

Supplementary table 1. Variants identified in core-promoters between -100 to +100 in the individual genome

Motif	Gene	Chr	Position	Strand	Ref.	Variant	T	B	N	From TSS	Position in motif	Motif	dbSNP144	Frequency (1000g EUR)
Variants in motifs														
BRE	CEP63	chr3	134205071	+	G	T	+	+	+	25	2	GCACGCC	rs1874883	0.6909
BRE	CISD2	chr4	103790186	+	G	T	+	+	+	52	2	CCGCGCC	rs223332	0.492
BRE	ANAPC13	chr3	134204834	-	GCCC	G	+	+	+	-3	6-7	CCACGCC	rs377262480	-
DPE	TTF2	chr1	117602960	+	C	A	+	+	+	12	4	GGACC	rs2244501	0.8757
DPE	TYW3	chr1	75198740	+	A	C	+	+	+	-96	3	GGATG	rs2345436	0.6859
DPE	TYW3	chr1	75198763	+	A	C	+	+	+	-73	3	GGATG	rs277372	1
DPE	KBTBD8	chr3	67048762	+	T	C	+	+	+	36	3	AGTCG	rs4856833	0.7644
DPE	TIPARP	chr3	156392135	+	G	A	+	+	+	-70	5	AGACG	rs66538320	0.4314
DPE	NFKB1	chr4	103422504	+	C	G	+	+	+	19	4	AGACA	rs72696119	0.4046
DPE	GRAMD3	chr5	125695874	+	C	G	+	+	+	87	4	AGACG	rs77944663	0.1869
DPE	UQCRQ	chr5	132202399	+	T	C	+	+	+	81	3	GGTTG	rs30178	0.7256
DPE	TREML4	chr6	41196156	+	C	T	+	+	+	95	2	AGATC	rs2803496	0.9135
DPE	CELF2	chr10	11047207	+	C	G	+	+	+	-52	4	AGACA	rs2773499	0.6203
DPE	ZNF215	chr11	6947628	+	GCGGG(G	G	+	+	+	-26	1-3	GGACG	rs6144196	-
DPE	ZP1	chr11	60635091	+	T	C	+	+	+	77	4	GGTTG	rs550479	0.999
DPE	EXOSC8	chr13	37574681	+	C	T	+	+	+	4	4	AGTCA	rs7334233	0.8966
DPE	LGALS17A	chr19	40170053	+	G	A	+	+	+	40	2	AGACA	rs8103033	0.3072
DPE	NDUFA3	chr19	54606209	+	T	G	+	+	+	50	4	GGTTC	rs254260	0.9831
INR	C12orf10	chr12	53693532	+	A	G	+	+	+	63	3	CCAATTC	rs1534284	1
INR	C12orf10	chr12	53693533	+	A	C	+	+	+	64	4	CCAATTC	rs1534283	1
INR	RPL27	chr17	41150521	+	C	T	+	+	+	76	7	TCAATCC	rs691997	1
INR	RPL27	chr17	41150521	+	C	T	+	+	+	76	7	TCAATCC	rs691997	1
INR	CYP4F8	chr19	15725981	+	T	TCCAG(+	+	+	-48	5	CTAGTCC	rs111417224	0.8917
Variants not in motifs														
	ISG15	chr1	948846	+	T	TA	+	+	+	-1			rs3841266	0.9791
	ISG15	chr1	948870	+	C	G	+	+	+	24			rs4615788	0.9573
	ISG15	chr1	948921	+	T	C	+	+	+	75			rs15842	0.9573
	CLCNKB	chr1	16370178	+	A	AGCTC	+	+	+	-53			rs140307022	0.4036
	CLCNKB	chr1	16370215	+	A	G	+	+	+	-16			rs868950	0.496
	CROCC	chr1	17248500	+	A	G	+	+	+	56			rs6683035	-
	CROCC	chr1	17248532	+	A	G	+	+	+	88			rs6586566	1
	CD52	chr1	26644399	+	C	T	+	+	+	-12			rs41285347	0.1899
	ZMYM1	chr1	35545022	+	G	GGC	+	+	+	59			rs72510664	1
	DNALI1	chr1	38022452	+	C	A	+	+	+	-68			rs2273014	0.4682
	NDUFS5	chr1	39491927	+	G	C	+	+	+	-40			rs1984600	0.833
	CCDC163P	chr1	45965703	-	G	T	+	+	+	49			rs3748643	0.6978
	MIR760	chr1	94312482	+	T	TC	+	+	+	95			rs5776191	1
	PSMB4	chr1	151372138	+	G	A	+	+	+	98			rs7172	0.835
	FMO2	chr1	171154303	+	A	C	+	+	+	-44			rs28369794	0.1799
	CACYBP	chr1	174968530	+	T	TC	+	+	+	-41			rs11398770	1
	LHX4	chr1	180199384	+	A	AAG	+	+	+	-49			rs138033992	0.4394
	RGS1	chr1	192544795	+	A	G	+	+	+	-62			rs2984920	0.8181
	DIEXF	chr1	210001233	+	C	T	+	+	+	-79			rs661849	0.7515

HHAT	chr1	210501504	+	T	A	+	+	+	-92	rs688585	0.5577
TAF1A	chr1	222763249	-	C	T	+	+	+	-13	rs3008652	1
EDARADD	chr1	236557771	+	G	A	+	+	+	92	rs966365	0.825
KIF26B	chr1	245318385	+	G	C	+	+	+	99	rs4658708	0.9533
OR2W3	chr1	248058797	+	T	G	+	+	+	-92	rs1856248	0.9801
C2orf48	chr2	10281903	+	G	GC	+	+	+	-78	rs5829249	1
KHK	chr2	27309659	+	A	C	+	+	+	49	rs6742004	0.6173
VIT	chr2	36923898	+	G	T	+	+	+	66	rs6544026	0.997
DHX57	chr2	39103032	-	G	GC	+	+	+	-11	rs35161265	1
MORN2	chr2	39103032	+	G	GC	+	+	+	-71	rs35161265	1
PNO1	chr2	68385097	+	A	G	+	+	+	93	rs2044693	0.6223
SH2D6	chr2	85662017	+	G	A	+	+	+	100	rs2271628	0.5298
GPLY	chr2	85921477	+	G	A	+	+	+	64	rs142960627	0.0298
NMS	chr2	101086894	+	G	A	+	+	+	-50	rs13385681	0.2048
ARHGAP15	chr2	143886953	+	T	C	+	+	+	55	rs354709	0.6123
ARPC2	chr2	219082119	+	G	T	+	+	+	-1	rs2271541	0.5199
CYP27A1	chr2	219646547	+	A	AC	+	+	+	76	rs11375701	1
MFF	chr2	228192223	+	A	AAGT	+	+	+	-5	rs10679131	0.992
SPATA3	chr2	231860848	+	A	G	+	+	+	10	rs6722863	0.9513
CHRND	chr2	233390937	+	A	G	+	+	+	68	rs2245601	0.4483
EAF1	chr3	15469001	+	A	C	+	+	+	-63	rs2290536	0.8231
METTL6	chr3	15469001	-	A	C	+	+	+	41	rs2290536	0.8231
RBMS3	chr3	29322802	+	A	AT	+	+	+	-1	rs11369412	0.9384
NRADDP	chr3	47053017	+	A	C	+	+	+	-15	rs936186	0.998
ZNF589	chr3	48282652	+	TGCGC	T	+	+	+	57	rs35806621	-
COL6A5	chr3	130064348	+	G	A	+	+	+	-11	rs4491952	1
ANAPC13	chr3	134204834	+	GCCC	G	+	+	+	-3	rs377262480	-
ANAPC13	chr3	134204841	-	C	G	+	+	+	-10	rs2370576	0.6909
CEP63	chr3	134204841	+	C	G	+	+	+	-56	rs2370576	0.6909
LOC100289361	chr3	142720221	+	T	TGGAC	+	+	+	89	rs3832221	0.6183
NMD3	chr3	160939141	+	C	T	+	+	+	43	rs28384382	0.2793
CCDC50	chr3	191046793	+	G	C	+	+	+	-81	rs6779820	0.2903
ZNF141	chr4	331693	+	G	GC	+	+	+	98	rs5855672	1
GPR78	chr4	8582217	+	G	C	+	+	+	1	rs4274827	0.3877
GPR78	chr4	8582234	+	C	T	+	+	+	18	rs17844775	0.3161
CLRN2	chr4	17516771	+	C	T	+	+	+	-17	rs2597784	1
KCNIP4-IT1	chr4	21854712	-	T	C	+	+	+	100	rs1398836	0.9891
TMPRSS11BNL	chr4	69083869	-	G	GA	+	+	+	-71	rs34548520	0.7296
MIR577	chr4	115577997	+	C	G	+	+	+	83	rs34115976	0.2028
USP38	chr4	144106031	+	T	TC	+	+	+	-39	rs70953714	1
GRIA2	chr4	158141805	+	ATGTG	A	+	+	+	-15	rs113291896	-
RXFP1	chr4	159442840	+	T	TTGTG1	+	+	+	-26	rs146007330	0.997
SLC6A18	chr5	1225564	+	T	C	+	+	+	95	rs7728646	0.7873
PRDM9	chr5	23507777	+	T	C	+	+	+	54	rs2914282	0.9732
RAD17	chr5	68665736	-	T	C	+	+	+	98	rs3756400	0.9453
MIR583	chr5	95414786	+	T	TTAAAA	+	+	+	-56	rs5869706	0.6362
ERAP2	chr5	96211741	+	T	G	+	+	+	98	rs1230358	0.5875
UQCQRQ	chr5	132202411	+	C	G	+	+	+	93	rs30177	0.7256

FAM53C	chr5	137673167	+	A	C	+	+	+	-57	rs3756766	0.7326
PCDHB2	chr5	140474190	+	T	TC	+	+	+	-1	rs5871764	1
HMGXB3	chr5	149380158	+	C	T	+	+	+	-11	rs3812008	0.5905
TIGD6	chr5	149380158	-	C	T	+	+	+	14	rs3812008	0.5905
HMGXB3	chr5	149380159	+	G	C	+	+	+	-10	rs3812009	0.7773
TIGD6	chr5	149380159	-	G	C	+	+	+	13	rs3812009	0.7773
MIR218-2	chr5	168195356	-	G	A	+	+	+	-96	rs11134527	0.2386
RIOK1	chr6	7390077	-	C	T	+	+	+	16	rs6597266	0.3459
BTN2A2	chr6	26383386	+	T	C	+	+	+	-53	rs9461249	0.1213
HLA-F-AS1	chr6	29716847	-	C	T	+	+	+	-21	rs1633082	0.4284
HLA-F-AS1	chr6	29716901	-	G	T	+	+	+	-75	rs1633081	0.4284
HLA-F-AS1	chr6	29716925	-	AG	A	+	+	+	-99	rs377019154	-
HLA-A	chr6	29910286	+	C	T	+	+	+	40	rs2916801	0.8171
TCF19	chr6	31126252	+	C	A	+	+	+	-51	rs3130456	0.6133
HCG27	chr6	31165566	+	T	C	+	+	+	30	rs3094609	0.8777
MICB	chr6	31465915	+	G	C	+	+	+	89	rs3828916	0.7684
VARS	chr6	31745284	-	C	T	+	+	+	-13	rs2736426	0.5507
SNORD48	chr6	31803064	+	CT	C	+	+	+	25	rs34103657	-
C6orf89	chr6	36853685	+	G	GC	+	+	+	46	rs11461876	0.999
TREML4	chr6	41196034	+	T	C	+	+	+	-28	rs6458202	0.7724
TREML4	chr6	41196040	+	T	C	+	+	+	-22	rs6458203	0.7714
TREML4	chr6	41196041	+	C	T	+	+	+	-21	rs6458204	0.7714
TREML4	chr6	41196095	+	C	T	+	+	+	34	rs6458205	0.7724
TREML4	chr6	41196104	+	C	CCTT	+	+	+	43	rs10700462	0.8917
GPR111	chr6	47624299	+	A	G	+	+	+	-27	rs9369730	0.6759
GLYATL3	chr6	49467595	+	G	C	+	+	+	-76	rs9463489	0.7495
GLYATL3	chr6	49467613	+	CT	C	+	+	+	-58	rs11325069	-
TPBG	chr6	83072871	+	A	G	+	+	+	-52	rs1570140	0.6382
PK1B	chr6	122793033	+	A	G	+	+	+	-29	rs1267941	0.8022
SERINC1	chr6	122793033	-	A	G	+	+	+	-7	rs1267941	0.8022
SMLR1	chr6	131148541	+	A	G	+	+	+	-4	rs4895897	0.7227
TCF21	chr6	134210185	+	T	TC	+	+	+	-74	rs5880195	1
TARID	chr6	134210185	+	T	TC	+	+	+	-41	rs5880195	1
CCDC28A	chr6	139094629	+	C	CG,CGC	+	+	+	-28	rs111500978	-
CCDC28A	chr6	139094638	+	A	G	+	+	+	-19	rs59299306	0.2833
OCM	chr7	5920394	+	T	TA	+	+	+	-35	rs201796201	0.3151
OCM	chr7	5920406	+	T	A	+	+	+	-23	rs10235465	0.5915
ING3	chr7	120590786	+	C	CG	+	+	+	-31	rs11408222	1
NDUFB2	chr7	140396472	+	C	CG	+	+	+	-9	rs57717083	-
WEE2-AS1	chr7	141437940	-	C	A	+	+	+	91	rs62486738	0.4125
PRSS3P2	chr7	142478755	+	T	C	+	+	+	-2	rs73742441	0.998
PRSS3P2	chr7	142478771	+	A	AC	+	+	+	15	rs201689354	-
GALNTL5	chr7	151653523	+	C	G	+	+	+	60	rs11762439	0.6213
C8orf48	chr8	13424385	+	C	A	+	+	+	34	rs10095899	1
RHOBTB2	chr8	22845013	+	G	C	+	+	+	84	rs2430804	0.8708
UBXN8	chr8	30601611	+	TC	T	+	+	+	-71	rs3217273	-
MIR486	chr8	41517958	-	A	AG	+	+	+	-4	rs59908561	1
CPNE3	chr8	87526691	+	T	TC	+	+	+	36	rs77927763	1

DCSTAMP	chr8	105351998	+	A	C	+	+	+	-26	rs2458415	0.7624
LY6K	chr8	143781474	+	T	TTTTG	+	+	+	-55	rs200730553	-
KIAA1875	chr8	145162598	+	G	C	+	+	+	-31	rs10091401	0.9115
DMRTA1	chr9	22446828	+	A	G	+	+	+	-12	rs655497	0.3032
TRMT10B	chr9	37753709	+	T	C	+	+	+	-91	rs7847996	1
TRMT10B	chr9	37753724	+	C	G	+	+	+	-76	rs7861704	1
ZNF189	chr9	104161154	+	C	A	+	+	+	19	rs2253258	0.8847
CYLC2	chr9	105757558	+	A	G	+	+	+	-35	rs10739861	0.7187
OR13F1	chr9	107266596	+	T	C	+	+	+	53	rs7049042	0.7475
OR1N2	chr9	125315376	+	C	CT	+	+	+	-73	rs11412445	0.6451
OR1N2	chr9	125315418	+	G	C	+	+	+	-31	rs1411270	0.2376
OR1N2	chr9	125315542	+	C	T	+	+	+	94	rs1831369	0.2376
RNU6ATAC	chr9	137029687	-	G	A	+	+	+	-1	rs67051032	0.1471
CCDC183	chr9	139690840	+	G	A	+	+	+	51	rs1055995	0.6233
AKR1C3	chr10	5136651	+	C	G	+	+	+	84	rs12529	0.4046
FAM208B	chr10	5726837	+	G	A	+	+	+	37	rs7900687	1
ARL5B	chr10	18948299	+	TG	T	+	+	+	-14	rs10711928	-
MIR604	chr10	29834095	-	G	A	+	+	+	-69	rs4463752	0.4602
RSU1P2	chr10	45649975	-	A	AATG	+	+	+	70	rs4027063	0.8499
ANKRD30BP3	chr10	45650114	+	C	A	+	+	+	5	rs3851259	0.8519
GPRIN2	chr10	46993499	+	T	C	+	+	+	-47	rs3127806	0.9026
GPRIN2	chr10	46993508	+	A	C	+	+	+	-38	rs3127807	0.9026
MSMB	chr10	51549545	+	G	T	+	+	+	-8	rs4935176	0.999
CISD1	chr10	60028838	+	G	GC	+	+	+	-24	rs67338868	-
ZNF365	chr10	64133907	+	C	CG	+	+	+	-9	rs3215033	-
C10orf11	chr10	77542558	+	C	T	+	+	+	40	rs2133705	0.492
LDB3	chr10	88428303	+	G	A	+	+	+	-18	rs2803556	0.1551
FLJ37201	chr10	91457753	-	C	T	+	+	+	-68	rs7089150	0.501
OLMALINC	chr10	102133333	+	CT	C	+	+	+	1	rs60426037	-
RPEL1	chr10	105005683	+	T	TATAA	+	+	+	40	rs55923607	-
MIR4680	chr10	112657917	+	GTT	GGT	+	+	+	70	-	-
VT11A	chr10	114206754	+	G	C	+	+	+	-2	rs3824624	0.7097
ZDHH6	chr10	114206754	-	G	C	+	+	+	-37	rs3824624	0.7097
PNLIPRP3	chr10	118187399	+	T	G	+	+	+	-25	rs10787669	0.9026
PNLIPRP3	chr10	118187405	+	T	C	+	+	+	-19	rs10787670	0.9036
PNLIPRP2	chr10	118380511	+	A	G	+	+	+	47	rs3010502	1
CYP2E1	chr10	135340866	+	T	TC	+	+	+	-1	rs11445593	1
ZNF215	chr11	6947628	+	GCGGGG	G	+	+	+	-26	rs6144196	-
CALCB	chr11	15095130	+	G	T	+	+	+	-16	rs1540148	0.7396
C11orf58	chr11	16760244	+	T	G	+	+	+	97	rs1846936	0.8052
LINC00294	chr11	33097652	+	G	A	+	+	+	-44	rs2273550	0.1471
CAT	chr11	34460472	+	A	T	+	+	+	1	rs7943316	0.669
CAT	chr11	34460541	+	T	C	+	+	+	70	rs1049982	0.669
OR4C16	chr11	55339676	+	G	T	+	+	+	73	rs12800642	0.2117
OR8K1	chr11	56113516	+	T	C	+	+	+	2	rs1905055	0.673
BBS1	chr11	66278059	+	C	G	+	+	+	-60	rs1791688	1
OMP	chr11	76813961	+	C	T	+	+	+	76	rs2233546	0.0517
C11orf54	chr11	93474678	+	G	C	+	+	+	-82	rs630648	0.9901

TAF1D	chr11	93474678	-	G	C	+	+	+	26	rs630648	0.9901
MED17	chr11	93517329	+	A	G	+	+	+	-76	rs655208	0.999
PGR	chr11	100999838	-	A	AG	+	+	+	31	rs11437764	0.999
NCAM1	chr11	112831965	+	T	TC	+	+	+	-4	rs11214438	1
CD3G	chr11	118215076	+	AGGCT	A	+	+	+	18	rs140947880	-
TRAPPC4	chr11	118889247	+	A	AG	+	+	+	7	rs11440855	1
LINC00942	chr12	1609719	+	A	G	+	+	+	63	rs10848499	0.4781
LINC00942	chr12	1609729	+	A	G	+	+	+	73	rs10848500	0.4761
C1RL-AS1	chr12	7260825	+	A	AC	+	+	+	-79	rs35898229	0.0905
EMP1	chr12	13349588	+	CT	C	+	+	+	-14	rs11285488	-
LINC00592	chr12	52604705	+	G	A	+	+	+	-9	rs61541205	0.3181
HOXC-AS1	chr12	54393770	+	A	G	+	+	+	25	rs56368105	0.4245
HOXC-AS1	chr12	54393774	+	G	A	+	+	+	21	rs12817092	0.5676
HOXC-AS1	chr12	54393783	+	G	C	+	+	+	12	rs56154542	0.4095
NEUROD4	chr12	55413630	+	G	A	+	+	+	-99	rs1488033	0.2465
SLC39A5	chr12	56623839	+	G	GC	+	+	+	20	rs11403568	-
OS9	chr12	58087737	+	T	G	+	+	+	-1	rs4760168	0.6799
MIR3652	chr12	104324148	-	G	A	+	+	+	-55	rs2722187	0.8857
HSP90B1	chr12	104324148	+	G	A	+	+	+	37	rs2722187	0.8857
RPL21P28	chr13	27825753	+	G	C	+	+	+	61	rs3118727	0.9056
ATP5EP2	chr13	28519354	+	A	C	+	+	+	12	rs2504220	0.8658
EXOSC8	chr13	37574714	+	C	T	+	+	+	37	rs9547715	0.8946
GPC6	chr13	93879087	+	G	A	+	+	+	10	rs319522	0.4523
RPPH1	chr14	20811577	-	A	G	+	+	+	-7	rs2297619	0.8618
MRPL52	chr14	23299009	+	G	GC	+	+	+	-83	rs5807191	1
GEMIN2	chr14	39583481	+	A	G	+	+	+	-7	rs2277458	0.828
GNG2	chr14	52326938	+	C	CA	+	+	+	-84	rs140848378	0.2127
SLIRP	chr14	78174473	+	A	C	+	+	+	60	rs11159286	0.9642
SNORA11B	chr14	91592748	+	C	CTTCTT	+	+	+	-22	rs57615276	0.831
UNC79	chr14	93799587	+	C	CCGGG	+	+	+	23	rs143806161	-
TCL1B	chr14	96152728	+	T	C	+	+	+	-26	rs11160284	0.4483
LINC01550;C14	chr14	98444369	-	T	C	+	+	+	93	rs8016584	1
SNORD114-2	chr14	101418193	+	TG	T	+	+	+	1	rs10713875	-
CRIP1	chr14	105953204	+	T	C	+	+	+	-53	rs12323571	1
CRIP1	chr14	105953324	+	C	T	+	+	+	68	rs7160340	0.9692
CRIP1	chr14	105953331	+	GC	G	+	+	+	75	rs34296176	-
SNORD115-1	chr15	25415809	+	C	T	+	+	+	-61	rs2739838	0.7584
SCAND2P	chr15	85174600	+	G	T	+	+	+	-91	rs4842977	0.8191
SCAND2P	chr15	85174631	+	G	A	+	+	+	-60	rs3825877	0.5537
MPG	chr16	126982	+	A	AG	+	+	+	-36	rs11390587	-
UBE2I	chr16	1359217	+	A	G	+	+	+	64	rs4984805	0.8857
ZNF174	chr16	3451101	+	G	A	+	+	+	-89	rs1230965	0.8509
ZSCAN32	chr16	3451101	-	G	A	+	+	+	-36	rs1230965	0.8509
PRMT7	chr16	68344945	+	G	C	+	+	+	69	rs3743741	0.502
HSBP1	chr16	83841560	+	G	T	+	+	+	53	rs3743623	0.4165
ENO3	chr17	4854480	+	C	T	+	+	+	97	rs366577	0.5636
GUCY2D	chr17	7906020	+	CG	C	+	+	+	33	rs33942683	-
GUCY2D	chr17	7906038	+	GC	G	+	+	+	51	rs33914314	-

COX10-AS1	chr17	13972811	+	G	A	+	+	+	-36	rs6502330	1
SNORD65	chr17	16344600	+	T	C	+	+	+	61	rs4617905	0.6461
FOXN1	chr17	26850929	+	A	C	+	+	+	-30	rs483434	0.9602
KRTAP9-4	chr17	39405960	+	T	C	+	+	+	22	rs11655750	0.7336
KRTAP9-9	chr17	39411670	+	T	TACCTC	+	+	+	35	-	0.5805
RPL27	chr17	41150465	+	TG	T	+	+	+	20	rs11305686	-
RPL27	chr17	41150471	+	G	C	+	+	+	26	rs9899458	1
GOSR2	chr17	45000547	+	G	C	+	+	+	62	rs183199	0.998
ATP5G1	chr17	46970083	+	G	GA	+	+	+	-65	rs35130875	0.5586
DLX4	chr17	48046626	+	T	TG	+	+	+	65	rs71146955	1
KIF2B	chr17	51900262	+	G	A	+	+	+	24	rs12939320	0.4622
PSMC5	chr17	61904724	+	T	C	+	+	+	-46	rs2665834	0.5984
PSMC5	chr17	61904728	+	G	A	+	+	+	-42	rs2727287	0.5984
GGA3	chr17	73257830	-	C	T	+	+	+	-88	rs2279161	0.8022
MRPS7	chr17	73257830	+	C	T	+	+	+	82	rs2279161	0.8022
SNORD1A	chr17	74557804	+	GT	G	+	+	+	90	rs60161580	-
TSPAN10	chr17	79609410	+	G	T	+	+	+	80	rs7406219	0.2853
MIR1-2	chr18	19408950	-	C	T	+	+	+	100	rs9989532	0.9801
RIOK3	chr18	21032796	+	C	A	+	+	+	10	rs6507666	0.9235
KIAA1468	chr18	59854476	+	AG	A	+	+	+	-48	rs11342642	-
SERPINB13	chr18	61254525	+	A	AT	+	+	+	-9	rs3216123	0.7256
ZNF407	chr18	72343008	+	T	C	+	+	+	90	rs7243081	1
SNORD105	chr19	10218332	+	A	G	+	+	+	6	rs2305789	0.1213
OR10H2	chr19	15838746	+	A	G	+	+	+	-88	rs11672695	0.5
OR10H2	chr19	15838754	+	AG	A	+	+	+	-80	rs34728106	-
HPN-AS1	chr19	35597215	-	C	A	+	+	+	-7	rs10422803	0.4254
BCKDHA	chr19	41903675	+	A	G	+	+	+	-19	rs892043	0.9414
GIPR	chr19	46171497	+	GT	G	+	+	+	-5	rs34125392	-
ZNF175	chr19	52074537	+	A	G	+	+	+	7	rs3752132	0.7535
ZNF701	chr19	53073605	+	A	G	+	+	+	80	rs193040	0.668
LOC284379	chr19	54106756	-	C	T	+	+	+	-5	rs13344462	0.1551
LOC284379	chr19	54106763	-	C	T	+	+	+	-12	rs13344463	0.1541
ZNF444	chr19	56652592	+	G	A	+	+	+	58	rs3745836	0.9652
WISP2	chr20	43343908	+	G	A	+	+	+	24	rs1980803	0.7366
WISP2	chr20	43343930	+	T	G	+	+	+	46	rs1980804	1
CD40	chr20	44746982	+	T	C	+	+	+	90	rs1883832	0.7406
ZFAS1	chr20	47895197	-	C	T	+	+	+	19	rs479474	0.837
MC3R	chr20	54823779	+	G	T	+	+	+	-9	rs13044293	1
IFNAR1	chr21	34697264	+	T	C	+	+	+	51	rs2850015	0.7087
KRTAP10-7	chr21	46020473	+	C	CTCAT	+	+	+	-24	rs113686885	0.9394
KRTAP10-7	chr21	46020527	+	C	T	+	+	+	31	rs1211103	0.9354
DEPDC5	chr22	32150038	+	A	AG	+	+	+	30	rs138284	1
ATF4	chr22	39916626	+	T	TC	+	+	+	58	rs35920692	0.3171
SERHL	chr22	42896554	+	TGGGGCT		+	+	+	-31	rs71311440	-
MIR4763	chr22	46509402	+	A	G	+	+	+	-44	rs4823513	0.998
MIR532	chrX	49767832	+	A	G	+	+	+	79	rs456615	1
MIR532	chrX	49767835	+	A	G	+	+	+	82	rs456617	1
MIR532	chrX	49767832	+	A	G	+	+	+	79	rs456615	1

MIR532	chrX	49767835	+	A	G	+	+	+	82	rs456617	1
FLJ44635	chrX	71364064	+	A	G	+	+	+	31	rs6525579	0.2833
PIN4	chrX	71401607	+	G	A	+	+	+	82	rs6525589	0.97
PIN4	chrX	71401614	+	C	A	+	+	+	89	rs7058353	0.97
TCEAL4	chrX	102840421	+	G	T	+	+	+	3	rs221931	0.4817
CLDN2	chrX	106163512	+	A	AC	+	+	+	-94	-	0.0039
NDUFA1	chrX	119005705	+	C	G	+	+	+	-29	rs708463	0.5548
RNF113A	chrX	119005705	-	C	G	+	+	+		rs708463	0.5548
LINC00893	chrX	148621334	-	G	C	+	+	+	-22	rs12116320	0.9217
