E-03	0.072	patternA	PatternI
TRIM39	cg23623622	6	30294256	30311506	6	30139880	154376	10.10	44.0	9.66E-03	0.072	patternA	PatternI
GPSM3	cg11348335	6	32158543	32163300	6	32939525	776225	10.00	2722.7	9.85E-03	0.072	patternA	PatternI
STK11	cg16238993	19	1189406	1228428	19	1132372	57034	9.99	46.7	9.86E-03	0.072	patternA	PatternI
RAB3A	cg23264278	19	18307594	18314884	19	19051482	736598	9.99	8.4	9.87E-03	0.072	patternA	PatternI

TRIM39	cg0133639C	6	30294256	30311506	6	29895059	399197	9.84	27.4	1.02E-02	0.074	patternA	PatternI
GP3M3	cg06414921	6	32158543	32163300	6	31276504	882039	9.70	3923.2	1.05E-02	0.074	patternA	PatternI
ACTR1A	cg18505495	10	104238986	104262482	10	104179494	59492	9.70	58.7	1.05E-02	0.074	patternA	PatternI
SCYL1	cg15574972	11	65292548	65306175	11	65265134	27414	9.66	183.5	1.05E-02	0.074	patternA	PatternI
TBKBP1	cg20440414	17	45771447	45789416	17	46178346	388930	9.65	117.8	1.06E-02	0.074	patternA	PatternI
DDAH2	cg06099048	6	31694815	31698394	6	32164151	465757	9.64	314.7	1.06E-02	0.074	patternA	PatternI
MARK4	cg18304472	19	45582546	45808541	19	45844176	35635	9.62	8.5	1.06E-02	0.074	patternA	PatternI
SESN2	cg26040332	1	28586038	28609002	1	27960788	625250	9.57	36.6	1.07E-02	0.074	patternA	PatternI
SAFB	cg21575584	19	5623046	5668489	19	5690316	21827	9.46	71.0	1.10E-02	0.075	patternA	PatternI
DAXX	cg22065976	6	33286335	33297046	6	33589061	292015	9.45	443.9	1.10E-02	0.075	patternA	PatternI
XRCC3	cg08142571	14	104163946	104181841	14	104096390	67556	9.36	42.1	1.12E-02	0.075	patternA	PatternI
MIF4GD	cg05100739	17	73262309	73267308	17	72733163	529146	9.33	161.6	1.13E-02	0.075	patternA	PatternI
MRPL28	cg06525293	16	417384	420527	16	725532	305005	9.33	239.9	1.13E-02	0.075	patternA	PatternI
NLRX1	cg1476201C	11	119037277	119054725	11	118443311	593966	9.25	104.0	1.15E-02	0.075	patternA	PatternI
BCL3	cg04571944	19	45250962	45263301	19	45644563	381262	9.23	2365.1	1.15E-02	0.075	patternA	PatternIV
TSEN34	cg17892871	19	54693789	54697585	19	54618653	75136	9.21	651.8	1.16E-02	0.075	patternA	PatternI
MOB2	cg16328251	11	1490687	1522477	11	1770181	247704	9.21	20.1	1.16E-02	0.075	patternA	PatternI
ADAP1	cg09754845	7	937540	995043	7	1408818	413775	9.18	45.8	1.17E-02	0.075	patternA	PatternI
MVD	cg14752986	16	88718343	88729569	16	88717571	772	9.08	38.1	1.19E-02	0.075	patternA	PatternI
STK11	cg2157864C	19	1189406	1228428	19	590409	598997	9.04	42.5	1.20E-02	0.075	patternA	PatternIV
LRSAM1	cg21260583	9	130213765	130265780	9	130830463	564683	9.04	19.8	1.20E-02	0.075	patternA	PatternI
CAPG	cg15317609	2	85621871	85645555	2	85839182	193627	8.97	121.2	1.22E-02	0.075	patternA	PatternI
ZBTB45	cg0295505C	19	59024897	59050278	19	59070391	20113	8.96	12.5	1.22E-02	0.075	patternA	PatternI
SCYL1	cg15082918	11	65292548	65306175	11	66104153	797978	8.96	245.8	1.22E-02	0.075	patternA	PatternI
PLIN3	cg13357752	19	4838353	4867780	19	4639397	198956	8.96	80.4	1.22E-02	0.075	patternA	PatternI
CAPG	cg24504864	2	85621871	85645555	2	85665051	19496	8.92	104.6	1.23E-02	0.075	patternA	PatternI
SNAI3	cg14752986	16	88744090	88752901	16	88717571	26519	8.92	94.0	1.23E-02	0.075	patternA	PatternI
FLOT1	cg21636096	6	30695486	30710510	6	30313077	382409	8.89	743.4	1.24E-02	0.075	patternA	PatternI
UBE2M	cg21994576	19	59067079	59070327	19	58739778	327301	8.85	336.7	1.25E-02	0.075	patternA	PatternIV
NUBP2	cg06526921	16	1832902	1839192	16	2034455	195263	8.84	160.1	1.25E-02	0.075	patternA	PatternI
DAXX	cg06618123	6	33286335	33297046	6	33377795	80749	8.82	457.2	1.26E-02	0.075	patternA	PatternI
BCL3	cg07251576	19	45250962	45263301	19	45349316	86015	8.78	337.1	1.27E-02	0.075	patternA	PatternI

DAXX	cg01170201	6	33286335	33297046	6	32820976	465359	8.75	602.0	1.28E-02	0.075	patternA	PatternI
HDAC5	cg05951576	17	42154114	42201070	17	42083264	70850	8.71	107.9	1.29E-02	0.075	patternA	PatternI
DAPK3	cg26797585	19	3958451	3971121	19	3585609	372842	8.70	90.1	1.30E-02	0.075	patternA	PatternI
ATP6V0B	cg18540614	1	44440159	44443967	1	43833945	606214	8.65	2373.4	1.31E-02	0.075	patternA	PatternI
KRT23	cg09852679	17	39078948	39093886	17	38973067	105881	8.65	420.4	1.31E-02	0.075	patternA	PatternI
MED16	cg21578640	19	867962	893218	19	590409	277553	8.62	93.7	1.32E-02	0.075	patternA	PatternIV
ARID5A	cg12224898	2	97202480	97218375	2	96971451	231029	8.62	115.6	1.32E-02	0.075	patternA	PatternI
ZNF282	cg12857488	7	148892577	148923339	7	149195092	271753	8.61	12.1	1.32E-02	0.075	patternA	PatternI
SLC27A1	cg12526923	19	17579578	17616977	19	17439208	140370	8.55	6.4	1.34E-02	0.075	patternA	PatternI
FLOT2	cg26930529	17	27206353	27224697	17	26971994	234359	8.55	1270.2	1.34E-02	0.075	patternA	PatternI
TBC1D10B	cg10277268	16	30368423	30381585	16	30825733	444148	8.54	316.7	1.34E-02	0.075	patternA	PatternI
FLOT1	cg00124488	6	30695486	30710510	6	31509762	799252	8.50	326.2	1.35E-02	0.075	patternA	PatternI
DAXX	cg21352296	6	33286335	33297046	6	34216944	919898	8.47	382.9	1.36E-02	0.075	patternA	PatternI
HMG20B	cg16260977	19	3572775	3579086	19	3761708	182622	8.39	159.8	1.39E-02	0.075	patternA	PatternI
SH3GL1	cg14710040	19	4360367	4400544	19	3985464	374903	8.38	13.5	1.39E-02	0.075	patternA	PatternI
BRMS1	cg04321378	11	66104804	66112596	11	65819389	285415	8.33	40.0	1.41E-02	0.075	patternA	PatternI
SH3GL1	cg13357752	19	4360367	4400544	19	4639397	238853	8.31	21.7	1.42E-02	0.075	patternA	PatternI
FHOD1	cg03498383	16	67263290	67281561	16	68002044	720483	8.31	54.2	1.42E-02	0.075	patternA	PatternI
UBE2M	cg02955050	19	59067079	59070327	19	59070391	64	8.31	446.3	1.42E-02	0.075	patternA	PatternI
CCS	cg19626726	11	66360292	66373490	11	65668074	692218	8.28	19.8	1.43E-02	0.075	patternA	PatternI
ASPRV1	cg25631352	2	70187226	70189397	2	70995527	806130	8.28	97.4	1.43E-02	0.075	patternA	PatternI
GALK1	cg20715365	17	73747675	73761792	17	73900573	138781	8.28	47.1	1.43E-02	0.075	patternA	PatternI
MARK4	cg24836072	19	45582546	45808541	19	46498091	689550	8.28	7.8	1.43E-02	0.075	patternA	PatternI
HMG20B	cg07071609	19	3572775	3579086	19	4535315	956229	8.27	184.9	1.43E-02	0.075	patternA	PatternI
MXD3	cg02460251	5	176728462	176739758	5	176107427	621035	8.25	1127.6	1.44E-02	0.075	patternA	PatternI
HSF1	cg13490753	8	145515280	145538385	8	145825518	287133	8.22	237.7	1.45E-02	0.075	patternA	PatternI
TNFRSF12A	cg09935998	16	3068446	3072384	16	3054327	14119	8.22	23.7	1.45E-02	0.075	patternA	PatternI
TNFRSF10C	cg20460852	8	22941868	22974950	8	23082822	107872	8.22	1750.2	1.45E-02	0.075	patternA	PatternI
IL4R	cg10290107	16	27324989	27376099	16	27561132	185033	8.21	183.1	1.45E-02	0.075	patternA	PatternI
SPNS2	cg23899285	17	4402133	4442330	17	4699393	257063	8.21	2.8	1.45E-02	0.075	patternA	PatternI
B3GALT4	cg22065976	6	33244917	33252609	6	33589061	336452	8.18	98.4	1.46E-02	0.075	patternA	PatternI
TRIM39	cg23168870	6	30294256	30311506	6	30523692	212186	8.18	47.7	1.46E-02	0.075	patternA	PatternI

UBE2M	cg02344833	19	59067079	59070327	19	58545285	521794	8.16	436.6	1.47E-02	0.075	patternA	PatternI
TNFAIP8L2	cg07367563	1	151129105	151132225	1	151032068	97037	8.15	790.4	1.47E-02	0.075	patternA	PatternI
PANK4	cg04407228	1	2439972	2458039	1	1710158	729814	8.13	16.1	1.48E-02	0.075	patternA	PatternI
COPE	cg09374949	19	19010323	19030206	19	18548964	461359	8.09	334.8	1.49E-02	0.075	patternA	PatternI
B3GALT4	cg14560317	6	33244917	33252609	6	32940489	304428	8.05	124.4	1.51E-02	0.075	patternA	PatternI
FUT7	cg14095044	9	139924626	139927462	9	140314220	386758	7.98	2737.0	1.53E-02	0.075	patternA	PatternIII
HCK	cg08728520	20	30639991	30689659	20	31331105	641446	7.97	522.9	1.54E-02	0.075	patternA	PatternI
RXRB	cg27196273	6	33161365	33168630	6	32632992	528373	7.97	171.5	1.54E-02	0.075	patternA	PatternI
ZNF609	cg18650670	15	64752941	64978264	15	65689152	710888	-7.96	-5.1	1.54E-02	0.075	patternA	PatternIV
BTBD2	cg07492258	19	1985447	2034880	19	1748825	236622	7.96	78.8	1.54E-02	0.075	patternA	PatternI
CYSTM1	cg11268983	5	139554227	139661637	5	140262304	600667	7.96	12.9	1.54E-02	0.075	patternA	PatternI
MED16	cg16238993	19	867962	893218	19	1132372	239154	7.94	102.7	1.55E-02	0.075	patternA	PatternI
CCS	cg10498476	11	66360292	66373490	11	66035147	325145	7.92	26.9	1.56E-02	0.075	patternA	PatternI
PPP4C	cg15853475	16	30087299	30096698	16	29757565	329734	7.92	604.9	1.56E-02	0.075	patternA	PatternI
HSPA1L	cg13964363	6	31777396	31783437	6	32157454	374017	7.90	53.8	1.56E-02	0.075	patternA	PatternIV
INTS5	cg07747515	11	62414320	62420774	11	61659326	754994	7.90	81.5	1.57E-02	0.075	patternA	PatternI
PRR14	cg15853475	16	30662038	30667761	16	29757565	904473	7.89	480.3	1.57E-02	0.075	patternA	PatternI
LYPLA2	cg09896346	1	24117460	24122029	1	23751195	366265	7.88	496.4	1.57E-02	0.075	patternA	PatternI
TSPO	cg24407859	22	43547520	43559248	22	43411083	136437	7.86	645.9	1.58E-02	0.075	patternA	PatternI
XRCC3	cg15649561	14	104163946	104181841	14	103852292	311654	7.84	127.7	1.59E-02	0.075	patternA	PatternI
RAB3A	cg09374949	19	18307594	18314884	19	18548964	234080	7.80	22.5	1.60E-02	0.075	patternA	PatternI
RNF5	cg06099048	6	32146131	32151930	6	32164151	12221	7.74	353.0	1.63E-02	0.076	patternA	PatternI
ZNF467	cg06842319	7	149461271	149470568	7	150453731	983163	-7.72	-4074.3	1.64E-02	0.076	patternA	PatternII
MPV17L2	cg23264278	19	18303992	18307758	19	19051482	743724	7.72	21.1	1.64E-02	0.076	patternA	PatternI
B3GALT4	cg12770425	6	33244917	33252609	6	33585071	332462	7.68	119.2	1.66E-02	0.076	patternA	PatternII
PGM1	cg14800796	1	64058947	64125916	1	63833137	225810	7.55	18.1	1.71E-02	0.078	patternA	PatternI
VPS37C	cg07747515	11	60897728	60929089	11	61659326	730237	7.55	32.9	1.71E-02	0.078	patternA	PatternI
PLIN3	cg21575584	19	4838353	4867780	19	5690316	822536	7.53	167.4	1.72E-02	0.078	patternA	PatternI
CTDP1	cg27121095	18	77439801	77514510	18	77155145	284656	7.51	26.7	1.73E-02	0.078	patternA	PatternI
MIF4GD	cg05145649	17	73262309	73267308	17	73127468	134841	7.48	147.8	1.74E-02	0.079	patternA	PatternI
MIF4GD	cg20715365	17	73262309	73267308	17	73900573	633265	7.45	87.7	1.75E-02	0.079	patternA	PatternI
RNF5	cg11348335	6	32146131	32151930	6	32939525	787595	7.43	171.0	1.76E-02	0.079	patternA	PatternI

GPSM3	cg27196273	6	32158543	32163300	6	32632992	469692	7.42	2773.0	1.77E-02	0.079	patternA	PatternI
KRAS	cg26397265	12	25357723	25403870	12	25348258	9465	-7.41	-30.4	1.77E-02	0.079	patternV	PatternIV
CUEDC2	cg26894311	10	104183002	104192418	10	104153930	29072	7.38	26.8	1.79E-02	0.079	patternA	PatternI
NFKBIE	cg20275500	6	44225903	44233500	6	44237955	4455	7.38	39.0	1.79E-02	0.079	patternA	PatternI
GPSM3	cg14560317	6	32158543	32163300	6	32940489	777189	7.35	5980.4	1.80E-02	0.079	patternA	PatternI
SLC27A1	cg09374949	19	17579578	17616977	19	18548964	931987	7.35	18.0	1.80E-02	0.079	patternA	PatternI
ADAP1	cg01587709	7	937540	995043	7	1570155	575112	7.34	18.3	1.80E-02	0.079	patternA	PatternI
HLX	cg20796294	1	221051699	221058401	1	220219430	832269	7.34	608.3	1.81E-02	0.079	patternA	PatternI
DOK4	cg12469332	16	57505863	57521239	16	58283784	762545	7.28	12.1	1.83E-02	0.079	patternA	PatternI
RNASEK	cg02705837	17	6915736	6917851	17	7554666	636815	7.28	2858.6	1.84E-02	0.079	patternA	PatternI
COPE	cg23264278	19	19010323	19030206	19	19051482	21276	7.28	123.9	1.84E-02	0.079	patternA	PatternI
CAPG	cg19130836	2	85621871	85645555	2	86426474	780919	7.27	108.5	1.84E-02	0.079	patternA	PatternIII
GNA15	cg14710040	19	3136191	3163767	19	3985464	821697	7.22	10.2	1.86E-02	0.079	patternA	PatternI
FXR2	cg20347916	17	7494548	7518189	17	7621118	102929	7.21	25.2	1.87E-02	0.079	patternA	PatternI
MARK4	cg07251576	19	45582546	45808541	19	45349316	233230	7.20	6.8	1.87E-02	0.079	patternA	PatternI
PPP4C	cg10277268	16	30087299	30096698	16	30825733	729035	7.19	790.6	1.88E-02	0.079	patternA	PatternI
MLLT1	cg02301978	19	6212966	6279959	19	7069707	789748	7.19	43.3	1.88E-02	0.079	patternA	PatternI
DAPK3	cg13357752	19	3958451	3971121	19	4639397	668276	7.16	42.3	1.89E-02	0.079	patternA	PatternI
VPS37C	cg25994096	11	60897728	60929089	11	61348278	419189	7.14	34.0	1.91E-02	0.079	patternA	PatternI
STARD3	cg24204940	17	37793318	37819737	17	36904473	888845	7.13	33.0	1.91E-02	0.079	patternA	PatternI
SESN2	cg08139234	1	28586038	28609002	1	29240631	631629	7.13	13.8	1.91E-02	0.079	patternA	PatternI
FLOT1	cg24322638	6	30695486	30710510	6	30524987	170499	7.10	745.1	1.93E-02	0.079	patternA	PatternI
CYSTM1	cg26882009	5	139554227	139661637	5	140346106	684469	7.09	11.7	1.93E-02	0.079	patternA	PatternI
HDAC5	cg04496106	17	42154114	42201070	17	41561072	593042	7.07	107.9	1.94E-02	0.079	patternA	PatternI
SH3GL1	cg16260977	19	4360367	4400544	19	3761708	598659	7.05	36.7	1.95E-02	0.079	patternA	PatternI
RNF5	cg13964363	6	32146131	32151930	6	32157454	5524	7.02	458.2	1.97E-02	0.079	patternA	PatternIV
PRCC	cg00472324	1	156720402	156770607	1	156052196	668206	7.02	22.0	1.97E-02	0.079	patternA	PatternI
HSPA1L	cg06099048	6	31777396	31783437	6	32164151	380714	7.01	41.1	1.97E-02	0.079	patternA	PatternI
SMAD5	cg15028653	5	135468534	135524435	5	134824531	644003	-6.97	-5.6	2.00E-02	0.079	patternV	PatternIV
HMG20B	cg14710040	19	3572775	3579086	19	3985464	406378	6.94	58.1	2.01E-02	0.079	patternA	PatternI
FUT7	cg14788802	9	139924626	139927462	9	140446233	518771	6.93	1251.3	2.02E-02	0.079	patternA	PatternI
SNAI3	cg06757180	16	88744090	88752901	16	88914674	161773	6.93	179.0	2.02E-02	0.079	patternA	PatternI

TBC1D10B	cg04603809	16	30368423	30381585	16	29874120	494303	6.92	237.2	2.02E-02	0.079	patternA	PatternI
RXRB	cg23011817	6	33161365	33168630	6	33422290	253660	6.92	287.0	2.02E-02	0.079	patternA	PatternI
BRMS1	cg19626726	11	66104804	66112596	11	65668074	436730	6.92	75.1	2.02E-02	0.079	patternA	PatternI
CD2AP	cg09215818	6	47445525	47594999	6	48415237	820238	-6.91	-7.5	2.03E-02	0.079	patternV	PatternII
BCL3	cg18304472	19	45250962	45263301	19	45844176	580875	6.91	418.6	2.03E-02	0.079	patternA	PatternI
ASPRV1	cg25336731	2	70187226	70189397	2	70520884	331487	6.90	170.9	2.04E-02	0.079	patternA	PatternI
RNASEK	cg19488133	17	6915736	6917851	17	7297863	380012	6.88	3939.1	2.05E-02	0.079	patternA	PatternI
ATP6V0D1	cg24654547	16	67471917	67515140	16	68057165	542025	6.84	280.6	2.07E-02	0.080	patternA	PatternI
NR2F6	cg16572859	19	17342692	17356749	19	18263815	907066	6.82	13.3	2.09E-02	0.080	patternA	PatternI
HDAC5	cg14559369	17	42154114	42201070	17	42976850	775780	6.71	79.6	2.15E-02	0.082	patternA	PatternI
TALDO1	cg24440302	11	747329	765024	11	406829	340500	6.70	1716.3	2.15E-02	0.082	patternA	PatternI
TRIM39	cg26161170	6	30294256	30311506	6	30313174	1668	6.70	32.2	2.16E-02	0.082	patternA	PatternI
BCL3	cg23048660	19	45250962	45263301	19	45004795	246167	6.68	460.9	2.17E-02	0.082	patternA	PatternI
TRIM39	cg24322638	6	30294256	30311506	6	30524987	213481	6.60	46.5	2.22E-02	0.083	patternA	PatternI
PANX2	cg04705716	22	50609160	50618723	22	51020991	402268	6.59	184.2	2.23E-02	0.083	patternA	PatternI
ST3GAL4	cg14123737	11	126225535	126310239	11	126225373	162	6.58	13.8	2.24E-02	0.083	patternA	PatternI
TP53I11	cg03487637	11	44907454	44972840	11	45940039	967199	6.57	96.9	2.24E-02	0.083	patternA	PatternI
GNA15	cg19244855	19	3136191	3163767	19	3029152	107039	6.56	11.1	2.25E-02	0.083	patternA	PatternI
GALK1	cg05145649	17	73747675	73761792	17	73127468	620207	6.55	78.8	2.25E-02	0.083	patternA	PatternI
DDA1	cg16572859	19	17420327	17434110	19	18263815	829705	6.53	48.0	2.26E-02	0.083	patternA	PatternI
BTBD2	cg16238993	19	1985447	2034880	19	1132372	853075	6.53	64.5	2.27E-02	0.083	patternA	PatternI
SH3GL1	cg07071609	19	4360367	4400544	19	4535315	134771	6.52	42.3	2.27E-02	0.083	patternA	PatternI
USF1	cg26146390	1	161009041	161015767	1	160068471	940570	6.51	273.8	2.28E-02	0.083	patternA	PatternI
TBC1D10B	cg00352195	16	30368423	30381585	16	30773975	392390	6.49	219.4	2.29E-02	0.083	patternA	PatternI
ANO10	cg10283155	3	43396351	43733086	3	42642604	753747	6.49	1.2	2.29E-02	0.083	patternA	PatternI
ARID3B	cg23152885	15	74833518	74890472	15	74422282	411236	6.49	25.9	2.29E-02	0.083	patternA	PatternI
LIMK2	cg06494227	22	31608225	31676066	22	30752758	855467	6.47	134.6	2.30E-02	0.083	patternA	PatternI
PHF23	cg20347916	17	7138347	7143041	17	7621118	478077	6.46	284.6	2.31E-02	0.083	patternA	PatternI
CYSTM1	cg12588763	5	139554227	139661637	5	139555533	1306	6.46	13.7	2.31E-02	0.083	patternA	PatternI
SLC29A2	cg04321378	11	66129992	66139685	11	65819389	310603	6.45	4.7	2.32E-02	0.083	patternA	PatternI
BRMS1	cg15574972	11	66104804	66112596	11	65265134	839670	6.44	115.5	2.33E-02	0.083	patternA	PatternI
MPV17L2	cg12526923	19	18303992	18307758	19	17439208	864784	6.44	19.9	2.33E-02	0.083	patternA	PatternI

TBC1D10B	cg03466485	16	30368423	30381585	16	30411736	30151	6.43	199.3	2.33E-02	0.083	patternA	PatternI
VPS37C	cg15454066	11	60897728	60929089	11	61595377	666288	6.41	36.5	2.35E-02	0.083	patternA	PatternI
PLIN3	cg1471004C	19	4838353	4867780	19	3985464	852889	6.41	49.4	2.35E-02	0.083	patternA	PatternI
KLF16	cg07492258	19	1852399	1863567	19	1748825	103574	6.40	231.6	2.36E-02	0.083	patternA	PatternI
MVD	cg0675718C	16	88718343	88729569	16	88914674	185105	6.39	72.2	2.36E-02	0.083	patternA	PatternI
TP53I11	cg08680146	11	44907454	44972840	11	45307938	335098	6.39	95.5	2.36E-02	0.083	patternA	PatternI
TRMT112	cg13972394	11	64083932	64085556	11	63448941	634991	6.35	807.9	2.39E-02	0.083	patternV	PatternI
ITGB8	cg10003623	7	20370325	20455377	7	19600886	769439	-6.35	-3.9	2.39E-02	0.083	patternV	PatternIII
DAXX	cg27196273	6	33286335	33297046	6	32632992	653343	6.30	256.6	2.43E-02	0.084	patternA	PatternI
YIPF1	cg12759997	1	54317392	54356407	1	54518742	162335	6.30	48.1	2.43E-02	0.084	patternA	PatternI
IFITM2	cg24440302	11	307631	315272	11	406829	91557	6.29	20851.7	2.43E-02	0.084	patternA	PatternI
CCDC85B	cg15082918	11	65657875	65659105	11	66104153	445048	6.28	774.6	2.44E-02	0.084	patternV	PatternI
CST7	cg19654195	20	24929866	24940564	20	24450361	479505	6.27	383.4	2.45E-02	0.084	patternA	PatternI
ATAD3A	cg2506604C	1	1447531	1470067	1	936229	511302	6.27	8.2	2.45E-02	0.084	patternA	PatternI
RNASEK	cg13545212	17	6915736	6917851	17	6617192	298544	6.26	3515.3	2.46E-02	0.084	patternA	PatternI
HCK	cg25803642	20	30639991	30689659	20	31349752	660093	6.17	415.5	2.53E-02	0.086	patternA	PatternI
PFKFB3	cg27222274	10	6186881	6277495	10	6962378	684883	6.13	11.8	2.56E-02	0.086	patternA	PatternI
FLYWCH2	cg0908003C	16	2933187	2949383	16	2820366	112821	6.12	53.4	2.56E-02	0.086	patternA	PatternII
ATP6V0D1	cg03498383	16	67471917	67515140	16	68002044	486904	6.12	247.9	2.57E-02	0.086	patternA	PatternI
DOK4	cg2736796C	16	57505863	57521239	16	56702038	803825	6.11	8.4	2.58E-02	0.086	patternA	PatternI
ZNF467	cg12857488	7	149461271	149470568	7	149195092	266179	6.08	558.6	2.60E-02	0.086	patternA	PatternI
ZNF219	cg23576507	14	21558205	21572881	14	21571844	1037	6.07	25.7	2.61E-02	0.086	patternA	PatternI
DAXX	cg11348335	6	33286335	33297046	6	32939525	346810	6.07	249.5	2.61E-02	0.086	patternA	PatternI
HDAC5	cg01065373	17	42154114	42201070	17	41476044	678070	6.06	118.0	2.61E-02	0.086	patternA	PatternIV
KCNQ1	cg16328251	11	2465914	2870339	11	1770181	695733	6.06	3.2	2.62E-02	0.086	patternA	PatternI
DAXX	cg23011817	6	33286335	33297046	6	33422290	125244	6.06	430.6	2.62E-02	0.086	patternA	PatternI
ACAA1	cg10495947	3	38144620	38178733	3	39148675	969942	6.04	95.2	2.63E-02	0.087	patternA	PatternI
B3GALT4	cg11348335	6	33244917	33252609	6	32939525	305392	6.03	55.5	2.64E-02	0.087	patternA	PatternI
COL9A3	cg06026331	20	61447596	61472511	20	60912101	535495	6.00	61.4	2.67E-02	0.087	patternA	PatternI
PRCC	cg02237987	1	156720402	156770607	1	156897441	126834	6.00	28.8	2.67E-02	0.087	patternA	PatternI
HSF1	cg00713939	8	145515280	145538385	8	144660590	854690	5.97	31.0	2.69E-02	0.087	patternA	PatternI
GPSM3	cg00124488	6	32158543	32163300	6	31509762	648781	5.97	2726.6	2.69E-02	0.087	patternA	PatternI

DVL2	cg19488133	17	7128660	7137864	17	7297863	159999	5.95	154.6	2.71E-02	0.088	patternA	PatternI
RILPL1	cg21131339	12	123955925	124018265	12	123848917	107008	5.94	6.5	2.72E-02	0.088	patternA	PatternI
MOB2	cg07333715	11	1490687	1522477	11	2292691	770214	5.91	23.4	2.74E-02	0.088	patternA	PatternI
CCNL1	cg15362595	3	156864297	156878549	3	156392089	472208	-5.91	-114.3	2.74E-02	0.088	patternV	PatternI
ZNF672	cg18411883	1	249132409	249143716	1	248710638	421771	5.90	223.0	2.75E-02	0.088	patternA	PatternIII
PPP4C	cg04603809	16	30087299	30096698	16	29874120	213179	5.90	591.1	2.76E-02	0.088	patternA	PatternI
RAB39A	cg14844619	11	107799229	107834208	11	107880372	46164	-5.87	-2.5	2.78E-02	0.088	patternV	PatternIV
BTBD2	cg05228284	19	1985447	2034880	19	2720847	685967	5.87	29.6	2.78E-02	0.088	patternA	PatternI
PACSIN2	cg24407859	22	43231418	43411151	22	43411083	68	5.87	33.4	2.78E-02	0.088	patternA	PatternI
TMUB1	cg06842319	7	150778167	150780633	7	150453731	324436	-5.86	-2254.5	2.79E-02	0.088	patternA	PatternII
NFKBIL1	cg23168870	6	31514647	31526606	6	30523692	990955	5.86	38.0	2.79E-02	0.088	patternA	PatternI
ZNF282	cg26820118	7	148892577	148923339	7	148036601	855976	5.85	14.6	2.80E-02	0.088	patternA	PatternI
HSPA1B	cg00124488	6	31795512	31798031	6	31509762	285750	5.83	152.8	2.82E-02	0.088	patternA	PatternI
ANXA9	cg16555184	1	150954493	150968110	1	149982714	971779	5.80	124.5	2.85E-02	0.089	patternA	PatternI
PPP4C	cg03466485	16	30087299	30096698	16	30411736	315038	5.78	497.6	2.86E-02	0.089	patternA	PatternI
UTF1	cg23105839	10	135043778	135045062	10	135050004	4942	5.76	40.9	2.88E-02	0.089	patternA	PatternI
HCK	cg00260888	20	30639991	30689659	20	30865478	175819	5.76	594.9	2.89E-02	0.089	patternA	PatternI
FKBPL	cg14560317	6	32096484	32098068	6	32940489	842421	5.75	103.9	2.90E-02	0.089	patternA	PatternI
DVL2	cg13545212	17	7128660	7137864	17	6617192	511468	5.74	138.3	2.90E-02	0.089	patternA	PatternI
AGPAT2	cg13696351	9	139567595	139581875	9	140063617	481742	5.70	90.7	2.95E-02	0.089	patternA	PatternI
MAD2L2	cg19602920	1	11734537	11751707	1	12079277	327570	5.68	26.9	2.96E-02	0.089	patternA	PatternI
KREMEN1	cg07391456	22	29469066	29564321	22	29702411	138090	5.68	14.7	2.96E-02	0.089	patternA	PatternI
FKBPL	cg11348335	6	32096484	32098068	6	32939525	841457	5.68	46.9	2.96E-02	0.089	patternA	PatternI
RNF5	cg27196273	6	32146131	32151930	6	32632992	481062	5.67	173.4	2.97E-02	0.089	patternA	PatternI
MSRA	cg04227985	8	9911778	10286401	8	9009105	902673	5.67	1.7	2.97E-02	0.089	patternA	PatternI
ZNF408	cg03487637	11	46722368	46727462	11	45940039	782329	5.67	66.0	2.97E-02	0.089	patternA	PatternI
S1PR4	cg16260977	19	3172344	3180329	19	3761708	581379	5.67	1463.4	2.97E-02	0.089	patternA	PatternI
CXCR1	cg15490781	2	219027568	219031718	2	219858271	826553	5.64	8788.9	3.00E-02	0.090	patternA	PatternI
SLC50A1	cg10445911	1	155107820	155111329	1	154971922	135898	5.64	117.7	3.01E-02	0.090	patternA	PatternI
GPSM3	cg01170201	6	32158543	32163300	6	32820976	657676	5.61	6345.7	3.04E-02	0.091	patternA	PatternI
INTS5	cg14638988	11	62414320	62420774	11	62476544	55770	5.60	63.1	3.04E-02	0.091	patternA	PatternI
HCK	cg05938437	20	30639991	30689659	20	30697524	7865	5.59	848.9	3.06E-02	0.091	patternA	PatternI

TPM2	cg00976036	9	35681989	35691017	9	34989696	692293	5.59	12.9	3.06E-02	0.091	patternA	PatternI
HSPA1L	cg27196273	6	31777396	31783437	6	32632992	849555	5.58	20.2	3.07E-02	0.091	patternA	PatternI
PPP4C	cg00352195	16	30087299	30096698	16	30773975	677277	5.57	546.3	3.08E-02	0.091	patternA	PatternI
HSPA1L	cg19579005	6	31777396	31783437	6	30782272	995124	5.56	46.0	3.09E-02	0.091	patternA	PatternIV
SLC29A2	cg23430644	11	66129992	66139685	11	65383542	746450	5.55	16.3	3.09E-02	0.091	patternA	PatternI
PRR14	cg10277268	16	30662038	30667761	16	30825733	157972	5.54	619.9	3.11E-02	0.091	patternA	PatternI
DAPK3	cg19244855	19	3958451	3971121	19	3029152	929299	5.52	28.5	3.13E-02	0.091	patternA	PatternI
RAB11FIP4	cg09460159	17	29718642	29865236	17	30771470	906234	5.51	23.7	3.14E-02	0.091	patternA	PatternI
SH2B2	cg09267051	7	101928405	101962178	7	100943468	984937	5.51	64.6	3.14E-02	0.091	patternA	PatternI
TAF10	cg07224992	11	6627526	6633898	11	6817449	183551	5.49	7800.4	3.16E-02	0.091	patternV	PatternII
CCS	cg15082918	11	66360292	66373490	11	66104153	256139	5.49	40.3	3.16E-02	0.091	patternA	PatternI
DAPK3	cg14710040	19	3958451	3971121	19	3985464	14343	5.48	26.0	3.17E-02	0.091	patternA	PatternI
TNFRSF10C	cg09951048	8	22941868	22974950	8	21966736	975132	5.46	2057.9	3.19E-02	0.091	patternA	PatternI
HMG20B	cg19244855	19	3572775	3579086	19	3029152	543623	5.46	63.0	3.19E-02	0.091	patternA	PatternI
PPP2R5D	cg06876672	6	42952237	42980080	6	42952166	71	5.46	35.2	3.19E-02	0.091	patternA	PatternI
TFEB	cg01289140	6	41651716	41703997	6	41862737	158740	5.44	25.7	3.21E-02	0.091	patternA	PatternI
MVB12A	cg16572859	19	17516531	17544533	19	18263815	719282	5.44	16.8	3.22E-02	0.091	patternA	PatternI
MPV17L2	cg16572859	19	18303992	18307758	19	18263815	40177	5.40	30.6	3.26E-02	0.092	patternA	PatternI
TUBA4A	cg25297849	2	220114433	220142892	2	219922998	191435	5.37	264.0	3.30E-02	0.093	patternA	PatternI
MARK4	cg18075720	19	45582546	45808541	19	45349207	233339	5.34	7.4	3.33E-02	0.094	patternA	PatternI
MFSD10	cg23927271	4	2932288	2936586	4	2471043	461245	5.33	203.1	3.35E-02	0.094	patternA	PatternI
GNA15	cg16260977	19	3136191	3163767	19	3761708	597941	5.33	27.3	3.35E-02	0.094	patternA	PatternI
DTX2	cg22610194	7	76090993	76135312	7	77045539	910227	5.31	16.8	3.37E-02	0.094	patternA	PatternI
FXR2	cg19488133	17	7494548	7518189	17	7297863	196685	5.30	28.6	3.38E-02	0.094	patternA	PatternI
ATG4D	cg19355182	19	10654571	10664094	19	10543010	111561	5.29	78.2	3.39E-02	0.094	patternA	PatternI
APC	cg09835486	5	112043195	112181936	5	112257968	76032	-5.29	-2.4	3.40E-02	0.094	patternA	PatternI
BLOC1S3	cg04571944	19	45682003	45685059	19	45644563	37440	5.29	72.2	3.40E-02	0.094	patternA	PatternIV
TUBA4A	cg15490781	2	220114433	220142892	2	219858271	256162	5.28	203.6	3.40E-02	0.094	patternA	PatternI
DVL2	cg20347916	17	7128660	7137864	17	7621118	483254	5.28	133.2	3.40E-02	0.094	patternA	PatternI
ZNF438	cg09639837	10	31109136	31320866	10	30722502	386634	5.28	3.9	3.41E-02	0.094	patternA	PatternI
CXCR1	cg25297849	2	219027568	219031718	2	219922998	891280	5.25	11331.3	3.44E-02	0.094	patternA	PatternI
B3GAT3	cg07747515	11	62382768	62389647	11	61659326	723442	5.25	101.3	3.45E-02	0.094	patternA	PatternI

NLRX1	cg15407505	11	119037277	119054725	11	119613061	558336	5.22	34.4	3.48E-02	0.095	patternA	PatternI
DAPK3	cg07071609	19	3958451	3971121	19	4535315	564194	5.19	81.8	3.51E-02	0.096	patternA	PatternI
SPHK1	cg04510639	17	74372665	74383941	17	74722764	338823	5.17	5.0	3.55E-02	0.096	patternA	PatternI
KRT23	cg06307169	17	39078948	39093886	17	38296698	782250	5.16	186.1	3.55E-02	0.096	patternA	PatternI
NFKBIL1	cg23897356	6	31514647	31526606	6	30688013	826634	5.12	37.5	3.61E-02	0.097	patternA	PatternI
MARK4	cg23048660	19	45582546	45808541	19	45004795	577751	5.12	9.2	3.61E-02	0.097	patternA	PatternI
TPRA1	cg02711849	3	127291912	127317094	3	126398161	893751	5.11	18.2	3.62E-02	0.097	patternA	PatternI
SIRT6	cg07071609	19	4174106	4182601	19	4535315	352714	5.10	94.8	3.64E-02	0.098	patternA	PatternI
MED16	cg07492258	19	867962	893218	19	1748825	855607	5.09	121.8	3.66E-02	0.098	patternA	PatternI
NFKBIL1	cg13964363	6	31514647	31526606	6	32157454	630848	5.08	42.5	3.66E-02	0.098	patternA	PatternIV
VPS37C	cg13973351	11	60897728	60929089	11	60928923	166	5.08	59.5	3.66E-02	0.098	patternA	PatternI
KREMEN1	cg04776735	22	29469066	29564321	22	29137963	331103	5.07	22.4	3.68E-02	0.098	patternA	PatternI
ACTR1A	cg26894311	10	104238986	104262482	10	104153930	85056	5.05	31.3	3.70E-02	0.098	patternA	PatternI
ASPSR1	cg22230229	17	79934683	79975282	17	79372254	562429	5.03	4.9	3.73E-02	0.099	patternA	PatternI
ZNF219	cg19983597	14	21558205	21572881	14	21852154	279273	5.01	15.8	3.76E-02	0.099	patternA	PatternI
TPRN	cg13696351	9	140086069	140098645	9	140063617	22452	4.99	23.2	3.78E-02	0.100	patternA	PatternI
CD59	cg12246353	11	33719807	33757991	11	33061158	658649	4.98	40.3	3.80E-02	0.100	patternA	PatternI
MIF4GD	cg05865679	17	73262309	73267308	17	73452251	184943	4.98	82.1	3.81E-02	0.100	patternA	PatternI
SIRT6	cg16260977	19	4174106	4182601	19	3761708	412398	4.97	81.8	3.81E-02	0.100	patternA	PatternI
TNIP2	cg23927271	4	2743375	2758103	4	2471043	272332	4.97	47.5	3.82E-02	0.100	patternA	PatternI
HCAR2	cg21618040	12	123185840	123187890	12	123921306	733416	4.93	730.7	3.88E-02	0.101	patternA	PatternI
PRR14	cg04603809	16	30662038	30667761	16	29874120	787918	4.92	463.8	3.89E-02	0.101	patternA	PatternI
FXR2	cg13545212	17	7494548	7518189	17	6617192	877356	4.92	25.5	3.90E-02	0.101	patternA	PatternI
PHF23	cg19488133	17	7138347	7143041	17	7297863	154822	4.88	322.5	3.96E-02	0.102	patternA	PatternI
FLOT1	cg23623622	6	30695486	30710510	6	30139880	555606	4.84	680.6	4.02E-02	0.104	patternA	PatternI
OSBPL8	cg11264102	12	76745577	76953589	12	77157695	204106	-4.83	-9.6	4.03E-02	0.104	patternV	PatternI
DDAH2	cg06414921	6	31694815	31698394	6	31276504	418311	4.81	213.4	4.06E-02	0.104	patternA	PatternI
FLYWCH2	cg06526921	16	2933187	2949383	16	2034455	898732	4.81	18.3	4.06E-02	0.104	patternA	PatternI
STARD3	cg15393197	17	37793318	37819737	17	37213172	580146	4.79	35.6	4.09E-02	0.104	patternA	PatternI
KRT23	cg12041100	17	39078948	39093886	17	38337188	741760	-4.78	-398.0	4.11E-02	0.105	patternA	PatternII
NFKBIL1	cg10628782	6	31514647	31526606	6	31620229	93623	4.77	77.5	4.12E-02	0.105	patternA	PatternIV
TFEB	cg10260072	6	41651716	41703997	6	42421084	717087	4.76	47.9	4.15E-02	0.105	patternA	PatternI

RNF5	cg06414921	6	32146131	32151930	6	31276504	869627	4.75	240.5	4.15E-02	0.105	patternA	PatternI
RXRB	cg04014576	6	33161365	33168630	6	34112818	944188	4.75	180.2	4.16E-02	0.105	patternA	PatternI
HCAR2	cg26494424	12	123185840	123187890	12	124118326	930436	4.73	1776.8	4.19E-02	0.105	patternA	PatternI
SGTA	cg19244855	19	2754712	2783369	19	3029152	245783	4.73	16.9	4.19E-02	0.105	patternA	PatternI
B3GALT4	cg21352296	6	33244917	33252609	6	34216944	964335	4.72	82.7	4.21E-02	0.106	patternA	PatternI
PRR14	cg00352195	16	30662038	30667761	16	30773975	106214	4.72	428.7	4.22E-02	0.106	patternA	PatternI
SLC50A1	cg25017976	1	155107820	155111329	1	154947060	160760	4.70	104.5	4.24E-02	0.106	patternA	PatternI
ASPSCR1	cg11252953	17	79934683	79975282	17	80358829	383547	4.68	11.0	4.27E-02	0.106	patternA	PatternI
CYSTM1	cg03317235	5	139554227	139661637	5	139423324	130903	4.68	18.5	4.27E-02	0.106	patternA	PatternI
FLYWCH2	cg00064051	16	2933187	2949383	16	3314045	364662	4.68	6.3	4.28E-02	0.106	patternA	PatternI
RXRB	cg19156220	6	33161365	33168630	6	33244752	76122	-4.68	-473.2	4.28E-02	0.106	patternA	PatternIII
MAP3K2	cg09131629	2	128056306	128146041	2	128433309	287268	-4.67	-14.9	4.29E-02	0.106	patternV	PatternI
RPS28	cg16906204	19	8386042	8388224	19	8509784	121560	4.67	3405.1	4.29E-02	0.106	patternA	PatternI
ZNF467	cg16174274	7	149461271	149470568	7	148679906	781365	4.66	569.7	4.30E-02	0.106	patternA	PatternI
MAP1LC3A	cg00783946	20	33134658	33148149	20	33872414	724265	4.66	23.8	4.30E-02	0.106	patternA	PatternI
DDAH2	cg27196273	6	31694815	31698394	6	32632992	934598	4.63	151.5	4.35E-02	0.106	patternA	PatternI
DBN1	cg02460251	5	176883609	176901402	5	176107427	776182	4.63	49.1	4.37E-02	0.106	patternA	PatternI
SPNS2	cg06345277	17	4402133	4442330	17	5342595	900265	4.62	2.5	4.37E-02	0.106	patternA	PatternI
SLC50A1	cg01032200	1	155107820	155111329	1	155290641	179312	-4.62	-22.9	4.38E-02	0.106	patternA	PatternII
S1PR4	cg14710040	19	3172344	3180329	19	3985464	805135	4.62	527.8	4.38E-02	0.106	patternA	PatternI
SLC25A1	cg02207496	22	19163095	19166343	22	18894280	268815	4.60	248.0	4.42E-02	0.107	patternA	PatternI
HSPA1L	cg06414921	6	31777396	31783437	6	31276504	500892	4.59	28.0	4.43E-02	0.107	patternA	PatternI
ALPL	cg17196364	1	21835858	21904905	1	21617006	218852	4.58	226.1	4.45E-02	0.107	patternA	PatternI
TRMT112	cg03074984	11	64083932	64085556	11	64126431	40875	4.58	642.4	4.46E-02	0.107	patternV	PatternI
FLOT1	cg23168870	6	30695486	30710510	6	30523692	171794	4.57	738.8	4.46E-02	0.107	patternA	PatternI
ZNF775	cg12857488	7	150065879	150109558	7	149195092	870787	4.56	48.7	4.49E-02	0.108	patternA	PatternI
PHF23	cg13545212	17	7138347	7143041	17	6617192	521155	4.55	287.4	4.51E-02	0.108	patternA	PatternI
SULT1A1	cg09351569	16	28616903	28634946	16	28632419	2527	-4.54	-281.4	4.52E-02	0.108	patternA	PatternII
MSRB1	cg06526921	16	1988211	1993327	16	2034455	41128	4.54	4264.5	4.53E-02	0.108	patternA	PatternI
MAP3K2	cg00906167	2	128056306	128146041	2	128615801	469760	-4.50	-11.1	4.60E-02	0.109	patternV	PatternI
INTS5	cg06558326	11	62414320	62420774	11	62391084	23236	4.48	144.8	4.64E-02	0.110	patternA	PatternI
SLC29A2	cg10498476	11	66129992	66139685	11	66035147	94845	4.47	11.8	4.66E-02	0.110	patternA	PatternI

PRR14	cg03466485	16	30662038	30667761	16	30411736	250302	4.46	387.8	4.67E-02	0.110	patternA	PatternI
FUT7	cg13696351	9	139924626	139927462	9	140063617	136155	4.46	1404.3	4.68E-02	0.110	patternA	PatternI
IMPDH1	cg2191363C	7	128032331	128050306	7	128828599	778293	4.43	376.9	4.73E-02	0.111	patternA	PatternI
ZNF775	cg06842319	7	150065879	150109558	7	150453731	344173	-4.43	-350.6	4.74E-02	0.111	patternA	PatternII
MPV17L2	cg11610754	19	18303992	18307758	19	18722595	414837	4.41	37.7	4.77E-02	0.112	patternA	PatternI
SLC29A2	cg19626726	11	66129992	66139685	11	65668074	461918	4.41	8.7	4.78E-02	0.112	patternA	PatternI
DTNBP1	cg03156064	6	15523032	15663289	6	15630603	32686	4.40	19.7	4.79E-02	0.112	patternA	PatternII
ATG4D	cg01284702	19	10654571	10664094	19	11039163	375069	4.38	40.0	4.84E-02	0.112	patternA	PatternI
LRSAM1	cg01475855	9	130213765	130265780	9	131084770	818990	4.38	13.3	4.84E-02	0.112	patternA	PatternI
TAF10	cg13301069	11	6627526	6633898	11	6624877	2649	4.38	729.4	4.85E-02	0.112	patternV	PatternIII
FLOT1	cg2616117C	6	30695486	30710510	6	30313174	382312	4.37	499.0	4.85E-02	0.112	patternA	PatternI
SLC29A2	cg15574972	11	66129992	66139685	11	65265134	864858	4.37	13.4	4.86E-02	0.112	patternA	PatternI
HMGAI	cg04263436	6	34204650	34214008	6	33245467	959183	4.37	339.3	4.86E-02	0.112	patternA	PatternI
S1PR4	cg19244855	19	3172344	3180329	19	3029152	143192	4.36	576.4	4.87E-02	0.112	patternA	PatternI
PPME1	cg1081926C	11	73882144	73965748	11	74022742	56994	4.36	1.9	4.88E-02	0.112	patternA	PatternI
DAPK3	cg16260977	19	3958451	3971121	19	3761708	196743	4.36	69.7	4.88E-02	0.112	patternA	PatternI
FLOT1	cg0133639C	6	30695486	30710510	6	29895059	800427	4.36	420.4	4.88E-02	0.112	patternA	PatternI
SLC50A1	cg06193775	1	155107820	155111329	1	155145882	34553	4.35	103.5	4.89E-02	0.112	patternA	PatternI
FBXL19	cg27609508	16	30934376	30960104	16	30905407	28969	4.34	10.4	4.92E-02	0.112	patternA	PatternI
TRIM39	cg21636096	6	30294256	30311506	6	30313077	1571	4.33	44.8	4.94E-02	0.112	patternA	PatternI
TSEN34	cg15680557	19	54693789	54697585	19	54704426	6841	4.33	348.6	4.95E-02	0.112	patternA	PatternI
CCNL1	cg09250741	3	156864297	156878549	3	156893021	14472	-4.33	-77.6	4.95E-02	0.112	patternV	PatternI
SPHK1	cg05865679	17	74372665	74383941	17	73452251	920414	4.31	7.3	4.97E-02	0.112	patternA	PatternI
CUEDC2	cg18505495	10	104183002	104192418	10	104179494	3508	4.31	47.4	4.99E-02	0.112	patternA	PatternI
UBAP1	cg00976036	9	34179003	34252521	9	34989696	737175	4.30	25.8	5.00E-02	0.112	patternA	PatternI
FKBPL	cg01170201	6	32096484	32098068	6	32820976	722908	4.29	109.1	5.03E-02	0.113	patternA	PatternI
NUDC	cg26040332	1	27226729	27273353	1	27960788	687435	4.29	30.2	5.04E-02	0.113	patternA	PatternI
ASPSR1	cg15523177	17	79934683	79975282	17	79269242	665441	4.29	12.6	5.04E-02	0.113	patternA	PatternI
FBXL19	cg16947339	16	30934376	30960104	16	30546198	388178	4.27	18.1	5.07E-02	0.113	patternA	PatternI
B3GALT4	cg06618123	6	33244917	33252609	6	33377795	125186	4.26	97.8	5.08E-02	0.113	patternA	PatternI
WDR46	cg04263436	6	33246885	33257304	6	33245467	1418	4.26	74.3	5.09E-02	0.113	patternA	PatternI
WDR46	cg12770425	6	33246885	33257304	6	33585071	327767	4.25	68.0	5.12E-02	0.113	patternA	PatternII

SPHK1	cg20715365	17	74372665	74383941	17	73900573	472092	4.24	7.6	5.15E-02	0.114	patternA	PatternI
ATAD3A	cg04407228	1	1447531	1470067	1	1710158	240091	4.22	5.0	5.19E-02	0.114	patternA	PatternI
TRIM39	cg19579005	6	30294256	30311506	6	30782272	470766	4.22	45.0	5.19E-02	0.114	patternA	PatternIV
CDA	cg17196364	1	20915441	20945401	1	21617006	671605	4.20	201.1	5.23E-02	0.115	patternA	PatternI
ECHS1	cg23105839	10	135175984	135187193	10	135050004	125980	4.19	63.4	5.25E-02	0.115	patternA	PatternI
WDR46	cg01170201	6	33246885	33257304	6	32820976	425909	4.18	76.0	5.28E-02	0.115	patternA	PatternI
HCAR2	cg00871673	12	123185840	123187890	12	122516220	669620	4.18	2063.7	5.28E-02	0.115	patternA	PatternI
GNA13	cg03182819	17	63006833	63052957	17	63053327	370	-4.17	-29.9	5.30E-02	0.116	patternV	PatternI
HMGA1	cg06618123	6	34204650	34214008	6	33377795	826855	4.16	262.8	5.32E-02	0.116	patternA	PatternI
UTF1	cg04652645	10	135043778	135045062	10	135049999	4937	4.12	49.6	5.41E-02	0.118	patternA	PatternI
BRMS1	cg25753024	11	66104804	66112596	11	67070913	958317	4.11	125.6	5.43E-02	0.118	patternA	PatternIV
HMGA1	cg07156929	6	34204650	34214008	6	34856927	642919	4.10	317.6	5.47E-02	0.118	patternA	PatternI
WNK2	cg07525971	9	95947198	96082854	9	95858482	88716	4.07	0.4	5.53E-02	0.120	patternA	PatternI
B3GAT3	cg14638988	11	62382768	62389647	11	62476544	86897	4.04	78.0	5.61E-02	0.121	patternA	PatternI
SLC29A2	cg15082918	11	66129992	66139685	11	66104153	25839	4.04	17.9	5.61E-02	0.121	patternA	PatternI
HSPA1B	cg06414921	6	31795512	31798031	6	31276504	519008	4.03	209.9	5.64E-02	0.121	patternA	PatternI
TNFRSF12A	cg00064051	16	3068446	3072384	16	3314045	241661	4.03	13.9	5.65E-02	0.121	patternA	PatternI
USF1	cg04975598	1	161009041	161015767	1	160039909	969132	4.02	500.9	5.66E-02	0.121	patternA	PatternI
SLC50A1	cg11750116	1	155107820	155111329	1	155057442	50378	4.02	88.4	5.66E-02	0.121	patternA	PatternI
NFE2	cg11426224	12	54685895	54694905	12	54567248	118647	4.02	1006.1	5.67E-02	0.121	patternA	PatternI
WDR46	cg23011817	6	33246885	33257304	6	33422290	164986	3.97	54.8	5.79E-02	0.123	patternA	PatternI
CCDC61	cg04571944	19	46498339	46524576	19	45644563	853776	3.97	249.5	5.79E-02	0.123	patternA	PatternIV
FKBP1	cg13964363	6	32096484	32098068	6	32157454	59386	3.97	122.2	5.79E-02	0.123	patternA	PatternIV
MVB12A	cg12526923	19	17516531	17544533	19	17439208	77323	3.96	10.6	5.82E-02	0.123	patternA	PatternI
CCDC85B	cg10498476	11	65657875	65659105	11	66035147	376042	3.93	489.5	5.91E-02	0.125	patternV	PatternI
DAXX	cg04014576	6	33286335	33297046	6	34112818	815772	3.92	267.0	5.93E-02	0.125	patternA	PatternI
INTS5	cg15454066	11	62414320	62420774	11	61595377	818943	3.90	86.8	5.99E-02	0.126	patternA	PatternI
MYPOP	cg04571944	19	46393278	46405862	19	45644563	748715	3.88	96.2	6.04E-02	0.127	patternA	PatternIV
TUBA4A	cg01506492	2	220114433	220142892	2	219232590	881843	3.88	193.7	6.04E-02	0.127	patternA	PatternI
BTBD2	cg19244855	19	1985447	2034880	19	3029152	994272	3.87	22.3	6.07E-02	0.127	patternA	PatternI
AXIN1	cg06525293	16	337440	402673	16	725532	322859	3.87	18.8	6.08E-02	0.127	patternA	PatternI
ANXA9	cg07367563	1	150954493	150968110	1	151032068	63958	3.87	126.6	6.09E-02	0.127	patternA	PatternI

NFKBIL1	cg24322638	6	31514647	31526606	6	30524987	989660	3.85	36.1	6.12E-02	0.127	patternA	PatternI
ADAT3	cg07492258	19	1905377	1913444	19	1748825	156552	3.83	25.6	6.19E-02	0.129	patternA	PatternI
WDR46	cg14560317	6	33246885	33257304	6	32940489	306396	3.80	70.0	6.29E-02	0.131	patternA	PatternI
RFX2	cg21575584	19	5993175	6199583	19	5690316	302859	3.79	7.6	6.31E-02	0.131	patternA	PatternI
HIPK3	cg15892658	11	33278218	33378569	11	33757569	379000	-3.78	-18.3	6.35E-02	0.131	patternV	PatternI
MICU1	cg14931764	10	74127098	74385899	10	74952899	567000	3.76	19.2	6.41E-02	0.132	patternA	PatternIII
HSPA1B	cg27196273	6	31795512	31798031	6	32632992	834961	3.75	148.2	6.44E-02	0.132	patternA	PatternI
CXCR1	cg01506492	2	219027568	219031718	2	219232590	200872	3.74	8291.3	6.45E-02	0.132	patternA	PatternI
HMGA1	cg22065976	6	34204650	34214008	6	33589061	615589	3.74	251.8	6.45E-02	0.132	patternA	PatternI
PDZD7	cg26482199	10	102767440	102790890	10	101990787	776653	3.74	4.1	6.45E-02	0.132	patternA	PatternII
CCDC85B	cg23430644	11	65657875	65659105	11	65383542	274333	3.74	659.1	6.46E-02	0.132	patternV	PatternI
CCDC85B	cg04321378	11	65657875	65659105	11	65819389	160284	3.74	190.1	6.47E-02	0.132	patternV	PatternI
HMGA1	cg21352296	6	34204650	34214008	6	34216944	2936	3.74	217.7	6.48E-02	0.132	patternA	PatternI
TRIM39	cg12478978	6	30294256	30311506	6	30710766	399260	-3.73	-74.3	6.48E-02	0.132	patternA	PatternIII
ATG4D	cg07742633	19	10654571	10664094	19	10047209	607362	3.73	41.3	6.50E-02	0.132	patternA	PatternI
SPNS2	cg24751717	17	4402133	4442330	17	4642944	200614	3.72	2.0	6.53E-02	0.132	patternA	PatternI
PLIN3	cg07071609	19	4838353	4867780	19	4535315	303038	3.70	149.4	6.58E-02	0.133	patternA	PatternI
TAF10	cg17121955	11	6627526	6633898	11	6411382	216144	3.68	855.5	6.64E-02	0.134	patternV	PatternI
TNFRSF10C	cg04394254	8	22941868	22974950	8	22422816	519052	3.61	1797.5	6.89E-02	0.139	patternA	PatternI
WDR46	cg22065976	6	33246885	33257304	6	33589061	331757	3.60	55.0	6.93E-02	0.139	patternA	PatternI
COPE	cg02860168	19	19010323	19030206	19	19462266	432060	3.59	293.2	6.94E-02	0.139	patternA	PatternI
ECHS1	cg04652645	10	135175984	135187193	10	135049999	125985	3.59	77.6	6.97E-02	0.140	patternA	PatternI
DAXX	cg12770425	6	33286335	33297046	6	33585071	288025	3.58	506.6	7.00E-02	0.140	patternA	PatternII
LRSAM1	cg00995988	9	130213765	130265780	9	130495533	229753	3.56	25.4	7.05E-02	0.141	patternA	PatternI
BLVRA	cg10045804	7	43798279	43846939	7	44621958	775019	3.54	10.6	7.14E-02	0.142	patternA	PatternIII
ALAS1	cg09166903	3	52232102	52248343	3	52090762	141340	3.53	70.1	7.15E-02	0.142	patternA	PatternI
HIPK3	cg12246353	11	33278218	33378569	11	33061158	217060	-3.53	-19.8	7.16E-02	0.142	patternV	PatternI
RNF5	cg00124488	6	32146131	32151930	6	31509762	636369	3.53	164.7	7.17E-02	0.142	patternA	PatternI
RILPL1	cg09593767	12	123955925	124018265	12	124457669	439404	3.53	7.6	7.19E-02	0.142	patternA	PatternI
DOK4	cg06080402	16	57505863	57521239	16	57481519	24344	3.53	17.9	7.19E-02	0.142	patternA	PatternI
COL9A3	cg16714055	20	61447596	61472511	20	61051341	396255	3.52	16.5	7.22E-02	0.142	patternA	PatternI
GPSM3	cg13964363	6	32158543	32163300	6	32157454	1089	3.51	6850.8	7.23E-02	0.142	patternA	PatternIV

DDAH2	cg00124488	6	31694815	31698394	6	31509762	185053	3.51	145.8	7.24E-02	0.142	patternA	PatternI
NUDC	cg27547812	1	27226729	27273353	1	26437414	789315	3.51	15.2	7.25E-02	0.142	patternA	PatternI
MPV17L2	cg09374949	19	18303992	18307758	19	18548964	241206	3.50	53.5	7.28E-02	0.143	patternA	PatternI
TRIM39	cg01365762	6	30294256	30311506	6	30457827	146321	3.49	51.3	7.33E-02	0.143	patternA	PatternI
HCAR2	cg16097051	12	123185840	123187890	12	124068991	881101	3.48	1409.6	7.36E-02	0.144	patternA	PatternI
DDAH2	cg13964363	6	31694815	31698394	6	32157454	459060	3.47	383.6	7.41E-02	0.144	patternA	PatternIV
HSPA1L	cg00124488	6	31777396	31783437	6	31509762	267634	3.46	19.2	7.42E-02	0.144	patternA	PatternI
PPARD	cg07156929	6	35310335	35395968	6	34856927	453408	3.46	13.4	7.43E-02	0.144	patternA	PatternI
EFNA1	cg10445911	1	155099936	155107333	1	154971922	128014	3.46	4.7	7.44E-02	0.144	patternA	PatternI
TMED5	cg16010723	1	93615299	93646285	1	92764349	850950	-3.44	-23.4	7.50E-02	0.145	patternV	PatternI
RXRB	cg12770425	6	33161365	33168630	6	33585071	416441	3.44	333.7	7.51E-02	0.145	patternA	PatternII
ASPSCR1	cg17917959	17	79934683	79975282	17	79197229	737454	3.43	13.9	7.53E-02	0.145	patternA	PatternI
B3GALT4	cg27196273	6	33244917	33252609	6	32632992	611925	3.43	54.1	7.54E-02	0.145	patternA	PatternI
ECHS1	cg24382527	10	135175984	135187193	10	135090367	85617	3.43	53.1	7.55E-02	0.145	patternA	PatternI
ZNF684	cg13784898	1	40997233	41013841	1	41827425	813584	-3.41	-4.0	7.62E-02	0.146	patternV	PatternI
ASPSCR1	cg24975666	17	79934683	79975282	17	80416629	441347	3.40	12.0	7.68E-02	0.147	patternA	PatternI
ASPSCR1	cg05255149	17	79934683	79975282	17	80675120	699838	3.37	13.1	7.80E-02	0.149	patternA	PatternI
TUBA4A	cg26544277	2	220114433	220142892	2	220083865	30568	3.35	165.2	7.85E-02	0.150	patternA	PatternI
PLEKHN1	cg25066040	1	901877	911245	1	936229	24984	3.35	3.7	7.87E-02	0.150	patternA	PatternI
FAM161B	cg08201755	14	74398204	74417117	14	74960113	542996	3.34	13.5	7.89E-02	0.150	patternA	PatternIII
FLOT1	cg23897356	6	30695486	30710510	6	30688013	7473	3.34	708.2	7.91E-02	0.150	patternA	PatternI
ARID3B	cg24527973	15	74833518	74890472	15	74988445	97973	-3.33	-71.7	7.94E-02	0.150	patternA	PatternIV
TPRN	cg14788802	9	140086069	140098645	9	140446233	347588	3.33	19.3	7.95E-02	0.150	patternA	PatternI
AKAP8L	cg13404054	19	15490859	15529952	19	15311666	179193	3.33	37.2	7.97E-02	0.150	patternA	PatternI
B3GAT3	cg06558326	11	62382768	62389647	11	62391084	1437	3.32	177.3	7.98E-02	0.150	patternA	PatternI
PPP2R5D	cg10260072	6	42952237	42980080	6	42421084	531153	3.32	19.7	7.98E-02	0.150	patternA	PatternI
NUBP2	cg09080030	16	1832902	1839192	16	2820366	981174	3.32	428.4	7.98E-02	0.150	patternA	PatternII
RNF5	cg10628782	6	32146131	32151930	6	31620229	525902	3.32	788.1	8.01E-02	0.150	patternA	PatternIV
HEYL	cg21011110	1	40089825	40105617	1	40157436	51819	3.32	1.1	8.01E-02	0.150	patternA	PatternI
SLC50A1	cg00472324	1	155107820	155111329	1	156052196	940867	3.31	66.0	8.03E-02	0.150	patternA	PatternI
TMED7	cg14470895	5	114949205	114968689	5	115152431	183742	-3.31	-24.2	8.05E-02	0.150	patternV	PatternI
UTF1	cg24382527	10	135043778	135045062	10	135090367	45305	3.30	33.2	8.09E-02	0.151	patternA	PatternI

MSRA	cg15301489	8	9911778	10286401	8	11058770	772369	3.29	1.9	8.13E-02	0.151	patternA	PatternI
HSPA1L	cg10628782	6	31777396	31783437	6	31620229	157167	3.28	92.0	8.16E-02	0.152	patternA	PatternIV
FIBCD1	cg19203369	9	133777825	133814673	9	133814378	295	-3.28	-0.3	8.18E-02	0.152	patternV	PatternI
NFKBIL1	cg06099048	6	31514647	31526606	6	32164151	637545	3.27	31.1	8.21E-02	0.152	patternA	PatternI
CCDC61	cg09120986	19	46498339	46524576	19	47249219	724643	3.26	70.4	8.28E-02	0.153	patternA	PatternI
HMGA1	cg23011817	6	34204650	34214008	6	33422290	782360	3.25	243.1	8.28E-02	0.153	patternA	PatternI
TBKBP1	cg08457495	17	45771447	45789416	17	45771936	489	3.24	59.5	8.34E-02	0.154	patternA	PatternI
CPNE1	cg00783946	20	34213953	34252878	20	33872414	341539	3.24	72.0	8.35E-02	0.154	patternV	PatternI
FAM161B	cg15079605	14	74398204	74417117	14	73704078	694126	3.23	13.0	8.41E-02	0.154	patternA	PatternIII
NFKBIL1	cg11046887	6	31514647	31526606	6	31870245	343639	3.23	33.5	8.42E-02	0.154	patternA	PatternIII
CCDC61	cg24836072	19	46498339	46524576	19	46498091	248	3.22	39.9	8.46E-02	0.154	patternA	PatternI
ASPSCR1	cg20140052	17	79934683	79975282	17	79367844	566839	3.22	11.3	8.46E-02	0.154	patternA	PatternI
DAXX	cg19156220	6	33286335	33297046	6	33244752	41583	-3.22	-683.2	8.46E-02	0.154	patternA	PatternIII
SAC3D1	cg23430644	11	64808373	64812300	11	65383542	571242	3.19	36.9	8.56E-02	0.156	patternA	PatternI
UBAP1	cg20741293	9	34179003	34252521	9	34958139	705618	3.19	24.9	8.58E-02	0.156	patternA	PatternIII
RILPL1	cg21618040	12	123955925	124018265	12	123921306	34619	3.19	3.8	8.59E-02	0.156	patternA	PatternI
BANP	cg18665648	16	87982850	88110924	16	87799740	183110	3.18	4.9	8.63E-02	0.156	patternA	PatternI
ATP6V0D1	cg06092312	16	67471917	67515140	16	68345214	830074	3.17	517.4	8.66E-02	0.156	patternA	PatternIV
ADAT3	cg16238993	19	1905377	1913444	19	1132372	773005	3.17	20.6	8.66E-02	0.156	patternA	PatternI
SAC3D1	cg03074984	11	64808373	64812300	11	64126431	681942	3.17	28.1	8.67E-02	0.156	patternA	PatternI
AXIN1	cg07664667	16	337440	402673	16	778351	375678	3.16	19.0	8.70E-02	0.157	patternA	PatternI
HEYL	cg15728256	1	40089825	40105617	1	40254184	148567	3.16	0.8	8.74E-02	0.157	patternA	PatternIII
ZNF821	cg16503601	16	71893583	71929239	16	71929079	160	3.15	7.2	8.77E-02	0.157	patternA	PatternI
DDAH2	cg10628782	6	31694815	31698394	6	31620229	74586	3.14	692.4	8.82E-02	0.158	patternA	PatternIV
DDAH2	cg19579005	6	31694815	31698394	6	30782272	912543	3.13	328.0	8.87E-02	0.159	patternA	PatternIV
ZNF467	cg11490987	7	149461271	149470568	7	149535717	65149	3.12	690.4	8.91E-02	0.159	patternA	PatternI
RILPL1	cg26494424	12	123955925	124018265	12	124118326	100061	3.12	9.2	8.93E-02	0.159	patternA	PatternI
CDK5	cg06842319	7	150750899	150755617	7	150453731	297168	-3.11	-250.0	8.96E-02	0.160	patternA	PatternII
IL4R	cg08495403	16	27324989	27376099	16	28222985	846886	3.11	65.1	8.97E-02	0.160	patternA	PatternI
MAML3	cg23924007	4	140637907	141075338	4	140099401	538506	3.10	1.7	9.00E-02	0.160	patternA	PatternI
PPARD	cg18353713	6	35310335	35395968	6	35310441	106	3.08	6.6	9.10E-02	0.161	patternA	PatternI
FKBP4	cg04235126	12	2904119	2914576	12	3600216	685640	3.06	46.8	9.23E-02	0.163	patternA	PatternI

B3GAT3	cg15454066	11	62382768	62389647	11	61595377	787391	3.05	106.2	9.30E-02	0.164	patternA	PatternI
TRIOBP	cg12942139	22	38093011	38172563	22	37823517	269494	3.04	17.7	9.32E-02	0.164	patternA	PatternIII
TRAPPC6A	cg18304472	19	45666186	45681495	19	45844176	162681	3.04	19.7	9.35E-02	0.165	patternA	PatternI
CCDC61	cg18304472	19	46498339	46524576	19	45844176	654163	3.03	42.8	9.40E-02	0.165	patternA	PatternI
TRIM39	cg06414921	6	30294256	30311506	6	31276504	964998	3.02	26.5	9.46E-02	0.166	patternA	PatternI
SPNS2	cg19506535	17	4402133	4442330	17	4853363	411033	2.99	2.1	9.59E-02	0.168	patternA	PatternI
HEYL	cg19320564	1	40089825	40105617	1	40157253	51636	2.99	0.6	9.61E-02	0.168	patternA	PatternI
FLYWCH2	cg09935998	16	2933187	2949383	16	3054327	104944	2.98	9.6	9.65E-02	0.169	patternA	PatternI
ZNF699	cg01329093	19	9404951	9420514	19	9546029	125515	-2.97	-20.1	9.70E-02	0.169	patternV	PatternII
DDAH2	cg12478978	6	31694815	31698394	6	30710766	984049	-2.97	-544.5	9.70E-02	0.169	patternA	PatternIII
BLVRA	cg10410146	7	43798279	43846939	7	44112411	265472	-2.97	-18.0	9.70E-02	0.169	patternA	PatternII
ADAT3	cg05228284	19	1905377	1913444	19	2720847	807403	2.94	9.4	9.87E-02	0.171	patternA	PatternI
WDR46	cg06618123	6	33246885	33257304	6	33377795	120491	2.94	54.9	9.91E-02	0.172	patternA	PatternI
PTDSS2	cg24440302	11	448268	491393	11	406829	41439	2.93	6.9	9.96E-02	0.173	patternA	PatternI
DENND1A	cg08758850	9	126141933	126692431	9	127533554	841123	2.92	1.6	9.99E-02	0.173	patternA	PatternI
WDR46	cg21352296	6	33246885	33257304	6	34216944	959640	2.92	46.0	1.00E-01	0.173	patternA	PatternI
WDR46	cg11348335	6	33246885	33257304	6	32939525	307360	2.92	30.3	1.00E-01	0.173	patternA	PatternI
FBXL19	cg10277268	16	30934376	30960104	16	30825733	108643	2.91	21.0	1.00E-01	0.173	patternA	PatternI
TDG	cg20282533	12	104359582	104382652	12	104618451	235799	2.91	18.6	1.01E-01	0.173	patternV	PatternII
DOK4	cg27524972	16	57505863	57521239	16	57279645	226218	2.90	10.3	1.01E-01	0.174	patternA	PatternI
TPRN	cg14095044	9	140086069	140098645	9	140314220	215575	2.90	40.9	1.01E-01	0.174	patternA	PatternIII
TRAPPC6A	cg24836072	19	45666186	45681495	19	46498091	816596	2.89	18.0	1.02E-01	0.174	patternA	PatternI
VAV1	cg02301978	19	6772725	6857377	19	7069707	212330	2.88	64.2	1.03E-01	0.175	patternA	PatternI
PDZD7	cg26439963	10	102767440	102790890	10	102587110	180330	2.86	1.6	1.04E-01	0.177	patternA	PatternI
ZNF609	cg10599479	15	64752941	64978264	15	65321629	343365	-2.85	-3.5	1.04E-01	0.177	patternA	PatternII
ASPCR1	cg05921834	17	79934683	79975282	17	80709563	734281	2.85	5.2	1.04E-01	0.177	patternA	PatternIII
EFNA1	cg06193775	1	155099936	155107333	1	155145882	38549	2.84	4.1	1.05E-01	0.178	patternA	PatternI
HMGA1	cg04014576	6	34204650	34214008	6	34112818	91832	2.84	152.3	1.05E-01	0.178	patternA	PatternI
HMGA1	cg27374423	6	34204650	34214008	6	34759890	545882	2.83	109.6	1.05E-01	0.178	patternA	PatternI
TSPAN33	cg21913630	7	128784712	128808671	7	128828599	19928	2.83	15.9	1.06E-01	0.178	patternA	PatternI
EFNA1	cg25017976	1	155099936	155107333	1	154947060	152876	2.82	4.1	1.06E-01	0.179	patternA	PatternI
KRAS	cg09908986	12	25357723	25403870	12	25404321	451	-2.80	-16.3	1.07E-01	0.181	patternV	PatternI

MED23	cg0104391C	6	131895106	131949369	6	132834340	884971	2.79	60.0	1.08E-01	0.181	patternV	PatternIII
MARK4	cg04571944	19	45582546	45808541	19	45644563	62017	2.78	43.1	1.08E-01	0.182	patternA	PatternIV
CCDC85B	cg19626726	11	65657875	65659105	11	65668074	8969	2.78	341.9	1.09E-01	0.183	patternV	PatternI
ZNF282	cg16174274	7	148892577	148923339	7	148679906	212671	2.77	11.3	1.09E-01	0.183	patternA	PatternI
EFNA1	cg0103220C	1	155099936	155107333	1	155290641	183308	-2.76	-0.9	1.10E-01	0.184	patternA	PatternII
SLC25A1	cg16901519	22	19163095	19166343	22	18560646	602449	2.75	233.2	1.11E-01	0.185	patternA	PatternI
EDEM3	cg02430413	1	184659365	184724047	1	185014391	290344	-2.74	-17.6	1.11E-01	0.185	patternV	PatternI
FBXL19	cg00352195	16	30934376	30960104	16	30773975	160401	2.73	14.5	1.12E-01	0.187	patternA	PatternI
YOD1	cg08128274	1	207217194	207226325	1	206832043	385151	-2.71	-15.5	1.13E-01	0.189	patternV	PatternI
HSPA1B	cg06099048	6	31795512	31798031	6	32164151	366120	2.70	281.9	1.14E-01	0.189	patternA	PatternI
CCDC85B	cg15574972	11	65657875	65659105	11	65265134	392741	2.69	523.8	1.15E-01	0.190	patternV	PatternI
S100A11	cg07367563	1	152004982	152020383	1	151032068	972914	2.68	3689.8	1.15E-01	0.191	patternA	PatternI
LYST	cg01789743	1	235824341	236046940	1	236159467	112527	-2.68	-57.0	1.16E-01	0.191	patternV	PatternIII
HMGA1	cg12770425	6	34204650	34214008	6	33585071	619579	2.65	288.2	1.18E-01	0.194	patternA	PatternII
VPS37C	cg17517598	11	60897728	60929089	11	61659090	730001	2.65	52.6	1.18E-01	0.194	patternA	PatternIV
TRAF2	cg13696351	9	139776364	139821059	9	140063617	242558	2.65	10.6	1.18E-01	0.194	patternA	PatternI
MAML3	cg18065318	4	140637907	141075338	4	140201433	436474	2.63	0.4	1.19E-01	0.196	patternA	PatternI
MYO5A	cg26158897	15	52599480	52821247	15	53083135	261888	-2.61	-5.2	1.21E-01	0.198	patternA	PatternI
CCDC85B	cg10105999	11	65657875	65659105	11	65337913	319962	2.59	526.1	1.22E-01	0.200	patternV	PatternIII
RBAK	cg08740107	7	5085452	5109119	7	5834372	725253	2.59	24.6	1.23E-01	0.200	patternV	PatternII
STARD3	cg1204110C	17	37793318	37819737	17	38337188	517451	-2.59	-74.4	1.23E-01	0.200	patternA	PatternII
TMED5	cg05797295	1	93615299	93646285	1	93913477	267192	-2.58	-25.2	1.23E-01	0.201	patternV	PatternI
PRCC	cg14892118	1	156720402	156770607	1	156561431	158971	-2.57	-16.9	1.24E-01	0.201	patternA	PatternII
RAB39A	cg18391757	11	107799229	107834208	11	108093451	259243	-2.57	-0.9	1.24E-01	0.201	patternV	PatternI
PDZD7	cg1866878C	10	102767440	102790890	10	102883165	92275	2.57	0.6	1.24E-01	0.202	patternA	PatternI
WDR46	cg27196273	6	33246885	33257304	6	32632992	613893	2.55	30.3	1.25E-01	0.203	patternA	PatternI
ZNF282	cg11490987	7	148892577	148923339	7	149535717	612378	2.54	14.1	1.26E-01	0.204	patternA	PatternI
PPARD	cg27374423	6	35310335	35395968	6	34759890	550445	2.54	4.6	1.27E-01	0.204	patternA	PatternI
B3GALT4	cg1915622C	6	33244917	33252609	6	33244752	165	-2.54	-145.0	1.27E-01	0.204	patternA	PatternIII
SPINK8	cg06212498	3	48348336	48369831	3	49045151	675320	2.53	3.0	1.27E-01	0.205	patternA	PatternI
SAC3D1	cg10105999	11	64808373	64812300	11	65337913	525613	2.53	29.9	1.27E-01	0.205	patternA	PatternIII
FBXL19	cg03466485	16	30934376	30960104	16	30411736	522640	2.52	13.0	1.28E-01	0.205	patternA	PatternI

ZNF12	cg08740107	7	6728064	6746554	7	5834372	893692	2.52	70.2	1.28E-01	0.205	patternV	PatternII
NFKBIL1	cg06414921	6	31514647	31526606	6	31276504	238143	2.52	20.6	1.28E-01	0.205	patternA	PatternI
ZNF770	cg00332155	15	35270542	35280488	15	35837878	557390	-2.52	-33.3	1.28E-01	0.205	patternV	PatternI
MAD2L2	cg20059492	1	11734537	11751707	1	12603854	852147	2.51	141.4	1.28E-01	0.205	patternA	PatternII
BANP	cg0675718C	16	87982850	88110924	16	88914674	803750	2.51	17.2	1.29E-01	0.206	patternA	PatternI
B3GALT4	cg0401457C	6	33244917	33252609	6	34112818	860209	2.51	55.0	1.29E-01	0.206	patternA	PatternI
C6orf120	cg0164580C	6	170102233	170106401	6	170189779	83378	2.50	70.9	1.29E-01	0.206	patternV	PatternII
EFNA1	cg1175011C	1	155099936	155107333	1	155057442	42494	2.50	3.4	1.29E-01	0.206	patternA	PatternI
TRAF2	cg14788802	9	139776364	139821059	9	140446233	625174	2.49	9.1	1.30E-01	0.207	patternA	PatternI
RILPL1	cg16097051	12	123955925	124018265	12	124068991	50726	2.49	7.2	1.31E-01	0.207	patternA	PatternI
BANP	cg1475298C	16	87982850	88110924	16	88717571	606647	2.49	8.9	1.31E-01	0.207	patternA	PatternI
RFX2	cg0230197C	19	5993175	6199583	19	7069707	870124	2.47	4.7	1.32E-01	0.209	patternA	PatternI
UBE4A	cg1476201C	11	118230300	118269926	11	118443311	173385	-2.46	-40.8	1.33E-01	0.209	patternV	PatternI
VCPIP1	cg14353137	8	67540722	67579452	8	67873799	294347	-2.46	-7.8	1.33E-01	0.210	patternV	PatternI
PANK3	cg0713699C	5	167975500	168006605	5	168728081	721476	-2.46	-23.5	1.33E-01	0.210	patternV	PatternI
SAC3D1	cg1962672C	11	64808373	64812300	11	65668074	855774	2.45	19.0	1.34E-01	0.210	patternA	PatternI
TRAPPC6A	cg0725157C	19	45666186	45681495	19	45349316	316870	2.45	15.0	1.34E-01	0.210	patternA	PatternI
GSS	cg0078394C	20	33516236	33543620	20	33872414	328794	2.45	9.1	1.34E-01	0.210	patternA	PatternI
ATG4B	cg12903924	2	242576628	242613272	2	242448061	128567	2.45	39.4	1.34E-01	0.210	patternA	PatternIV
SPINK8	cg2293456C	3	48348336	48369831	3	48884614	514783	2.44	2.0	1.35E-01	0.211	patternA	PatternI
MIF4GD	cg2383837C	17	73262309	73267308	17	72732946	529363	2.41	170.9	1.38E-01	0.215	patternA	PatternII
MYO5A	cg1435438C	15	52599480	52821247	15	52043967	555513	-2.40	-3.6	1.39E-01	0.216	patternA	PatternI
PPP1R12A	cg0067798C	12	80167343	80329240	12	80084523	82820	-2.40	-7.3	1.39E-01	0.216	patternV	PatternI
RAB36	cg1336139C	22	23487513	23506537	22	24114971	608434	2.40	8.8	1.39E-01	0.216	patternA	PatternI
ZBTB41	cg25634004	1	197122810	197169672	1	197744519	574847	-2.39	-2.4	1.39E-01	0.216	patternV	PatternI
ADD3	cg2177075C	10	111756126	111895323	10	112440394	545071	2.39	129.9	1.39E-01	0.216	patternV	PatternII
SLFN11	cg21745612	17	33677324	33700720	17	32907636	769688	-2.38	-149.7	1.40E-01	0.217	patternV	PatternII
SAC3D1	cg15574972	11	64808373	64812300	11	65265134	452834	2.38	29.1	1.41E-01	0.217	patternA	PatternI
BCL2L12	cg13861524	19	50168823	50177173	19	50836391	659218	-2.38	-84.5	1.41E-01	0.217	patternA	PatternIII
ZNF770	cg1038648C	15	35270542	35280488	15	35047189	223353	-2.37	-77.8	1.41E-01	0.217	patternV	PatternI
IREB2	cg12654502	15	78729773	78793798	15	78730523	750	-2.37	-12.7	1.41E-01	0.217	patternV	PatternI
MYO5A	cg12067522	15	52599480	52821247	15	52405000	194480	-2.37	-2.0	1.42E-01	0.218	patternA	PatternI

YOD1	cg1505715C	1	207217194	207226325	1	206680618	536576	-2.35	-22.1	1.43E-01	0.220	patternV	PatternI
TRAF2	cg14095044	9	139776364	139821059	9	140314220	493161	2.33	19.4	1.45E-01	0.223	patternA	PatternIII
PPIP5K2	cg19788741	5	102455853	102548500	5	101632310	823543	-2.32	-9.7	1.46E-01	0.223	patternV	PatternI
ZNF821	cg1782310C	16	71893583	71929239	16	71918263	10976	2.32	4.5	1.46E-01	0.224	patternA	PatternI
SPNS2	cg11475493	17	4402133	4442330	17	4613604	171274	2.31	3.1	1.47E-01	0.224	patternA	PatternIII
WSB1	cg15710971	17	25621102	25640657	17	25621084	18	-2.31	-74.3	1.47E-01	0.224	patternV	PatternI
ALAS1	cg18509826	3	52232102	52248343	3	52017385	214717	2.30	62.6	1.48E-01	0.226	patternA	PatternI
ZNF770	cg18459189	15	35270542	35280488	15	35261784	8758	-2.30	-78.8	1.49E-01	0.226	patternV	PatternI
ZNF292	cg0413738C	6	87862551	87973914	6	88182602	208688	-2.30	-6.7	1.49E-01	0.226	patternV	PatternI
SEPSECS	cg01793416	4	25121627	25162204	4	25823590	661386	-2.29	-29.4	1.49E-01	0.226	patternV	PatternIII
NR1H2	cg13861524	19	50832910	50886239	19	50836391	3481	-2.29	-150.2	1.50E-01	0.227	patternA	PatternIII
HSPA1B	cg13964363	6	31795512	31798031	6	32157454	359423	2.28	352.2	1.50E-01	0.227	patternA	PatternIV
TRAPPC6A	cg1807572C	19	45666186	45681495	19	45349207	316979	2.25	16.4	1.53E-01	0.231	patternA	PatternI
FLOT1	cg12478978	6	30695486	30710510	6	30710766	256	-2.25	-1073.8	1.53E-01	0.231	patternA	PatternIII
RAB39A	cg15648026	11	107799229	107834208	11	107461798	337431	-2.24	-1.0	1.55E-01	0.233	patternV	PatternI
FLOT1	cg19579005	6	30695486	30710510	6	30782272	71762	2.24	639.9	1.55E-01	0.233	patternA	PatternIV
RALY	cg24253482	20	32581452	32696114	20	33064396	368282	-2.23	-101.7	1.55E-01	0.233	patternA	PatternIII
YOD1	cg1279644C	1	207217194	207226325	1	207224331	1994	-2.23	-22.1	1.56E-01	0.233	patternV	PatternI
DDX21	cg11279933	10	70715884	70744829	10	71211301	466472	-2.21	-33.0	1.57E-01	0.235	patternV	PatternI
LIMK2	cg14948714	22	31608225	31676066	22	31741883	65817	2.21	106.6	1.57E-01	0.235	patternA	PatternIII
UTF1	cg22887949	10	135043778	135045062	10	134683495	360283	-2.21	-104.4	1.57E-01	0.235	patternA	PatternII
BBS10	cg11264102	12	76738254	76742222	12	77157695	415473	-2.20	-32.0	1.59E-01	0.237	patternV	PatternI
CCS	cg25753024	11	66360292	66373490	11	67070913	697423	2.20	29.3	1.59E-01	0.237	patternA	PatternIV
AMN	cg08142571	14	103388993	103399933	14	104096390	696457	2.19	2.7	1.60E-01	0.238	patternA	PatternI
SEPSECS	cg1816110C	4	25121627	25162204	4	24473977	647650	-2.19	-2.6	1.60E-01	0.238	patternV	PatternI
GPSM3	cg10628782	6	32158543	32163300	6	31620229	538314	2.17	11345.8	1.62E-01	0.240	patternA	PatternIV
HEYL	cg09938328	1	40089825	40105617	1	39325620	764205	2.17	1.2	1.62E-01	0.241	patternA	PatternI
EFNA1	cg00472324	1	155099936	155107333	1	156052196	944863	2.16	2.5	1.63E-01	0.242	patternA	PatternI
FHOD1	cg26480675	16	67263290	67281561	16	66461075	802215	2.14	119.6	1.66E-01	0.245	patternA	PatternII
TRIM39	cg0887991C	6	30294256	30311506	6	29974319	319937	2.14	34.7	1.66E-01	0.245	patternA	PatternIV
KIAA1586	cg12152867	6	56911347	56920023	6	56708725	202622	-2.12	-6.2	1.68E-01	0.247	patternV	PatternI
GNPTAB	cg06192289	12	102139275	102224716	12	102513805	289089	-2.11	-38.8	1.69E-01	0.250	patternV	PatternII

TOB1	cg18454685	17	48939584	48945339	17	48639239	300345	-2.10	-81.9	1.70E-01	0.250	patternV	PatternI
ZNF787	cg27482605	19	56598732	56632649	19	55677760	920972	2.09	86.8	1.71E-01	0.252	patternA	PatternIV
NFKBIL1	cg00124488	6	31514647	31526606	6	31509762	4885	2.08	13.8	1.73E-01	0.253	patternA	PatternI
TOB1	cg13497650	17	48939584	48945339	17	48351646	587938	-2.08	-62.6	1.73E-01	0.254	patternV	PatternI
HMGA1	cg19156220	6	34204650	34214008	6	33244752	959898	-2.07	-369.3	1.75E-01	0.256	patternA	PatternIII
NRP2	cg04647948	2	206546714	206662857	2	206950423	287566	-2.06	-0.8	1.76E-01	0.256	patternV	PatternIV
SLC30A1	cg00787537	1	211744910	211752084	1	211307839	437071	-2.06	-188.2	1.76E-01	0.256	patternV	PatternIV
DDAH2	cg27070869	6	31694815	31698394	6	32122779	424385	2.06	257.9	1.76E-01	0.256	patternA	PatternII
TRAPPC6A	cg23048660	19	45666186	45681495	19	45004795	661391	2.05	19.7	1.76E-01	0.257	patternA	PatternI
ASPSR1	cg20462759	17	79934683	79975282	17	80010313	35031	2.05	21.4	1.77E-01	0.257	patternA	PatternIV
HSPA1L	cg11046887	6	31777396	31783437	6	31870245	86808	2.05	37.3	1.77E-01	0.257	patternA	PatternIII
KREMEN1	cg11408359	22	29469066	29564321	22	29602004	37683	-2.05	-24.6	1.77E-01	0.257	patternA	PatternIII
TOB1	cg14929100	17	48939584	48945339	17	48206884	732700	-2.04	-104.1	1.78E-01	0.258	patternV	PatternI
PPP1CB	cg11495753	2	28974506	29025806	2	30006577	980771	2.03	106.6	1.79E-01	0.258	patternV	PatternIII
RAB11FIP2	cg25987923	10	119764427	119806114	10	119302050	462377	-2.03	-4.5	1.79E-01	0.258	patternV	PatternI
GALE	cg25880573	1	24122089	24127271	1	24073129	48960	2.03	149.8	1.79E-01	0.258	patternA	PatternIII
SMG1	cg11698816	16	18816175	18937776	16	19535587	597811	-2.01	-9.4	1.82E-01	0.262	patternV	PatternI
ZNF518A	cg09345397	10	97889472	97965044	10	98610861	645817	-2.01	-91.8	1.82E-01	0.262	patternV	PatternIII
PLEKHN1	cg04407228	1	901877	911245	1	1710158	798913	2.01	2.0	1.83E-01	0.262	patternA	PatternI
USP1	cg14800796	1	62901968	62917475	1	63833137	915662	-2.00	-50.0	1.83E-01	0.262	patternV	PatternI
MAML3	cg09038155	4	140637907	141075338	4	139937227	700680	2.00	1.0	1.83E-01	0.262	patternA	PatternI
RAB39A	cg18204760	11	107799229	107834208	11	107461044	338185	-1.99	-0.4	1.85E-01	0.265	patternV	PatternI
CTDP1	cg23281729	18	77439801	77514510	18	78005477	490967	1.99	23.7	1.85E-01	0.265	patternA	PatternIII
MTHFD2	cg15270558	2	74425689	74444692	2	74881167	436475	-1.98	-6.6	1.86E-01	0.265	patternV	PatternI
SLFN5	cg21745612	17	33570055	33600674	17	32907636	662419	-1.97	-449.5	1.88E-01	0.267	patternV	PatternII
ZNF524	cg27482605	19	56111388	56114504	19	55677760	433628	1.96	459.4	1.88E-01	0.268	patternA	PatternIV
RNF5	cg11046887	6	32146131	32151930	6	31870245	275886	1.96	314.5	1.89E-01	0.268	patternA	PatternIII
U2SURP	cg23069822	3	142683339	142779567	3	143692006	912439	-1.96	-17.6	1.89E-01	0.268	patternV	PatternIV
WDR46	cg04014576	6	33246885	33257304	6	34112818	855514	1.95	30.2	1.91E-01	0.271	patternA	PatternI
AMN	cg16082877	14	103388993	103399933	14	103011332	377661	1.93	5.8	1.93E-01	0.274	patternA	PatternI
AMN	cg15649561	14	103388993	103399933	14	103852292	452359	1.92	8.0	1.95E-01	0.276	patternA	PatternI
INTS5	cg03922588	11	62414320	62420774	11	62473871	53097	1.91	79.0	1.96E-01	0.277	patternA	PatternIV

MLLT1	cg18732869	19	6212966	6279959	19	6739680	459721	1.91	27.7	1.96E-01	0.277	patternA	PatternIII
FLOT1	cg01209655	6	30695486	30710510	6	30041081	654405	-1.89	-1397.4	1.99E-01	0.281	patternA	PatternIII
FLOT1	cg10628782	6	30695486	30710510	6	31620229	909719	1.88	1276.7	2.01E-01	0.283	patternA	PatternIV
SLC25A46	cg05797914	5	110073837	110100857	5	110702850	601993	1.87	166.7	2.03E-01	0.285	patternV	PatternII
MIER3	cg12654349	5	56215429	56267502	5	56205094	10335	-1.87	-3.0	2.03E-01	0.285	patternV	PatternI
SLC25A46	cg07312116	5	110073837	110100857	5	110074930	1093	-1.86	-28.2	2.04E-01	0.287	patternV	PatternI
TOB1	cg25244778	17	48939584	48945339	17	48228521	711063	-1.85	-62.5	2.05E-01	0.288	patternV	PatternI
KLHL9	cg21004841	9	21329670	21335379	9	21995327	659948	-1.85	-56.1	2.06E-01	0.288	patternV	PatternI
ZNF444	cg11781339	19	56643968	56672262	19	56092040	551928	1.84	9.9	2.08E-01	0.291	patternA	PatternI
FKBPL	cg10628782	6	32096484	32098068	6	31620229	476255	1.83	188.0	2.09E-01	0.292	patternA	PatternIV
SIGLEC7	cg13861524	19	51645556	51656783	19	50836391	809165	-1.82	-199.6	2.11E-01	0.294	patternA	PatternIII
GSTCD	cg10346535	4	106629935	106768885	4	106629853	82	-1.81	-0.6	2.11E-01	0.294	patternV	PatternI
ZNF677	cg17892871	19	53731577	53758151	19	54618653	860502	-1.81	-1.9	2.11E-01	0.294	patternV	PatternI
NUDT21	cg06080402	16	56463045	56486111	16	57481519	995408	-1.81	-31.6	2.11E-01	0.294	patternV	PatternI
MBNL2	cg01941219	13	97873688	98046374	13	98795021	748647	-1.81	-1.3	2.12E-01	0.294	patternV	PatternI
CPEB4	cg06928134	5	173315283	173388979	5	173384132	4847	-1.80	-21.8	2.14E-01	0.296	patternV	PatternIII
PIKFYVE	cg08862564	2	209130991	209223475	2	208395069	735922	-1.79	-8.0	2.15E-01	0.297	patternV	PatternI
YTHDC2	cg12373617	5	112849380	112930982	5	113698140	767158	-1.79	-4.5	2.15E-01	0.298	patternV	PatternI
DBN1	cg07286681	5	176883609	176901402	5	176660615	222994	1.79	585.6	2.16E-01	0.298	patternA	PatternII
AFF4	cg05970164	5	132211071	132299326	5	131992018	219053	-1.77	-12.9	2.19E-01	0.302	patternV	PatternI
CD84	cg26146390	1	160510885	160549306	1	160068471	442414	-1.76	-19.0	2.20E-01	0.302	patternV	PatternI
RAP1B	cg10835308	12	69004619	69054372	12	68726120	278499	-1.76	-28.9	2.20E-01	0.302	patternV	PatternI
GSTCD	cg25223851	4	106629935	106768885	4	106395307	234628	-1.75	-0.7	2.22E-01	0.305	patternV	PatternI
CD38	cg09190466	4	15779898	15854853	4	16598089	743236	-1.74	-32.7	2.24E-01	0.307	patternV	PatternIII
BRIP1	cg12999453	17	59758627	59940882	17	59482319	276308	-1.74	-0.4	2.24E-01	0.307	patternV	PatternI
SH2B2	cg05005422	7	101928405	101962178	7	101650989	277416	1.74	306.1	2.24E-01	0.307	patternA	PatternIII
WDR36	cg07312116	5	110427414	110466200	5	110074930	352484	-1.73	-11.0	2.26E-01	0.309	patternV	PatternI
SLC29A2	cg10105999	11	66129992	66139685	11	65337913	792079	1.72	11.0	2.27E-01	0.309	patternA	PatternIII
DVL2	cg21696827	17	7128660	7137864	17	6541594	587066	1.72	212.6	2.27E-01	0.309	patternA	PatternIV
NUDT21	cg27524972	16	56463045	56486111	16	57279645	793534	-1.72	-18.3	2.27E-01	0.309	patternV	PatternI
MED23	cg21975007	6	131895106	131949369	6	132128965	179596	-1.72	-7.6	2.28E-01	0.311	patternV	PatternI
SLC29A2	cg25753024	11	66129992	66139685	11	67070913	931228	1.71	12.2	2.29E-01	0.311	patternA	PatternIV

TRAPPC10	cg1640035C	21	45432200	45526433	21	46414569	888136	1.71	86.0	2.29E-01	0.311	patternV	PatternIII
APC	cg21606957	5	112043195	112181936	5	111753754	289441	-1.71	-1.6	2.30E-01	0.312	patternA	PatternIII
ABCB10	cg1204831C	1	229652329	229694442	1	229762093	67651	-1.70	-11.1	2.31E-01	0.313	patternV	PatternI
USF1	cg08992717	1	161009041	161015767	1	160681615	327426	1.69	839.1	2.33E-01	0.315	patternA	PatternII
WDR46	cg1915622C	6	33246885	33257304	6	33244752	2133	-1.69	-75.3	2.34E-01	0.316	patternA	PatternIII
PAPOLG	cg11349992	2	60983365	61029220	2	61108895	79675	-1.68	-5.1	2.35E-01	0.317	patternV	PatternI
TGFB3	cg10096873	1	92145902	92371892	1	92546470	174578	-1.68	-1.4	2.35E-01	0.317	patternV	PatternI
KIAA1586	cg27378522	6	56911347	56920023	6	56820052	91295	-1.68	-6.9	2.36E-01	0.317	patternV	PatternI
SH2B2	cg06216309	7	101928405	101962178	7	101603359	325046	1.67	203.3	2.36E-01	0.317	patternA	PatternIII
IL7R	cg12739682	5	35852797	35879705	5	36876863	997158	-1.67	-476.9	2.36E-01	0.317	patternV	PatternI
MEX3C	cg20227886	18	48700920	48744674	18	48405353	295567	-1.67	-5.7	2.37E-01	0.317	patternV	PatternI
XPO1	cg11349992	2	61704984	61765761	2	61108895	596089	-1.67	-10.6	2.37E-01	0.317	patternV	PatternI
ZNF772	cg21994576	19	57978031	57988938	19	58739778	750840	-1.66	-5.8	2.38E-01	0.318	patternV	PatternIV
C6orf120	cg08470742	6	170102233	170106401	6	169653905	448328	-1.66	-68.2	2.38E-01	0.318	patternV	PatternI
FKBP4	cg1161247C	12	2904119	2914576	12	3068051	153475	1.64	88.6	2.42E-01	0.323	patternA	PatternIV
CCNT1	cg22517087	12	49082247	49110681	12	49208544	97863	-1.63	-7.1	2.44E-01	0.325	patternV	PatternI
CD84	cg04975598	1	160510885	160549306	1	160039909	470976	-1.62	-34.7	2.46E-01	0.328	patternV	PatternI
ARID5B	cg13381235	10	63661059	63856703	10	64120814	264111	1.62	7.1	2.47E-01	0.328	patternA	PatternII
TRAPPC11	cg03973167	4	184580420	184634745	4	185394988	760243	-1.62	-8.9	2.47E-01	0.328	patternV	PatternI
ZNF772	cg02344833	19	57978031	57988938	19	58545285	556347	-1.61	-7.4	2.49E-01	0.330	patternV	PatternI
TDG	cg13702005	12	104359582	104382652	12	103889789	469793	-1.60	-12.0	2.50E-01	0.331	patternV	PatternI
YTHDC2	cg09835486	5	112849380	112930982	5	112257968	591412	-1.60	-6.0	2.50E-01	0.331	patternV	PatternI
FEM1B	cg26825559	15	68570141	68588203	15	67814090	756051	-1.60	-23.2	2.51E-01	0.331	patternV	PatternI
WDR36	cg05797914	5	110427414	110466200	5	110702850	236650	1.60	62.8	2.51E-01	0.331	patternV	PatternII
RAP1B	cg09516963	12	69004619	69054372	12	68042445	962174	-1.59	-9.8	2.53E-01	0.334	patternV	PatternI
B3GAT3	cg03922588	11	62382768	62389647	11	62473871	84224	1.59	93.0	2.53E-01	0.334	patternA	PatternIV
GTF3C3	cg27452117	2	197627756	197664449	2	197036434	591322	-1.58	-6.5	2.56E-01	0.336	patternV	PatternI
KLHL22	cg13813874	22	20783528	20850170	22	20849595	575	1.57	11.0	2.57E-01	0.338	patternA	PatternI
GPSM3	cg27070869	6	32158543	32163300	6	32122779	35764	1.57	4141.8	2.57E-01	0.338	patternA	PatternII
VAV1	cg18732869	19	6772725	6857377	19	6739680	33045	1.57	41.6	2.58E-01	0.338	patternA	PatternIII
KCNA3	cg25847024	1	111214310	111217655	1	111991376	773721	-1.57	-63.1	2.58E-01	0.338	patternV	PatternI
IL6ST	cg12654349	5	55230923	55290821	5	56205094	914273	-1.56	-16.0	2.58E-01	0.338	patternV	PatternI

TGFB3	cg16010723	1	92145902	92371892	1	92764349	392457	-1.56	-3.2	2.58E-01	0.338	patternV	PatternI
DDX21	cg27570978	10	70715884	70744829	10	70231996	483888	-1.55	-59.7	2.61E-01	0.340	patternV	PatternIV
RNF5	cg27070869	6	32146131	32151930	6	32122779	23352	1.55	261.1	2.61E-01	0.340	patternA	PatternII
RHO	cg12048310	1	228870824	228882416	1	229762093	879677	-1.55	-37.2	2.61E-01	0.340	patternV	PatternI
COL5A3	cg07742633	19	10070237	10121147	19	10047209	23028	1.55	0.3	2.61E-01	0.340	patternA	PatternI
COL5A3	cg19355182	19	10070237	10121147	19	10543010	421863	1.54	0.5	2.64E-01	0.342	patternA	PatternI
SRSF6	cg25649000	20	42086568	42092245	20	41817903	268665	-1.54	-131.7	2.64E-01	0.342	patternV	PatternI
SLC35B3	cg01815076	6	8413301	8435794	6	8435968	174	-1.54	-11.8	2.64E-01	0.343	patternV	PatternI
CD84	cg10021668	1	160510885	160549306	1	159751259	759626	-1.53	-18.2	2.65E-01	0.343	patternV	PatternI
ZKSCAN1	cg18231159	7	99613204	99639312	7	99214508	398696	-1.53	-29.2	2.65E-01	0.343	patternV	PatternI
PPM1A	cg03540606	14	60712470	60765805	14	60982016	216211	-1.53	-8.7	2.67E-01	0.344	patternV	PatternI
ALAS1	cg00455242	3	52232102	52248343	3	52872820	624477	-1.52	-100.5	2.67E-01	0.344	patternA	PatternII
GNPTAB	cg11144990	12	102139275	102224716	12	102455902	231186	-1.52	-11.0	2.68E-01	0.344	patternV	PatternI
TOB1	cg23614229	17	48939584	48945339	17	48638594	300990	-1.52	-31.3	2.68E-01	0.344	patternV	PatternI
NRP2	cg13582873	2	206546714	206662857	2	207024197	361340	-1.52	-0.5	2.68E-01	0.344	patternV	PatternI
NFKBIL1	cg27070869	6	31514647	31526606	6	32122779	596173	1.52	24.4	2.68E-01	0.344	patternA	PatternII
CMTR2	cg03564166	16	71315292	71323618	16	70380888	934404	-1.51	-61.2	2.70E-01	0.346	patternV	PatternI
RAP2A	cg01941219	13	98086476	98121382	13	98795021	673639	-1.50	-7.2	2.72E-01	0.348	patternV	PatternI
HSPA1L	cg27070869	6	31777396	31783437	6	32122779	339342	1.50	30.0	2.73E-01	0.349	patternA	PatternII
LYPLA2	cg25880573	1	24117460	24122029	1	24073129	44331	1.49	1912.6	2.74E-01	0.350	patternA	PatternIII
CAPG	cg04593571	2	85621871	85645555	2	85361052	260819	1.49	176.5	2.75E-01	0.350	patternA	PatternIV
MFSD10	cg03469578	4	2932288	2936586	4	3735986	799400	-1.49	-1858.0	2.75E-01	0.350	patternA	PatternII
INTS5	cg17517598	11	62414320	62420774	11	61659090	755230	1.49	106.8	2.75E-01	0.350	patternA	PatternIV
COL5A3	cg01284702	19	10070237	10121147	19	11039163	918016	1.49	0.3	2.76E-01	0.350	patternA	PatternI
XPR1	cg26280553	1	180601140	180859387	1	180882276	22889	-1.48	-0.4	2.76E-01	0.351	patternA	PatternI
PNRC2	cg09896346	1	24285599	24289952	1	23751195	534404	-1.48	-157.6	2.78E-01	0.353	patternV	PatternI
CD38	cg04764131	4	15779898	15854853	4	16228633	373780	-1.47	-7.8	2.78E-01	0.353	patternV	PatternI
ZNF772	cg01268824	19	57978031	57988938	19	58220818	231880	-1.47	-3.4	2.79E-01	0.353	patternV	PatternI
NUDT21	cg27367960	16	56463045	56486111	16	56702038	215927	-1.46	-12.9	2.81E-01	0.355	patternV	PatternI
PDIK1L	cg27547812	1	26437664	26452034	1	26437414	250	-1.46	-6.3	2.81E-01	0.355	patternV	PatternI
SREK1	cg05902997	5	65435799	65479443	5	65440515	4716	-1.46	-12.9	2.82E-01	0.355	patternV	PatternI
NRP2	cg01399068	2	206546714	206662857	2	207630025	967168	-1.46	-0.2	2.83E-01	0.356	patternV	PatternI

RBAK	cg23432654	7	5085452	5109119	7	5595804	486685	-1.46	-10.0	2.83E-01	0.356	patternV	PatternI
BLOC1S6	cg05785653	15	45879321	45908197	15	45695817	183504	-1.45	-22.4	2.83E-01	0.356	patternV	PatternIV
MTHFD2	cg08430329	2	74425689	74444692	2	73430374	995315	-1.45	-6.9	2.84E-01	0.357	patternV	PatternII
RNASEK	cg21696827	17	6915736	6917851	17	6541594	374142	1.45	4981.3	2.85E-01	0.357	patternA	PatternIV
TUBA4A	cg22980611	2	220114433	220142892	2	220144208	1316	1.44	175.9	2.85E-01	0.358	patternA	PatternIII
MYBL1	cg14353137	8	67474410	67526482	8	67873799	347317	-1.44	-12.2	2.86E-01	0.358	patternV	PatternI
CDK5	cg17806882	7	150750899	150755617	7	150216872	534027	1.44	125.5	2.86E-01	0.358	patternA	PatternII
ZNF24	cg26141063	18	32912176	32925446	18	32870200	41976	-1.44	-28.0	2.87E-01	0.358	patternV	PatternI
PANK4	cg02328713	1	2439972	2458039	1	2704354	246315	-1.44	-141.3	2.87E-01	0.358	patternA	PatternII
CD38	cg02183671	4	15779898	15854853	4	15779999	101	-1.43	-9.7	2.88E-01	0.358	patternV	PatternI
SPTLC1	cg07525971	9	94794281	94877666	9	95858482	980816	-1.43	-1.8	2.88E-01	0.358	patternA	PatternI
GTF2H3	cg09593767	12	124118375	124147153	12	124457669	310516	-1.43	-4.9	2.89E-01	0.358	patternV	PatternI
DCAF17	cg02227919	2	172290727	172341562	2	171569132	721595	-1.43	-3.7	2.89E-01	0.358	patternV	PatternI
PURA	cg26882009	5	139487362	139496321	5	140346106	849785	-1.43	-10.2	2.89E-01	0.358	patternV	PatternI
BAG5	cg15649561	14	104022881	104029168	14	103852292	170589	-1.43	-52.8	2.89E-01	0.358	patternV	PatternI
MSRB1	cg09080030	16	1988211	1993327	16	2820366	827039	1.42	9099.2	2.90E-01	0.360	patternA	PatternII
TNFRSF12A	cg09080030	16	3068446	3072384	16	2820366	248080	1.42	87.6	2.91E-01	0.360	patternA	PatternII
GSAP	cg22610194	7	76940068	77045717	7	77045539	178	-1.42	-3.7	2.92E-01	0.361	patternV	PatternI
MAP1LC3A	cg24253482	20	33134658	33148149	20	33064396	70262	-1.42	-52.3	2.92E-01	0.361	patternA	PatternIII
TDG	cg07994320	12	104359582	104382652	12	104850524	467872	-1.41	-6.6	2.93E-01	0.361	patternV	PatternI
LMAN1	cg05598816	18	56995055	57027194	18	57026567	627	-1.41	-16.1	2.93E-01	0.361	patternV	PatternI
FLOT1	cg08879910	6	30695486	30710510	6	29974319	721167	1.41	469.4	2.93E-01	0.361	patternA	PatternIV
TRAPPC6A	cg04571944	19	45666186	45681495	19	45644563	21623	1.41	85.9	2.94E-01	0.361	patternA	PatternIV
ZKSCAN1	cg19989222	7	99613204	99639312	7	98741665	871539	-1.41	-25.8	2.94E-01	0.361	patternV	PatternI
TSPAN33	cg07293445	7	128784712	128808671	7	128550623	234089	1.39	15.7	2.99E-01	0.366	patternA	PatternII
TXK	cg04127233	4	48068410	48136273	4	47839619	228791	-1.39	-10.7	3.00E-01	0.368	patternV	PatternI
DDAH2	cg11046887	6	31694815	31698394	6	31870245	171851	1.38	240.3	3.01E-01	0.368	patternA	PatternIII
TXK	cg22803211	4	48068410	48136273	4	48833130	696857	-1.38	-9.9	3.01E-01	0.368	patternV	PatternI
ZNF677	cg15680557	19	53731577	53758151	19	54704426	946275	-1.38	-0.9	3.02E-01	0.368	patternV	PatternI
PURA	cg11268983	5	139487362	139496321	5	140262304	765983	-1.38	-11.0	3.02E-01	0.368	patternV	PatternI
RBAK	cg24239690	7	5085452	5109119	7	5635953	526834	-1.38	-6.9	3.02E-01	0.368	patternV	PatternI
MOB1B	cg22674793	4	71768043	71888166	4	71570323	197720	-1.38	-2.2	3.03E-01	0.368	patternV	PatternI

ZNF699	cg16906204	19	9404951	9420514	19	8509784	895167	-1.37	-5.8	3.05E-01	0.371	patternV	PatternI
DFFB	cg12133393	1	3773845	3801993	1	3816695	14702	-1.37	-12.7	3.05E-01	0.371	patternV	PatternI
GTF2H3	cg21131339	12	124118375	124147153	12	123848917	269458	-1.36	-3.9	3.06E-01	0.371	patternV	PatternI
KLHL22	cg22258863	22	20783528	20850170	22	21058570	208400	1.36	6.8	3.06E-01	0.371	patternA	PatternI
BTBD1	cg08939095	15	83685174	83736106	15	83953068	216962	-1.36	-8.8	3.07E-01	0.371	patternV	PatternI
MEX3C	cg27092705	18	48700920	48744674	18	48556386	144534	-1.35	-7.4	3.10E-01	0.375	patternV	PatternI
ECHS1	cg22887949	10	135175984	135187193	10	134683495	492489	-1.34	-135.5	3.12E-01	0.377	patternA	PatternII
SRSF10	cg09896346	1	24291294	24307417	1	23751195	540099	-1.33	-63.6	3.14E-01	0.378	patternV	PatternI
CUL4A	cg16476991	13	113862552	113919399	13	114831404	912005	-1.33	-18.5	3.16E-01	0.381	patternV	PatternI
BRMS1	cg10105999	11	66104804	66112596	11	65337913	766891	1.32	81.8	3.17E-01	0.381	patternA	PatternIII
ZNF280D	cg18132228	15	56922379	57210769	15	56035476	886903	-1.32	-2.3	3.17E-01	0.381	patternV	PatternI
RAB12	cg16647169	18	8609443	8639379	18	9474995	835616	-1.32	-10.8	3.18E-01	0.383	patternV	PatternI
ZNF700	cg08305551	19	12035883	12061588	19	12978611	917023	-1.32	-24.9	3.19E-01	0.383	patternV	PatternI
FXR2	cg21696827	17	7494548	7518189	17	6541594	952954	1.31	34.9	3.21E-01	0.384	patternA	PatternIV
ECHS1	cg26450254	10	135175984	135187193	10	134218408	957576	1.31	123.9	3.21E-01	0.384	patternA	PatternIII
HOOK1	cg13093249	1	60280458	60342050	1	59281922	998536	-1.31	-1.5	3.21E-01	0.384	patternV	PatternI
FEM1B	cg17827166	15	68570141	68588203	15	68522236	47905	-1.30	-15.0	3.23E-01	0.386	patternV	PatternI
ZNF699	cg07742633	19	9404951	9420514	19	10047209	626695	-1.29	-3.9	3.26E-01	0.389	patternV	PatternI
RHOA	cg07663280	1	228870824	228882416	1	228270405	600419	-1.29	-16.7	3.27E-01	0.390	patternV	PatternI
ELK4	cg03142956	1	205577071	205601090	1	205012349	564722	-1.28	-27.0	3.28E-01	0.390	patternV	PatternIII
ZNF23	cg17823100	16	71481500	71496998	16	71918263	421265	-1.28	-7.4	3.28E-01	0.390	patternV	PatternI
TSEN34	cg27482605	19	54693789	54697585	19	55677760	980175	1.28	1538.3	3.30E-01	0.392	patternA	PatternIV
CD84	cg00329300	1	160510885	160549306	1	161008462	459156	-1.27	-17.3	3.31E-01	0.393	patternV	PatternI
PNRC2	cg25880573	1	24285599	24289952	1	24073129	212470	-1.27	-762.6	3.31E-01	0.393	patternV	PatternIII
PURA	cg12588763	5	139487362	139496321	5	139555533	59212	-1.27	-11.3	3.32E-01	0.393	patternV	PatternI
ZNF775	cg17806882	7	150065879	150109558	7	150216872	107314	1.27	157.2	3.33E-01	0.394	patternA	PatternII
TRIOBP	cg18443229	22	38093011	38172563	22	38082335	10676	-1.26	-121.1	3.34E-01	0.394	patternA	PatternIII
CCNT1	cg07923666	12	49082247	49110681	12	49932857	822176	-1.26	-6.5	3.34E-01	0.394	patternV	PatternI
PHF23	cg21696827	17	7138347	7143041	17	6541594	596753	1.26	386.7	3.35E-01	0.395	patternA	PatternIV
KLHL42	cg20263570	12	27932953	27955973	12	28657738	701765	1.26	37.3	3.36E-01	0.396	patternV	PatternII
ZNF280D	cg00395929	15	56922379	57210769	15	57181938	28831	1.25	3.5	3.39E-01	0.398	patternV	PatternII
PANX2	cg14274482	22	50609160	50618723	22	50913571	294848	1.25	203.5	3.39E-01	0.398	patternA	PatternIII

ZKSCAN1	cg1187489C	7	99613204	99639312	7	99534075	79129	-1.25	-32.8	3.39E-01	0.398	patternV	PatternIV
DCP1A	cg00455242	3	53317447	53381654	3	52872820	444627	1.24	10.4	3.39E-01	0.398	patternA	PatternII
ST3GAL4	cg0753004E	11	126225535	126310239	11	126165567	59968	1.24	298.4	3.40E-01	0.398	patternA	PatternII
BAG5	cg08142571	14	104022881	104029168	14	104096390	67222	-1.24	-16.1	3.40E-01	0.399	patternV	PatternI
CMTR2	cg1782310C	16	71315292	71323618	16	71918263	594645	-1.24	-27.4	3.41E-01	0.399	patternV	PatternI
SRSF10	cg25880573	1	24291294	24307417	1	24073129	218165	-1.24	-318.5	3.42E-01	0.400	patternV	PatternIII
SCYL1	cg1010599C	11	65292548	65306175	11	65337913	31738	1.23	123.3	3.43E-01	0.400	patternA	PatternIII
FKBPL	cg2707086C	6	32096484	32098068	6	32122779	24711	1.23	64.3	3.44E-01	0.400	patternA	PatternII
B3GAT3	cg1751759E	11	62382768	62389647	11	61659090	723678	1.23	122.7	3.44E-01	0.400	patternA	PatternIV
GTF2H3	cg26494424	12	124118375	124147153	12	124118326	49	-1.23	-5.6	3.44E-01	0.400	patternV	PatternI
IMPDH1	cg09776122	7	128032331	128050306	7	128603393	553087	-1.23	-2140.1	3.44E-01	0.400	patternA	PatternII
PRPF38B	cg0156406E	1	109234945	109244425	1	110198568	954143	-1.23	-67.9	3.45E-01	0.400	patternV	PatternI
GLCE	cg1782716C	15	69452923	69564556	15	68522236	930687	-1.22	-0.9	3.46E-01	0.402	patternV	PatternI
CMTR2	cg16503601	16	71315292	71323618	16	71929079	605461	-1.21	-40.1	3.48E-01	0.404	patternV	PatternI
GTF2H3	cg2161804C	12	124118375	124147153	12	123921306	197069	-1.21	-2.3	3.49E-01	0.405	patternV	PatternI
TP53INP1	cg1147477E	8	95938200	95961639	8	95487352	450848	-1.21	-54.7	3.50E-01	0.405	patternV	PatternII
MXD3	cg07286681	5	176728462	176739758	5	176660615	67847	1.20	10784.8	3.53E-01	0.407	patternA	PatternII
ZNF23	cg16503601	16	71481500	71496998	16	71929079	432081	-1.20	-10.5	3.53E-01	0.407	patternV	PatternI
VPS36	cg17143642	13	52986737	53024763	13	52026804	959933	-1.20	-10.4	3.54E-01	0.408	patternV	PatternI
TNIP2	cg0346957E	4	2743375	2758103	4	3735986	977883	-1.19	-387.7	3.56E-01	0.410	patternA	PatternII
FGFR1OP2	cg1964737C	12	27091316	27119583	12	26146815	944501	1.19	219.8	3.57E-01	0.411	patternV	PatternII
BTBD1	cg22805152	15	83685174	83736106	15	83736134	28	-1.19	-5.6	3.57E-01	0.411	patternV	PatternI
HP1BP3	cg17196364	1	21069154	21113816	1	21617006	503190	-1.18	-24.5	3.58E-01	0.411	patternV	PatternI
GTF2H3	cg16097051	12	124118375	124147153	12	124068991	49384	-1.18	-4.5	3.59E-01	0.411	patternV	PatternI
ZKSCAN1	cg1801340E	7	99613204	99639312	7	100487659	848347	-1.18	-12.5	3.59E-01	0.411	patternV	PatternI
ZNF700	cg25818882	19	12035883	12061588	19	12886379	824791	-1.18	-22.9	3.60E-01	0.413	patternV	PatternI
GPSM3	cg11046887	6	32158543	32163300	6	31870245	288298	1.17	3904.0	3.63E-01	0.414	patternA	PatternIII
FKBPL	cg11046887	6	32096484	32098068	6	31870245	226239	1.17	68.5	3.63E-01	0.414	patternA	PatternIII
CASP8AP2	cg18640564	6	90539613	90584155	6	90142888	396725	-1.16	-7.8	3.65E-01	0.416	patternV	PatternI
BRIP1	cg1955751E	17	59758627	59940882	17	60704641	763759	-1.16	-0.3	3.65E-01	0.416	patternV	PatternI
TMED5	cg1639426C	1	93615299	93646285	1	93811744	165459	-1.15	-13.5	3.70E-01	0.421	patternV	PatternIII
TSPAN33	cg09776122	7	128784712	128808671	7	128603393	181319	-1.14	-92.0	3.71E-01	0.422	patternA	PatternII

IMPDH1	cg07293445	7	128032331	128050306	7	128550623	500317	1.13	311.9	3.75E-01	0.426	patternA	PatternII
LTN1	cg21277945	21	30300466	30365270	21	30191751	108715	1.13	91.1	3.76E-01	0.427	patternV	PatternII
TRAPPC10	cg21887544	21	45432200	45526433	21	45431138	1062	1.12	31.4	3.79E-01	0.430	patternV	PatternIII
ATXN7	cg25137613	3	63850233	63989138	3	63849764	469	-1.11	-2.7	3.82E-01	0.433	patternV	PatternI
ENPP4	cg09101258	6	46097730	46114436	6	46713411	598975	-1.10	-64.5	3.85E-01	0.436	patternV	PatternIII
RBAK	cg00730085	7	5085452	5109119	7	5115365	6246	1.10	110.6	3.86E-01	0.436	patternV	PatternII
ZYG11B	cg13984393	1	53192126	53293014	1	52831958	360168	-1.10	-2.0	3.87E-01	0.437	patternA	PatternI
TXK	cg07522516	4	48068410	48136273	4	48492196	355923	-1.09	-6.9	3.89E-01	0.439	patternV	PatternI
RBAK	cg11896795	7	5085452	5109119	7	5465465	356346	-1.08	-2.9	3.93E-01	0.443	patternV	PatternI
ZKSCAN8	cg27658416	6	28109688	28127250	6	28603033	475783	-1.08	-22.1	3.94E-01	0.444	patternV	PatternI
NKTR	cg10283155	3	42642106	42690227	3	42642604	498	-1.07	-32.6	3.97E-01	0.447	patternV	PatternI
RBM25	cg15079605	14	73525144	73588122	14	73704078	115956	-1.07	-23.2	3.98E-01	0.448	patternV	PatternIII
ZNF700	cg01284702	19	12035883	12061588	19	11039163	996720	-1.06	-21.0	4.00E-01	0.449	patternV	PatternI
TMUB1	cg17806882	7	150778167	150780633	7	150216872	561295	1.06	890.2	4.00E-01	0.449	patternA	PatternII
COL5A3	cg09700868	19	10070237	10121147	19	10562169	441022	1.06	1.3	4.01E-01	0.449	patternA	PatternIII
CCNT1	cg14029489	12	49082247	49110681	12	49689463	578782	-1.06	-16.8	4.01E-01	0.449	patternV	PatternII
RFX2	cg18732869	19	5993175	6199583	19	6739680	540097	1.06	2.5	4.01E-01	0.449	patternA	PatternIII
POLR2M	cg00395929	15	57884231	58074960	15	57181938	702293	1.05	4.0	4.03E-01	0.450	patternV	PatternII
CCNT1	cg12020201	12	49082247	49110681	12	50017283	906602	-1.05	-4.9	4.05E-01	0.453	patternV	PatternI
ZNF655	cg11874899	7	99156029	99174076	7	99534075	359999	-1.04	-74.4	4.06E-01	0.453	patternV	PatternIV
ZNF655	cg18231159	7	99156029	99174076	7	99214508	40432	-1.04	-59.5	4.06E-01	0.453	patternV	PatternI
PURA	cg03317235	5	139487362	139496321	5	139423324	64038	-1.03	-13.7	4.10E-01	0.456	patternV	PatternI
HUS1	cg23633700	7	47735328	48019178	7	48016735	2443	-1.03	-15.1	4.12E-01	0.458	patternV	PatternIII
UTF1	cg26450254	10	135043778	135045062	10	134218408	825370	1.03	67.4	4.12E-01	0.458	patternA	PatternIII
YTHDF3	cg23906935	8	64081112	64125346	8	63984459	96653	0.99	51.7	4.25E-01	0.471	patternV	PatternII
ZNF655	cg19989222	7	99156029	99174076	7	98741665	414364	-0.97	-52.4	4.33E-01	0.480	patternV	PatternI
PRELID1	cg07286681	5	176730775	176733960	5	176660615	70160	0.97	17020.9	4.33E-01	0.480	patternA	PatternII
CNOT6L	cg00611818	4	78634541	78740769	4	78074683	559858	0.97	38.2	4.36E-01	0.483	patternV	PatternIII
SPINK8	cg08206271	3	48348336	48369831	3	47646780	701556	0.96	4.3	4.37E-01	0.483	patternA	PatternII
ZKSCAN8	cg15743358	6	28109688	28127250	6	28303923	176673	-0.96	-23.0	4.39E-01	0.484	patternV	PatternI
TRIM39	cg01209655	6	30294256	30311506	6	30041081	253175	-0.96	-61.3	4.39E-01	0.485	patternA	PatternIII
ZNF444	cg27482605	19	56643968	56672262	19	55677760	966208	0.94	26.1	4.46E-01	0.492	patternA	PatternIV

CNTRL	cg13569051	9	123837141	123939888	9	124051703	111815	-0.93	-52.6	4.50E-01	0.495	patternV	PatternIII
HEYL	cg17784876	1	40089825	40105617	1	39464086	625739	0.93	6.4	4.51E-01	0.497	patternA	PatternII
CD38	cg04408998	4	15779898	15854853	4	15684672	95226	0.92	16.3	4.53E-01	0.498	patternV	PatternII
UPF3A	cg16476991	13	115047059	115071283	13	114831404	215655	-0.92	-17.0	4.57E-01	0.501	patternV	PatternI
CD84	cg08992717	1	160510885	160549306	1	160681615	132309	-0.91	-51.5	4.57E-01	0.501	patternV	PatternII
ANKRD40	cg13497650	17	48770551	48785285	17	48351646	418905	-0.91	-16.0	4.58E-01	0.502	patternV	PatternI
HSPA1B	cg10628782	6	31795512	31798031	6	31620229	175283	0.90	408.8	4.62E-01	0.506	patternA	PatternIV
ANKRD40	cg18454685	17	48770551	48785285	17	48639239	131312	-0.89	-20.4	4.69E-01	0.513	patternV	PatternI
ZKSCAN8	cg25474372	6	28109688	28127250	6	28762125	634875	-0.88	-18.5	4.70E-01	0.513	patternV	PatternIII
ANKRD40	cg25244778	17	48770551	48785285	17	48228521	542030	-0.88	-16.1	4.73E-01	0.516	patternV	PatternI
ZNF700	cg07812877	19	12035883	12061588	19	11531469	504414	-0.87	-74.2	4.76E-01	0.519	patternV	PatternII
ANKRD40	cg14929100	17	48770551	48785285	17	48206884	563667	-0.86	-25.6	4.80E-01	0.523	patternV	PatternI
ZKSCAN8	cg27219662	6	28109688	28127250	6	28891728	764478	-0.85	-18.0	4.84E-01	0.527	patternV	PatternI
ZNF467	cg17806882	7	149461271	149470568	7	150216872	746304	0.85	1363.0	4.86E-01	0.528	patternA	PatternII
ZNF623	cg00713939	8	144718183	144735900	8	144660590	57593	-0.84	-5.4	4.88E-01	0.530	patternV	PatternI
ZKSCAN8	cg08926828	6	28109688	28127250	6	28757569	630319	-0.84	-10.7	4.90E-01	0.532	patternV	PatternI
ZKSCAN8	cg08377819	6	28109688	28127250	6	28956268	829018	-0.83	-10.3	4.92E-01	0.534	patternV	PatternI
EDRF1	cg27630209	10	127408084	127452712	10	127748305	295593	0.83	50.6	4.94E-01	0.535	patternV	PatternIII
MATR3	cg12588763	5	138609441	138667360	5	139555533	888173	-0.80	-10.3	5.09E-01	0.550	patternV	PatternI
CD2AP	cg09101258	6	47445525	47594999	6	46713411	732114	-0.80	-8.1	5.09E-01	0.550	patternV	PatternIII
ANKH	cg06444178	5	14704910	14871887	5	14871469	418	-0.80	-5.8	5.10E-01	0.550	patternA	PatternII
TOB1	cg25180585	17	48939584	48945339	17	49230756	285417	-0.79	-57.7	5.10E-01	0.551	patternV	PatternIV
GPR35	cg12903924	2	241544848	241570676	2	242448061	877385	0.78	6.9	5.16E-01	0.557	patternA	PatternIV
ARHGAP5	cg12474182	14	32545320	32628934	14	33403952	775018	-0.78	-4.8	5.17E-01	0.557	patternV	PatternIII
SP4	cg17777998	7	21467652	21554440	7	21510481	42829	-0.77	-13.8	5.23E-01	0.563	patternV	PatternIII
MED23	cg05332565	6	131895106	131949369	6	131642853	252253	0.76	108.1	5.27E-01	0.566	patternV	PatternIII
ZNF354C	cg10832470	5	178487416	178510538	5	179105290	594752	-0.74	-13.4	5.36E-01	0.576	patternV	PatternIII
HSPA1B	cg11046887	6	31795512	31798031	6	31870245	72214	0.74	159.2	5.37E-01	0.576	patternA	PatternIII
UBASH3B	cg04883609	11	122526383	122685181	11	122073934	452449	-0.74	-3.3	5.38E-01	0.577	patternA	PatternII
DBN1	cg11302624	5	176883609	176901402	5	176788169	95440	-0.72	-65.9	5.45E-01	0.583	patternA	PatternII
CCDC170	cg02364518	6	151815165	151942328	6	152547148	604820	-0.72	-3.0	5.47E-01	0.585	patternV	PatternII
MATR3	cg03317235	5	138609441	138667360	5	139423324	755964	-0.68	-12.5	5.65E-01	0.604	patternV	PatternI

ANKRD40	cg23614229	17	48770551	48785285	17	48638594	131957	-0.68	-7.2	5.66E-01	0.604	patternV	PatternI
MAP3K2	cg25501666	2	128056306	128146041	2	127640322	415984	0.68	21.5	5.68E-01	0.606	patternV	PatternII
PANX2	cg08760073	22	50609160	50618723	22	51021304	402581	-0.68	-432.2	5.68E-01	0.606	patternA	PatternIV
PDIK1L	cg08948442	1	26437664	26452034	1	26014468	423196	0.67	17.4	5.73E-01	0.610	patternV	PatternII
AMBRA1	cg03487637	11	46417964	46615675	11	45940039	477925	0.66	1.1	5.75E-01	0.611	patternA	PatternI
CUL4A	cg10997500	13	113862552	113919399	13	113974988	55589	-0.66	-132.2	5.78E-01	0.614	patternV	PatternII
AKAP7	cg05332565	6	131456806	131604675	6	131642853	38178	0.65	6.9	5.84E-01	0.620	patternA	PatternIII
ITPR2	cg19647370	12	26490342	26986131	12	26146815	343527	0.62	5.2	5.96E-01	0.632	patternA	PatternII
RPTOR	cg09680719	17	78518619	78940171	17	77796831	721788	-0.61	-1.7	6.01E-01	0.637	patternA	PatternI
SMARCE1	cg12041100	17	38781214	38804760	17	38337188	444026	0.60	14.1	6.09E-01	0.644	patternV	PatternII
ZKSCAN8	cg12408601	6	28109688	28127250	6	27841665	268023	-0.60	-32.8	6.09E-01	0.644	patternV	PatternIV
KRAS	cg19647370	12	25357723	25403870	12	26146815	742945	0.58	63.4	6.19E-01	0.654	patternV	PatternII
HSPA1B	cg27070869	6	31795512	31798031	6	32122779	324748	0.57	116.4	6.28E-01	0.663	patternA	PatternII
RPS27L	cg03624661	15	63418071	63450220	15	63569529	119309	0.57	2.8	6.29E-01	0.663	patternA	PatternI
MYO7B	cg25501666	2	128293378	128395304	2	127640322	653056	-0.56	-7.6	6.31E-01	0.665	patternA	PatternII
S100A11	cg27204614	1	152004982	152020383	1	152481862	461479	-0.56	-4724.4	6.33E-01	0.666	patternA	PatternII
MEX3C	cg26557404	18	48700920	48744674	18	47721899	979021	-0.54	-4.0	6.41E-01	0.674	patternV	PatternIII
NLRX1	cg09194364	11	119037277	119054725	11	119612475	557750	0.53	37.0	6.47E-01	0.679	patternA	PatternII
SHISA8	cg04809988	22	42307297	42310570	22	41940355	366942	0.53	4.5	6.50E-01	0.682	patternA	PatternII
ZNF609	cg03028236	15	64752941	64978264	15	65669811	691547	-0.53	-0.5	6.50E-01	0.682	patternA	PatternI
ESR1	cg02364518	6	151977826	152450754	6	152547148	96394	-0.53	-3.2	6.52E-01	0.683	patternA	PatternII
LEPR	cg02619167	1	65886248	66107242	1	65613297	272951	-0.52	-0.6	6.57E-01	0.687	patternA	PatternI
IL6ST	cg15431103	5	55230923	55290821	5	55457410	166589	0.49	15.4	6.74E-01	0.704	patternV	PatternII
EHMT1	cg13696351	9	140513444	140764468	9	140063617	449827	0.49	1.3	6.74E-01	0.704	patternA	PatternI
COL5A3	cg01329093	19	10070237	10121147	19	9546029	524208	-0.48	-0.5	6.77E-01	0.706	patternA	PatternII
TPT1	cg13717880	13	45911008	45915505	13	45563580	347428	-0.47	-223.9	6.82E-01	0.711	patternV	PatternI
GCNT1	cg13661740	9	79034752	79122332	9	79635912	513580	-0.46	-0.2	6.92E-01	0.721	patternA	PatternI
MBNL1	cg26591958	3	151961617	152183569	3	151160047	801570	-0.44	-43.3	7.03E-01	0.731	patternV	PatternII
TRAPPC10	cg12094974	21	45432200	45526433	21	46323812	797379	-0.44	-15.0	7.05E-01	0.732	patternV	PatternII
TOP3B	cg07644571	22	22311397	22337213	22	22307395	4002	0.44	2.7	7.05E-01	0.732	patternA	PatternI
IL12RB2	cg07195508	1	67773047	67862583	1	67390935	382112	-0.44	-0.3	7.06E-01	0.732	patternA	PatternI
MXD3	cg11302624	5	176728462	176739758	5	176788169	48411	-0.43	-948.6	7.06E-01	0.732	patternA	PatternII

ZNF609	cg22159557	15	64752941	64978264	15	65067668	89404	-0.43	-0.5	7.11E-01	0.736	patternA	PatternI
ZNF609	cg14179433	15	64752941	64978264	15	65809620	831356	-0.43	-1.0	7.11E-01	0.736	patternA	PatternI
EHMT1	cg14788802	9	140513444	140764468	9	140446233	67211	0.41	1.0	7.23E-01	0.748	patternA	PatternI
IL12RB2	cg23251970	1	67773047	67862583	1	68298816	436233	-0.40	-0.2	7.27E-01	0.751	patternA	PatternI
ZFP2	cg10832470	5	178322895	178360213	5	179105290	745077	0.40	0.4	7.27E-01	0.751	patternA	PatternIII
ARID5B	cg02852210	10	63661059	63856703	10	63017479	643580	-0.38	-2.7	7.39E-01	0.762	patternA	PatternIII
MIER3	cg15431103	5	56215429	56267502	5	55457410	758019	0.38	2.1	7.43E-01	0.766	patternV	PatternII
TBKBP1	cg05526642	17	45771447	45789416	17	46595118	805702	-0.37	-66.2	7.46E-01	0.767	patternA	PatternIII
EHMT1	cg14095044	9	140513444	140764468	9	140314220	199224	0.36	1.9	7.56E-01	0.777	patternA	PatternIII
UTF1	cg03897392	10	135043778	135045062	10	134803718	240060	-0.29	-27.5	8.00E-01	0.822	patternA	PatternII
ADD3	cg03871549	10	111756126	111895323	10	112403448	508125	0.29	62.4	8.02E-01	0.824	patternV	PatternII
RANBP6	cg13930177	9	6011043	6015618	9	5996654	14389	0.28	78.1	8.04E-01	0.825	patternV	PatternII
AKAP7	cg21975007	6	131456806	131604675	6	132128965	524290	-0.25	-0.1	8.23E-01	0.843	patternA	PatternI
PRELID1	cg11302624	5	176730775	176733960	5	176788169	54209	-0.25	-1028.4	8.23E-01	0.843	patternA	PatternII
ZNF236	cg03659519	18	74534563	74682683	18	74961966	279283	0.25	0.6	8.25E-01	0.844	patternV	PatternII
ATG4D	cg09700868	19	10654571	10664094	19	10562169	92402	0.25	40.4	8.28E-01	0.846	patternA	PatternIII
ATG4D	cg07812877	19	10654571	10664094	19	11531469	867375	0.24	28.7	8.32E-01	0.849	patternA	PatternII
PPIP5K2	cg05587118	5	102455853	102548500	5	102201664	254189	-0.23	-2.2	8.37E-01	0.854	patternV	PatternIII
UBASH3B	cg08181212	11	122526383	122685181	11	122177231	349152	0.22	1.2	8.45E-01	0.862	patternA	PatternII
ANKRD40	cg25180585	17	48770551	48785285	17	49230756	445471	-0.19	-6.2	8.65E-01	0.880	patternV	PatternIV
TMX1	cg09669049	14	51706880	51722759	14	52455814	733055	0.19	60.7	8.67E-01	0.882	patternV	PatternIII
ATP6V0D1	cg00323316	16	67471917	67515140	16	66785861	686056	0.17	70.0	8.80E-01	0.895	patternA	PatternII
PRPF38B	cg21947298	1	109234945	109244425	1	109289127	44702	-0.15	-33.9	8.95E-01	0.908	patternV	PatternIV
SMARCE1	cg06307169	17	38781214	38804760	17	38296698	484516	0.14	1.6	9.02E-01	0.915	patternV	PatternI
ZNF736	cg24495177	7	63767837	63815238	7	64362326	547088	0.14	3.1	9.03E-01	0.915	patternV	PatternIII
HLX	cg22535327	1	221051699	221058401	1	220312424	739275	-0.13	-280.1	9.05E-01	0.916	patternA	PatternII
ECHS1	cg03897392	10	135175984	135187193	10	134803718	372266	-0.13	-19.3	9.12E-01	0.922	patternA	PatternII
PRPF4B	cg12529922	6	4021501	4065217	6	3222140	799361	0.12	14.9	9.15E-01	0.925	patternV	PatternII
MYO5A	cg12421755	15	52599480	52821247	15	53080933	259686	-0.12	-0.7	9.17E-01	0.926	patternA	PatternIII
RPTOR	cg20140052	17	78518619	78940171	17	79367844	427673	-0.09	-0.1	9.40E-01	0.948	patternA	PatternI
RPTOR	cg17917959	17	78518619	78940171	17	79197229	257058	-0.08	-0.1	9.43E-01	0.950	patternA	PatternI
BLOC1S6	cg08436772	15	45879321	45908197	15	45725215	154106	0.08	7.0	9.45E-01	0.952	patternV	PatternIII

PPM1A	cg26068585	14	60712470	60765805	14	60637976	74494	-0.07	-4.0	9.47E-01	0.953	patternV	PatternII
ZKSCAN8	cg14913178	6	28109688	28127250	6	27521267	588421	-0.07	-1.9	9.52E-01	0.957	patternV	PatternIII
TMX3	cg22506586	18	66340925	66382535	18	65398512	942413	0.06	5.3	9.55E-01	0.959	patternV	PatternIII
RPTOR	cg15523177	17	78518619	78940171	17	79269242	329071	-0.06	-0.1	9.58E-01	0.961	patternA	PatternI
RPTOR	cg22230229	17	78518619	78940171	17	79372254	432083	0.02	0.0	9.86E-01	0.989	patternA	PatternI
SMARCE1	cg09852679	17	38781214	38804760	17	38973067	168307	-0.02	-0.4	9.89E-01	0.990	patternV	PatternI
RPTOR	cg11523661	17	78518619	78940171	17	77916043	602576	-0.01	0.0	9.91E-01	0.992	patternA	PatternI
FHOD1	cg00323316	16	67263290	67281561	16	66785861	477429	0.00	0.0	1.00E+00	1.000	patternA	PatternII