

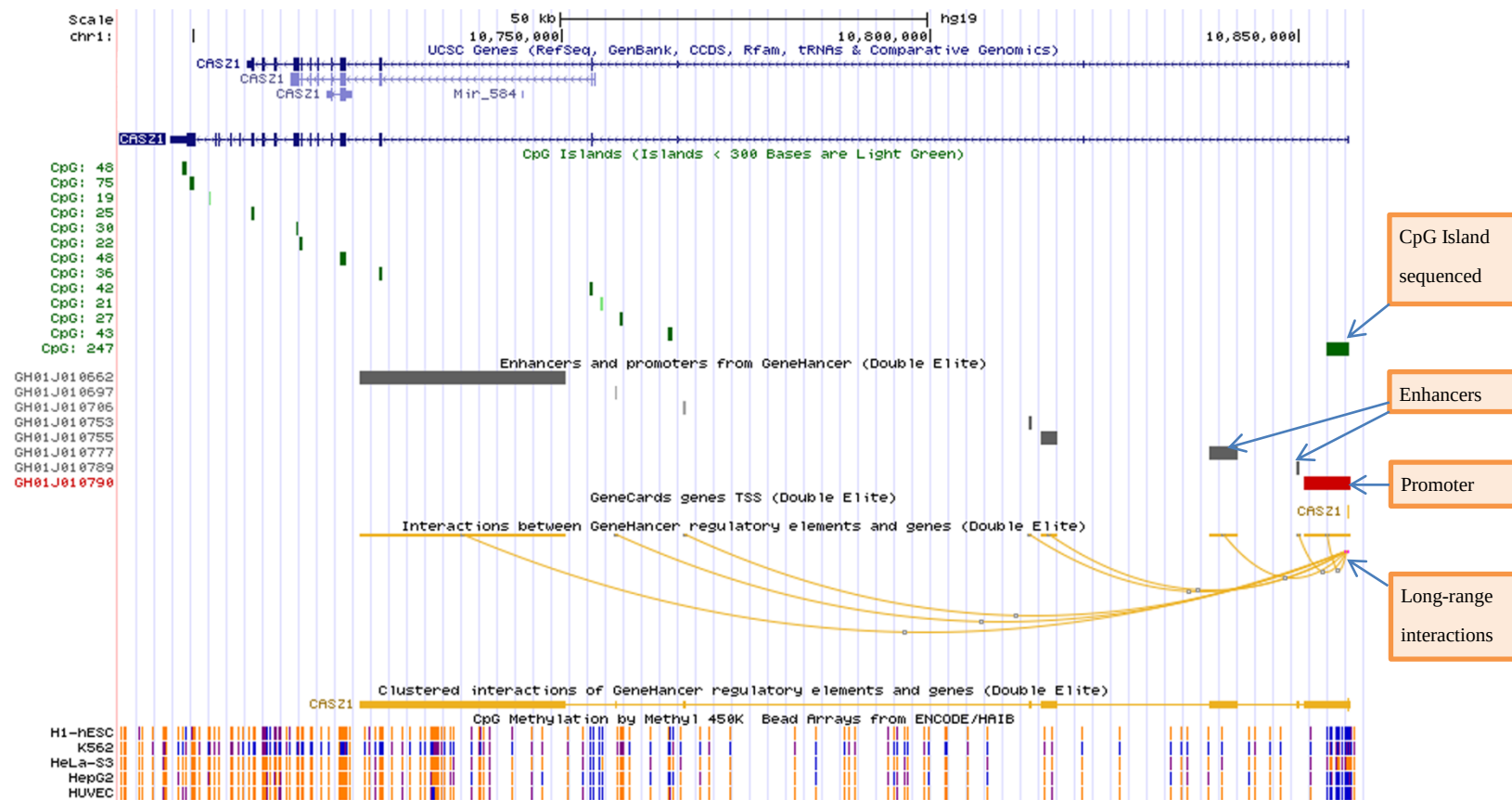


Figure e-1 The genomic region of the *CASZ1* gene.

After genomic sequence evaluation in the *CASZ1* gene region (from 2 kilo bases upstream of the transcription start site to 1 kilo bases downstream of the first exon), a genomic fragment at 5' end of *CASZ1* was sequenced (chr1: 10856805-10856994, length: 190bp). The sequenced fragment is located at a CpG island (chr1:10853895-10856964). This CpG island overlaps the promoter (chr1:10850682-10857058) of *CASZ1* gene. In the track named "Enhancers and promoters from GeneHancer", red and gray colors represent promoters and enhancers, respectively. The track "Interactions between GeneHancer regulatory elements and genes" shows the long-range interactions between the promoter (chr1:10850682-10857058) and its target enhancers in *CASZ1* gene.

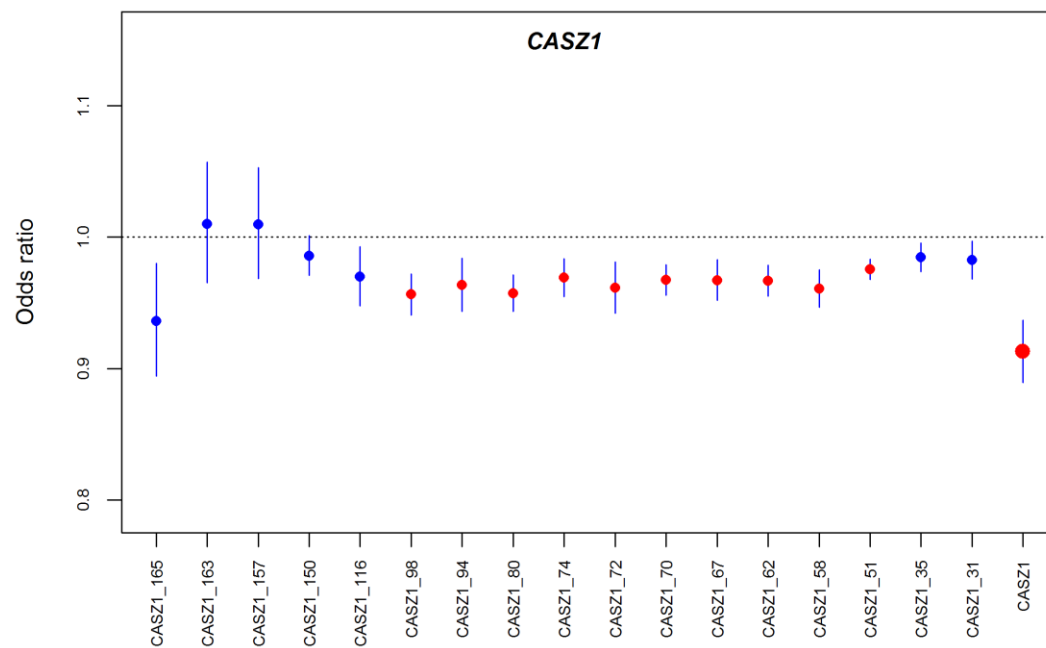


Figure e-2 The odds ratios for the association between CASZ1 methylations and IS

The figure shows the odds ratios for each of the CpG sites which were assessed by logistic regression model. The associations were unadjusted for covariates. The methylation levels of 14 of the 17 sites were nominally associated with IS and 10 of these sites were significantly associated with IS in univariate analysis ($P < 3.0 \times 10^{-3}$, Bonferroni correction).

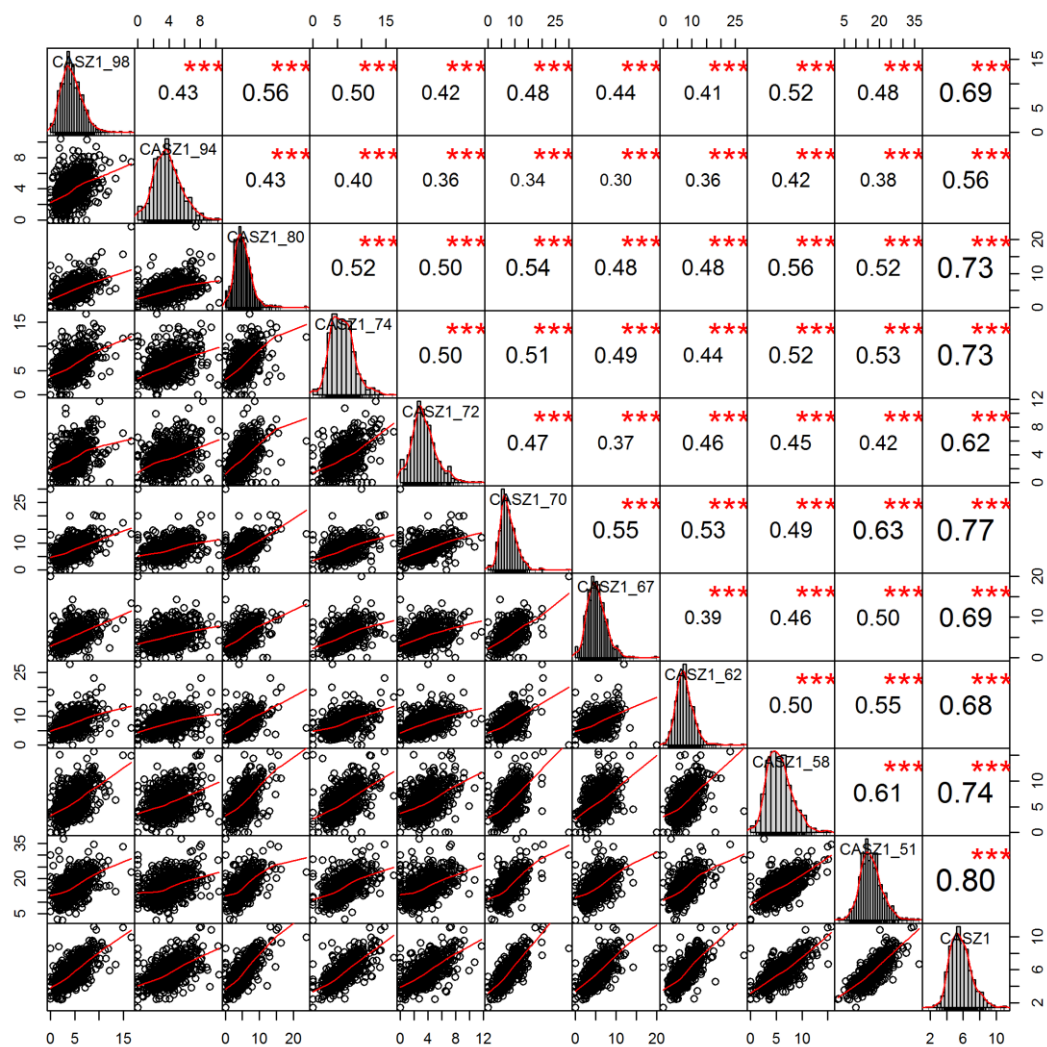


Figure e-3 The correlation between the IS-associated methylation sites

The IS-associated methylation sites were significantly correlated.

Table e-1 The SBP-associated methylations identified by Mendelian randomization analysis

probeID	Gene	CHR	Probe_bp	topSNP	topSNP_bp	A1	A2	Freq	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI	nsnp_HEIDI
cg05598010	GLTPD1	1	1261797	rs2649589	1311716	G	A	0.0777778	0.0255186	0.00489757	1.88E-07	-1.13696	0.0580581	2.16E-85	-0.0224447	0.00445748	4.77E-07	7.73E-01	20
cg21118819	AURKAIP1	1	1287259	rs2649589	1311716	G	A	0.0777778	0.0255186	0.00489757	1.88E-07	-2.15514	0.0428583	0.00E+00	-0.0118408	0.00228468	2.19E-07	8.45E-01	20
cg23982607	GNB1	1	1823379	rs6664664	1751264	A	G	0.527778	0.0124259	0.00246534	4.65E-07	-1.05015	0.024068	0.00E+00	-0.0118325	0.00236322	5.53E-07	1.18E-01	19
cg15833286	CFAP74	1	1873499	rs2803327	1873525	T	C	0.461111	-0.0130798	0.00249188	1.53E-07	-0.540031	0.0320649	1.20E-63	0.0242205	0.00483324	5.41E-07	7.66E-01	20
cg17747265	CFAP74	1	1875780	rs2803328	1874326	G	C	0.511494	0.0127733	0.00248305	2.69E-07	-1.08102	0.0236935	0.00E+00	-0.011816	0.00231151	3.19E-07	6.88E-01	20
cg03396347	CFAP74	1	1875803	rs2803328	1874326	G	C	0.511494	0.0127733	0.00248305	2.69E-07	-1.09964	0.0232532	0.00E+00	-0.0116159	0.00227138	3.15E-07	7.01E-01	20
cg00546117	RERE	1	8445545	rs3765971	8445360	C	T	0.314607	-0.0164056	0.00258682	2.27E-10	-1.02618	0.0272656	5.467584e-310	0.0159871	0.00255636	4.01E-10	5.46E-01	20
cg12760995	CASZ1	1	10789713	rs880315	10796866	C	T	0.348315	-0.0196031	0.00260784	5.62E-14	-0.655694	0.0321263	1.37E-92	0.0298967	0.00423839	1.74E-12	3.31E-01	19
cg15622917	CASZ1	1	10796823	rs880315	10796866	C	T	0.348315	-0.0196031	0.00260784	5.62E-14	0.255772	0.0339702	5.10E-14	-0.0766429	0.0144075	1.04E-07	4.81E-01	10
cg16988262	DDI2	1	15930761	rs998032	15989918	C	T	0.288889	0.0141585	0.00276109	2.93E-07	1.10215	0.0279672	0.00E+00	0.0128462	0.0025263	3.68E-07	8.64E-01	20
cg03753284	MED8	1	43855912	rs11210839	43845658	G	A	0.420455	-0.0144234	0.00252206	1.07E-08	1.06795	0.024819	0.00E+00	-0.0135056	0.00238235	1.44E-08	3.75E-01	20
cg18762505	FGGY	1	59646049	rs11207423	59650829	C	G	0.3	0.0214098	0.0027592	8.56E-15	-0.302695	0.0359495	3.76E-17	-0.0707306	0.0123958	1.16E-08	3.29E-01	20
cg05010058	CEP68	2	65284262	rs2723065	65279414	G	A	0.311111	0.017639	0.00254149	3.92E-12	0.462491	0.0328113	4.05E-45	0.0381391	0.00612524	4.77E-10	7.23E-02	20
cg24986868	CCDC148	2	159312599	rs11674284	159372889	G	A	0.238889	0.0144784	0.00274817	1.38E-07	0.865286	0.0339976	6.81E-143	0.0167325	0.00324336	2.48E-07	6.52E-01	20
cg14426788	PKP4	2	159312727	rs3771600	159404780	G	C	0.238889	0.0143979	0.00275184	1.68E-07	0.692523	0.0354833	7.90E-85	0.0207905	0.00411396	4.33E-07	5.03E-01	20
cg25608061	HOXD3	2	177027291	rs2301301	177032267	C	T	0.294444	-0.0147144	0.00264574	2.68E-08	-1.01701	0.0284097	1.18E-280	0.0144683	0.00263269	3.89E-08	6.39E-01	20
cg00586420	HOXD3	2	177034761	rs13017511	177035395	G	A	0.294444	-0.0147441	0.00264552	2.50E-08	0.423932	0.0344782	9.56E-35	-0.0347794	0.00685157	3.85E-07	1.19E-01	20
cg00278547	HOXD3	2	177037212	rs9141	177037970	C	T	0.283333	-0.0143573	0.00265295	6.24E-08	-0.557784	0.0338352	4.68E-61	0.0257399	0.00500596	2.72E-07	3.70E-01	20
cg22934308	HOXD3	2	177038617	rs13017511	177035395	G	A	0.294444	-0.0147441	0.00264552	2.50E-08	-0.558172	0.0341183	3.70E-60	0.026415	0.00500709	1.32E-07	1.60E-01	20
cg26754761	HOXD-AS1	2	177040938	rs13017511	177035395	G	A	0.294444	-0.0147441	0.00264552	2.50E-08	-1.11066	0.0262988	0.00E+00	0.0132751	0.0024026	3.29E-08	9.96E-01	20
cg19180624	HOXD1	2	177053297	rs6759499	177052949	A	G	0.261111	-0.0148498	0.00271114	4.32E-08	0.46454	0.0350559	4.43E-40	-0.0319667	0.00631509	4.15E-07	8.94E-01	20
cg21415385	VGLL4	3	11604056	rs6442260	11590751	A	G	0.375	0.0170944	0.00256971	2.89E-11	0.442913	0.033063	6.38E-41	0.0385954	0.00647781	2.55E-09	9.97E-01	20
cg02648746	ULK4	3	42004678	rs1716645	41970480	T	C	0.215909	0.0197524	0.00335912	4.10E-09	-0.447323	0.0438087	1.77E-24	-0.0441569	0.00866557	3.48E-07	9.99E-01	20
cg03852670	SLC10A4	4	48484997	rs776584	48633500	G	C	0.477778	0.0169592	0.00246583	6.09E-12	-0.467379	0.0323744	3.04E-47	-0.0362858	0.00584399	5.33E-10	1.13E-01	20
cg18074184	SLC10A4	4	48485090	rs2945330	48606526	C	A	0.472222	0.0172913	0.00246691	2.40E-12	-0.558713	0.0324012	1.25E-66	-0.0309484	0.00476618	8.40E-11	1.79E-01	20
cg19283196	SLC10A4	4	48485233	rs1712767	48663375	A	G	0.466667	0.0173308	0.0024642	2.03E-12	-0.484688	0.0321559	2.44E-51	-0.0357566	0.0056103	1.85E-10	3.38E-01	20
cg19065831	SLC10A4	4	48485289	rs6836632	48485075	A	G	0.471264	-0.0174445	0.00246481	1.47E-12	0.23746	0.0320793	1.34E-13	-0.0734628	0.0143609	3.13E-07	3.60E-01	20
cg19247841	SLC10A4	4	48485301	rs992423	48481976	T	C	0.466667	-0.0176214	0.00246582	8.94E-13	0.387136	0.0309958	8.47E-36	-0.0455173	0.00733826	5.55E-10	9.60E-01	20
cg19212779	FRYL	4	48777471	rs12645501	48506163	A	T	0.527778	0.0174541	0.00246529	1.45E-12	0.265317	0.0328087	6.12E-16	0.0657857	0.0123497	9.99E-08	9.66E-01	20
cg22571664	NPR3	5	32713112	rs1421811	32714270	G	C	0.443182	0.0282547	0.00252372	4.34E-29	-0.198881	0.0327788	1.30E-09	-0.142068	0.0266326	9.59E-08	6.31E-02	15
cg18693985	CPEB4	5	173351052	rs17696407	173387335	A	C	0.298851	0.0139389	0.00267978	1.98E-07	-1.08859	0.0284082	0.00E+00	-0.0128045	0.00248427	2.55E-07	4.71E-01	20
cg15454374	HLA-B	6	31325455	rs2769	31321882	A	G	0.160714	-0.0171606	0.00324123	1.19E-07	0.683111	0.0431218	1.61E-56	-0.0251213	0.0050028	5.13E-07	1.23E-01	20
cg21112943	CSNK2B	6	31633196	rs3749953	31713124	G	A	0.172222	0.0223132	0.00382366	5.37E-09	-0.482111	0.0486351	3.66E-23	-0.0462823	0.00920331	4.93E-07	8.55E-02	10

cg22727233	LY6G6C	6	31688428	rs2242665	31839309	C	T	0.533333	0.015495	0.00246213	3.11E-10	0.371631	0.0324184	2.01E-30	0.0416946	0.00755792	3.45E-08	1.05E-01	20
cg25270367	TNXB	6	32022898	rs2857009	32019746	C	G	0.688889	-0.0182221	0.00269539	1.38E-11	-0.863058	0.0333174	5.99E-148	0.0211134	0.00322767	6.10E-11	1.01E-01	20
cg05598103	TNXB	6	32022929	rs2071295	32038700	T	C	0.277778	-0.0179778	0.00269525	2.56E-11	0.648054	0.0357825	2.61E-73	-0.0277412	0.00443209	3.87E-10	1.36E-01	20
cg11032077	TNXB	6	32032728	rs204883	32032743	A	G	0.35	-0.0180436	0.00252833	9.59E-13	-0.824946	0.0297193	1.40E-169	0.0218724	0.00316451	4.79E-12	6.25E-02	20
cg14669361	TNXB	6	32038747	rs2071295	32038700	T	C	0.277778	-0.0179778	0.00269525	2.56E-11	0.288302	0.0363773	2.28E-15	-0.0623575	0.0122191	3.34E-07	2.83E-01	20
cg13798746	TNXB	6	32038887	rs185819	32050067	C	T	0.416667	-0.0150224	0.00246431	1.09E-09	0.28874	0.0329508	1.91E-18	-0.0520274	0.0103968	5.61E-07	8.84E-02	20
cg08362880	TNXB	6	32053600	rs2269426	32076499	A	G	0.294444	-0.0148093	0.00255802	7.07E-09	0.385682	0.0333217	5.55E-31	-0.0383976	0.00741584	2.25E-07	7.32E-02	20
cg07088771	TNXB	6	32057846	rs7766862	32033007	A	G	0.278409	-0.0181227	0.00269703	1.83E-11	-1.04759	0.0310662	2.84E-249	0.0172995	0.00262513	4.40E-11	1.25E-01	20
cg15657588	TNXB	6	32075763	rs204883	32032743	A	G	0.35	-0.0180436	0.00252833	9.59E-13	0.317962	0.032981	5.38E-22	-0.0567477	0.00989327	9.69E-09	5.20E-01	20
cg00188055	TNXB	6	32076079	rs2269426	32076499	A	G	0.294444	-0.0148093	0.00255802	7.07E-09	0.516453	0.0335458	1.76E-53	-0.028675	0.00529168	6.00E-08	1.31E-01	20
cg09872737	TNXB	6	32076270	rs2269426	32076499	A	G	0.294444	-0.0148093	0.00255802	7.07E-09	0.589837	0.0330763	3.94E-71	-0.0251074	0.00455965	3.66E-08	6.46E-02	20
cg18049167	PPT2	6	32121261	rs2071295	32038700	T	C	0.277778	-0.0179778	0.00269525	2.56E-11	0.285914	0.0366081	5.71E-15	-0.0628783	0.0123968	3.93E-07	1.95E-01	20
cg12585943	PPT2	6	32121368	rs2071295	32038700	T	C	0.277778	-0.0179778	0.00269525	2.56E-11	0.286932	0.0368112	6.46E-15	-0.0626552	0.0123631	4.02E-07	1.41E-01	20
cg17229678	PPT2	6	32121555	rs2071295	32038700	T	C	0.277778	-0.0179778	0.00269525	2.56E-11	0.427506	0.0359226	1.17E-32	-0.0420527	0.00722733	5.94E-09	1.67E-01	20
cg27134827	PPT2	6	32121566	rs2071295	32038700	T	C	0.277778	-0.0179778	0.00269525	2.56E-11	0.403189	0.0366181	3.40E-28	-0.044589	0.00781578	1.16E-08	1.96E-01	20
cg09198277	NOTCH4	6	32187662	rs1009382	32026107	C	T	0.383333	0.0170729	0.00269734	2.46E-10	-0.349479	0.0347678	9.02E-24	-0.0488524	0.00912086	8.50E-08	5.58E-02	20
cg19988162	C6orf10	6	32303790	rs2857009	32019746	C	G	0.688889	-0.0182221	0.00269539	1.38E-11	-0.403666	0.0363683	1.26E-28	0.0451416	0.00781837	7.75E-09	1.00E-01	20
cg10846853	HLA-DQB1	6	32632859	rs6941112	31946614	A	G	0.272222	-0.0157993	0.00270828	5.43E-09	0.40434	0.0369728	7.74E-28	-0.0390743	0.00759141	2.64E-07	1.25E-01	20
cg05283184	IRAK1BP1	6	79620031	rs2174742	79610101	T	G	0.455056	-0.0137832	0.0024643	2.23E-08	-1.07841	0.0254747	0.00E+00	0.0127811	0.00230499	2.94E-08	8.39E-01	20
cg18132916	IRAK1BP1	6	79620363	rs9352683	79718795	G	T	0.445122	-0.0138466	0.00246319	1.90E-08	-0.586582	0.031722	2.42E-76	0.0236056	0.00438898	7.52E-08	8.53E-01	20
cg09184832	IRAK1BP1	6	79620586	rs3805747	79672522	G	A	0.455056	-0.0137671	0.00246339	2.29E-08	-0.541741	0.0327717	2.20E-61	0.0254127	0.0048	1.19E-07	7.45E-01	20
cg11833968	IRAK1BP1	6	79620685	rs9352683	79718795	G	T	0.445122	-0.0138466	0.00246319	1.90E-08	-0.438417	0.0324377	1.26E-41	0.0315832	0.00608496	2.10E-07	9.56E-01	20
cg08737367	HOXA13	7	27243221	rs2023844	27243238	G	A	0.0505618	0.0340781	0.00470105	4.21E-13	-0.957087	0.0600945	4.16E-57	-0.0356061	0.00539669	4.17E-11	6.12E-01	20
cg06795527	HOXA13	7	27245018	rs2023843	27243221	C	T	0.05	0.0347516	0.00469606	1.36E-13	0.63099	0.0625063	5.82E-24	0.0550748	0.0092279	2.40E-09	9.29E-01	20
cg14228300	IGFBP3	7	45961074	rs1496499	45979023	G	T	0.333333	0.0151915	0.00247205	7.99E-10	-0.426127	0.0325854	4.44E-39	-0.0356502	0.00640981	2.67E-08	7.24E-01	20
cg04812164	IGFBP3	7	45977344	rs2965074	45983129	T	G	0.337079	0.0155469	0.00247211	3.20E-10	0.716135	0.0305338	1.21E-121	0.0217095	0.00357396	1.24E-09	1.49E-01	20
cg15741354	PRAG1	8	8146129	rs1107832	8146083	A	T	0.402597	0.0133701	0.00252667	1.21E-07	0.896897	0.0297954	4.59E-199	0.0149071	0.00286032	1.87E-07	4.83E-01	20
cg02520399	PRAG1	8	8168661	rs2979181	8323088	T	A	0.576389	-0.0154771	0.00246384	3.35E-10	0.316593	0.0316196	1.34E-23	-0.0488864	0.00918716	1.03E-07	5.90E-01	20
cg27000590	PRAG1	8	8182003	rs7817376	8380530	C	T	0.477778	-0.0146601	0.00246142	2.59E-09	-0.346302	0.0322349	6.39E-27	0.0423333	0.00812696	1.90E-07	4.16E-01	20
cg04654363	CLDN23	8	8581213	rs1703982	8598388	A	T	0.483146	-0.0171415	0.00246582	3.62E-12	-0.235212	0.0323167	3.38E-13	0.0728768	0.0144968	4.98E-07	9.91E-01	20
cg21290162	TNKS	8	9741960	rs17150693	9741652	G	C	0.178161	-0.0145629	0.00285242	3.30E-07	-0.927841	0.0344426	7.73E-160	0.0156955	0.00312898	5.27E-07	3.52E-01	20
cg06620390	MSRA	8	10192943	rs6982308	10193772	C	G	0.405556	-0.0182523	0.00246588	1.35E-13	0.351867	0.0311634	1.45E-29	-0.0518728	0.00837964	6.00E-10	6.25E-01	20
cg02319733	MSRA	8	10282549	rs14879	10286273	G	A	0.233333	-0.0162274	0.00268779	1.57E-09	0.764047	0.0329469	5.71E-119	-0.0212388	0.0036351	5.14E-09	5.71E-02	20
cg12940923	MSRA	8	10282607	rs14879	10286273	G	A	0.233333	-0.0162274	0.00268779	1.57E-09	0.92987	0.0306481	3.38E-202	-0.0174513	0.00294717	3.19E-09	6.09E-02	20
cg21915799	MSRA	8	10282809	rs11250007	10285086	C	G	0.222222	-0.0155513	0.00269827	8.25E-09	0.606365	0.0343096	6.73E-70	-0.0256468	0.00468055	4.27E-08	1.82E-01	20

cg24036517	SOX7	8	10585394	rs7814757	10675188	T	C	0.353933	-0.0182314	0.00251606	4.30E-13	0.263369	0.0325954	6.48E-16	-0.0692239	0.0128323	6.87E-08	6.40E-01	20
cg26161004	BLK	8	11413186	rs4841562	11425077	T	C	0.350649	-0.0143153	0.00253926	1.73E-08	0.377108	0.0325811	5.55E-31	-0.0379607	0.00748976	4.01E-07	5.47E-02	20
cg24861686	BLK	8	11418058	rs804280	11612698	C	A	0.522222	0.0164883	0.00249318	3.76E-11	0.289734	0.031443	3.13E-20	0.0569084	0.0105919	7.75E-08	7.76E-01	20
cg05635807	BLK	8	11422167	rs7834638	11420295	C	T	0.327586	-0.0158719	0.00257962	7.62E-10	0.32864	0.031959	8.39E-25	-0.0482957	0.00914717	1.29E-07	1.42E-01	20
cg12840336	BLK	8	11422730	rs4841561	11418773	T	C	0.364706	-0.0151636	0.0025914	4.88E-09	-0.511979	0.0319288	7.28E-58	0.0296176	0.00538802	3.86E-08	1.39E-01	20
cg16810626	GATA4	8	11594003	rs1390950	11595829	C	T	0.366667	-0.0179655	0.00256153	2.33E-12	0.508108	0.0320341	1.17E-56	-0.0353577	0.00551216	1.41E-10	6.86E-02	20
cg16331727	NEIL2	8	11630219	rs4840581	11635569	T	C	0.359551	-0.017502	0.00247295	1.47E-12	-0.51788	0.0314195	4.88E-61	0.0337954	0.00519672	7.86E-11	5.61E-02	20
cg04897713	DEFB136	8	11832762	rs11998678	11830150	T	C	0.38764	-0.015978	0.00246688	9.37E-11	0.414407	0.0305239	5.52E-42	-0.0385563	0.00659553	5.04E-09	3.46E-01	20
cg25777549	EBF2	8	25902400	rs7835016	25889501	A	C	0.288889	0.0191139	0.00291007	5.10E-11	0.323991	0.037013	2.07E-18	0.0589951	0.0112293	1.49E-07	2.22E-01	20
cg24295381	EBF2	8	25902594	rs11778076	25913258	G	A	0.694444	0.018044	0.00282123	1.60E-10	0.339043	0.0362064	7.66E-21	0.0532204	0.0100768	1.28E-07	6.14E-01	19
cg08373250	NOV	8	120438409	rs6996275	120415378	A	G	0.127778	-0.0179422	0.00296594	1.46E-09	-1.52611	0.0203748	0.00E+00	0.0117568	0.0019498	1.64E-09	1.43E-01	20
cg11691535	TSNARE1	8	143425682	rs11985182	143456488	G	A	0.388889	0.0143099	0.0026024	3.83E-08	-0.563741	0.0326667	9.85E-67	-0.0253838	0.00484497	1.61E-07	5.53E-01	20
cg01005506	ADO	10	64565768	rs1848797	64552934	G	A	0.322222	0.0177227	0.00251195	1.73E-12	-0.277818	0.0330933	4.66E-17	-0.0637926	0.0118108	6.62E-08	1.44E-01	20
cg12474798	ADO	10	64565772	rs1848797	64552934	G	A	0.322222	0.0177227	0.00251195	1.73E-12	-0.265151	0.032893	7.57E-16	-0.0668401	0.0125898	1.10E-07	1.42E-01	20
cg00972288	SIRT1	10	69644348	rs12355259	69704101	C	T	0.233333	-0.0145029	0.00258086	1.92E-08	-0.834566	0.0297075	1.20E-173	0.0173778	0.00315372	3.58E-08	1.65E-01	20
cg02286717	SYNPO2L	10	75415704	rs3740293	75406141	C	A	0.105556	-0.0236427	0.00356469	3.31E-11	-1.1454	0.042387	8.07E-161	0.0206415	0.00320456	1.18E-10	4.08E-01	20
cg09521743	SYNPO2L	10	75415752	rs11000728	75404300	G	C	0.105556	-0.0238076	0.00357037	2.60E-11	-0.686537	0.0454863	1.79E-51	0.0346778	0.00568546	1.06E-09	7.17E-01	20
cg19154600	SYNPO2L	10	75415868	rs3740293	75406141	C	A	0.105556	-0.0236427	0.00356469	3.31E-11	-0.709943	0.0453134	2.53E-55	0.0333023	0.00545247	1.01E-09	2.43E-01	20
cg23083424	SYNPO2L	10	75415875	rs3740293	75406141	C	A	0.105556	-0.0236427	0.00356469	3.31E-11	-0.810601	0.0454556	3.93E-71	0.0291669	0.0046919	5.09E-10	3.74E-01	20
cg07699608	CHCHD1	10	75541558	rs11000771	75524458	G	T	0.102273	-0.022754	0.00363412	3.82E-10	0.690514	0.0436713	2.59E-56	-0.0329523	0.00566053	5.84E-09	2.23E-01	20
cg03493300	CNNM2	10	104813866	rs11191543	104824387	A	G	0.0611111	0.0498069	0.00463957	7.03E-27	1.26096	0.0564871	2.21E-110	0.0394991	0.00408274	3.86E-22	5.46E-01	20
cg09803321	NT5C2	10	104913480	rs11191593	104939215	C	T	0.0611111	0.0508515	0.00462314	3.89E-28	0.732841	0.0600347	2.85E-34	0.0693896	0.00849177	3.05E-16	7.77E-01	20
cg25462858	INA	10	105032988	rs1163073	105022934	C	T	0.308989	0.0158746	0.00264236	1.88E-09	-0.324563	0.0344521	4.48E-21	-0.0489107	0.00965588	4.08E-07	8.51E-02	20
cg11005552	OBFC1	10	105648138	rs12765878	105669622	C	T	0.544444	0.0135426	0.00246035	3.71E-08	0.827695	0.0287292	1.60E-182	0.0163618	0.0030263	6.43E-08	3.48E-01	20
cg08687540	LSP1	11	1890204	rs592373	1890990	G	A	0.338889	0.0250485	0.00254638	7.87E-23	0.208307	0.0333945	4.44E-10	0.120248	0.0228265	1.38E-07	4.22E-01	12
cg24552015	LSP1	11	1892038	rs592373	1890990	G	A	0.338889	0.0250485	0.00254638	7.87E-23	0.200421	0.0336771	2.66E-09	0.124979	0.0245447	3.54E-07	5.52E-02	12
cg07734975	SWAP70	11	9780844	rs360137	9773568	T	C	0.41954	0.0143265	0.00248905	8.63E-09	0.400001	0.0320845	1.13E-35	0.0358162	0.00685377	1.73E-07	5.06E-02	20
cg26365553	MADD	11	47290613	rs2279238	47282024	T	C	0.0965909	0.0248756	0.00339894	2.51E-13	0.445249	0.0445575	1.64E-23	0.0558689	0.00946224	3.54E-09	8.67E-01	20
cg23844623	MADD	11	47290730	rs1051006	47306585	A	G	0.111111	0.0235824	0.00323195	2.96E-13	0.336062	0.0411446	3.14E-16	0.0701727	0.0128957	5.28E-08	9.83E-01	20
cg06294321	C11orf31	11	57508677	rs11604333	57467035	G	C	0.168675	0.0136319	0.00261762	1.91E-07	0.876729	0.0295186	7.47E-194	0.0155486	0.00303121	2.91E-07	1.44E-01	20
cg211033440	SIPA1	11	65409861	rs12801636	65391317	A	G	0.222222	0.0150898	0.0029495	3.12E-07	-0.953621	0.034479	2.23E-168	-0.0158237	0.00314542	4.89E-07	6.44E-01	20
cg05252626	ADAMTS8	11	130271817	rs747249	130271647	A	G	0.383333	-0.0199579	0.00257451	9.06E-15	0.335499	0.0335638	1.59E-23	-0.0594872	0.00971091	9.02E-10	1.03E-01	20
cg04671971	ADAMTS8	11	130271905	rs4936098	130280667	A	G	0.394444	-0.0204443	0.00255556	1.25E-15	0.433647	0.0335545	3.31E-38	-0.047145	0.00693088	1.03E-11	1.02E-01	20
cg110366797	HOXC4	12	54441509	rs7297416	54443090	C	A	0.235632	0.0149517	0.00269092	2.76E-08	-0.512758	0.0340215	2.49E-51	-0.0291594	0.00559321	1.85E-07	5.06E-01	18
cg10240950	C12orf76	12	110486919	rs11064829	110481056	G	A	0.0555556	0.0251626	0.00474615	1.15E-07	-2.23881	0.0374461	0.00E+00	-0.0112393	0.00212826	1.29E-07	2.85E-01	20

cg24530795	FAM109A	12	111807189	rs10849938	111800059	C	T	0.252874	0.0197863	0.00293007	1.45E-11	0.587307	0.0391145	5.85E-51	0.0336899	0.00547032	7.34E-10	4.04E-01	20
cg10833066	FAM109A	12	111807467	rs7398833	111786892	C	T	0.25	0.0200577	0.00292754	7.33E-12	1.42872	0.0249338	0.00E+00	0.0140389	0.00206366	1.03E-11	8.00E-01	20
cg26359133	SH2B3	12	111847419	rs2238154	111882485	A	C	0.233333	0.0217264	0.00302025	6.33E-13	0.505864	0.0387161	5.15E-39	0.0429491	0.00681554	2.95E-10	8.57E-01	20
cg08577424	BRAP	12	112123256	rs642898	112141233	G	A	0.338889	0.0180106	0.00274157	5.06E-11	-0.939058	0.0321796	3.30E-187	-0.0191794	0.00299255	1.46E-10	5.63E-02	20
cg04952827	ULK3	15	75135187	rs9210	75128501	T	C	0.30814	-0.0200937	0.00276899	3.98E-13	-0.266329	0.035218	3.96E-14	0.0754468	0.0144094	1.64E-07	1.83E-01	20
cg06330618	FES	15	91428456	rs2521501	91437388	T	A	0.366667	-0.0284173	0.00264871	7.54E-27	0.344489	0.0342291	7.95E-24	-0.0824912	0.0112383	2.13E-13	5.03E-02	12
cg06505273	TNRC6A	16	24850292	rs12924246	24844629	G	A	0.197368	0.0236571	0.00311329	3.00E-14	0.8592	0.0373269	3.06E-117	0.0275339	0.00381581	5.36E-13	8.62E-01	20
cg01109535	SLC5A11	16	24856104	rs2303084	24834581	C	G	0.151685	0.0238728	0.00310649	1.54E-14	0.755931	0.037914	1.90E-88	0.0315807	0.00440418	7.47E-13	8.09E-01	20
cg04399565	SLC5A11	16	24856162	rs200541	24733141	A	G	0.161111	0.0238507	0.00310909	1.71E-14	0.575308	0.0396482	1.04E-47	0.0414573	0.00611298	1.19E-11	3.89E-01	20
cg02428538	SLC5A11	16	24856791	rs1862450	24856775	A	G	0.155172	0.0222032	0.0031038	8.47E-13	-0.666987	0.037633	2.76E-70	-0.0332888	0.00501822	3.28E-11	5.02E-02	20
cg00339695	SLC5A11	16	24857497	rs2303083	24835168	A	G	0.151163	0.0241753	0.00311126	7.86E-15	0.915692	0.0369035	6.47E-136	0.0264011	0.00356042	1.21E-13	7.43E-01	20
cg23280807	SLC5A11	16	24857579	rs2303084	24834581	C	G	0.151685	0.0238728	0.00310649	1.54E-14	0.798895	0.0381253	1.71E-97	0.0298823	0.00414173	5.40E-13	6.19E-01	20
cg04756594	SLC5A11	16	24857601	rs2303084	24834581	C	G	0.151685	0.0238728	0.00310649	1.54E-14	0.825684	0.037826	1.24E-105	0.0289127	0.00398867	4.21E-13	6.81E-01	20
cg26870567	SLC5A11	16	24862006	rs12924246	24844629	G	A	0.197368	0.0236571	0.00311329	3.00E-14	0.333058	0.0394762	3.26E-17	0.0710299	0.01258	1.64E-08	3.50E-01	20
cg04022912	SLC5A11	16	24864984	rs1862450	24856775	A	G	0.155172	0.0222032	0.0031038	8.47E-13	0.316117	0.0400909	3.15E-15	0.0702374	0.0132571	1.17E-07	3.11E-01	20
cg06028605	SLC5A11	16	24865363	rs2303084	24834581	C	G	0.151685	0.0238728	0.00310649	1.54E-14	1.06897	0.0347126	3.06E-208	0.0223325	0.00299517	8.91E-14	9.50E-01	20
cg01435766	SLC5A11	16	24870053	rs189919	24737741	G	A	0.155172	0.0238356	0.00310871	1.76E-14	0.276874	0.0392079	1.64E-12	0.0860882	0.0165736	2.05E-07	2.27E-01	20
cg05552543	CFDP1	16	75322715	rs4993969	75411521	A	T	0.45	0.0170522	0.00250599	1.02E-11	0.286665	0.033066	4.34E-18	0.0594848	0.0111113	8.66E-08	8.53E-01	20
cg03315344	CHST6	16	75512273	rs977987	75506593	G	A	0.416667	0.0160008	0.00255095	3.56E-10	-0.518974	0.0327527	1.52E-56	-0.0308316	0.00528649	5.47E-09	5.43E-02	20
cg02555788	TNXB	16	75550118	rs3851734	75371920	T	C	0.44186	0.0174983	0.0025059	2.90E-12	-0.307156	0.0337836	9.74E-20	-0.0569688	0.0102869	3.06E-08	3.24E-01	20
cg07891658	BANP	16	87996731	rs4843750	88003095	T	G	0.247126	-0.0150531	0.00261155	8.22E-09	-0.377869	0.0337402	4.11E-29	0.0398368	0.00777291	2.97E-07	7.71E-01	20
cg06915872	BANP	16	87998081	rs4843750	88003095	T	G	0.247126	-0.0150531	0.00261155	8.22E-09	-0.397498	0.0342226	3.45E-31	0.0378696	0.00733447	2.43E-07	5.45E-01	20
cg05703749	BANP	16	88027707	rs7206128	88028533	C	G	0.272727	-0.0144989	0.00259053	2.18E-08	0.59195	0.0320663	4.32E-76	-0.0244935	0.00457298	8.50E-08	8.49E-01	20
cg27546431	MYO1C	17	1372751	rs2302457	1370720	T	C	0.482759	-0.0140746	0.00252386	2.45E-08	0.423196	0.0331206	2.19E-37	-0.0332579	0.00650706	3.20E-07	4.62E-01	20
cg01160692	HIC1	17	1959620	rs8076897	1985050	T	C	0.428571	-0.0195215	0.002614	8.16E-14	-0.24139	0.0353878	9.02E-12	0.0808713	0.0160569	4.74E-07	2.66E-01	20
cg13768953	DLG4	17	7114967	rs507506	7118322	A	G	0.461111	0.0149139	0.00249372	2.23E-09	-0.635976	0.0305777	4.45E-96	-0.0234504	0.00407998	9.05E-09	3.77E-01	20
cg03613822	DLG4	17	7115140	rs507506	7118322	A	G	0.461111	0.0149139	0.00249372	2.23E-09	-0.908081	0.0271361	1.61E-245	-0.0164235	0.00278965	3.93E-09	1.52E-01	20
cg04106389	DLG4	17	7117241	rs507506	7118322	A	G	0.461111	0.0149139	0.00249372	2.23E-09	0.325887	0.0327368	2.40E-23	0.045764	0.00892686	2.95E-07	2.86E-01	20
cg17892169	TNFSF12	17	7452644	rs9899183	7452977	C	T	0.224719	-0.0154692	0.00276545	2.22E-08	-0.444352	0.0352148	1.67E-36	0.0348129	0.00680766	3.16E-07	9.78E-02	20
cg20961037	NMT1	17	43096356	rs1053733	43183028	A	G	0.45	-0.0220213	0.00249565	1.11E-18	0.230827	0.0310318	1.02E-13	-0.0954017	0.0167747	1.29E-08	7.82E-02	20
cg17117718	CRHR1	17	43663208	rs17426174	43830938	C	G	0.177778	0.0170535	0.00293477	6.22E-09	1.51707	0.0218543	0.00E+00	0.0112411	0.00194126	7.01E-09	1.87E-01	20
cg05727186	CRHR1	17	43697356	rs17426174	43830938	C	G	0.177778	0.0170535	0.00293477	6.22E-09	-0.489117	0.0390897	6.36E-36	-0.0348659	0.00661559	1.36E-07	4.91E-01	20
cg03954353	CRHR1	17	43715162	rs1876831	43907745	T	C	0.166667	0.0168006	0.00293409	1.03E-08	0.485366	0.0398609	4.15E-34	0.0346143	0.00668015	2.20E-07	5.06E-01	20
cg01882395	C17orf69	17	43717810	rs16940665	43907896	C	T	0.178161	0.016801	0.00293409	1.03E-08	0.557487	0.0395908	4.95E-45	0.030137	0.00568159	1.13E-07	7.67E-01	20
cg23762722	CRHR1	17	43817897	rs17689882	43906828	A	G	0.177778	0.0166917	0.00293559	1.30E-08	-0.605948	0.0372129	1.30E-59	-0.0275464	0.00513149	7.96E-08	8.09E-01	20

cg16228356	CRHR1	17	43848958	rs17689882	43906828	A	G	0.177778	0.0166917	0.00293559	1.30E-08	-0.917366	0.0361815	8.00E-142	-0.0181953	0.0032795	2.89E-08	6.94E-01	20
cg15295732	MAPT-AS1	17	43942128	rs17426174	43830938	C	G	0.177778	0.0170535	0.00293477	6.22E-09	-0.71024	0.0384257	2.81E-76	-0.0240109	0.00433147	2.97E-08	1.53E-01	20
cg05301556	MAPT	17	43971177	rs17689882	43906828	A	G	0.177778	0.0166917	0.00293559	1.30E-08	-0.560656	0.0395165	1.09E-45	-0.0297717	0.00564081	1.31E-07	4.38E-01	20
cg16520312	MAPT	17	43971471	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	-0.582147	0.0391601	5.50E-50	-0.028842	0.00540109	9.29E-08	6.30E-01	20
cg23202277	MAPT	17	43971911	rs17689882	43906828	A	G	0.177778	0.0166917	0.00293559	1.30E-08	0.40725	0.0378102	4.72E-27	0.0409864	0.00815109	4.95E-07	5.11E-01	20
cg00891649	MAPT	17	43972573	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	-0.719009	0.0376119	1.84E-81	-0.023352	0.00426001	4.21E-08	9.16E-01	20
cg18878992	MAPT	17	43974344	rs17689882	43906828	A	G	0.177778	0.0166917	0.00293559	1.30E-08	0.78288	0.0364289	1.91E-102	0.0213209	0.00387876	3.87E-08	6.74E-01	20
cg14202850	MAPT	17	43974869	rs1876831	43907745	T	C	0.166667	0.0168006	0.00293409	1.03E-08	0.413833	0.0391352	3.92E-26	0.0405976	0.00806277	4.77E-07	5.97E-01	20
cg24801230	MAPT	17	43978533	rs17426174	43830938	C	G	0.177778	0.0170535	0.00293477	6.22E-09	-1.59176	0.0183089	0.00E+00	-0.0107136	0.00184784	6.71E-09	2.07E-01	20
cg18228076	MAPT	17	43983362	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	-1.48391	0.0234206	0.00E+00	-0.0113149	0.00198549	1.21E-08	6.53E-01	20
cg02228913	MAPT	17	44058016	rs17689882	43906828	A	G	0.177778	0.0166917	0.00293559	1.30E-08	-1.38642	0.0268195	0.00E+00	-0.0120394	0.00213016	1.59E-08	4.12E-01	20
cg00846647	MAPT	17	44060252	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	-1.1857	0.0317859	1.49E-304	-0.0141607	0.00250375	1.55E-08	5.98E-01	20
cg21705961	MAPT	17	44060775	rs17689882	43906828	A	G	0.177778	0.0166917	0.00293559	1.30E-08	-0.736163	0.0364129	6.92E-91	-0.0226739	0.0041424	4.41E-08	6.68E-01	20
cg01934064	MAPT	17	44064242	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	0.548858	0.0391165	1.00E-44	0.0305913	0.00577375	1.17E-07	2.29E-01	20
cg07368061	MAPT	17	44090862	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	-0.833463	0.0368556	3.14E-113	-0.0201452	0.00363164	2.90E-08	7.25E-01	20
cg09764761	MAPT	17	44105544	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	-0.751977	0.0378559	8.31E-88	-0.0223282	0.00406086	3.83E-08	7.91E-01	20
cg19832721	KANSL1	17	44249866	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	1.27989	0.0298133	0.00E+00	0.0131186	0.00231294	1.41E-08	5.11E-01	20
cg08670715	KANSL1	17	44341754	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	0.474749	0.0389596	3.71E-34	0.0353667	0.00682836	2.23E-07	1.56E-01	20
cg05159804	KANSL1	17	44343776	rs4640231	43912786	C	G	0.177778	0.0167903	0.00293436	1.05E-08	-1.09975	0.0336783	6.91E-234	-0.0152674	0.00270887	1.74E-08	4.61E-01	20
cg16759221	GOSR2	17	45003025	rs1662596	44993118	A	G	0.305556	-0.0176369	0.00252812	3.04E-12	-0.413405	0.0312046	4.62E-40	0.0426625	0.00691141	6.71E-10	2.90E-01	20
cg26170930	GOSR2	17	45020358	rs11655668	45007632	A	G	0.286517	-0.0165089	0.00259083	1.87E-10	-0.307817	0.0335294	4.29E-20	0.0536322	0.0102455	1.65E-07	7.84E-02	20
cg24434387	GOSR2	17	45051692	rs1662576	44996245	T	C	0.305556	-0.0175525	0.00252659	3.74E-12	0.256858	0.0326186	3.42E-15	-0.0683354	0.0131173	1.89E-07	7.67E-01	20
cg08010546	GOSR2	17	45060287	rs9905068	45069046	T	C	0.202247	-0.0205301	0.00282547	3.71E-13	0.287759	0.0368745	6.01E-15	-0.0713447	0.0134162	1.05E-07	1.18E-01	20
cg01544580	CBX1	17	46180269	rs7212202	46132723	C	G	0.205556	0.0172983	0.00305702	1.53E-08	0.626069	0.0379436	3.67E-61	0.02763	0.00516204	8.67E-08	1.52E-01	20
cg00730441	TBX2	17	59483863	rs2240736	59485393	C	T	0.283333	0.0177021	0.00279212	2.30E-10	-0.498815	0.0360969	1.96E-43	-0.0354883	0.00615852	8.29E-09	1.88E-01	20
cg18271897	SEPT11	17	75316784	rs1436138	75316880	G	A	0.333333	0.0156605	0.00257426	1.18E-09	0.676813	0.0327852	1.11E-94	0.0231386	0.00396521	5.37E-09	2.99E-01	20
cg15661536	SEPT10	17	75317185	rs1436138	75316880	G	A	0.333333	0.0156605	0.00257426	1.18E-09	0.614424	0.0332144	2.11E-76	0.0254881	0.00441046	7.51E-09	9.04E-02	20
cg17278466	USP36	17	76798203	rs7218899	76739850	C	T	0.494444	-0.0150613	0.00246707	1.03E-09	0.503341	0.0318463	2.86E-56	-0.0299226	0.00525431	1.23E-08	9.26E-01	20
cg15465367	USP36	17	76798307	rs1057040	76799795	G	A	0.488506	-0.015562	0.00246221	2.61E-10	0.464698	0.0315885	5.48E-49	-0.0334884	0.00576683	6.36E-09	4.49E-01	20
cg23834688	USP36	17	76798392	rs7215260	76677481	A	G	0.482353	-0.0144877	0.00246274	4.04E-09	0.415357	0.0321107	2.85E-38	-0.0348801	0.00651359	8.56E-08	8.04E-01	20
cg27089789	AP3D1	19	2136986	rs2238600	2140034	T	G	0.0174419	-0.0334704	0.00623937	8.13E-08	-1.88369	0.0749543	2.27E-139	0.0177685	0.00338694	1.55E-07	1.37E-01	11
cg02092181	DOT1L	19	2162766	rs3810409	2180515	A	G	0.0340909	-0.0362508	0.00629394	8.44E-09	0.98879	0.0833848	1.95E-32	-0.0366618	0.00707641	2.21E-07	1.24E-01	10
cg01401641	TSHZ3	19	31839171	rs12610813	31850047	G	A	0.333333	-0.0146505	0.00253085	7.10E-09	0.357472	0.0335649	1.74E-26	-0.0409836	0.00805809	3.66E-07	5.68E-01	20
cg15637286	TSHZ3	19	31845176	rs12610813	31850047	G	A	0.333333	-0.0146505	0.00253085	7.10E-09	-0.399887	0.0329542	6.92E-34	0.0366366	0.00701217	1.74E-07	5.06E-01	20
cg05381795	OPRL1	20	62713085	rs6010717	62714783	C	G	0.287356	-0.0140741	0.0025404	3.03E-08	-0.430314	0.0333169	3.67E-38	0.0327066	0.00642378	3.55E-07	7.76E-01	19

Table e-2 The DBP-associated methylations identified by Mendelian randomization analysis

probeID	Gene	CHR	Probe_bp	topSNP	topSNP_bp	A1	A2	Freq	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI	nsnp_HEIDI
cg00401797	PRDM16	1	3315193	rs6670123	3326796	G	C	0.194444	-0.0278034	0.00360732	1.29E-14	-0.333846	0.0481973	4.31E-12	0.0832822	0.0161654	2.58E-07	7.60E-02	11
cg05968369	PRDM16	1	3320446	rs2493292	3328659	T	C	0.2	-0.0284462	0.00355151	1.15E-15	0.316661	0.0470609	1.71E-11	-0.0898318	0.0174362	2.58E-07	5.21E-01	12
cg00546117	RERE	1	8445545	rs3765971	8445360	C	T	0.314607	-0.0182217	0.0025881	1.92E-12	-1.02618	0.0272656	5.467584e-310	0.0177568	0.00256582	4.50E-12	7.26E-02	20
cg00786138	RERE	1	8470722	rs301799	8489302	C	T	0.361111	0.0177789	0.00249901	1.13E-12	0.291001	0.0327514	6.38E-19	0.0610957	0.0110013	2.80E-08	5.23E-01	20
cg01447281	RERE	1	8482689	rs301806	8482078	C	T	0.359551	0.0175329	0.0024953	2.12E-12	0.315327	0.0328174	7.36E-22	0.0556024	0.00980349	1.41E-08	6.88E-01	20
cg00120948	RERE	1	8484417	rs301805	8481016	T	G	0.356322	0.0178376	0.00249852	9.40E-13	0.321335	0.0332695	4.52E-22	0.0555109	0.00966897	9.40E-09	8.06E-01	20
cg12760995	CASZ1	1	10789713	rs880315	10796866	C	T	0.348315	-0.0173676	0.00260922	2.81E-11	-0.655694	0.0321263	1.37E-92	0.0264874	0.0041856	2.48E-10	4.21E-01	19
cg03753284	MED8	1	43855912	rs11210839	43845658	G	A	0.420455	-0.0140859	0.00252336	2.38E-08	1.06795	0.024819	0.00E+00	-0.0131896	0.0023826	3.10E-08	1.23E-01	20
cg26915799	IPO9	1	201852272	rs2250377	201860626	A	G	0.272222	-0.0165649	0.00259918	1.85E-10	-0.473801	0.0334667	1.68E-45	0.0349617	0.00601602	6.19E-09	8.85E-01	20
cg24645447	SDCCAG8	1	243426679	rs12741781	243428152	G	T	0.306818	-0.0250065	0.00262994	1.95E-21	-0.353099	0.033779	1.42E-25	0.0708201	0.0100685	2.01E-12	2.31E-01	20
cg15440661	THADA	2	43395871	rs10167465	43397176	G	A	0.432584	-0.0151388	0.00256258	3.47E-09	-0.329885	0.0330927	2.09E-23	0.0458911	0.00902976	3.73E-07	8.84E-01	20
cg23009780	ADRA2B	2	96774492	rs2312955	96777168	T	G	0.3	-0.0183798	0.0026052	1.73E-12	0.426019	0.0332484	1.38E-37	-0.0431431	0.00698091	6.40E-10	6.52E-02	20
cg25074764	ADRA2B	2	96778750	rs11687113	96658588	G	A	0.327778	-0.0158506	0.00256883	6.82E-10	-0.408943	0.0320454	2.69E-37	0.0387599	0.0069774	2.77E-08	1.41E-01	20
cg18369288	ADRA2B	2	96780655	rs2301707	96931846	C	T	0.288889	-0.0172714	0.00262424	4.66E-11	-0.355052	0.0346303	1.15E-24	0.0486447	0.00878295	3.05E-08	1.12E-01	20
cg24986868	CCDC148	2	159312599	rs11674284	159372889	G	A	0.238889	0.0179974	0.00274952	5.93E-11	0.865286	0.0339976	6.81E-143	0.0207994	0.00328099	2.31E-10	2.68E-01	20
cg14426788	CCDC148	2	159312727	rs3771600	159404780	G	C	0.238889	0.0180381	0.0027532	5.70E-11	0.692523	0.0354833	7.90E-85	0.0260469	0.00419364	5.26E-10	2.76E-01	20
cg09072756	PKP4	2	159343691	rs11695939	159376514	T	C	0.227273	0.0180173	0.0027511	5.80E-11	-0.351207	0.0371147	3.00E-21	-0.0513011	0.00952637	7.24E-08	2.96E-01	20
cg02324737	DYNC112	2	172543905	rs11904009	172627343	G	T	0.308989	0.0155734	0.00273754	1.28E-08	-0.476985	0.0349005	1.60E-42	-0.0326496	0.0062166	1.50E-07	9.92E-01	20
cg19010139	ULK4	3	41695019	rs1613233	41945144	A	G	0.222222	-0.0311883	0.00336071	1.70E-20	0.382352	0.0445251	8.90E-18	-0.0815697	0.0129416	2.92E-10	9.65E-01	20
cg02108620	ULK4	3	42002230	rs17218103	41943724	G	A	0.188889	-0.0312534	0.00350926	5.32E-19	-0.450936	0.0449873	1.20E-23	0.0693079	0.0104102	2.78E-11	8.62E-01	20
cg03022575	ULK4	3	42003672	rs17283677	41926148	G	A	0.188889	-0.0312133	0.00350959	5.94E-19	0.463375	0.0441878	9.97E-26	-0.0673608	0.00993114	1.18E-11	5.11E-01	20
cg02648746	ULK4	3	42004678	rs1716645	41970480	T	C	0.215909	-0.0309602	0.00336059	3.20E-20	-0.447323	0.0438087	1.77E-24	0.0692121	0.0101186	7.91E-12	9.95E-01	20
cg27405988	CDC25A	3	48171915	rs6797587	48197614	A	G	0.322222	0.0158503	0.00261969	1.45E-09	-0.36431	0.0342851	2.26E-26	-0.0435077	0.00827484	1.46E-07	3.29E-01	20
cg08146865	NME6	3	48335857	rs7653336	48369464	A	T	0.256098	0.0162894	0.00264917	7.81E-10	-1.4075	0.0146802	0.00E+00	-0.0115733	0.00188605	8.45E-10	1.83E-01	20
cg11946769	NME6	3	48343235	rs11718350	48360992	G	T	0.294444	0.0162838	0.00264949	7.96E-10	-0.331654	0.0342512	3.56E-22	-0.0490987	0.00946205	2.11E-07	7.80E-02	20
cg20734569	SPINK8	3	48348370	rs7653336	48369464	A	T	0.256098	0.0162894	0.00264917	7.81E-10	-1.02908	0.0283644	3.27E-288	-0.0158291	0.00261103	1.34E-09	2.72E-01	20
cg08510456	BSN	3	49591008	rs9875617	49634696	A	G	0.234568	0.0161992	0.00266757	1.26E-09	0.327074	0.0351059	1.20E-20	0.0495276	0.00973537	3.63E-07	4.13E-01	20
cg08166588	AMIGO3	3	49757438	rs2352974	49890613	T	C	0.533333	-0.0152055	0.00247019	7.49E-10	0.481271	0.0324815	1.14E-49	-0.0315945	0.00555796	1.31E-08	2.63E-01	20
cg05666287	RNF123	3	49757470	rs2271961	49878113	C	T	0.533333	-0.0158193	0.00246047	1.28E-10	0.383958	0.0329544	2.26E-31	-0.0412006	0.00731909	1.81E-08	3.06E-01	20
cg21612339	GMPPB	3	49761620	rs11130221	49819102	G	C	0.534483	-0.016117	0.0024598	5.68E-11	0.96806	0.0267765	3.29E-286	-0.0166488	0.00258235	1.14E-10	2.17E-01	20
cg19381811	UBA7	3	49851713	rs2352974	49890613	T	C	0.533333	-0.0152055	0.00247019	7.49E-10	0.35928	0.0325969	3.00E-28	-0.0423222	0.00787498	7.69E-08	2.39E-01	20
cg24308560	MST1R	3	49941425	rs2230590	49936102	C	T	0.522222	-0.0135384	0.00246234	3.84E-08	-0.509048	0.0318382	1.53E-57	0.0265955	0.00511516	2.00E-07	5.54E-01	20
cg27360567	MST1R	3	49941613	rs11713193	49924424	A	G	0.522222	-0.0135369	0.00246078	3.78E-08	-0.427047	0.0328684	1.35E-38	0.0316989	0.00625754	4.07E-07	9.93E-02	20

cg07735586	SLMAP	3	57945651	rs1522387	57946096	G	A	0.493827	-0.0154872	0.00247548	3.95E-10	-1.00031	0.0256306	0.00E+00	0.0154824	0.0025063	6.52E-10	1.42E-01	20
cg24033633	SLMAP	3	57945695	rs1675380	57944507	G	C	0.458824	-0.0152159	0.00247511	7.88E-10	-1.19086	0.0202575	0.00E+00	0.0127773	0.00208976	9.70E-10	9.04E-02	20
cg02936049	ZBTB38	3	141102599	rs1344673	141125234	T	C	0.938889	-0.0312261	0.00572466	4.91E-08	-1.41227	0.0706979	8.88E-89	0.0221106	0.00420192	1.42E-07	3.43E-01	13
cg03651493	NPR3	5	32714243	rs1421811	32714270	G	C	0.443182	0.018894	0.0025253	7.35E-14	-0.260408	0.0327073	1.70E-15	-0.0725553	0.0133074	4.97E-08	2.08E-01	14
cg05885484	CSNK1G3	5	122847316	rs2173683	122841745	A	C	0.8	-0.0193102	0.00298354	9.67E-11	-0.670929	0.0374713	1.08E-71	0.0287813	0.00472849	1.15E-09	2.62E-01	20
cg20708411	CSNK1G3	5	122847581	rs2173683	122841745	A	C	0.8	-0.0193102	0.00298354	9.67E-11	-0.787256	0.0367988	1.53E-101	0.0245285	0.00395943	5.83E-10	2.60E-01	20
cg26117521	EBF1	5	158460303	rs7734385	158460212	A	G	0.511111	0.0156712	0.00248746	2.98E-10	0.317864	0.0324173	1.07E-22	0.0493016	0.00930161	1.16E-07	2.48E-01	20
cg18693985	CPEB4	5	173351052	rs17696407	173387335	A	C	0.298851	0.022834	0.00268097	1.64E-17	-1.08859	0.0284082	0.00E+00	-0.0209757	0.00252288	9.24E-17	1.75E-01	20
cg21438527	HIST1H4D	6	26189355	rs17598658	26175866	C	A	0.111111	0.0226202	0.00400903	1.68E-08	2.08275	0.0289071	0.00E+00	0.0108607	0.00193077	1.85E-08	2.23E-01	20
cg14345882	BTN3A2	6	26364793	rs9379859	26369549	T	C	0.140449	0.0198991	0.00360325	3.34E-08	1.69143	0.0317358	0.00E+00	0.0117647	0.00214171	3.95E-08	1.16E-01	20
cg16479474	ZNF165	6	28041457	rs149900	28014597	T	C	0.258427	0.0220572	0.00285604	1.14E-14	0.344287	0.0395455	3.15E-18	0.0640664	0.0110891	7.59E-09	5.43E-01	20
cg05261824	ZNF165	6	28046730	rs9348793	28084189	A	G	0.252809	0.0221228	0.00286459	1.14E-14	-0.418814	0.0392612	1.45E-26	-0.0528225	0.00844409	3.96E-10	8.19E-01	20
cg09156207	ZSCAN12L1	6	28058724	rs9295760	28147385	A	G	0.320513	0.0214786	0.00269933	1.77E-15	0.638644	0.035448	1.45E-72	0.0336316	0.00462053	3.37E-13	4.43E-01	20
cg11517269	ZSCAN12L1	6	28058789	rs203877	28048624	C	T	0.333333	0.0210273	0.00269713	6.40E-15	0.793921	0.0334693	2.20E-124	0.0264854	0.00357601	1.30E-13	7.81E-01	20
cg12623302	ZSCAN12L1	6	28058802	rs203877	28048624	C	T	0.333333	0.0210273	0.00269713	6.40E-15	0.852313	0.0328509	2.08E-148	0.0246709	0.00330426	8.24E-14	7.23E-01	20
cg18105139	ZSCAN12L1	6	28058856	rs200973	27858421	G	A	0.183333	0.0263231	0.00309881	2.00E-17	0.849765	0.0398562	7.29E-101	0.0309769	0.00392544	2.99E-15	4.48E-01	20
cg03597347	ZSCAN12L1	6	28058909	rs1904841	28108085	T	C	0.241573	0.0226237	0.0028661	2.95E-15	0.892067	0.0356651	4.49E-138	0.025361	0.00336907	5.17E-14	9.65E-01	20
cg17849569	ZSCAN12L1	6	28058911	rs1904841	28108085	T	C	0.241573	0.0226237	0.0028661	2.95E-15	0.929376	0.0354235	1.03E-151	0.0243429	0.00322045	4.07E-14	9.85E-01	20
cg02631126	ZSCAN12L1	6	28058918	rs9295760	28147385	A	G	0.320513	0.0214786	0.00269933	1.77E-15	0.887636	0.0329859	1.70E-159	0.0241975	0.00317119	2.34E-14	9.97E-01	20
cg12740337	ZSCAN12L1	6	28058973	rs200973	27858421	G	A	0.183333	0.0263231	0.00309881	2.00E-17	1.00298	0.038117	1.36E-152	0.026245	0.00324662	6.28E-16	4.94E-01	20
cg06952873	ZSCAN12L1	6	28059208	rs9295760	28147385	A	G	0.320513	0.0214786	0.00269933	1.77E-15	0.805802	0.0339794	2.56E-124	0.0266549	0.00353341	4.57E-14	5.21E-01	20
cg08851530	ZSCAN12L1	6	28072375	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	1.76903	0.0627604	8.42E-175	0.0155739	0.00282103	3.38E-08	7.55E-02	20
cg10876282	ZSCAN16	6	28092338	rs1631552	28089699	A	C	0.327778	0.0211735	0.00269802	4.25E-15	0.747529	0.0321726	2.02E-119	0.0283247	0.00380957	1.04E-13	2.50E-01	20
cg18032046	ZSCAN16	6	28092343	rs9295760	28147385	A	G	0.320513	0.0214786	0.00269933	1.77E-15	-0.50838	0.0357322	6.18E-46	-0.0422491	0.00608364	3.79E-12	8.58E-01	20
cg01566283	ZNF192	6	28109239	rs1904840	28108232	T	C	0.255556	0.0224292	0.00286673	5.13E-15	-0.530219	0.0390065	4.40E-42	-0.0423018	0.00623834	1.19E-11	1.51E-01	20
cg22143856	ZNF389	6	28129313	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	0.886626	0.0368094	3.43E-128	0.0253266	0.00340009	9.42E-14	2.93E-01	20
cg23281280	ZNF389	6	28129359	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	1.04662	0.0348354	2.55E-198	0.0214549	0.00283068	3.47E-14	2.48E-01	20
cg19592336	ZNF389	6	28129416	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	1.0556	0.0345612	7.04E-205	0.0212725	0.00280373	3.27E-14	3.65E-01	20
cg12963246	ZNF389	6	28129442	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	1.07099	0.0343069	6.10E-214	0.0209668	0.00275979	3.02E-14	3.77E-01	20
cg20151795	ZNF389	6	28129481	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	0.755976	0.0367329	4.12E-94	0.0297036	0.00405761	2.47E-13	4.01E-01	20
cg23161317	ZNF389	6	28129485	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	0.972804	0.0356511	6.09E-164	0.023083	0.003066	5.12E-14	4.03E-01	20
cg17949981	ZNF389	6	28129498	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	0.473497	0.0384051	6.32E-35	0.0474242	0.00717316	3.81E-11	3.60E-01	20
cg08968635	ZNF389	6	28129556	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	0.638796	0.0382598	1.40E-62	0.0351524	0.00495719	1.33E-12	7.77E-01	20
cg26335602	ZNF389	6	28129616	rs9295761	28147987	G	A	0.267442	0.0224552	0.00286684	4.79E-15	0.765672	0.0380939	7.44E-90	0.0293275	0.00401848	2.92E-13	1.80E-01	20
cg15407162	ZNF193	6	28192457	rs9461443	28194629	T	A	0.303371	0.0232321	0.00282836	2.15E-16	-0.247063	0.0390277	2.44E-10	-0.0940331	0.0187536	5.33E-07	4.60E-01	20

cg01192291	ZKSCAN4	6	28220797	rs9380069	28203300	G	A	0.164773	0.0204583	0.00340285	1.83E-09	-0.569774	0.0452073	2.02E-36	-0.035906	0.00661696	5.75E-08	8.59E-01	20
cg21251018	NKAPL	6	28226885	rs200965	27866384	A	G	0.183333	0.0261222	0.00310665	4.17E-17	0.325584	0.0432203	4.95E-14	0.0802317	0.0142996	2.01E-08	3.27E-01	20
cg17017591	ZBED9	6	28557765	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	1.1079	0.0693255	1.73E-57	0.0248676	0.00468329	1.10E-07	3.88E-01	20
cg01400884	ZBED9	6	28583971	rs2079705	28323968	A	G	0.0852273	0.0289074	0.00488538	3.28E-09	1.05062	0.0698861	4.45E-51	0.0275147	0.00499725	3.67E-08	7.19E-01	20
cg02246609	ZBED9	6	28584003	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	0.915739	0.0707909	2.83E-38	0.0300858	0.00582829	2.44E-07	4.76E-01	20
cg01309870	ZBED9	6	28584035	rs2394101	28447519	G	T	0.0813953	0.027911	0.00486989	9.97E-09	1.02523	0.0673866	2.85E-52	0.027224	0.00507589	8.17E-08	4.17E-01	20
cg04626491	ZBED9	6	28584053	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	1.08085	0.0696993	3.09E-54	0.0254898	0.00481688	1.21E-07	2.57E-01	20
cg09470274	ZBED9	6	28584057	rs7770236	28450437	A	G	0.0852273	0.0275166	0.00486904	1.59E-08	0.893486	0.068155	2.90E-39	0.0307969	0.00593427	2.11E-07	4.58E-01	20
cg20450471	ZBED9	6	28584061	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	1.04839	0.0695047	2.07E-51	0.026279	0.00498247	1.33E-07	3.64E-01	20
cg03682719	ZBED9	6	28584103	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	0.841437	0.0703055	5.21E-33	0.0327425	0.00642734	3.50E-07	4.39E-01	20
cg20839206	ZBED9	6	28584121	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	0.933737	0.070321	3.10E-40	0.0295059	0.00569273	2.18E-07	3.14E-01	20
cg22121557	ZBED9	6	28584138	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	0.975712	0.070132	5.32E-44	0.0282365	0.00541072	1.80E-07	2.86E-01	20
cg03858673	ZBED9	6	28584155	rs7770236	28450437	A	G	0.0852273	0.0275166	0.00486904	1.59E-08	0.807268	0.068631	6.09E-32	0.0340861	0.00669154	3.51E-07	5.51E-01	20
cg24114014	ZBED9	6	28584167	rs7770236	28450437	A	G	0.0852273	0.0275166	0.00486904	1.59E-08	0.865213	0.0684897	1.39E-36	0.0318033	0.00616501	2.49E-07	5.35E-01	20
cg04645150	ZBED9	6	28584172	rs4540253	28383714	T	G	0.0833333	0.0275507	0.00489383	1.81E-08	0.937702	0.0703277	1.48E-40	0.0293811	0.0056651	2.14E-07	3.85E-01	20
cg19918208	LINC01623	6	28828364	rs13197574	28060239	C	T	0.105556	0.0234387	0.00383334	9.70E-10	-0.801308	0.0497066	1.82E-58	-0.0292506	0.0051164	1.08E-08	1.71E-01	20
cg16677399	LINC01623	6	28830902	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-1.5694	0.0393995	0.00E+00	-0.0154563	0.00246751	3.75E-10	9.05E-01	20
cg00903577	LINC01623	6	28831109	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-1.35644	0.0434751	1.05E-213	-0.0178829	0.00287705	5.11E-10	9.45E-01	20
cg06608359	LINC01623	6	28831300	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-0.934182	0.0488195	1.28E-81	-0.0259663	0.00431282	1.74E-09	9.53E-01	20
cg19343530	LINC01623	6	28831388	rs13207345	28265572	T	C	0.0111111	0.0244412	0.00382565	1.67E-10	-0.413238	0.050205	1.86E-16	-0.0591455	0.0117192	4.49E-07	2.91E-01	20
cg13269645	HCG14	6	28864832	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	0.997239	0.0457035	1.51E-105	0.0243244	0.00399366	1.12E-09	9.60E-01	20
cg03270340	TRIM27	6	28891204	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-1.22406	0.0447924	2.00E-164	-0.019817	0.00320734	6.47E-10	8.89E-01	20
cg20373401	ZNF311	6	28983164	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-0.906158	0.0480706	2.91E-79	-0.0267693	0.00445289	1.84E-09	1.36E-01	20
cg02675264	ZNF311	6	28984246	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	0.425744	0.0507414	4.84E-17	0.056976	0.0112606	4.20E-07	3.98E-01	20
cg14132236	ZNF311	6	28984254	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	0.428481	0.0507098	2.92E-17	0.0566121	0.0111602	3.92E-07	4.94E-01	20
cg27490993	ZNF311	6	28984269	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	0.468631	0.0506832	2.32E-20	0.0517618	0.0098962	1.69E-07	2.01E-01	20
cg11935738	GABBR1	6	29520752	rs7752448	28301099	G	A	0.106742	0.0210897	0.00368355	1.03E-08	0.517282	0.0474087	1.02E-27	0.0407702	0.00804178	3.98E-07	7.47E-02	20
cg08065408	GABBR1	6	29520774	rs13217619	28306671	C	T	0.105556	0.0243485	0.0038201	1.85E-10	0.59924	0.0485151	4.78E-35	0.0406323	0.00717365	1.48E-08	4.00E-01	20
cg09641376	GABBR1	6	29520965	rs13217619	28306671	C	T	0.105556	0.0243485	0.0038201	1.85E-10	0.513799	0.0492077	1.60E-25	0.0473891	0.00871079	5.32E-08	1.44E-01	20
cg12749246	GABBR1	6	29521013	rs13195291	28169241	A	G	0.105556	0.0236987	0.00383226	6.26E-10	0.466262	0.0510891	7.08E-20	0.050827	0.00992822	3.06E-07	6.38E-01	20
cg06343355	GABBR1	6	29521023	rs13195291	28169241	A	G	0.105556	0.0236987	0.00383226	6.26E-10	0.449927	0.0509192	9.91E-19	0.0526723	0.0103962	4.05E-07	1.14E-01	20
cg16690356	HCG9	6	29945948	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-1.4105	0.0427358	6.88E-239	-0.0171976	0.00276095	4.70E-10	3.88E-01	20
cg25721950	TRIM31	6	30074078	rs13197633	28174757	A	G	0.105556	0.0238767	0.00384591	5.36E-10	0.592368	0.0493661	3.57E-33	0.0403072	0.00730993	3.51E-08	4.84E-01	20
cg04073296	TRIM31	6	30074080	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	0.408947	0.0499848	2.81E-16	0.0593162	0.0118329	5.36E-07	7.98E-01	20
cg03403996	TRIM31	6	30074162	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-1.20578	0.0440939	1.21E-164	-0.0201174	0.00325587	6.46E-10	3.56E-01	20

cg11100081	TRIM31	6	30079307	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-1.24727	0.0441222	8.45E-176	-0.0194483	0.00314241	6.06E-10	1.33E-01	20
cg06657028	TRIM31	6	30080495	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	-1.28214	0.0440856	5.89E-186	-0.0189193	0.00305288	5.75E-10	7.30E-01	20
cg08116408	TRIM40	6	30112776	rs2232423	28366151	G	A	0.123596	0.0242572	0.00382433	2.26E-10	0.60955	0.0505725	1.87E-33	0.0397953	0.00708975	1.99E-08	9.32E-01	20
cg05074385	TRIM15	6	30137208	rs13217619	28306671	C	T	0.105556	0.0243485	0.0038201	1.85E-10	-1.38839	0.0402844	2.72E-260	-0.0175373	0.00279813	3.67E-10	1.75E-01	20
cg18200389	TRIM26	6	30170340	rs13208096	28225311	G	C	0.0783133	0.0245072	0.00382774	1.53E-10	0.445887	0.0506232	1.27E-18	0.0549629	0.0106129	2.23E-07	3.53E-01	20
cg26074202	HLA-L	6	30227912	rs13217619	28306671	C	T	0.105556	0.0243485	0.0038201	1.85E-10	0.457978	0.0477828	9.28E-22	0.0531652	0.0100172	1.11E-07	1.89E-01	20
cg01554625	TUBB	6	30688579	rs2233980	31079644	A	G	0.174419	0.0218171	0.00341147	1.61E-10	-0.371574	0.0423063	1.59E-18	-0.0587153	0.0113571	2.34E-07	9.21E-01	20
cg20802826	LINC00243	6	30782080	rs2233980	31079644	A	G	0.174419	0.0218171	0.00341147	1.61E-10	-0.815547	0.0309536	5.49E-153	-0.0267515	0.00430451	5.14E-10	7.19E-02	20
cg19579005	LINC00243	6	30782272	rs3094222	31081434	G	A	0.196203	0.0216832	0.00341372	2.13E-10	-0.654825	0.0420324	1.01E-54	-0.033113	0.00562982	4.06E-09	5.87E-02	20
cg16537676	DDR1	6	30851624	rs3130557	31094703	T	C	0.177778	0.0221604	0.00340981	8.10E-11	0.484728	0.0433297	4.72E-29	0.0457172	0.00813539	1.91E-08	8.47E-02	20
cg26146308	DDR1	6	30851884	rs2233980	31079644	A	G	0.174419	0.0218171	0.00341147	1.61E-10	0.747026	0.0418786	3.59E-71	0.0292053	0.00485136	1.74E-09	5.52E-02	20
cg06893977	DDR1	6	30851928	rs3094222	31081434	G	A	0.196203	0.0216832	0.00341372	2.13E-10	0.386942	0.0422912	5.72E-20	0.0560374	0.0107399	1.81E-07	4.65E-01	20
cg15848685	VAR52	6	30882641	rs3094222	31081434	G	A	0.196203	0.0216832	0.00341372	2.13E-10	0.826773	0.0404209	5.52E-93	0.0262263	0.00432347	1.31E-09	9.77E-02	20
cg26672776	SFTA2	6	30899568	rs2233974	31080016	G	C	0.211111	0.0195386	0.00310095	2.96E-10	-1.11162	0.0317222	5.13E-269	-0.0175768	0.00283432	5.60E-10	1.43E-01	20
cg13561028	SFTA2	6	30899649	rs2233980	31079644	A	G	0.174419	0.0218171	0.00341147	1.61E-10	-1.42647	0.0304207	0.00E+00	-0.0152944	0.00241368	2.35E-10	8.15E-02	20
cg04390683	SFTA2	6	30900149	rs3132556	31078809	T	A	0.222222	0.0196475	0.00309429	2.16E-10	-1.13866	0.0311745	4.38E-292	-0.0172549	0.00275823	3.96E-10	1.94E-01	20
cg25107000	HLA-B	6	31275643	rs2523591	31326960	A	G	0.627778	-0.0133331	0.00251603	1.16E-07	0.662623	0.0313731	5.13E-99	-0.0201217	0.00391477	2.75E-07	1.92E-01	20
cg14801238	HLA-B	6	31275664	rs2523591	31326960	A	G	0.627778	-0.0133331	0.00251603	1.16E-07	0.599194	0.0320473	5.22E-78	-0.0222517	0.00436442	3.42E-07	1.56E-01	20
cg26343358	HLA-B	6	31275666	rs2523591	31326960	A	G	0.627778	-0.0133331	0.00251603	1.16E-07	0.727611	0.0304395	2.82E-126	-0.0183245	0.00354189	2.30E-07	1.12E-01	20
cg27071793	HLA-B	6	31275718	rs2523591	31326960	A	G	0.627778	-0.0133331	0.00251603	1.16E-07	0.586727	0.0318447	8.34E-76	-0.0227246	0.0044621	3.53E-07	1.35E-01	20
cg03709428	HLA-B	6	31275741	rs2523591	31326960	A	G	0.627778	-0.0133331	0.00251603	1.16E-07	0.685484	0.0309196	6.70E-109	-0.0194506	0.00377384	2.55E-07	2.21E-01	20
cg12076350	HLA-B	6	31275791	rs2523591	31326960	A	G	0.627778	-0.0133331	0.00251603	1.16E-07	0.591609	0.0319136	1.02E-76	-0.022537	0.00442322	3.48E-07	6.20E-02	20
cg17554194	HLA-B	6	31324972	rs2523589	31327334	T	G	0.444444	-0.017697	0.00246291	6.72E-13	0.439096	0.029816	4.33E-49	-0.0403033	0.00624108	1.06E-10	9.22E-02	20
cg26706521	HLA-B	6	31325085	rs2523589	31327334	T	G	0.444444	-0.017697	0.00246291	6.72E-13	-0.579859	0.0310501	7.92E-78	0.0305195	0.00455098	2.00E-11	8.52E-02	20
cg04981410	HLA-B	6	31325427	rs2523589	31327334	T	G	0.444444	-0.017697	0.00246291	6.72E-13	0.421054	0.0301403	2.38E-44	-0.0420303	0.0065778	1.66E-10	2.91E-01	20
cg00218406	HCP5	6	31431407	rs3130614	31476458	A	T	0.16092	0.0257705	0.00355714	4.34E-13	0.379848	0.045113	3.77E-17	0.0678443	0.012354	3.98E-08	4.53E-01	20
cg18808777	HCP5	6	31431503	rs3130614	31476458	A	T	0.16092	0.0257705	0.00355714	4.34E-13	0.353156	0.0452068	5.63E-15	0.0729719	0.0137371	1.08E-07	5.16E-01	20
cg21684411	HCP5	6	31431573	rs3094005	31465047	T	G	0.831461	0.0255018	0.00353505	5.45E-13	0.370118	0.0450585	2.14E-16	0.0689018	0.0127116	5.95E-08	8.45E-01	20
cg05182583	BAT2	6	31598464	rs3115672	31727897	T	C	0.614458	0.0254461	0.0036151	1.94E-12	0.755441	0.0449667	2.44E-63	0.0336838	0.00518847	8.47E-11	1.23E-01	7
cg09423426	CSNK2B	6	31633492	rs3115672	31727897	T	C	0.614458	0.0254461	0.0036151	1.94E-12	-0.527528	0.0459836	1.82E-30	-0.0482365	0.00804001	1.98E-09	1.28E-01	6
cg19240857	LY6G6E	6	31683109	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.393056	0.0466625	3.66E-17	-0.0667409	0.0121857	4.33E-08	2.44E-01	20
cg20288341	LY6G6D	6	31683131	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.388125	0.0471018	1.72E-16	-0.0675888	0.0124572	5.77E-08	5.22E-01	20
cg21506565	C6orf25	6	31691506	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.343668	0.0471436	3.10E-13	-0.0772653	0.0149819	2.51E-07	2.41E-01	20
cg22235293	C6orf25	6	31691539	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.33262	0.0470569	1.57E-12	-0.0798316	0.015724	3.83E-07	1.44E-01	20
cg07014308	C6orf25	6	31691597	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.326782	0.046951	3.40E-12	-0.081258	0.016134	4.74E-07	1.23E-01	20

cg00406022	C6orf25	6	31691696	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.349387	0.0469837	1.04E-13	-0.0760005	0.0145921	1.91E-07	2.50E-01	20
cg26749976	C6orf25	6	31691717	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.332929	0.0473426	2.03E-12	-0.0787943	0.0156528	4.81E-07	9.87E-02	20
cg23895220	C6orf25	6	31691870	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.349831	0.0470428	1.03E-13	-0.075904	0.0145734	1.90E-07	2.56E-01	20
cg01338864	C6orf25	6	31691905	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.334907	0.0466681	7.16E-13	-0.0792866	0.015496	3.11E-07	9.32E-02	20
cg00718684	C6orf25	6	31692026	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.354931	0.0471266	5.02E-14	-0.0739098	0.0141922	1.91E-07	4.41E-01	20
cg03658690	C6orf25	6	31692260	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.370905	0.0469657	2.85E-15	-0.0715915	0.013358	8.35E-08	1.49E-01	20
cg26114961	C6orf25	6	31692295	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.362051	0.046759	9.72E-15	-0.0733422	0.013811	1.09E-07	7.94E-02	20
cg21286967	DDAH2	6	31696710	rs389883	31947460	G	T	0.359551	0.0212066	0.00262914	7.29E-16	-0.260854	0.0344262	3.53E-14	-0.0812968	0.0147207	3.34E-08	1.02E-01	20
cg03608520	DDAH2	6	31696720	rs389883	31947460	G	T	0.359551	0.0212066	0.00262914	7.29E-16	-0.256768	0.0345258	1.03E-13	-0.0825906	0.0151054	4.56E-08	1.72E-01	20
cg16704889	DDAH2	6	31696729	rs389883	31947460	G	T	0.359551	0.0212066	0.00262914	7.29E-16	-0.274356	0.0343927	1.50E-15	-0.0772958	0.013628	1.41E-08	1.27E-01	20
cg18402034	DDAH2	6	31698651	rs3130614	31476458	A	T	0.16092	0.0257705	0.00355714	4.34E-13	-0.365573	0.0439884	9.52E-17	-0.0704934	0.0129084	4.73E-08	1.48E-01	20
cg00657529	DDAH2	6	31698687	rs3117577	31727474	G	A	0.107955	0.0255329	0.00361367	1.60E-12	-0.660198	0.0449619	8.22E-49	-0.0386746	0.00607436	1.93E-10	8.31E-01	20
cg04387059	DDAH2	6	31698722	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.425637	0.0466882	7.75E-20	-0.0623243	0.0109274	1.17E-08	1.37E-01	20
cg11093373	DDAH2	6	31698899	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	-0.410654	0.0467327	1.53E-18	-0.0640305	0.0114482	2.23E-08	3.88E-01	20
cg18909389	CLIC1	6	31701110	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.71886	0.0450573	2.66E-57	-0.0369022	0.00555223	3.00E-11	4.19E-01	20
cg13026137	CLIC1	6	31701260	rs3117577	31727474	G	A	0.107955	0.0255329	0.00361367	1.60E-12	-0.488102	0.0454741	7.08E-27	-0.0523106	0.0088636	3.60E-09	5.39E-01	20
cg12257344	CLIC1	6	31701288	rs3117577	31727474	G	A	0.107955	0.0255329	0.00361367	1.60E-12	-0.665278	0.0448957	1.12E-49	-0.0383793	0.0060177	1.80E-10	9.04E-01	20
cg21769117	CLIC1	6	31705273	rs3130614	31476458	A	T	0.16092	0.0257705	0.00355714	4.34E-13	-0.490549	0.0447598	5.98E-28	-0.052534	0.00869247	1.51E-09	6.93E-01	20
cg20640261	MSH5	6	31707019	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.411488	0.0464003	7.43E-19	-0.0644673	0.0114281	1.69E-08	2.50E-01	20
cg23634079	MSH5	6	31712195	rs3117577	31727474	G	A	0.107955	0.0255329	0.00361367	1.60E-12	-1.80251	0.0219734	0.00E+00	-0.0141652	0.00201222	1.93E-12	8.67E-01	20
cg00686197	C6orf27	6	31733619	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.331956	0.0471086	1.83E-12	-0.0799128	0.0157508	3.90E-07	4.30E-01	20
cg06991565	C6orf27	6	31733799	rs3117577	31727474	G	A	0.107955	0.0255329	0.00361367	1.60E-12	-0.583873	0.0457071	2.28E-37	-0.0437302	0.0070728	6.29E-10	3.46E-01	20
cg00330953	C6orf27	6	31733810	rs3117577	31727474	G	A	0.107955	0.0255329	0.00361367	1.60E-12	-0.785668	0.0445577	1.38E-69	-0.0324983	0.00495502	5.43E-11	3.00E-01	20
cg09630142	C6orf27	6	31733889	rs3117577	31727474	G	A	0.107955	0.0255329	0.00361367	1.60E-12	-0.63625	0.0455404	2.34E-44	-0.0401303	0.00636465	2.88E-10	3.47E-01	20
cg03560996	C6orf27	6	31733908	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.621856	0.0457744	4.90E-42	-0.0426586	0.00662614	1.21E-10	1.88E-01	20
cg10158997	C6orf27	6	31734106	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.556934	0.0461329	1.48E-33	-0.0476313	0.0076166	4.01E-10	8.11E-02	20
cg13187827	C6orf27	6	31734192	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	-0.691668	0.0457851	1.46E-51	-0.0380159	0.00581508	6.26E-11	1.79E-01	20
cg19593741	C6orf27	6	31734217	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.635316	0.0458786	1.31E-43	-0.0417548	0.00645835	1.01E-10	1.81E-01	20
cg25264948	C6orf27	6	31734232	rs3115672	31727897	T	C	0.614458	0.0254461	0.0036151	1.94E-12	-0.621875	0.0455222	1.74E-42	-0.0409183	0.00653952	3.92E-10	1.11E-01	5
cg10095777	C6orf27	6	31734292	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.563578	0.0465129	8.63E-34	-0.0470698	0.00751944	3.86E-10	2.53E-01	20
cg23287992	C6orf27	6	31734390	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.596502	0.0460266	2.06E-38	-0.0444718	0.00698402	1.92E-10	5.57E-01	20
cg00848392	C6orf27	6	31734401	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.484859	0.0462521	1.03E-25	-0.0547118	0.00912372	2.01E-09	2.60E-01	20
cg25843346	VAR5	6	31762555	rs521977	31836827	T	G	0.627778	0.0183827	0.00262993	2.76E-12	0.281412	0.0336329	5.90E-17	0.065323	0.0121774	8.13E-08	9.00E-02	20
cg04659729	VAR5	6	31762688	rs521977	31836827	T	G	0.627778	0.0183827	0.00262993	2.76E-12	0.284271	0.0337746	3.87E-17	0.0646661	0.0120258	7.56E-08	7.47E-02	20
cg05571472	C6orf48	6	31802104	rs1150753	32059867	G	A	0.111111	0.0265063	0.00363535	3.08E-13	0.404433	0.0471463	9.63E-18	0.0655394	0.011797	2.77E-08	7.39E-01	20

cg16505946	ZBTB12	6	31870305	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	0.573719	0.0440841	1.02E-38	0.0462378	0.00725406	1.84E-10	6.78E-01	20
cg20069688	DOM3Z	6	31941049	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	-0.470909	0.046305	2.71E-24	-0.0558376	0.00945707	3.54E-09	7.41E-01	20
cg03661299	STK19	6	31947216	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.420547	0.0470105	3.69E-19	-0.0631406	0.0111664	1.56E-08	8.37E-01	20
cg21415604	C4B;C4A	6	31948433	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	0.47367	0.0469481	6.17E-24	0.0560593	0.0094812	3.37E-09	3.31E-01	20
cg04771084	CYP21A2	6	31973255	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-1.26866	0.0384522	1.02E-238	-0.0209305	0.00293766	1.04E-12	4.98E-01	20
cg06002203	TNXA	6	31976720	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.677961	0.0444025	1.24E-52	-0.0391284	0.00593391	4.28E-11	1.46E-01	20
cg21722170	TNXA	6	31977443	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	0.684243	0.0455105	4.34E-51	0.0384284	0.00588347	6.51E-11	8.76E-01	20
cg27449793	CYP21A2	6	32006074	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	0.443764	0.0469059	3.06E-21	0.0598372	0.010356	7.56E-09	1.28E-01	20
cg05045332	TNXB	6	32012897	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	0.532899	0.0455756	1.39E-31	0.0497796	0.00803032	5.68E-10	4.58E-01	20
cg02432444	TNXB	6	32016214	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.412349	0.0461336	3.96E-19	-0.064396	0.0113924	1.58E-08	8.08E-02	20
cg19964491	TNXB	6	32016236	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.518279	0.0463775	5.39E-29	-0.0506154	0.00835532	1.38E-09	2.37E-01	20
cg11493661	TNXB	6	32016239	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.44277	0.0466475	2.27E-21	-0.0592472	0.0103202	9.42E-09	1.34E-01	20
cg08661360	TNXB	6	32016247	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.554886	0.0463507	5.01E-33	-0.0472762	0.00765522	6.59E-10	8.01E-01	20
cg05473289	TNXB	6	32016257	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.526677	0.0464248	7.88E-30	-0.0498084	0.00818619	1.17E-09	5.57E-01	20
cg05298224	TNXB	6	32016360	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.647939	0.0461173	7.73E-45	-0.0404867	0.00631232	1.42E-10	5.80E-01	20
cg09474017	TNXB	6	32016368	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.619731	0.0458157	1.09E-41	-0.0423295	0.00665363	1.99E-10	5.53E-01	20
cg04293778	TNXB	6	32016426	rs1150753	32059867	G	A	0.111111	0.0265063	0.00363535	3.08E-13	-0.394892	0.0463773	1.67E-17	-0.0671228	0.0121199	3.06E-08	7.34E-02	20
cg15398152	TNXB	6	32016535	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.374367	0.0470769	1.83E-15	-0.0709294	0.0131924	7.59E-08	1.22E-01	20
cg241138857	TNXB	6	32055079	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.33333	0.0463932	6.73E-13	-0.0795832	0.01553	2.98E-07	6.62E-01	20
cg26695758	TNXB	6	32063607	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	-0.443469	0.0467647	2.47E-21	-0.0592925	0.0102931	8.39E-09	9.12E-02	20
cg20414186	TNXB	6	32064491	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.326276	0.0469864	3.81E-12	-0.0813837	0.0161785	4.90E-07	2.66E-01	20
cg03556669	TNXB	6	32064497	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.402953	0.0467292	6.51E-18	-0.0658974	0.0118301	2.54E-08	6.08E-01	20
cg24882324	TNXB	6	32064508	rs389883	31947460	G	T	0.359551	0.0212066	0.00262914	7.29E-16	-0.260872	0.0347959	6.52E-14	-0.0812913	0.0148034	3.99E-08	1.86E-01	20
cg15196197	TNXB	6	32064573	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.398864	0.0464583	9.05E-18	-0.0665076	0.0119484	2.60E-08	8.98E-01	20
cg13400512	TNXB	6	32064578	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	-0.475321	0.0462818	9.60E-25	-0.0553192	0.00933849	3.15E-09	7.03E-01	20
cg12694372	TNXB	6	32064582	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.503299	0.0464059	2.09E-27	-0.0527591	0.00871435	1.41E-09	7.50E-01	20
cg15265085	TNXB	6	32064588	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.504927	0.0461071	6.56E-28	-0.0525373	0.00864031	1.20E-09	6.99E-01	20
cg21642103	TNXB	6	32064656	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.450522	0.0464051	2.78E-22	-0.0588817	0.0100821	5.21E-09	6.86E-01	20
cg21342636	TNXB	6	32064671	rs3117577	31727474	G	A	0.107955	0.0255329	0.00361367	1.60E-12	-0.404778	0.0461583	1.80E-18	-0.0630788	0.0114648	3.76E-08	5.95E-01	20
cg01485117	TNXB	6	32064677	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.431615	0.0465169	1.72E-20	-0.061461	0.0107027	9.33E-09	6.84E-01	20
cg27081346	TNXB	6	32064692	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	-0.48663	0.0463266	8.25E-26	-0.0540337	0.00905433	2.41E-09	6.62E-01	20
cg15793329	TNXB	6	32064749	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.540476	0.0463861	2.25E-31	-0.0485366	0.0079173	8.76E-10	4.90E-01	20
cg21289669	TNXB	6	32064764	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	-0.496386	0.0465137	1.38E-26	-0.0529717	0.00883166	2.00E-09	7.65E-01	20
cg18330047	TNXB	6	32064783	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.487912	0.0466049	1.20E-25	-0.0537656	0.00905535	2.90E-09	6.41E-01	20
cg15014577	TNXB	6	32064785	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.433482	0.046463	1.06E-20	-0.0611964	0.0106344	8.69E-09	9.08E-01	20

cg18102337	TNXB	6	32064810	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.643899	0.0458517	8.49E-45	-0.0411982	0.00635305	8.89E-11	5.92E-01	20
cg01033871	TNXB	6	32064837	rs1150753	32059867	G	A	0.111111	0.0265063	0.00363535	3.08E-13	-0.511267	0.0464775	3.81E-28	-0.0518444	0.00853061	1.22E-09	5.38E-01	20
cg05889186	TNXB	6	32064842	rs1150753	32059867	G	A	0.111111	0.0265063	0.00363535	3.08E-13	-0.568848	0.0460968	5.50E-35	-0.0465965	0.00742289	3.44E-10	6.80E-01	20
cg15745284	TNXB	6	32064923	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.493886	0.0467401	4.25E-26	-0.0531152	0.00891934	2.60E-09	4.71E-01	20
cg07518714	TNXB	6	32064945	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.515221	0.0467479	3.02E-28	-0.0509158	0.00843958	1.61E-09	4.84E-01	20
cg00355613	TNXB	6	32064956	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.555735	0.0464621	5.68E-33	-0.0472039	0.0076453	6.65E-10	6.88E-01	20
cg17272563	PRRT1	6	32116548	rs521977	31836827	T	G	0.627778	0.0183827	0.00262993	2.76E-12	0.244284	0.0336038	3.61E-13	0.0752515	0.0149352	4.69E-07	2.25E-01	20
cg05525649	PBX2	6	32156269	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	0.478081	0.0467215	1.42E-24	0.0549999	0.00929594	3.29E-09	5.58E-02	20
cg08293075	PBX2	6	32156294	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	0.44305	0.0472257	6.50E-21	0.0593487	0.0103441	9.61E-09	9.22E-02	20
cg11103845	PBX2	6	32157230	rs3094222	31081434	G	A	0.196203	0.0216832	0.00341372	2.13E-10	-0.418458	0.0430298	2.36E-22	-0.0518169	0.0097438	1.05E-07	2.22E-01	20
cg00442389	GPSM3	6	32160074	rs433061	32014828	A	G	0.111111	0.0265536	0.00363895	2.95E-13	-0.602105	0.0459097	2.70E-39	-0.0441013	0.00691622	1.81E-10	1.20E-01	20
cg16390049	NOTCH4	6	32165089	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.493083	0.0465366	3.12E-26	-0.0532018	0.00892613	2.52E-09	2.72E-01	20
cg08828723	NOTCH4	6	32165176	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.458701	0.0468349	1.19E-22	-0.0571896	0.00985046	6.41E-09	5.32E-02	20
cg06891815	NOTCH4	6	32165237	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-0.509513	0.0463702	4.37E-28	-0.0514862	0.0085419	1.67E-09	3.63E-01	20
cg24697648	NOTCH4	6	32188317	rs389883	31947460	G	T	0.359551	0.0212066	0.00262914	7.29E-16	0.239518	0.035053	8.31E-12	0.0885386	0.0169819	1.85E-07	9.11E-02	20
cg09177461	C6orf10	6	32280185	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	0.382439	0.0465863	2.23E-16	0.0685936	0.0126631	6.07E-08	1.27E-01	20
cg21241195	C6orf10	6	32289357	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-1.33369	0.0376816	2.14E-274	-0.0196694	0.0027845	1.62E-12	5.43E-02	20
cg17851230	C6orf10	6	32289373	rs521977	31836827	T	G	0.627778	0.0183827	0.00262993	2.76E-12	-0.287185	0.0337505	1.75E-17	-0.0640099	0.0118512	6.62E-08	6.77E-02	20
cg13966843	C6orf10	6	32336160	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	-1.36794	0.0371055	1.61E-297	-0.019177	0.00271055	1.50E-12	5.94E-02	20
cg08882389	HLA-DRA	6	32410690	rs497309	31892484	C	A	0.105556	0.0265275	0.00362845	2.66E-13	-0.426319	0.0460071	1.93E-20	-0.0622246	0.0108412	9.49E-09	8.98E-01	20
cg25645491	HLA-DRA	6	32411067	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	0.750905	0.0453986	1.88E-61	0.0349351	0.00528635	3.88E-11	7.30E-01	20
cg06423300	HLA-DQB2	6	32729059	rs1150753	32059867	G	A	0.111111	0.0265063	0.00363535	3.08E-13	-0.771843	0.0457605	7.87E-64	-0.0343416	0.00513119	2.19E-11	5.60E-01	20
cg24421410	HLA-DMA	6	32920220	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	0.829479	0.0439214	1.50E-79	0.0316258	0.00469577	1.64E-11	1.89E-01	20
cg02806715	HLA-DMA	6	32920567	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	0.839939	0.0440663	5.35E-81	0.0313051	0.00461884	1.22E-11	1.86E-01	20
cg08735211	HLA-DMA	6	32920657	rs1270942	31918860	G	A	0.105556	0.0262944	0.00362599	4.13E-13	0.751873	0.0446848	1.57E-63	0.0349719	0.00525142	2.75E-11	8.82E-02	20
cg24129356	HLA-DMA	6	32920735	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	0.858458	0.0438391	2.20E-85	0.0305582	0.00451705	1.33E-11	2.03E-01	20
cg03520342	HLA-DMA	6	32920784	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	0.972585	0.0428819	6.97E-114	0.0269723	0.00392596	6.41E-12	8.76E-02	20
cg07151443	HLA-DMA	6	32920962	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	0.965613	0.0429541	6.50E-112	0.0271671	0.00395756	6.67E-12	1.58E-01	20
cg14833385	HLA-DMA	6	32921142	rs1269852	32080191	C	G	0.111111	0.0262329	0.00363894	5.65E-13	0.555599	0.0463219	3.81E-33	0.0472155	0.00764153	6.46E-10	4.01E-01	20
cg23262351	IRAK1BP1	6	79576851	rs9350792	79587173	G	A	0.311111	-0.0178214	0.00253716	2.16E-12	-0.350494	0.0334838	1.22E-25	0.0508465	0.00871757	5.46E-09	5.30E-01	20
cg18132916	IRAK1BP1	6	79620363	rs9352683	79718795	G	T	0.445122	-0.0162112	0.0024644	4.77E-11	-0.586582	0.031722	2.42E-76	0.0276367	0.00445922	5.73E-10	1.04E-01	20
cg11833968	IRAK1BP1	6	79620685	rs9352683	79718795	G	T	0.445122	-0.0162112	0.0024644	4.77E-11	-0.438417	0.0324377	1.26E-41	0.0369767	0.00625156	3.32E-09	2.39E-01	20
cg03039315	C6orf204	6	118973136	rs11153763	118938738	G	A	0.449438	-0.0136042	0.00247098	3.68E-08	-1.03809	0.0248068	0.00E+00	0.013105	0.00240082	4.80E-08	5.97E-01	20
cg21191810	C6orf204	6	118973309	rs9320649	118693665	G	A	0.44382	-0.0132161	0.00248874	1.09E-07	-0.849644	0.0294005	1.23E-183	0.0155549	0.0029782	1.76E-07	7.81E-01	20
cg18833306	C6orf204	6	118973337	rs7764272	118692498	A	C	0.438889	-0.0131849	0.00248765	1.16E-07	-0.743423	0.0305851	1.66E-130	0.0177354	0.00342484	2.24E-07	1.82E-01	20

cg05564266	C6orf204	6	118973597	rs9320649	118693665	G	A	0.44382	-0.0132161	0.00248874	1.09E-07	-0.695216	0.0315167	7.89E-108	0.0190101	0.00368208	2.43E-07	6.41E-01	20
cg08737367	HOXA13	7	27243221	rs2023844	27243238	G	A	0.0505618	0.0273407	0.00470358	6.15E-09	-0.957087	0.0600945	4.16E-57	-0.0285666	0.00523157	4.75E-08	4.08E-01	20
cg06795527	HOXA13	7	27245018	rs2023843	27243221	C	T	0.05	0.027646	0.0046986	4.01E-09	0.63099	0.0625063	5.82E-24	0.0438137	0.00861896	3.71E-07	5.80E-01	20
cg14228300	IGFBP3	7	45961074	rs1496499	45979023	G	T	0.333333	-0.0160928	0.00247331	7.70E-11	-0.426127	0.0325854	4.44E-39	0.0377652	0.0064829	5.70E-09	8.18E-02	20
cg23193639	IGFBP3	7	45961078	rs11977526	46008110	A	G	0.270588	-0.0179527	0.00251055	8.64E-13	0.280106	0.0335078	6.30E-17	-0.0640926	0.0117948	5.51E-08	2.87E-01	20
cg04812164	IGFBP3	7	45977344	rs2965074	45983129	T	G	0.337079	-0.0161629	0.00247337	6.38E-11	0.716135	0.0305338	1.21E-121	-0.0225696	0.00358533	3.07E-10	1.14E-01	20
cg04305808	ZKSCAN1	7	99614209	rs7788746	99612405	G	T	0.377778	-0.0149267	0.00260673	1.03E-08	-0.36802	0.0351408	1.15E-25	0.0405595	0.00807278	5.05E-07	5.59E-01	20
cg18683606	SRRT	7	100471612	rs12705092	100473550	A	G	0.136364	-0.0222846	0.00317536	2.26E-12	0.88627	0.0379624	1.51E-120	-0.0251442	0.00374121	1.81E-11	6.96E-02	20
cg15741354	PRAG1	8	8146129	rs1107832	8146083	A	T	0.402597	0.0158459	0.00252793	3.65E-10	0.896897	0.0297954	4.59E-199	0.0176675	0.00287899	8.43E-10	4.54E-01	20
cg02520399	PRAG1	8	8168661	rs2979181	8323088	T	A	0.576389	-0.0158861	0.0024651	1.16E-10	0.316593	0.0316196	1.34E-23	-0.0501782	0.00925972	5.99E-08	6.22E-01	20
cg27000590	PRAGMIN	8	8182003	rs7817376	8380530	C	T	0.477778	-0.0164226	0.00246265	2.59E-11	-0.346302	0.0322349	6.39E-27	0.0474228	0.00836995	1.46E-08	5.79E-01	20
cg08447380	PRAGMIN	8	8185703	rs7826238	8387095	T	G	0.438889	-0.0171346	0.00246638	3.73E-12	0.237417	0.0315927	5.69E-14	-0.0721709	0.0141474	3.37E-07	9.77E-01	20
cg04654363	CLDN23	8	8581213	rs1703982	8598388	A	T	0.483146	-0.0177979	0.00246708	5.44E-13	-0.235212	0.0323167	3.38E-13	0.0756675	0.0147681	3.00E-07	7.11E-01	20
cg18237548	ERI1	8	8860050	rs2288671	8860894	C	T	0.411111	-0.0174592	0.00247817	1.86E-12	-0.236572	0.0319906	1.41E-13	0.0738008	0.0144682	3.38E-07	6.23E-01	20
cg17522401	MSRA	8	9791214	rs10503396	9780861	A	G	0.127778	-0.0216771	0.00385404	1.86E-08	-0.607408	0.0492671	6.33E-35	0.0356879	0.00697416	3.10E-07	7.14E-01	20
cg06620390	MSRA	8	10192943	rs6982308	10193772	C	G	0.405556	-0.0215813	0.00246707	2.19E-18	0.351867	0.0311634	1.45E-29	-0.0613337	0.00886944	4.67E-12	2.46E-01	20
cg21915799	MSRA	8	10282809	rs11250007	10285086	C	G	0.222222	-0.0161123	0.00269964	2.40E-09	0.606365	0.0343096	6.73E-70	-0.026572	0.00469919	1.56E-08	1.63E-01	20
cg24036517	SOX7	8	10585394	rs7814757	10675188	T	C	0.353933	-0.0187383	0.00251735	9.82E-14	0.263369	0.0325954	6.48E-16	-0.0711485	0.0129961	4.38E-08	7.44E-01	20
cg21725652	XKR6	8	10918152	rs6601561	10961433	T	C	0.461111	0.0158577	0.00247193	1.41E-10	-0.343587	0.0312366	3.84E-28	-0.0461534	0.00832867	3.00E-08	3.85E-01	20
cg09528494	BLK	8	11338675	rs998683	11353000	A	G	0.266667	-0.017836	0.00278766	1.57E-10	0.330964	0.0366928	1.88E-19	-0.053891	0.0103267	1.80E-07	4.77E-01	20
cg14702231	BLK	8	11413234	rs7007439	11415794	T	A	0.644444	-0.0145009	0.00254426	1.20E-08	0.43798	0.0320671	1.80E-42	-0.0331086	0.00629456	1.44E-07	7.30E-02	20
cg24861686	BLK	8	11418058	rs804280	11612698	C	A	0.522222	0.0168916	0.00249445	1.28E-11	0.289734	0.031443	3.13E-20	0.0583004	0.0106842	4.85E-08	7.64E-01	20
cg05635807	BLK	8	11422167	rs7834638	11420295	C	T	0.327586	-0.0165885	0.00258091	1.30E-10	0.32864	0.031959	8.39E-25	-0.0504762	0.00926116	5.03E-08	2.30E-01	20
cg12840336	BLK	8	11422730	rs4841561	11418773	T	C	0.364706	-0.0157795	0.00259272	1.16E-09	-0.511979	0.0319288	7.28E-58	0.0308206	0.00541661	1.27E-08	1.58E-01	20
cg04880278	GATA4	8	11597172	rs7838131	11596163	G	A	0.422222	-0.0192869	0.00249272	1.02E-14	-0.29154	0.0323259	1.90E-19	0.0661552	0.0112655	4.30E-09	5.43E-02	20
cg11465442	DEFB136	8	11832261	rs10088415	11830825	G	A	0.561111	0.0169862	0.0024628	5.32E-12	-0.294353	0.0318569	2.47E-20	-0.0577069	0.0104407	3.26E-08	4.38E-01	20
cg04897713	DEFB136	8	11832762	rs11998678	11830150	T	C	0.38764	-0.0188033	0.00246808	2.57E-14	0.414407	0.0305239	5.52E-42	-0.045374	0.00682935	3.05E-11	6.32E-01	20
cg24126361	SLC25A37	8	23398346	rs6987271	23399773	G	A	0.311111	-0.0150175	0.00288906	2.02E-07	-1.39816	0.0244746	0.00E+00	0.0107409	0.00207487	2.26E-07	9.07E-02	20
cg08373250	NOV	8	120438409	rs6996275	120415378	A	G	0.127778	0.0252409	0.0029673	1.80E-17	-1.52611	0.0203748	0.00E+00	-0.0165394	0.00195686	2.86E-17	9.39E-01	20
cg11691535	TSNARE1	8	143425682	rs11985182	143456488	G	A	0.388889	0.0140131	0.00260374	7.38E-08	-0.563741	0.0326667	9.85E-67	-0.0248573	0.00483807	2.78E-07	3.78E-01	20
cg24267699	ABO	9	136151359	rs674302	136146664	A	T	0.35	0.016764	0.00264071	2.18E-10	0.907902	0.0334486	3.05E-162	0.0184645	0.00298708	6.35E-10	2.44E-01	20
cg14271713	SURF6	9	136153846	rs529565	136149500	C	T	0.35	0.0163702	0.00264293	5.87E-10	-0.515857	0.0366061	4.25E-45	-0.031734	0.00559643	1.42E-08	1.21E-01	20
cg01005506	ADO	10	64565768	rs1848797	64552934	G	A	0.322222	0.018397	0.00251323	2.48E-13	-0.277818	0.0330933	4.66E-17	-0.0662197	0.0120024	3.44E-08	5.19E-01	20
cg12474798	ADO	10	64565772	rs1848797	64552934	G	A	0.322222	0.018397	0.00251323	2.48E-13	-0.265151	0.032893	7.57E-16	-0.0693832	0.0128034	5.99E-08	8.13E-01	20
cg22903908	EGR2	10	64578919	rs7078554	64595034	A	T	0.444444	0.0151146	0.00246512	8.72E-10	-0.334164	0.032975	3.91E-24	-0.0452311	0.00862216	1.56E-07	4.52E-01	20

cg00210538	JMJD1C	10	65245820	rs7923544	65182256	G	T	0.511236	0.0153366	0.00246574	4.98E-10	-0.325309	0.03268	2.41E-23	-0.0471447	0.00893766	1.33E-07	8.01E-02	20
cg03493300	CNNM2	10	104813866	rs11191543	104824387	A	G	0.0611111	0.0372898	0.00464234	9.58E-16	1.26096	0.0564871	2.21E-110	0.0295725	0.00391268	4.09E-14	2.05E-01	20
cg04367197	ARNTL	11	13300320	rs900144	13294268	C	T	0.331461	0.0138612	0.00248417	2.41E-08	-0.443435	0.031494	5.04E-45	-0.0312587	0.00602597	2.13E-07	5.82E-02	20
cg06552810	DCDC5	11	31128660	rs1407258	31059839	A	T	0.408046	0.0147597	0.00255806	7.94E-09	1.14165	0.0236141	0.00E+00	0.0129284	0.00225656	1.01E-08	2.46E-01	20
cg26647111	DCDC5	11	31128758	rs1407258	31059839	A	T	0.408046	0.0147597	0.00255806	7.94E-09	0.849054	0.0301714	3.09E-174	0.0173837	0.00307551	1.58E-08	2.45E-01	20
cg14844989	DCDC1	11	31128820	rs1407258	31059839	A	T	0.408046	0.0147597	0.00255806	7.94E-09	1.03576	0.0264776	0.00E+00	0.0142501	0.00249645	1.14E-08	2.22E-01	20
cg06492744	SIPA1	11	65406254	rs12801636	65391317	A	G	0.222222	0.0186699	0.00295095	2.51E-10	0.320145	0.0380055	3.65E-17	0.0583171	0.0115279	4.22E-07	6.87E-02	17
cg24147428	SIPA1	11	65409760	rs12801636	65391317	A	G	0.222222	0.0186699	0.00295095	2.51E-10	-0.832263	0.0361496	2.76E-117	-0.0224327	0.00367714	1.06E-09	3.21E-01	20
cg211033440	SIPA1	11	65409861	rs12801636	65391317	A	G	0.222222	0.0186699	0.00295095	2.51E-10	-0.953621	0.034479	2.23E-168	-0.0195779	0.0031744	6.94E-10	6.16E-02	20
cg24468199	SIPA1	11	65410028	rs12801636	65391317	A	G	0.222222	0.0186699	0.00295095	2.51E-10	-0.484683	0.038322	1.15E-36	-0.0385199	0.00680769	1.53E-08	1.84E-01	20
cg16535667	SIPA1	11	65410126	rs12801636	65391317	A	G	0.222222	0.0186699	0.00295095	2.51E-10	-0.48853	0.0384944	6.64E-37	-0.0382165	0.00674946	1.49E-08	2.37E-01	20
cg22806934	UBASH3B	11	122577359	rs12577260	122506129	G	C	0.129213	-0.0239244	0.00373911	1.57E-10	0.503111	0.048233	1.79E-25	-0.0475529	0.0087188	4.92E-08	8.05E-01	20
cg03907575	DIP2B	12	50898411	rs2700482	51083265	T	C	0.366667	-0.0147352	0.0025868	1.23E-08	0.646977	0.0322909	2.68E-89	-0.0227755	0.00415674	4.27E-08	5.98E-02	20
cg20014596	DIP2B	12	50898483	rs2700480	51022431	T	A	0.359551	-0.0147556	0.00258439	1.13E-08	0.578718	0.0327692	8.46E-70	-0.025497	0.00469329	5.55E-08	1.73E-01	20
cg19993006	FAM109A	12	111807180	rs7297186	111778178	C	T	0.25	0.023994	0.00288474	9.01E-17	0.281413	0.038358	2.19E-13	0.0852626	0.0154966	3.75E-08	1.21E-01	20
cg24530795	FAM109A	12	111807189	rs10849938	111800059	C	T	0.252874	0.0256745	0.00293144	1.99E-18	0.587307	0.0391145	5.85E-51	0.0437156	0.0057784	3.87E-14	6.12E-02	20
cg10833066	FAM109A	12	111807467	rs7398833	111786892	C	T	0.25	0.0256501	0.00292891	2.00E-18	1.42872	0.0249338	0.00E+00	0.0179532	0.00207383	4.84E-18	7.08E-02	20
cg26359133	SH2B3	12	111847419	rs2238154	111882485	A	C	0.233333	0.0268604	0.00302168	6.18E-19	0.505864	0.0387161	5.15E-39	0.0530981	0.00722462	1.99E-13	3.28E-01	20
cg16427983	ABCB9	12	123453858	rs655293	123528405	G	A	0.2	0.0202094	0.00302692	2.45E-11	-0.3387	0.0385628	1.59E-18	-0.0596676	0.0112258	1.07E-07	7.72E-02	20
cg08176694	PITPNM2	12	123519157	rs655293	123528405	G	A	0.2	0.0202094	0.00302692	2.45E-11	0.418417	0.0389537	6.51E-27	0.0482996	0.00851782	1.42E-08	3.27E-01	20
cg27473871	PITPNM2	12	123636279	rs1727294	123616514	A	G	0.186747	0.0204675	0.00301134	1.07E-11	0.345174	0.0380156	1.09E-19	0.0592962	0.0108976	5.29E-08	2.47E-01	20
cg16389456	PITPNM2	12	123636548	rs655293	123528405	G	A	0.2	0.0202094	0.00302692	2.45E-11	0.333467	0.038795	8.28E-18	0.0606039	0.0114937	1.34E-07	3.00E-01	20
cg10672416	C12orf65	12	123718706	rs4460848	123677810	A	G	0.197674	0.0204259	0.00286574	1.02E-12	-0.417465	0.0374833	8.25E-29	-0.0489284	0.00815003	1.93E-09	3.49E-01	20
cg00585698	CDK2AP1	12	123750864	rs7313483	123726834	C	T	0.238095	0.0208245	0.0030216	5.52E-12	-0.435354	0.0378512	1.29E-30	-0.0478335	0.00809117	3.38E-09	8.56E-01	20
cg21153102	CHAC1	15	41252147	rs2306083	41347658	A	G	0.35	-0.0151249	0.00246887	9.01E-10	0.986521	0.0263387	4.94E-307	-0.0153316	0.00253586	1.49E-09	5.50E-02	20
cg14158153	SPTBN5	15	42141147	rs1122884	42132896	T	C	0.3	0.0158881	0.0026582	2.28E-09	0.353559	0.0352425	1.10E-23	0.0449377	0.00875164	2.82E-07	2.18E-01	20
cg20552236	CSK	15	75090958	rs1378940	75083494	C	A	0.365169	-0.0263797	0.00263898	1.60E-23	-0.236309	0.0340613	3.98E-12	0.111632	0.0195862	1.20E-08	6.21E-01	20
cg14664628	CSK	15	75095509	rs3765066	75140854	G	A	0.373563	-0.0270898	0.00262782	6.48E-25	0.289663	0.0331515	2.38E-18	-0.0935217	0.0140308	2.64E-11	1.48E-01	20
cg04952827	ULK3	15	75135187	rs9210	75128501	T	C	0.30814	-0.0287332	0.00277018	3.35E-25	-0.266329	0.035218	3.96E-14	0.107886	0.0176555	9.92E-10	2.81E-01	20
cg10852096	ADAMTS7	15	79043040	rs11072793	79006442	G	A	0.233333	0.0196111	0.00289119	1.18E-11	0.729406	0.0362612	5.42E-90	0.0268864	0.00418305	1.30E-10	1.95E-01	20
cg22753661	ADAMTS7	15	79092743	rs2277547	79082431	G	A	0.25	0.0194588	0.0028233	5.50E-12	-0.726597	0.0354038	1.34E-93	-0.0267807	0.00409891	6.42E-11	8.49E-02	20
cg12645284	ADAMTS7	15	79092878	rs2277547	79082431	G	A	0.25	0.0194588	0.0028233	5.50E-12	-0.730899	0.0353986	1.02E-94	-0.0266231	0.0040723	6.25E-11	6.19E-02	20
cg03209642	FES	15	91427605	rs2521501	91437388	T	A	0.366667	-0.0265716	0.00265014	1.18E-23	0.207984	0.0347662	2.20E-09	-0.127758	0.0248683	2.79E-07	1.79E-01	11
cg06330618	FES	15	91428456	rs2521501	91437388	T	A	0.366667	-0.0265716	0.00265014	1.18E-23	0.344489	0.0342291	7.95E-24	-0.0771334	0.0108591	1.22E-12	8.28E-02	12
cg10421029	FBXL19	16	30936028	rs7200879	30947572	G	A	0.238889	-0.0178351	0.0028814	6.03E-10	-0.375222	0.0368606	2.45E-24	0.0475322	0.0089874	1.23E-07	4.70E-01	20

cg04018474	STX1B	16	31008003	rs2303223	31075175	A	G	0.372093	0.0138557	0.00254028	4.92E-08	-0.436523	0.033286	2.73E-39	-0.031741	0.0063026	4.75E-07	4.89E-01	20
cg00596184	VPS4A	16	69350052	rs3817030	69350035	C	A	0.321839	0.0149754	0.00279868	8.76E-08	-1.31437	0.0240356	0.00E+00	-0.0113936	0.00213947	1.01E-07	8.82E-01	20
cg27025247	SMG6	17	2207482	rs1885986	2203175	G	C	0.294444	0.0155117	0.0025883	2.06E-09	0.390189	0.0340316	1.97E-30	0.0397543	0.00748498	1.09E-07	3.34E-01	20
cg21745320	SRR	17	2207495	rs17834627	2198892	C	T	0.294444	0.0157033	0.00258847	1.31E-09	0.390441	0.034333	5.75E-30	0.0402194	0.00751397	8.67E-08	3.42E-01	20
cg18334121	TSR1	17	2234844	rs8081273	2222325	T	C	0.316092	0.0151008	0.00255673	3.50E-09	-0.401891	0.0330261	4.55E-34	-0.0375743	0.00707149	1.08E-07	1.23E-01	20
cg03644378	CYB5D1	17	7761459	rs17807204	7784295	G	A	0.1	-0.0288034	0.00464809	5.77E-10	0.822378	0.0585429	7.99E-45	-0.0350245	0.00617753	1.43E-08	6.25E-02	20
cg18271897	SEPT9	17	75316784	rs1436138	75316880	G	A	0.333333	0.0156504	0.00257558	1.23E-09	0.676813	0.0327852	1.11E-94	0.0231237	0.00396688	5.57E-09	1.24E-01	20
cg15661536	SEPT9	17	75317185	rs1436138	75316880	G	A	0.333333	0.0156504	0.00257558	1.23E-09	0.614424	0.0332144	2.11E-76	0.0254717	0.00441222	7.79E-09	8.88E-02	20
cg17278466	USP36	17	76798203	rs7218899	76739850	C	T	0.494444	-0.0135583	0.00246835	3.96E-08	0.503341	0.0318463	2.86E-56	-0.0269366	0.00519164	2.12E-07	8.53E-01	20
cg15465367	USP36	17	76798307	rs1057040	76799795	G	A	0.488506	-0.0136956	0.0024635	2.71E-08	0.464698	0.0315885	5.48E-49	-0.029472	0.00566721	1.99E-07	7.20E-01	20
cg23834688	USP36	17	76798392	rs7215260	76677481	A	G	0.482353	-0.0135534	0.00246402	3.79E-08	0.415357	0.0321107	2.85E-38	-0.0326307	0.00644638	4.15E-07	8.60E-01	20
cg21427119	HM13	20	30132790	rs6059899	30132626	T	G	0.132184	0.0174835	0.00340729	2.88E-07	-1.49988	0.0306448	0.00E+00	-0.0116566	0.00228416	3.34E-07	1.00E+00	20
cg03999872	STMN3	20	62272968	rs6089953	62291008	A	G	0.264368	0.0151529	0.00286246	1.20E-07	-0.774738	0.0334498	1.12E-118	-0.0195587	0.00379002	2.46E-07	9.02E-02	20
cg05172940	RTEL1-TNFR	20	62327534	rs2427533	62365866	T	C	0.235955	0.016762	0.0028558	4.38E-09	0.526313	0.0358066	6.57E-49	0.031848	0.00584266	5.01E-08	6.01E-01	20
cg18611245	ARFRP1	20	62338235	rs2738758	62349625	G	C	0.238889	0.0165999	0.00283029	4.49E-09	0.59212	0.0353978	8.25E-63	0.0280347	0.00506523	3.12E-08	1.81E-01	20
cg04078896	ZGPAT	20	62338273	rs2427533	62365866	T	C	0.235955	0.016762	0.0028558	4.38E-09	0.554181	0.035382	2.72E-55	0.0302464	0.00550313	3.88E-08	1.88E-01	20
cg04379041	ZGPAT	20	62364801	rs2738758	62349625	G	C	0.238889	0.0165999	0.00283029	4.49E-09	0.35905	0.0358015	1.14E-23	0.0462328	0.00913175	4.13E-07	3.25E-01	20
cg19841423	LIME1	20	62366755	rs2427533	62365866	T	C	0.235955	0.016762	0.0028558	4.38E-09	0.643731	0.034409	4.24E-78	0.0260388	0.00464954	2.14E-08	2.98E-01	20
cg14977069	LIME1	20	62367698	rs2427533	62365866	T	C	0.235955	0.016762	0.0028558	4.38E-09	0.432269	0.0359145	2.30E-33	0.0387768	0.00735022	1.32E-07	4.69E-01	20
cg06653796	LIME1	20	62367805	rs2427533	62365866	T	C	0.235955	0.016762	0.0028558	4.38E-09	0.535794	0.035469	1.48E-51	0.0312844	0.00571824	4.48E-08	4.79E-01	20
cg21201401	LIME1	20	62367884	rs2427533	62365866	T	C	0.235955	0.016762	0.0028558	4.38E-09	0.392512	0.0361267	1.69E-27	0.0427044	0.00826951	2.42E-07	3.79E-01	20
cg24631526	LIME1	20	62367961	rs2427533	62365866	T	C	0.235955	0.016762	0.0028558	4.38E-09	0.51322	0.0352641	5.54E-48	0.0326604	0.00599996	5.23E-08	2.60E-01	20
cg13301327	ZBTB46	20	62387416	rs6011098	62398935	C	T	0.184932	0.0167534	0.00314038	9.57E-08	-1.6196	0.0176969	0.00E+00	-0.0103441	0.00194227	1.01E-07	8.17E-02	20
cg07774293	TCEA2	20	62694326	rs6062342	62695878	C	A	0.25	-0.0171836	0.00280494	9.01E-10	-0.318603	0.035339	1.96E-19	0.0539342	0.0106441	4.04E-07	7.96E-01	18

Table e-3 Characteristics of IS cases and controls

Characteristics	Cases (n = 1,207)	Controls (n = 1,269)	<i>P</i> values
Age, year	61.0±11.87	60.8±12.05	0.7766
Male, %	53.35	54.85	1
Smokers, %	36.12	38.3	1
Drinkers, %	28.75	26.48	1
SBP, mmHg	174.3±18.67	134.4±23.90	0
DBP, mmHg	101.7±11.88	80.6±13.12	3.0×10^{-291}
BMI, kg/m ²	25.2±3.30	22.2±3.23	4.6×10^{-102}
TC, mmol/L	5.12±1.17	4.62±0.94	1.1×10^{-31}
TG, mmol/L	1.91±4.27	1.50±1.09	7.8×10^{-4}
HDL-C, mmol/L	1.30±0.44	1.38±0.33	1.3×10^{-4}
LDL-C, mmol/L	2.96±1.01	2.61±0.77	4.6×10^{-22}
FBG, mmol/L	6.81±2.80	5.05±1.06	6.4×10^{-90}

Table e-4 Characteristics of the non-IS individuals

Characteristics	Hypertensive cases (n = 381)	Controls (n = 888)	<i>P</i> values
Age, year	66.1 ± 11.87	57.1 ± 11.04	8.35 × 10 ⁻³⁴
Male, %	51.97	57.25	0.0997
Smokers, %	35.01	33.08	0.5729
Drinkers, %	28.35	25.77	0.3674
SBP, mmHg	151.72 ± 17.85	117.87 ± 9.94	2.30 × 10 ⁻²⁰⁵
DBP, mmHg	87.92 ± 9.75	72.32 ± 7.20	7.10 × 10 ⁻¹³⁸
BMI, kg/m ²	23.02 ± 3.55	21.59 ± 2.87	2.49 × 10 ⁻¹²
TC, mmol/L	4.78 ± 0.97	4.49 ± 0.90	1.97 × 10 ⁻⁶
TG, mmol/L	1.70 ± 1.18	1.35 ± 0.95	3.90 × 10 ⁻⁷
HDL-C, mmol/L	1.34 ± 0.33	1.38 ± 0.33	0.0557
LDL-C, mmol/L	2.71 ± 0.76	2.52 ± 0.75	1.01 × 10 ⁻⁴
FBG, mmol/L	5.13 ± 1.01	4.95 ± 0.85	1.61 × 10 ⁻³

Table e-5 The associations between *CASZ1* methylations and BP and hypertension

Name*	Position [#]	SBP				DBP				Hypertension (381 cases and 888 controls at baseline)			
		Beta	<i>P</i> value	Beta†	<i>P</i> value†	Beta	<i>P</i> value	Beta†	<i>P</i> value†	OR(95%CI)	<i>P</i> value	OR(95%CI) †	<i>P</i> value†
CASZ1_165	10856830	0.0803	7.89E-01	0.1686	4.08E-01	-0.0729	6.59E-01	0.0094	9.38E-01	1.00(0.99,1.01)	5.93E-01	1.00(0.99,1.01)	6.75E-01
CASZ1_163	10856832	-0.3325	2.58E-01	-0.3559	7.42E-02	-0.1021	5.28E-01	-0.0831	4.87E-01	0.99(0.98,1.00)	1.53E-01	0.99(0.99,1.00)	2.69E-02
CASZ1_157	10856838	-0.2768	3.18E-01	-0.3603	5.53E-02	-0.1723	2.59E-01	-0.2133	5.87E-02	1.00(0.99,1.00)	2.86E-01	0.99(0.99,1.00)	4.05E-02
CASZ1_150	10856845	-0.2369	5.63E-02	-0.0848	3.14E-01	-0.1049	1.25E-01	-0.0205	6.84E-01	1.00(0.99,1.00)	1.87E-01	1.00(1.00,1.00)	8.78E-01
CASZ1_116	10856879	-0.1233	5.09E-01	-0.0684	5.89E-01	-0.0238	8.17E-01	-0.0076	9.20E-01	1.00(1.00,1.01)	6.56E-01	1.00(1.00,1.01)	3.56E-01
CASZ1_98	10856897	-0.5150	5.26E-04	-0.2305	2.27E-02	-0.2140	8.97E-03	-0.0598	3.25E-01	0.99(0.99,1.00)	2.25E-02	1.00(1.00,1.00)	4.43E-01
CASZ1_94	10856901	-0.0461	7.74E-01	-0.0351	7.47E-01	-0.0823	3.52E-01	-0.0631	3.33E-01	1.00(1.00,1.01)	6.44E-01	1.00(1.00,1.00)	4.90E-01
CASZ1_80	10856915	-0.4609	7.52E-04	-0.1981	3.34E-02	-0.1926	1.06E-02	-0.0464	4.06E-01	0.99(0.99,1.00)	5.13E-03	1.00(0.99,1.00)	1.79E-01
CASZ1_74	10856921	-0.3153	1.44E-02	-0.0993	2.57E-01	-0.1413	4.64E-02	-0.0525	3.17E-01	0.99(0.99,1.00)	1.16E-02	1.00(1.00,1.00)	1.76E-01
CASZ1_72	10856923	-0.1617	3.40E-01	0.0606	5.98E-01	-0.0540	5.63E-01	0.0629	3.61E-01	1.00(0.99,1.00)	4.95E-01	1.00(1.00,1.01)	4.93E-01
CASZ1_70	10856925	-0.3254	6.00E-03	-0.0990	2.19E-01	-0.1625	1.27E-02	-0.0676	1.61E-01	1.00(0.99,1.00)	5.36E-02	1.00(1.00,1.00)	7.32E-01
CASZ1_67	10856928	-0.4463	2.26E-03	-0.1702	8.68E-02	-0.2706	7.66E-04	-0.1233	3.87E-02	1.00(0.99,1.00)	4.97E-02	1.00(1.00,1.00)	8.36E-01
CASZ1_62	10856933	-0.1618	1.73E-01	0.0412	6.10E-01	-0.0616	3.46E-01	0.0325	5.02E-01	1.00(1.00,1.00)	5.86E-01	1.00(1.00,1.00)	1.38E-01
CASZ1_58	10856937	-0.6015	6.97E-06	-0.1551	8.99E-02	-0.2522	6.30E-04	-0.0646	2.39E-01	0.99(0.99,1.00)	3.48E-04	1.00(1.00,1.00)	4.80E-01
CASZ1_51	10856944	-0.2850	2.29E-04	-0.0871	9.70E-02	-0.1480	5.13E-04	-0.0468	1.38E-01	1.00(0.99,1.00)	1.02E-02	1.00(1.00,1.00)	8.33E-01
CASZ1_35	10856960	-0.0419	6.66E-01	0.0738	2.61E-01	-0.0756	1.58E-01	-0.0020	9.60E-01	1.00(1.00,1.00)	7.27E-01	1.00(1.00,1.00)	2.54E-01
CASZ1_31	10856964	-0.1803	1.71E-01	-0.1825	4.10E-02	-0.1111	1.25E-01	-0.0853	1.11E-01	1.00(0.99,1.00)	5.23E-01	1.00(1.00,1.00)	3.37E-01
CASZ1	-	-1.1674	3.43E-06	-0.3641	3.41E-02	-0.5893	2.08E-05	-0.1825	7.68E-02	0.99(0.98,1.00)	1.61E-03	1.00(0.99,1.00)	8.16E-01

CI: Confidence interval; DBP: Diastolic blood pressure; OR: Odds ratio; SBP: Systolic blood pressure.

*: The numbers in the names represented the position of the site in the genomic fragment sequenced.

#: GRCh37.p13.

†: Adjusted for IS status, sex, age, smoking, drinking, BMI, TC and FBG.