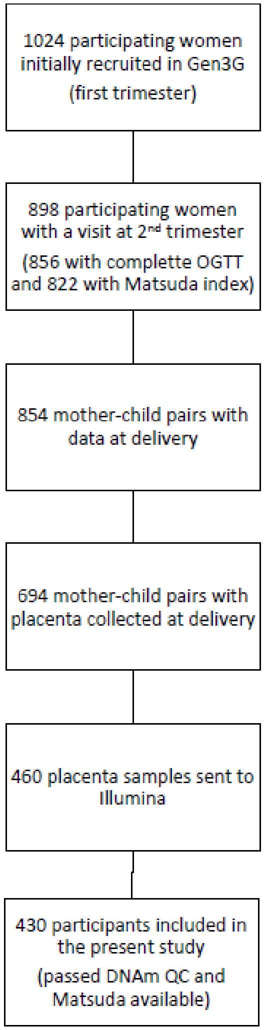
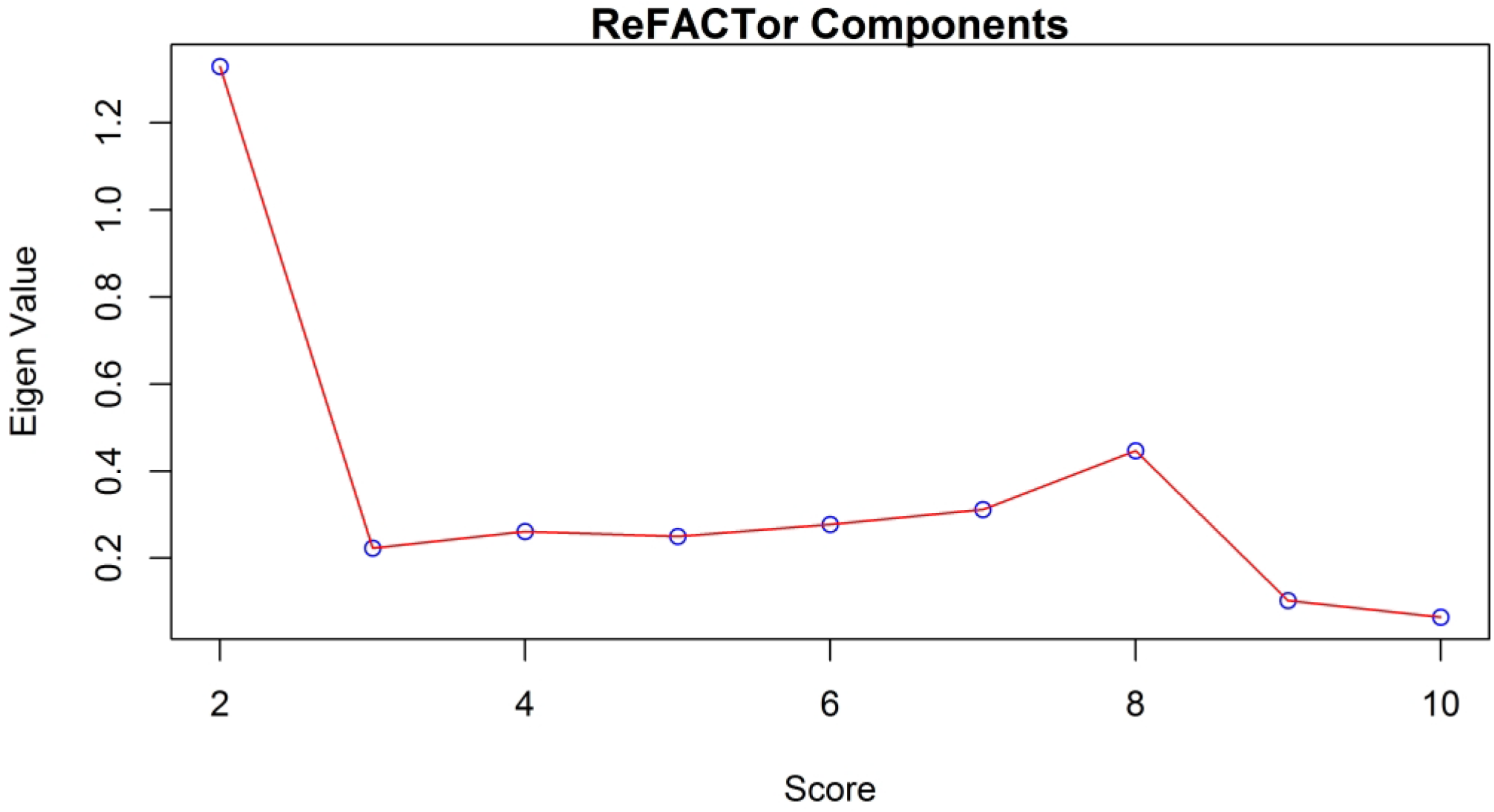
SUPPLEMENTARY DATA

Supplementary Figure 1. Participants flow chart included in current study



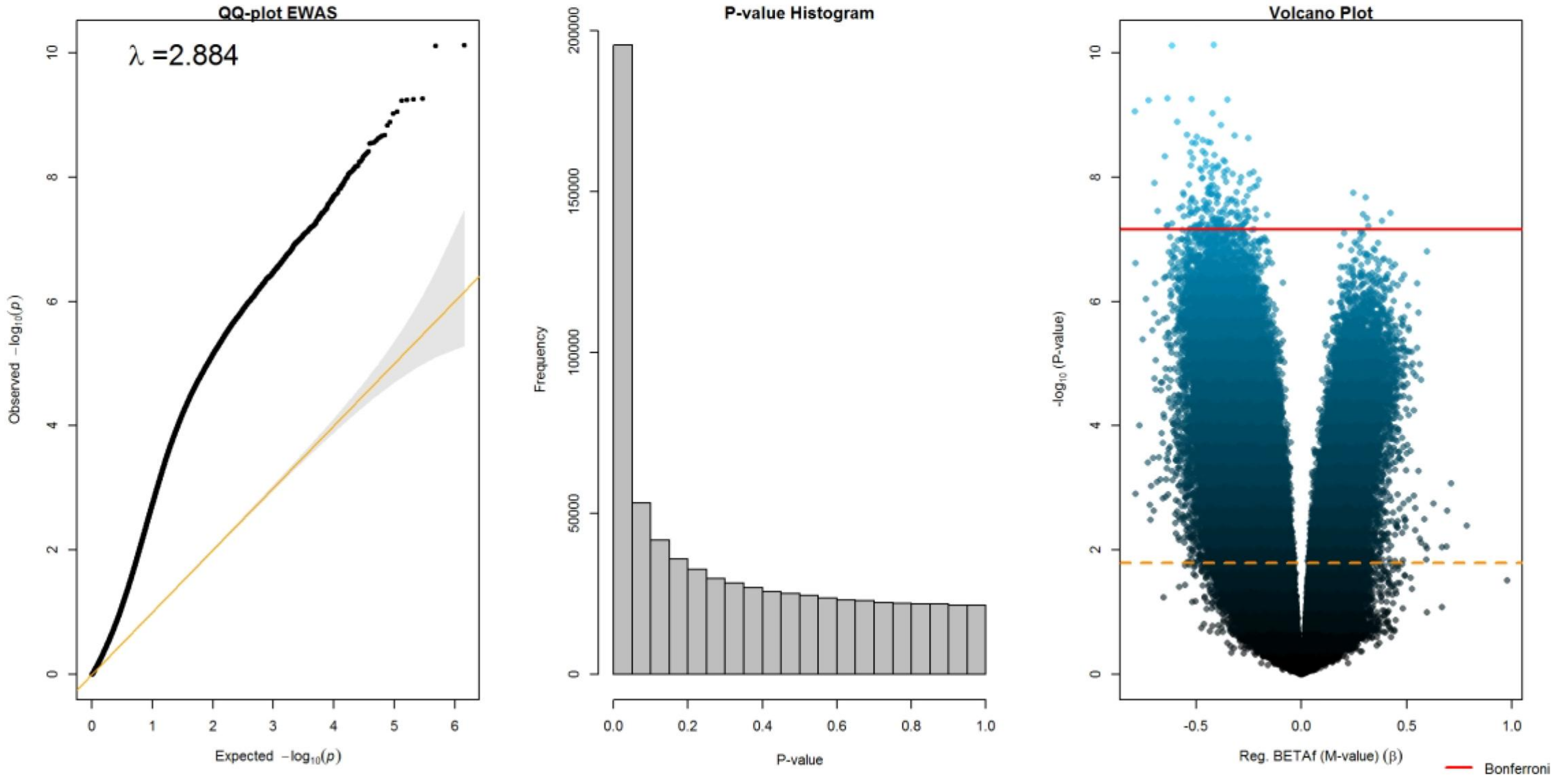
SUPPLEMENTARY DATA

Supplementary Figure 2.

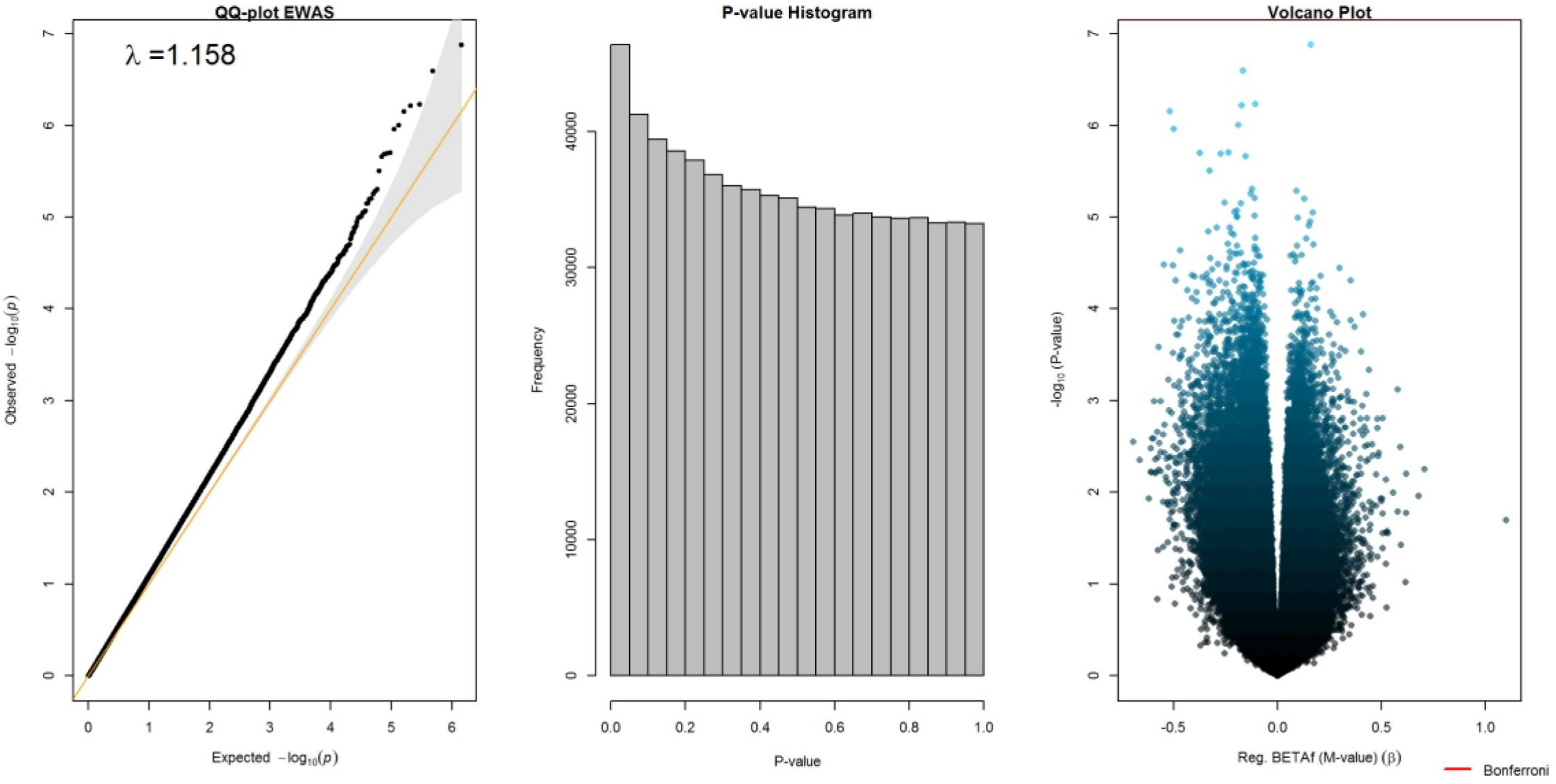


SUPPLEMENTARY DATA

Supplementary Figure 3.



SUPPLEMENTARY DATA



SUPPLEMENTARY DATA

Supplementary Table 1: Single Nucleotide Polymorphisms (SNPs) used to create genetic risk score (GRS) of insulin sensitivity

SNPs	chr position	annotated gene	initial association in Prokenpenko et al.	Association in Gen3G with Matsuda (ln)
			Beta	beta (SE)
rs1260326	2:27730940	*GCKR*	-0.067	-0.02307 (0.03824)
rs35767	12:102875569	*IGF1*	-0.080	0.01581 (0.05446)
rs459193	5:55806751	*ANKRD55/MAP3K1*	-0.053	-0.09932 (0.04122)
rs4846565	1:219722104	*LYPLAL1*	-0.044	-0.09431 (0.04130)
rs4865796	5:53272664	*ARL15*	-0.071	-0.01121 (0.04271)
rs6822892	4:157734675	*PDGFC*	-0.093	-0.006239 (0.040982)
rs7607980	2:165551201	*COBLL1*	-0.120	-0.09199 (0.05452)
rs1801282	3:12393125	*PPARG*	-0.084	-0.10657 (0.06494)

SUPPLEMENTARY DATA

Supplementary Table 2: Results from epigenome-wide analyses of maternal insulin sensitivity (Matsuda, ln-transformed) on placental DNA methylation (model adjusted for maternal age in years, gravid status [1 vs >1], smoking (yes/no in pregnancy), maternal body mass index [in kg/m2], child sex [m/f], and gestational age at birth in weeks)

						Illumina annotation	Humarray annotation			association with insulin sensitivity M-Value, Natural Log(Matsuda)			association with insulin sensitivity Beta-Value, Natural Log(Matsuda)		
CpG	chr	position (build 37)	position (cytoband)	Methylation Mean Beta-value	Relation to CpG Island	UCSC Ref Gene Name	Closest gene on the right	Closest gene on the left	Known imprinted genes in placenta*	coefficient	SE	p-value	coefficient	SE	p-value
cg00918900	1	1057335	p36.33	0.039	OpenSea		MIR200B	C1orf159		-0.522	0.084	5.55E-10	-0.011	0.002	2.70E-09
cg16140890	1	1082406	p36.33	0.116	OpenSea		MIR200B	C1orf159		-0.487	0.09	6.79E-08	-0.027	0.005	1.04E-07
cg21778193	1	1098070	p36.33	0.271	Island		MIR200B	C1orf159		-0.472	0.087	5.35E-08	-0.061	0.011	6.85E-09
cg14839558	1	1874488	p36.33	0.252	N_Shore		C1orf222	C1orf222		-0.476	0.088	5.67E-08	-0.057	0.010	2.45E-08
cg04131502	1	2845583	p36.32	0.076	N_Shore		ACTRT2	TTC34		-0.389	0.071	4.96E-08	-0.016	0.003	1.83E-07
cg11837181	1	3001002	p36.32	0.131	S_Shore	PRDM16	PRDM16	PRDM16		-0.413	0.076	5.18E-08	-0.028	0.005	1.11E-07
cg07686906	1	3353825	p36.32	0.226	S_Shelf	PRDM16	PRDM16	PRDM16		-0.351	0.057	5.75E-10	-0.040	0.006	7.12E-10
cg14494450	1	4190881	p36.32	0.106	N_Shore		AJAP1	LINC01134		-0.425	0.077	3.32E-08	-0.023	0.004	8.96E-08
cg09073467	1	6155515	p36.31	0.193	OpenSea	KCNAB2	KCNAB2	KCNAB2		-0.283	0.052	6.90E-08	-0.029	0.005	3.19E-08
cg00389386	1	6188136	p36.31	0.168	Island	CHD5	CHD5	CHD5		-0.308	0.056	4.33E-08	-0.028	0.005	1.53E-08
cg00386725	1	18617791	p36.13	0.099	OpenSea	IGSF21	IGSF21	IGSF21		-0.329	0.059	2.26E-08	-0.019	0.003	1.12E-08
cg12011250	1	30198037	p35.3	0.196	OpenSea		MATN1	PTPRU		-0.452	0.078	6.74E-09	-0.043	0.008	1.59E-08
cg26178126	1	37740931	p34.3	0.174	OpenSea		RPS29P6	RNA5SP43		-0.422	0.069	9.46E-10	-0.038	0.006	1.15E-09
cg07203271	1	53926112	p32.3	0.196	Island	DMRTB1	DMRTB1	DMRTB1		-0.394	0.072	4.68E-08	-0.040	0.007	3.20E-08
cg24064348	1	54181174	p32.3	0.238	OpenSea	GLIS1	GLIS1	GLIS1		-0.201	0.035	1.09E-08	-0.025	0.004	5.29E-09
cg08491066	1	156030669	q22	0.13	OpenSea	RAB25	RAB25	LAMTOR2		-0.318	0.059	6.63E-08	-0.022	0.004	6.84E-08
cg04847540	1	182754070	q25.3	0.055	OpenSea		NPL	RGS8		-0.437	0.079	2.59E-08	-0.011	0.002	9.29E-07
cg20659588	1	237963267	q43	0.165	OpenSea	RYR2	RYR2	RYR2		-0.433	0.075	8.42E-09	-0.036	0.006	2.75E-08
cg21307723	1	245215135	q44	0.807	OpenSea	EFCAB2	EFCAB2	RNU6-999P		0.294	0.053	3.95E-08	0.029	0.006	1.42E-07
cg07865738	2	3649447	p25.3	0.093	OpenSea	COLEC11	COLEC11	COLEC11		-0.560	0.099	1.80E-08	-0.024	0.005	1.59E-07
cg05444304	2	31442675	p23.1	0.934	OpenSea		RNA5SP90	CAPN14		0.306	0.055	2.12E-08	0.011	0.002	4.86E-08
cg04140215	2	60540175	p16.1	0.159	OpenSea		RNU1-32P	RNA5SP94		-0.432	0.073	2.82E-09	-0.035	0.006	7.64E-09
cg00460471	2	61437605	p15	0.176	OpenSea	USP34	USP34	AHSA2		-0.442	0.078	1.52E-08	-0.038	0.007	5.41E-08
cg04293688	2	75466188	p12	0.113	OpenSea		GAPDHP57	TACR1		-0.420	0.077	4.79E-08	-0.026	0.005	1.07E-07
cg02384870	2	216161208	q35	0.2	OpenSea		ATIC	ABCA12		-0.636	0.102	5.39E-10	-0.059	0.010	1.61E-09
cg16819051	2	229173235	q36.3	0.143	OpenSea		RPL7L1P10	SPHKAP	SPHKAP (maternal)	-0.382	0.071	6.38E-08	-0.027	0.005	1.08E-07
cg07728373	2	229266790	q36.3	0.087	OpenSea		RPL7L1P10	SPHKAP	SPHKAP (maternal)	-0.647	0.11	4.65E-09	-0.024	0.004	4.03E-08
cg16857113	3	1133865	p26.3	0.052	OpenSea	CNTN6	CNTN6	RN7SL120P	CNTN6 (maternal)	-0.422	0.075	1.86E-08	-0.011	0.002	6.94E-07
cg11294782	3	10487409	p25.3	0.065	OpenSea	ATP2B2	ATP2B2-IT1	MIR885		-0.293	0.051	1.21E-08	-0.011	0.002	1.94E-08
cg25721832	3	81913557	p12.2	0.085	OpenSea		RPL7AP23	GBE1		-0.351	0.061	7.75E-09	-0.016	0.003	2.75E-08
cg06751809	3	105047227	q13.11	0.562	OpenSea		ALCAM	TUBBP11		-0.726	0.117	5.89E-10	-0.114	0.018	1.30E-10
cg08389995	3	131645295	q22.1	0.085	OpenSea	CPNE4	MIR5704	CPNE4		-0.533	0.097	4.06E-08	-0.021	0.005	5.27E-06
cg08058801	3	147974120	q24	0.072	OpenSea		RPL38P1	HNRNPA1P20		-0.509	0.093	3.79E-08	-0.017	0.003	6.42E-08
cg16853336	3	149396490	q25.1	0.29	OpenSea	WWTR1	WWTR1	WWTR1-AS1		-0.244	0.042	9.01E-09	-0.033	0.006	1.23E-08
cg18861231	3	152057943	q25.1	0.079	OpenSea	MBNL1	TMEM14E	TMEM14E		-0.445	0.081	3.57E-08	-0.017	0.003	2.95E-07
cg00188627	3	159557779	q25.33	0.915	OpenSea	SCHIP1	SCHIP1	SCHIP1		0.384	0.07	5.01E-08	0.016	0.003	1.25E-06
cg25285919	3	188312215	q28	0.088	OpenSea	LPP	MIR28	LPP-AS1		-0.395	0.073	6.49E-08	-0.019	0.004	1.99E-07
cg20018106	4	21768009	p15.2	0.391	OpenSea	KCNIP4	KCNIP4	KCNIP4	KCNIP4 (maternal)	-0.526	0.097	6.74E-08	-0.083	0.015	1.14E-08
cg17756860	4	110510374	q25	0.102	OpenSea	CCDC109B	CCDC109B	CCDC109B		-0.430	0.076	1.39E-08	-0.022	0.004	3.84E-07
cg18650968	4	176340837	q34.2	0.049	OpenSea		TSEN2P1	ADAM29		-0.444	0.075	2.74E-09	-0.011	0.002	5.42E-07
cg02287371	5	1246274	p15.33	0.057	Island	SLC6A18	SLC6A18	SLC6A18		-0.497	0.09	3.31E-08	-0.016	0.003	1.50E-07
cg25314607	5	2148308	p15.33	0.096	OpenSea		IRX2	IRX4		-0.418	0.074	1.34E-08	-0.021	0.004	2.29E-08
cg14757962	5	2176287	p15.33	0.088	N_Shelf		IRX2	IRX4		-0.450	0.083	6.71E-08	-0.021	0.004	4.42E-08
cg13480617	5	35230725	p13.2	0.026	OpenSea	PRLR	PRLR	PRLR		-0.247	0.044	1.60E-08	-0.004	0.001	2.17E-07
cg23561197	5	125852064	q23.2	0.084	OpenSea		ALDH7A1	GRAMD3		-0.388	0.07	3.66E-08	-0.017	0.003	1.80E-08
cg26849382	5	140901022	q31.3	0.929	OpenSea	DIAPH1	DIAPH1	DIAPH1		0.317	0.059	6.15E-08	0.010	0.002	2.61E-07
cg17587481	5	152603672	q33.1	0.158	OpenSea		GRIA1	NMUR2		-0.557	0.102	4.23E-08	-0.043	0.008	1.68E-07
cg18682781	5	176277687	q35.2	0.15	OpenSea	UNC5A	HK3	UNC5A		-0.469	0.08	3.82E-09	-0.036	0.006	9.41E-09
cg06077821	5	180048893	q35.3	0.168	Island	FLT4	FLT4	FLT4		-0.416	0.064	7.54E-11	-0.036	0.006	1.32E-10
cg00078259	6	2656232	p25.2	0.128	OpenSea		MYLK4	C6orf195		-0.451	0.083	5.89E-08	-0.028	0.006	4.78E-07
cg14886500	6	23447204	p22.3	0.066	OpenSea		SPTLC1P2	RNU6-1060P		-0.504	0.09	2.54E-08	-0.015	0.003	3.24E-07
cg27652925	6	31740951	p21.33	0.47	OpenSea	C6orf27	VWA7	VWA7		-0.225	0.042	6.85E-08	-0.039	0.007	7.28E-08
cg01530082	6	32784327	p21.32	0.178	OpenSea	HLA-DOB	HLA-DOB	HLA-DOB		-0.447	0.081	2.93E-08	-0.040	0.007	2.79E-08
cg00045690	6	32825897	p21.32	0.197	S_Shelf	PSMB9	PSMB9	PSMB9		-0.558	0.099	1.93E-08	-0.049	0.010	2.08E-07
cg01948226	6	32829208	p21.32	0.098	OpenSea		PPP1R2P1	PSMB9		-0.455	0.077	4.27E-09	-0.023	0.004	2.58E-09
cg12954267	6	33093109	p21.32	0.13	OpenSea	HLA-DPB2	HLA-DPA3	HLA-DPB2		-0.467	0.078	2.56E-09	-0.029	0.005	1.10E-08
cg17226458	6	33780022	p21.31	0.149	OpenSea		LINC01016	MLN		-0.307	0.055	2.79E-08	-0.024	0.005	5.73E-08
cg17538538	6	106825021	q21	0.921	OpenSea		RNA5SP211	ATG5		0.311	0.057	4.64E-08	0.013	0.003	1.44E-07
cg12673377	7	1388271	p22.3	0.127	OpenSea		MICALL2	UNCX		-0.363	0.067	6.60E-08	-0.025	0.005	8.50E-08

cg26037026	7	1641922	p22.3	0.26	Island		TFAMP1	PSMG3-AS1		-0.349	0.065	6.71E-08	-0.044	0.008	1.80E-07
cg26225794	7	27717723	p15.2	0.05	OpenSea		TAX1BP1	HIBADH		-0.335	0.061	3.70E-08	-0.009	0.002	8.68E-07
cg11138231	7	99475824	q22.1	0.33	OpenSea	OR2AE1	TRIM4	OR2AE1		-0.564	0.102	3.01E-08	-0.077	0.014	4.91E-08
cg08582801	7	99588335	q22.1	0.117	OpenSea		ZKSCAN1	AZGP1P1		-0.255	0.046	3.48E-08	-0.018	0.003	1.60E-07
cg25903144	7	131609806	q32.3	0.097	OpenSea	LOC1019287	PLXNA4	PODXL	PODXL (maternal)	-0.520	0.093	2.27E-08	-0.023	0.004	1.81E-07
cg06981471	7	142982076	q34	0.116	N_Shelf	TMEM139	TMEM139	TMEM139		-0.304	0.055	3.73E-08	-0.018	0.003	2.05E-07
cg18616558	7	158798592	q36.3	0.163	Island		LINC00689	WDR60		-0.697	0.122	1.25E-08	-0.051	0.009	6.11E-08
cg24475484	8	1625395	p23.3	0.061	OpenSea	DLGAP2	DLGAP2	DLGAP2	DLGAP2 (maternal)	-0.414	0.072	7.35E-09	-0.013	0.002	6.68E-09
cg16513326	8	10877312	p23.1	0.143	S_Shelf	XKR6	MIR598	XKR6		-0.385	0.071	5.23E-08	-0.028	0.005	1.66E-07
cg15952840	8	11451312	p23.1	0.038	OpenSea		GATA4	LINC00208		-0.409	0.075	5.32E-08	-0.008	0.002	7.70E-07
cg14204490	8	33330967	p12	0.032	S_Shore	FUT10	TTI2	FUT10		-0.217	0.039	3.32E-08	-0.004	0.001	3.03E-08
cg05202700	8	38258250	p11.23	0.29	OpenSea	LETM2	LETM2	LETM2		-0.446	0.083	6.94E-08	-0.058	0.011	3.43E-08
cg24848724	8	142578640	q24.3	0.208	OpenSea		MIR4472-1	MROH5		-0.580	0.105	3.19E-08	-0.055	0.011	2.01E-07
cg03710412	8	142938779	q24.3	0.149	OpenSea		MIR4472-1	MROH5		-0.494	0.09	3.38E-08	-0.037	0.007	5.36E-08
cg09851596	8	143545214	q24.3	0.213	N_Shore	BAI1	BAI1	BAI1		-0.279	0.051	4.05E-08	-0.031	0.006	2.50E-08
cg04535454	8	144035192	q24.3	0.186	OpenSea		CDC42P3	CYP11B2		-0.345	0.064	5.61E-08	-0.032	0.006	4.06E-08
cg13022891	9	5817706	p24.1	0.168	OpenSea	ERMP1	ERMP1	ERMP1		-0.304	0.055	4.21E-08	-0.027	0.005	9.05E-08
cg05775586	9	28889354	p21.1	0.177	OpenSea	MIR873	RBMXP2	MIR873		-0.502	0.085	2.84E-09	-0.045	0.008	3.35E-09
cg05851077	9	29802712	p21.1	0.223	OpenSea		RBMXP2	MIR873		-0.790	0.129	8.76E-10	-0.075	0.013	1.29E-08
cg03275961	9	90386329	q21.33	0.112	OpenSea	CTSL3P	CTSL3P	CTSL		-0.353	0.063	2.72E-08	-0.022	0.004	4.20E-08
cg06830529	9	124960107	q33.2	0.19	OpenSea	MORN5	MORN5	MORN5		-0.363	0.062	5.64E-09	-0.035	0.006	1.04E-08
cg05389237	9	125314173	q33.2	0.134	OpenSea	OR1N2	OR1N2	OR1N1		-0.541	0.09	2.10E-09	-0.034	0.006	4.19E-09
cg03510150	9	130690744	q34.11	0.077	S_Shore	PIP5KL1	PIP5KL1	PIP5KL1		-0.225	0.04	1.43E-08	-0.011	0.002	3.89E-08
cg21927431	9	134678366	q34.13	0.147	OpenSea		MED27	EIF4A1P3		-0.358	0.063	1.20E-08	-0.027	0.005	5.05E-08
cg13449257	9	137355128	q34.2	0.301	N_Shore		COL5A1	RXRA		-0.378	0.069	4.81E-08	-0.052	0.009	1.73E-08
cg17224410	9	137852661	q34.3	0.171	OpenSea		OLFM1	FCN1		-0.404	0.074	4.91E-08	-0.035	0.006	4.27E-08
cg13463516	9	138632121	q34.3	0.231	S_Shelf	KCNT1	KCNT1	KCNT1		-0.368	0.064	8.37E-09	-0.043	0.008	1.35E-08
cg12760575	9	139158654	q34.3	0.528	N_Shore		GPSM1	QSOX2		-0.306	0.054	1.75E-08	-0.052	0.009	1.42E-08
cg08099672	9	139944162	q34.3	0.092	S_Shore	ENTPD2	ENTPD2	ENTPD2		-0.396	0.071	2.00E-08	-0.021	0.004	2.72E-08
cg14440140	9	140177567	q34.3	0.078	S_Shore		NRARP	TOR4A		-0.375	0.069	4.79E-08	-0.015	0.003	5.09E-08
cg14361947	9	140780551	q34.3	0.178	S_Shelf	CACNA1B	CACNA1B	CACNA1B		-0.218	0.04	4.68E-08	-0.021	0.004	9.75E-08
cg08511578	10	1403938	p15.3	0.133	N_Shore	ADARB2	ADARB2-AS1	ADARB2		-0.507	0.094	6.00E-08	-0.033	0.006	8.32E-08
cg20112984	10	1447183	p15.3	0.087	OpenSea	ADARB2	ADARB2-AS1	ADARB2		-0.469	0.082	1.02E-08	-0.020	0.004	3.71E-08
cg02831474	10	1783879	p15.3	0.065	S_Shelf		LINC00700	ADARB2		-0.613	0.094	7.64E-11	-0.019	0.003	3.86E-09
cg12697796	10	49954016	q11.23	0.157	OpenSea	WDFY4	WDFY4	WDFY4		-0.311	0.058	6.23E-08	-0.027	0.005	4.85E-08
cg08149223	10	50507130	q11.23	0.111	OpenSea	C10orf71	C10orf71	C10orf71-AS1		-0.285	0.05	1.01E-08	-0.018	0.003	2.41E-08
cg18233010	10	114911413	q25.3	0.92	OpenSea	TCF7L2	TCF7L2	TCF7L2		0.246	0.044	1.78E-08	0.012	0.002	3.32E-07
cg23521973	10	125117429	q26.13	0.089	OpenSea		GPR26	BUB3		-0.432	0.077	1.90E-08	-0.021	0.004	4.09E-08
cg00403246	10	134794753	q26.3	0.18	S_Shelf		GPR123	LINC01168		-0.248	0.045	4.40E-08	-0.024	0.005	1.05E-07
cg16608656	11	1082797	p15.5	0.121	N_Shore	MUC2	MUC2	MUC2		-0.458	0.083	3.07E-08	-0.028	0.005	1.04E-07
cg03568769	11	1800837	p15.5	0.108	OpenSea		RPL36AP39	CTSD		-0.400	0.071	1.51E-08	-0.023	0.004	2.34E-08
cg17985533	11	2019116	p15.5	0.136	N_Shore	H19;MIR675	H19	H19	H19 (paternal)	-0.265	0.048	3.44E-08	-0.020	0.004	1.01E-07
cg09701145	11	2019436	p15.5	0.226	N_Shore	MIR675;H19	H19	H19	H19 (paternal)	-0.367	0.064	9.76E-09	-0.042	0.007	3.79E-09
cg24073146	11	2543204	p15.5	0.177	OpenSea	KCNQ1	KCNQ1	KCNQ1	KCNQ1 (maternal)	-0.291	0.054	6.07E-08	-0.027	0.005	4.92E-08
cg00875983	11	3240213	p15.4	0.349	S_Shore	MRGPRG	MRGPRG-AS1	MRGPRG		-0.310	0.056	2.43E-08	-0.047	0.008	2.13E-08
cg15575356	11	47616757	p11.2	0.188	S_Shore	C1QTNF4	MTCH2	C1QTNF4		-0.274	0.049	2.54E-08	-0.027	0.005	6.17E-08
cg12161743	11	76750531	q13.5	0.138	N_Shore	B3GNT6	B3GNT6	B3GNT6		-0.412	0.076	6.35E-08	-0.031	0.006	7.25E-08
cg01124546	11	117515332	q23.3	0.243	OpenSea	DSCAML1	FXYD2	DSCAML1	DSCAML1 (maternal)	-0.284	0.053	6.13E-08	-0.035	0.007	7.59E-08
cg13625403	11	120008510	q23.3	0.249	Island	TRIM29	TRIM29	TRIM29		-0.511	0.095	6.66E-08	-0.059	0.011	1.97E-07
cg23519631	12	72690355	q21.1	0.185	OpenSea	TRHDE	TRHDE	TRHDE-AS1		-0.378	0.07	5.68E-08	-0.036	0.007	2.03E-07
cg23536293	12	99524459	q23.1	0.113	OpenSea	ANKS1B	ANKS1B	RNA5SP366		-0.614	0.113	5.63E-08	-0.033	0.007	2.71E-06
cg08737919	12	108840669	q23.3	0.073	OpenSea		FICD	CMKLR1		-0.333	0.06	2.41E-08	-0.012	0.002	8.65E-08
cg13116906	12	119552989	q24.23	0.055	OpenSea	SRRM4	SRRM4	SRRM4		-0.412	0.07	4.37E-09	-0.010	0.002	5.23E-08
cg06343669	12	132690782	q24.33	0.126	S_Shore	GALNT9	GALNT9	GALNT9		-0.472	0.082	1.05E-08	-0.029	0.005	5.05E-08
cg04907218	12	132826672	q24.33	0.173	N_Shore	GALNT9	GALNT9	GALNT9		-0.427	0.076	1.88E-08	-0.039	0.007	5.20E-09
cg02688867	12	133019854	q24.33	0.39	Island		MUC8	GALNT9		-0.380	0.07	6.06E-08	-0.060	0.011	9.19E-08
cg18617770	12	133035939	q24.33	0.229	OpenSea		MUC8	GALNT9		-0.329	0.06	3.73E-08	-0.038	0.007	6.02E-08
cg07435932	13	19648633	q12.11	0.095	OpenSea		RNA5SP24	PHF2P2		-0.532	0.096	3.12E-08	-0.024	0.004	6.21E-08
cg18042910	13	19662609	q12.11	0.71	OpenSea		RNA5SP24	PHF2P2		-0.462	0.083	2.37E-08	-0.062	0.011	2.44E-08
cg23359229	13	29976597	q12.3	0.049	OpenSea	MTUS2	MTUS2-AS1	GAPDHP69		-0.437	0.081	5.87E-08	-0.011	0.002	1.20E-06
cg06066032	13	48369175	q14.2	0.156	OpenSea		LINC00444	RPL27AP8		-0.528	0.09	4.05E-09	-0.039	0.007	2.23E-08
cg07080246	13	63306618	q21.31	0.347	OpenSea	LINC00448	LINC00376	LINC00448		-0.636	0.117	6.04E-08	-0.086	0.016	7.21E-08
cg13827123	13	93971495	q31.3	0.164	OpenSea	GPC6	HNRNPA1P29	GPC6	GPC6 (maternal)	-0.534	0.094	1.29E-08	-0.041	0.007	1.87E-08
cg24857040	13	113565214	q34	0.128	OpenSea		MCF2L	MCF2L	MCF2L (paternal)	-0.412	0.076	6.66E-08	-0.028	0.005	1.00E-07

cg11586089	14	66644923	q23.3	0.149	OpenSea		LINC00238	YBX1P1		-0.423	0.073	6.64E-09	-0.033	0.006	9.51E-09
cg13257690	14	101908752	q32.31	0.236	N_Shore		DIO3OS	LINC00524		-0.277	0.051	5.75E-08	-0.034	0.006	3.80E-08
cg11416433	15	25429261	q11.2	0.182	OpenSea	SNORD115-8	SNORD115-8	SNORD115-6		-0.316	0.053	2.15E-09	-0.031	0.005	1.26E-09
cg17905524	15	28305412	q13.1	0.104	OpenSea	OCA2	OCA2	OCA2	OCA2 (maternal)	-0.398	0.069	6.98E-09	-0.021	0.004	2.75E-08
cg05347757	15	51121020	q21.2	0.106	OpenSea		AP4E1	SPPL2A		-0.425	0.078	4.30E-08	-0.021	0.004	5.32E-07
cg25380707	15	86660946	q25.3	0.089	OpenSea	LINC01584	RNA5SP400	MIR548AP		-0.519	0.087	2.78E-09	-0.022	0.004	7.83E-09
cg01898225	15	99975141	q26.3	0.118	OpenSea		MEF2A	LRRC28		-0.346	0.062	2.30E-08	-0.023	0.004	9.45E-09
cg08792976	16	760528	p13.3	0.118	S_Shelf		METRN	FBXL16		-0.436	0.077	1.51E-08	-0.027	0.005	3.98E-08
cg21396983	16	1275423	p13.3	0.146	OpenSea	TPSG1	TPSB2	TPSG1		-0.481	0.083	7.39E-09	-0.035	0.006	7.43E-09
cg16444062	16	2770298	p13.3	0.144	Island	PRSS27	PRSS27	PRSS27		-0.529	0.098	6.81E-08	-0.038	0.007	9.03E-08
cg10964639	16	24043296	p12.2	0.141	OpenSea	PRKCB	PRKCB	PRKCB		-0.404	0.075	6.26E-08	-0.028	0.005	3.62E-08
cg08474716	16	27079640	p12.1	0.141	OpenSea	C16orf82	C16orf82	C16orf82		-0.523	0.09	6.57E-09	-0.035	0.006	3.11E-08
cg08239663	16	52688569	q12.2	0.092	OpenSea		CHD9	CASC16		-0.521	0.095	3.74E-08	-0.023	0.005	3.30E-07
cg00781180	16	73984002	q22.3	0.07	OpenSea		PSMD7	RPSAP56		-0.441	0.078	1.73E-08	-0.016	0.003	1.41E-07
cg01615861	16	85513978	q24.1	0.382	OpenSea		GSE1	MIR5093		-0.161	0.029	4.03E-08	-0.026	0.005	2.60E-08
cg06429120	16	86309214	q24.1	0.422	OpenSea	LINC01081	LINC01081	LINC01081		-0.682	0.124	3.51E-08	-0.103	0.019	4.50E-08
cg13254480	16	86513248	q24.1	0.099	OpenSea	FENDRR	FENDRR	FENDRR		-0.639	0.118	6.09E-08	-0.028	0.006	2.57E-07
cg08204714	16	87726461	q24.2	0.266	S_Shelf	JPH3	KLHDC4	JPH3		-0.265	0.049	5.32E-08	-0.034	0.006	7.84E-08
cg09640571	16	88388040	q24.2	0.225	OpenSea		ZNF469	BANP		-0.254	0.046	4.33E-08	-0.029	0.005	8.94E-08
cg01095004	16	88454883	q24.2	0.103	S_Shore		ZNF469	BANP		-0.518	0.093	2.18E-08	-0.028	0.005	6.55E-08
cg03699074	16	88849875	q24.3	0.891	N_Shore	FAM38A	PIEZO1	PIEZO1		0.422	0.077	3.74E-08	0.022	0.004	2.62E-07
cg08372350	16	88943191	q24.3	0.282	N_Shore	CBFA2T3	CBFA2T3	CBFA2T3		-0.452	0.078	5.69E-09	-0.059	0.010	1.65E-09
cg10877514	17	292539	p13.3	0.097	S_Shore	FAM101B	FAM101B	FAM101B		-0.474	0.082	7.87E-09	-0.022	0.004	3.02E-08
cg20612875	17	1094308	p13.3	0.319	OpenSea		ABR	ABR		-0.269	0.049	5.27E-08	-0.040	0.007	9.94E-08
cg16340422	17	17110120	p11.2	0.073	Island	PLD6	FLCN	PLD6		-0.394	0.068	6.58E-09	-0.015	0.003	3.23E-07
cg05790369	17	33202007	q12	0.185	OpenSea		CCT6B	TMEM132E		-0.443	0.079	1.83E-08	-0.042	0.008	5.24E-08
cg00903007	17	34068171	q12	0.271	Island	RASL10B	RASL10B	RASL10B		-0.252	0.042	2.34E-09	-0.033	0.005	1.25E-09
cg08357744	17	37559321	q12	0.082	S_Shore	FBXL20	MED1	FBXL20		-0.528	0.095	2.48E-08	-0.019	0.004	1.40E-06
cg27410679	17	43866278	q21.31	0.116	S_Shelf	CRHR1	CRHR1	CRHR1		-0.479	0.088	5.91E-08	-0.028	0.005	7.82E-08
cg14759277	17	48674158	q21.33	0.255	OpenSea	CACNA1G	CACNA1G	CACNA1G		-0.342	0.063	6.40E-08	-0.043	0.008	1.17E-07
cg18450810	17	51111066	q22	0.376	OpenSea		RPS2P48	C17orf112		-0.454	0.082	3.34E-08	-0.073	0.013	6.30E-08
cg10883064	17	60757346	q23.2	0.152	Island	MRC2	RNU6-446P	MRC2		-0.432	0.076	1.54E-08	-0.035	0.006	2.39E-08
cg02110836	17	71953083	q25.1	0.221	S_Shelf		RPL38	LINC00469		-0.226	0.039	8.26E-09	-0.026	0.004	3.85E-09
cg21347874	17	77122733	q25.3	0.06	OpenSea	HRNBP3	RBFOX3	RBFOX3		-0.471	0.086	4.51E-08	-0.015	0.003	6.04E-07
cg15867652	17	79011277	q25.3	0.081	S_Shore	BAIAP2	BAIAP2	BAIAP2		-0.502	0.093	6.32E-08	-0.018	0.004	3.23E-06
cg11086223	18	11487579	p11.21	0.197	OpenSea	LINC01255	NPIPB1P	PIEZO2		-0.353	0.064	4.12E-08	-0.036	0.007	7.13E-08
cg18216439	18	35132882	q12.2	0.088	OpenSea	CELF4	CELF4	CELF4		-0.397	0.073	5.80E-08	-0.018	0.004	2.55E-07
cg27332583	18	35150602	q12.2	0.145	S_Shelf		MIR4318	CELF4		-0.294	0.054	4.72E-08	-0.023	0.004	4.77E-08
cg12658750	18	75499382	q23	0.08	OpenSea		RNA5SP461	BDP1P		-0.327	0.057	8.97E-09	-0.015	0.003	1.43E-08
cg06495184	19	406256	p13.3	0.228	Island	C2CD4C	C2CD4C	C2CD4C		-0.383	0.063	1.46E-09	-0.044	0.007	5.12E-09
cg26238771	19	592158	p13.3	0.131	S_Shore	HCN2	HCN2	HCN2		-0.382	0.071	6.23E-08	-0.026	0.005	2.83E-07
cg20623853	19	1734365	p13.3	0.092	Island		ONECUT3	TCF3		-0.401	0.074	5.80E-08	-0.020	0.004	3.17E-07
cg18108190	19	2727822	p13.3	0.1	N_Shelf		SLC39A3	DIRAS1		-0.406	0.074	4.56E-08	-0.021	0.004	7.34E-08
cg12193237	19	3907913	p13.3	0.251	Island	ATCAY	RN7SL202P	ATCAY		-0.393	0.07	1.98E-08	-0.047	0.009	4.04E-08
cg11855710	19	29768180	q12	0.063	OpenSea		VSTM2B	RN7SL340P		-0.402	0.072	2.25E-08	-0.013	0.003	2.16E-07
cg24738497	19	36005395	q13.12	0.055	OpenSea	DMKN	SBSN	DMKN		-0.371	0.064	5.35E-09	-0.012	0.002	4.34E-09
cg09181711	19	51327196	q13.33	0.126	N_Shelf	KLK1	KLK15	KLK1		-0.497	0.083	2.23E-09	-0.031	0.006	2.55E-08
cg18184975	20	3644192	p13	0.093	S_Shelf	GFRA4	ADAM33	GFRA4		-0.387	0.072	6.33E-08	-0.020	0.004	2.01E-07
cg11177743	20	21545361	p11.22	0.133	OpenSea		PAX1	NKX2-2		-0.376	0.068	3.66E-08	-0.026	0.005	1.60E-07
cg01216882	20	31804277	q11.21	0.205	OpenSea	C20orf71	BPIFA3	BPIFA4P		-0.407	0.072	1.82E-08	-0.041	0.007	7.15E-09
cg11765907	20	43103949	q13.12	0.182	N_Shore	TTPAL	TTPAL	RPL37AP1		-0.258	0.046	2.04E-08	-0.025	0.005	3.97E-08
cg01864178	20	44662890	q13.12	0.31	S_Shore	SLC12A5	SLC12A5	SLC12A5		-0.450	0.081	2.70E-08	-0.061	0.012	1.37E-07
cg22509138	20	44809026	q13.12	0.123	S_Shelf	CDH22	CDH22	CDH22		-0.468	0.085	3.21E-08	-0.027	0.005	1.16E-07
cg09319487	20	56771178	q13.32	0.196	OpenSea		ANKRD60	C20orf85		-0.399	0.072	2.63E-08	-0.040	0.007	5.35E-08
cg09063835	20	58181392	q13.32	0.143	S_Shore	PHACTR3	PHACTR3	PHACTR3		-0.490	0.09	5.79E-08	-0.034	0.007	2.18E-07
cg05808230	20	61726456	q13.33	0.178	OpenSea		HAR1B	LINC01056	LINC01056 (paternal)	-0.426	0.074	1.02E-08	-0.038	0.007	6.16E-09
cg01618245	20	61990279	q13.33	0.1	N_Shore	CHRNA4	CHRNA4	CHRNA4		-0.523	0.095	3.66E-08	-0.025	0.005	2.38E-07
cg24600306	20	61990671	q13.33	0.162	N_Shore	CHRNA4	CHRNA4	CHRNA4		-0.277	0.051	5.78E-08	-0.024	0.004	5.37E-08
cg27625886	20	62060443	q13.33	0.129	S_Shore	KCNQ2	KCNQ2	KCNQ2		-0.514	0.088	4.93E-09	-0.033	0.006	4.33E-08
cg19450046	21	45712938	q22.3	0.304	N_Shore	AIRE	AIRE	AIRE		-0.366	0.066	3.27E-08	-0.051	0.009	5.78E-08
cg00046877	22	19702664	q11.21	0.182	S_Shore	SEPT5	SEPT5	SEPT5		-0.211	0.037	1.39E-08	-0.021	0.004	2.47E-08
cg23016281	22	27616620	q12.1	0.102	OpenSea		MN1	RNU6-1066P		-0.588	0.097	1.28E-09	-0.031	0.006	6.80E-07
cg00373987	22	37868968	q13.1	0.253	OpenSea	MFNG	MFNG	MFNG		-0.423	0.077	4.96E-08	-0.049	0.009	1.69E-07
cg13377560	22	43860820	q13.2	0.146	OpenSea	MPPED1	MPPED1	MPPED1		-0.367	0.068	6.08E-08	-0.027	0.005	1.87E-07
cg11821795	22	47611604	q13.31	0.064	S_Shelf		LINC00898	TBC1D22A		-0.437	0.081	6.78E-08	-0.013	0.003	3.88E-07

*ref: Sanchez---Delgado M, Court F, Vidal E, et al. Human Oocyte---Derived Methylation Differences Persist in the Placenta Revealing Widespread Transient Imprinting. *PLoS genetics.* 2016;12(11):e1006427

Supplementary Table 3. ReFACtor PCs and associations with Mastuda index and co-variables

	Pval_PC1	Pval_PC2	Pval_PC3	Pval_PC4	Pval_PC5	Pval_PC6	Pval_PC7	Pval_PC8	Pval_PC9	Pval_PC10
Matsuda index	<0.0001	0.011	0.495	0.123	0.021	0.068	0.603	0.822	0.505	0.932
Maternal age	0.202	0.080	0.715	0.642	0.726	0.034	0.225	0.614	0.432	0.163
Maternal BMI (V1)	0.314	0.700	0.407	0.570	0.756	0.433	0.801	0.367	0.971	0.193
Gravid status	0.635	0.338	0.289	0.351	0.598	0.212	0.146	0.350	0.299	0.307
Maternal Smoking	0.539	0.828	0.007	0.342	0.459	0.664	0.227	0.148	0.109	0.257
Gestational age at birth	0.289	0.736	<0.0001	0.344	0.090	0.585	0.003	0.180	0.744	0.694
Child sex	0.834	0.578	0.469	0.073	0.398	0.140	0.580	0.883	0.441	0.007

P-values from correlations if continuous variables, and from Kruskal-Wallis if categorical variables

SUPPLEMENTARY DATA

Supplementary Table 4. Results from Mendelian Randomization analyses, building genetic instrumental variables (GRS or single SNP) for DNA methylation at 188 CpGs identified in Model 1 using cis-- - SNPs within 500kb around each CpG site

SUPPLEMENTARY DATA

			GRS information on association with CpG and elastic net statistics (N = 418)									linear regression ln(matsuda) ~ GRS (N = 401)					TSLS results (N = 401)				linear regression ln(matsuda) ~ CpG (N = 401)		
CPG	chr	pos	Estimate	Std.Error	P.Value	r.square	Fstat	N of SNPs within ±500kb	N of SNPs MAF<0.05	N SNPs without duplicate	N of SNPs in GRS	estimate	SE	P_value	Rsquare	P_value adj for multiple testing	estimate	SE	P_value	P_value adj for multiple testing	estimate	SE	P_value
cg12658750	18	75499382	0.169	0.028	3.37E-09	0.081	36.5	16935	3291	1811	5	-0.079	0.023	0.0008	0.028	0.03	-0.448	0.142	0.0017	0.046	-0.150	0.039	1.45E-04
cg24475484	8	1625395	0.189	0.025	2.81E-13	0.120	57.0	25101	4134	2769	10	-0.046	0.014	0.0009	0.027	0.03	-0.242	0.074	0.0012	0.046	-0.103	0.025	5.09E-05
cg01618245	20	61990279	0.113	0.012	3.20E-20	0.185	94.3	18168	2970	1608	34	-0.022	0.007	0.0010	0.027	0.03	-0.195	0.059	0.0011	0.046	-0.106	0.025	3.31E-05
cg08099672	9	139944162	0.095	0.013	2.76E-12	0.111	51.9	17133	1692	1077	13	-0.034	0.010	0.0012	0.026	0.03	-0.342	0.107	0.0015	0.046	-0.156	0.036	1.97E-05
cg12673377	7	1388271	0.062	0.005	2.37E-27	0.246	135.8	20418	2694	1672	51	-0.015	0.004	0.0012	0.026	0.03	-0.238	0.073	0.0012	0.046	-0.150	0.036	3.07E-05
cg03699074	16	88849875	0.095	0.014	2.21E-11	0.102	47.3	21611	2782	1905	17	0.022	0.007	0.0030	0.022	0.07	0.224	0.078	0.0044	0.10	0.075	0.025	3.13E-03
cg24073146	11	2543204	0.108	0.017	1.35E-09	0.085	38.5	17447	2473	1698	6	-0.046	0.016	0.0039	0.021	0.07	-0.416	0.150	0.006	0.11	-0.140	0.042	8.89E-04
cg08511578	10	1403938	0.106	0.024	1.50E-05	0.044	19.2	17754	2647	1657	4	-0.034	0.013	0.0079	0.018	0.13	-0.327	0.134	0.015	0.16	-0.098	0.025	8.29E-05
cg11765907	20	43103949	0.047	0.005	1.50E-16	0.151	74.2	14001	1783	1041	27	-0.016	0.006	0.010	0.016	0.15	-0.324	0.125	0.010	0.16	-0.187	0.050	1.95E-04
cg02384870	2	216161208	0.175	0.033	1.53E-07	0.064	28.5	14134	1835	1063	5	-0.042	0.017	0.014	0.015	0.17	-0.243	0.100	0.016	0.16	-0.112	0.024	4.84E-06
cg21396983	16	1275423	0.079	0.009	1.39E-16	0.152	74.3	21550	2710	1738	24	-0.015	0.006	0.016	0.015	0.17	-0.182	0.074	0.014	0.16	-0.144	0.030	1.97E-06
cg09640571	16	88388040	0.031	0.004	1.75E-12	0.113	52.9	21289	3220	2169	27	-0.011	0.005	0.016	0.014	0.17	-0.356	0.147	0.016	0.16	-0.211	0.049	1.71E-05
cg24857040	13	113565214	0.079	0.008	5.26E-21	0.192	98.7	17276	2194	1324	26	-0.013	0.006	0.018	0.014	0.17	-0.169	0.071	0.017	0.16	-0.126	0.032	7.73E-05
cg20612875	17	1094308	0.035	0.003	4.26E-22	0.201	104.9	18826	2792	1917	39	-0.009	0.004	0.020	0.014	0.17	-0.252	0.106	0.017	0.16	-0.224	0.049	7.78E-06
cg23521973	10	125117429	0.079	0.011	7.45E-13	0.116	54.8	15015	2399	1336	17	-0.017	0.007	0.020	0.014	0.17	-0.212	0.090	0.019	0.16	-0.138	0.031	1.13E-05
cg14440140	9	140177567	0.081	0.008	8.24E-21	0.190	97.6	16195	1470	921	34	-0.013	0.006	0.025	0.012	0.19	-0.154	0.068	0.024	0.19	-0.109	0.030	3.10E-04
cg06429120	16	86309214	0.155	0.013	9.85E-28	0.249	138.1	22860	3698	2812	36	-0.015	0.007	0.027	0.012	0.19	-0.097	0.043	0.023	0.19	-0.101	0.021	1.86E-06
cg00460471	2	61437605	0.102	0.024	3.10E-05	0.041	17.7	13349	1511	814	3	-0.032	0.014	0.028	0.012	0.19	-0.319	0.151	0.035	0.21	-0.118	0.028	3.55E-05
cg02110836	17	71953083	0.057	0.005	2.91E-24	0.220	117.4	17019	2437	1629	30	-0.015	0.007	0.028	0.012	0.19	-0.265	0.119	0.026	0.19	-0.227	0.056	5.57E-05
cg06077821	5	180048893	0.047	0.005	2.68E-19	0.176	89.1	16657	2554	1497	34	-0.008	0.004	0.031	0.012	0.20	-0.178	0.081	0.028	0.19	-0.146	0.034	2.43E-05
cg00875983	11	3240213	0.071	0.008	1.34E-18	0.170	85.3	17171	2667	1744	20	-0.017	0.008	0.033	0.011	0.21	-0.237	0.109	0.031	0.20	-0.176	0.045	1.16E-04
cg14361947	9	140780551	0.056	0.007	5.95E-15	0.136	65.7	12059	978	679	24	-0.016	0.008	0.041	0.010	0.22	-0.295	0.144	0.041	0.21	-0.161	0.052	2.02E-03
cg00386725	1	18617791	0.095	0.012	6.12E-15	0.136	65.6	16267	2471	1494	12	-0.024	0.012	0.041	0.010	0.22	-0.248	0.120	0.038	0.21	-0.185	0.044	3.53E-05
cg10964639	16	24043296	0.059	0.008	4.62E-13	0.118	55.9	14736	2182	1222	24	-0.011	0.005	0.041	0.010	0.22	-0.182	0.088	0.039	0.21	-0.122	0.031	9.72E-05
cg11855710	19	29768180	0.148	0.021	1.85E-11	0.103	47.7	17654	3015	1361	10	-0.029	0.014	0.043	0.010	0.22	-0.199	0.096	0.039	0.21	-0.150	0.031	2.42E-06
cg12954267	6	33093109	0.092	0.026	4.69E-04	0.029	12.4	18517	6412	2328	3	-0.028	0.014	0.045	0.010	0.22	-0.321	0.174	0.07	0.27	-0.089	0.025	5.30E-04
cg00389386	1	6188136	0.062	0.007	8.31E-17	0.154	75.5	16477	1981	1136	22	-0.014	0.007	0.045	0.010	0.22	-0.234	0.115	0.043	0.21	-0.174	0.044	1.06E-04
cg21347874	17	77122733	0.083	0.012	6.99E-11	0.097	44.8	16022	2400	1721	13	-0.016	0.008	0.047	0.010	0.22	-0.188	0.093	0.044	0.21	-0.127	0.029	1.26E-05
cg27625886	20	62060443	0.135	0.015	8.29E-17	0.154	75.6	18081	2937	1609	17	-0.018	0.009	0.05	0.009	0.23	-0.128	0.064	0.048	0.23	-0.108	0.026	3.90E-05
cg11586089	14	66644923	0.090	0.010	2.11E-17	0.159	78.8	13997	1665	708	35	-0.013	0.007	0.06	0.009	0.25	-0.147	0.077	0.06	0.25	-0.110	0.030	2.96E-04
cg16340422	17	17110120	0.137	0.020	6.55E-11	0.098	45.0	13630	1744	1022	10	-0.025	0.013	0.06	0.009	0.26	-0.187	0.098	0.06	0.25	-0.124	0.029	2.89E-05
cg18861231	3	152057943	0.035	0.007	3.48E-07	0.061	26.8	13018	1777	676	18	-0.007	0.004	0.06	0.009	0.26	-0.195	0.106	0.07	0.27	-0.079	0.025	1.53E-03
cg03568769	11	1800837	0.074	0.005	1.28E-36	0.319	195.0	17582	2953	1759	66	-0.008	0.004	0.07	0.008	0.27	-0.104	0.057	0.07	0.27	-0.117	0.032	3.12E-04
cg12760575	9	139158654	0.110	0.013	5.14E-16	0.146	71.3	17109	1972	1300	15	-0.020	0.011	0.07	0.008	0.28	-0.185	0.102	0.07	0.27	-0.151	0.039	1.47E-04
cg26037026	7	1641922	0.194	0.055	0.000489	0.029	12.4	20490	2519	1493	1	-0.078	0.045	0.08	0.008	0.30	-0.406	0.241	0.09	0.30	-0.143	0.039	2.39E-04
cg14839558	1	1874488	0.141	0.017	3.66E-15	0.138	66.8	17112	1789	1113	19	-0.018	0.010	0.08	0.008	0.30	-0.133	0.075	0.08	0.29	-0.104	0.027	1.38E-04
cg24600306	20	61990671	0.070	0.007	5.23E-19	0.174	87.5	18172	2970	1608	24	-0.013	0.008	0.08	0.007	0.30	-0.193	0.110	0.08	0.29	-0.174	0.046	1.91E-04
cg16853336	3	149396490	0.040	0.006	6.82E-11	0.097	44.9	13981	2115	1079	19	-0.011	0.006	0.09	0.007	0.30	-0.270	0.157	0.09	0.30	-0.174	0.050	5.04E-04
cg08149223	10	50507130	0.043	0.007	1.56E-09	0.084	38.1	15782	2177	1029	16	-0.012	0.007	0.09	0.007	0.30	-0.273	0.159	0.09	0.30	-0.171	0.047	2.86E-04
cg00781180	16	73984002	0.218	0.037	4.82E-09	0.079	35.8	15775	1655	1261	6	-0.038	0.023	0.09	0.007	0.30	-0.177	0.103	0.09	0.30	-0.111	0.028	1.11E-04
cg16444062	16	2770298	0.236	0.053	1.03E-05	0.046	19.9	15567	1480	949	3	-0.047	0.029	0.10	0.007	0.32	-0.192	0.117	0.10	0.31	-0.105	0.026	4.92E-05
cg24738497	19	36005395	0.130	0.024	5.27E-08	0.069	30.7	14689	2074	1243	4	-0.028	0.017	0.10	0.007	0.32	-0.206	0.124	0.10	0.31	-0.149	0.034	1.20E-05
cg17756860	4	110510374	0.122	0.034	0.00034286	0.030	13.0	13975	1499	674	4	-0.032	0.020	0.11	0.007	0.32	-0.264	0.163	0.11	0.31	-0.128	0.028	6.14E-06
cg08737919	12	108840669	0.207	0.034	2.47E-09	0.082	37.2	14629	2021	914	6	-0.034	0.021	0.11	0.006	0.32	-0.163	0.101	0.11	0.31	-0.095	0.030	1.37E-03

cg12193237	19	3907913	0.048	0.005	8.51E-18	0.163	80.9	16921	2133	1364	36	-0.007	0.004	0.11	0.006	0.32	-0.147	0.090	0.10	0.31	-0.143	0.036	8.65E-05
cg07435932	13	19648633	0.381	0.127	0.00280574	0.021	9.0	16939	2652	1044	1	-0.102	0.065	0.12	0.006	0.34	-0.283	0.192	0.14	0.36	-0.091	0.025	2.94E-04
cg13449257	9	137355128	0.055	0.009	1.52E-08	0.074	33.3	18196	2544	1691	14	-0.011	0.007	0.13	0.006	0.36	-0.191	0.125	0.13	0.36	-0.145	0.034	2.35E-05
cg02287371	5	1246274	0.157	0.037	2.90E-05	0.041	17.9	17997	2289	1564	3	-0.033	0.022	0.13	0.006	0.36	-0.208	0.139	0.14	0.36	-0.097	0.028	4.76E-04
cg06751809	3	105047227	0.106	0.019	2.81E-08	0.072	32.0	14927	2475	943	13	-0.012	0.008	0.13	0.006	0.36	-0.115	0.075	0.13	0.36	-0.086	0.020	3.58E-05
cg01948226	6	32829208	0.092	0.015	1.24E-09	0.085	38.6	19534	8426	2926	10	-0.014	0.010	0.14	0.005	0.37	-0.159	0.106	0.13	0.36	-0.127	0.030	2.87E-05
cg00046877	22	19702664	0.065	0.009	2.83E-12	0.111	51.8	15502	2141	1221	12	-0.016	0.011	0.15	0.005	0.38	-0.248	0.168	0.14	0.36	-0.209	0.057	2.84E-04
cg01864178	20	44662890	0.087	0.014	1.25E-09	0.085	38.6	14114	1927	859	15	-0.012	0.009	0.16	0.005	0.38	-0.148	0.102	0.15	0.37	-0.129	0.029	1.16E-05
cg18682781	5	176277687	0.190	0.042	8.45E-06	0.047	20.3	14377	1242	712	3	-0.035	0.025	0.16	0.005	0.38	-0.181	0.127	0.16	0.37	-0.117	0.028	3.03E-05
cg13463516	9	138632121	0.035	0.005	5.61E-11	0.098	45.3	18674	2377	1670	24	-0.006	0.004	0.17	0.005	0.38	-0.163	0.115	0.16	0.37	-0.147	0.036	5.41E-05
cg09319487	20	56771178	0.148	0.012	4.59E-28	0.252	140.1	15943	2235	1345	28	-0.012	0.009	0.17	0.005	0.38	-0.083	0.060	0.16	0.37	-0.101	0.030	9.53E-04
cg08204714	16	87726461	0.201	0.064	0.00182003	0.023	9.8	21918	2969	2053	1	-0.093	0.067	0.17	0.005	0.38	-0.475	0.355	0.18	0.37	-0.180	0.049	2.58E-04
cg24064348	1	54181174	0.056	0.010	3.99E-08	0.070	31.3	13794	1697	881	8	-0.017	0.012	0.17	0.005	0.38	-0.310	0.224	0.17	0.37	-0.215	0.056	1.65E-04
cg18216439	18	35132882	0.209	0.065	0.0013874	0.024	10.4	13311	1742	916	1	-0.055	0.041	0.18	0.004	0.38	-0.280	0.212	0.19	0.37	-0.128	0.030	2.65E-05
cg04535454	8	144035192	0.049	0.009	2.17E-08	0.073	32.6	17157	2585	1321	16	-0.009	0.006	0.18	0.004	0.38	-0.175	0.129	0.18	0.37	-0.134	0.034	1.02E-04
cg08582801	7	99588335	0.041	0.009	6.73E-06	0.048	20.8	11898	913	363	7	-0.014	0.011	0.19	0.004	0.38	-0.332	0.247	0.18	0.37	-0.232	0.056	3.89E-05
cg27652925	6	31740951	0.049	0.010	1.90E-06	0.053	23.3	15655	5253	2035	8	-0.015	0.011	0.19	0.004	0.38	-0.307	0.230	0.18	0.37	-0.198	0.052	1.73E-04
cg09073467	1	6155515	0.073	0.006	1.34E-26	0.240	131.2	16527	2041	1179	36	-0.009	0.007	0.19	0.004	0.38	-0.126	0.095	0.18	0.37	-0.185	0.046	8.07E-05
cg08239663	16	52688569	0.210	0.044	2.29E-06	0.052	23.0	15429	2052	995	5	-0.028	0.022	0.19	0.004	0.38	-0.139	0.105	0.19	0.37	-0.092	0.023	1.05E-04
cg26225794	7	27717723	0.148	0.043	0.00074188	0.027	11.6	14250	1939	985	2	0.040	0.030	0.19	0.004	0.38	0.241	0.207	0.24	0.41	-0.121	0.033	3.24E-04
cg04293688	2	75466188	0.058	0.007	2.15E-14	0.131	62.8	15363	2334	1330	27	-0.006	0.005	0.19	0.004	0.38	-0.109	0.082	0.19	0.37	-0.115	0.029	1.11E-04
cg05202700	8	38258250	0.125	0.022	2.64E-08	0.072	32.2	12658	1326	661	8	-0.016	0.013	0.19	0.004	0.38	-0.125	0.095	0.19	0.37	-0.103	0.026	1.15E-04
cg15867652	17	79011277	0.119	0.012	9.22E-22	0.198	102.9	18385	2927	1635	23	-0.009	0.007	0.20	0.004	0.38	-0.075	0.057	0.19	0.37	-0.104	0.026	6.38E-05
cg00903007	17	34068171	0.020	0.002	2.67E-15	0.140	67.5	13632	1860	892	52	-0.004	0.003	0.20	0.004	0.38	-0.193	0.147	0.19	0.37	-0.215	0.054	9.47E-05
cg13377560	22	43860820	0.071	0.010	3.25E-12	0.110	51.5	16164	2593	1472	18	-0.010	0.008	0.21	0.004	0.39	-0.129	0.101	0.20	0.38	-0.142	0.036	8.46E-05
cg01095004	16	88454883	0.130	0.018	2.07E-12	0.112	52.5	21315	3131	2093	12	-0.014	0.011	0.21	0.004	0.39	-0.107	0.084	0.20	0.38	-0.105	0.028	2.43E-04
cg24848724	8	142578640	0.095	0.009	2.93E-21	0.194	100.1	16785	2282	1389	32	-0.007	0.005	0.21	0.004	0.39	-0.073	0.058	0.20	0.38	-0.088	0.025	3.51E-04
cg01898225	15	99975141	0.062	0.006	2.03E-19	0.178	89.8	15697	2792	1539	29	-0.007	0.006	0.22	0.004	0.39	-0.114	0.090	0.21	0.38	-0.179	0.038	2.86E-06
cg20018106	4	21768009	0.058	0.011	6.20E-08	0.068	30.4	16045	2280	975	13	-0.007	0.006	0.22	0.004	0.39	-0.123	0.097	0.21	0.38	-0.121	0.026	5.69E-06
cg18450810	17	51111066	0.214	0.045	3.11E-06	0.051	22.4	14484	2171	635	4	-0.034	0.027	0.22	0.004	0.39	-0.157	0.127	0.21	0.38	-0.104	0.028	2.82E-04
cg25285919	3	188312215	0.080	0.011	5.43E-13	0.118	55.5	14200	1596	1007	14	-0.009	0.007	0.22	0.004	0.39	-0.114	0.092	0.21	0.38	-0.114	0.031	2.51E-04
cg18184975	20	3644192	0.076	0.014	4.39E-08	0.070	31.1	14390	2558	1274	10	-0.011	0.009	0.23	0.004	0.39	-0.153	0.124	0.22	0.38	-0.138	0.032	2.40E-05
cg04131502	1	2845583	0.107	0.017	4.55E-10	0.089	40.8	17240	2079	1306	9	-0.014	0.012	0.25	0.003	0.42	-0.134	0.113	0.24	0.41	-0.136	0.033	6.26E-05
cg26849382	5	140901022	0.223	0.081	0.00651404	0.018	7.5	13286	1785	904	1	0.049	0.042	0.25	0.003	0.42	0.213	0.191	0.27	0.43	0.060	0.025	1.83E-02
cg16819051	2	229173235	0.189	0.063	0.00303083	0.021	8.9	14534	2218	867	1	-0.045	0.040	0.26	0.003	0.42	-0.235	0.208	0.26	0.43	-0.112	0.030	1.86E-04
cg25721832	3	81913557	0.089	0.015	2.94E-09	0.081	36.8	12811	1396	484	17	-0.012	0.010	0.27	0.003	0.43	-0.132	0.118	0.26	0.43	-0.101	0.033	2.13E-03
cg22509138	20	44809026	0.357	0.119	0.00283299	0.021	9.0	14092	1752	957	1	0.070	0.064	0.27	0.003	0.43	0.194	0.201	0.33	0.50	-0.107	0.026	3.62E-05
cg05808230	20	61726456	0.095	0.011	1.17E-15	0.143	69.4	18272	2767	1736	19	-0.009	0.008	0.27	0.003	0.43	-0.092	0.083	0.27	0.43	-0.131	0.032	4.96E-05
cg09063835	20	58181392	0.152	0.020	2.26E-13	0.121	57.5	15305	1716	1164	13	-0.013	0.012	0.28	0.003	0.43	-0.088	0.079	0.27	0.43	-0.117	0.027	1.78E-05
cg06066032	13	48369175	0.370	0.116	0.00154941	0.024	10.2	14559	2328	815	1	0.061	0.059	0.30	0.003	0.47	0.185	0.203	0.36	0.53	-0.098	0.025	7.18E-05
cg05389237	9	125314173	0.135	0.019	2.83E-12	0.111	51.9	13529	1515	817	17	-0.010	0.010	0.30	0.003	0.47	-0.078	0.074	0.29	0.46	-0.096	0.024	1.04E-04
cg17538538	6	106825021	0.131	0.026	8.85E-07	0.056	24.9	14420	2498	1195	4	0.020	0.021	0.33	0.002	0.50	0.151	0.152	0.32	0.49	0.133	0.037	3.46E-04
cg23519631	12	72690355	0.111	0.022	7.26E-07	0.057	25.3	12956	1472	563	8	-0.016	0.016	0.33	0.002	0.50	-0.144	0.144	0.32	0.49	-0.164	0.034	1.82E-06
cg08792976	16	760528	0.103	0.011	1.48E-19	0.179	90.6	22023	2572	1696	24	-0.008	0.008	0.34	0.002	0.50	-0.076	0.078	0.33	0.50	-0.137	0.033	3.27E-05
cg20623853	19	1734365	0.040	0.008	2.88E-07	0.061	27.2	17950	1888	1390	13	-0.006	0.006	0.34	0.002	0.50	-0.132	0.135	0.33	0.50	-0.148	0.036	5.67E-05
cg18042910	13	19662609	0.053	0.007	1.31E-13	0.124	58.7	17061	2665	1048	44	-0.004	0.004	0.37	0.002	0.53	-0.068	0.074	0.36	0.53	-0.107	0.026	4.78E-05
cg14204490	8	33330967	0.035	0.006	3.81E-10	0.090	41.2	13877	1541	509	27	0.006	0.007	0.37	0.002	0.53	0.176	0.204	0.39	0.55	-0.222	0.056	8.23E-05
cg01124546	11	117515332	0.065	0.009	5.51E-12	0.108	50.4	15525	2294	1396	13	-0.009	0.010	0.38	0.002	0.54	-0.135	0.150	0.37	0.53	-0.198	0.048	4.04E-05
cg00188627	3	159557779	0.133	0.022	1.50E-09	0.084	38.2	14587	1437	649	8	0.012	0.014	0.40	0.002	0.56	0.089	0.104	0.39	0.55	0.105	0.030	6.05E-04
cg03510150	9	130690744	0.058	0.008	5.78E-13	0.117	55.4	13396	1284	730	17	-0.007	0.009	0.42	0.002	0.59	-0.119	0.145	0.41	0.58	-0.200	0.050	8.62E-05
cg09701145	11	2019436	0.085	0.011	7.50E-13	0.116	54.8	17726	2869	1731	12	0.008	0.010	0.45	0.001	0.61	0.088	0.118	0.46	0.63	-0.174	0.039	1.03E-05
cg05775586	9	28889354	0.034	0.005	1.50E-12	0.113	53.3	15740	2741	1083	55	-0.002	0.003	0.47	0.001	0.64	-0.054	0.074	0.47	0.64	-0.098	0.026	1.85E-04

cg00373987	22	37868968	0.228	0.056	6.16E-05	0.038	16.4	15697	2077	1308	2	-0.027	0.039	0.49	0.001	0.65	-0.121	0.169	0.48	0.64	-0.144	0.033	1.38E-05
cg12161743	11	76750531	0.055	0.007	2.42E-14	0.131	62.5	13871	1984	1045	23	-0.004	0.005	0.49	0.001	0.65	-0.065	0.093	0.48	0.64	-0.147	0.033	1.38E-05
cg13827123	13	93971495	0.313	0.105	0.00304799	0.021	8.9	14374	2257	949	1	0.036	0.054	0.50	0.001	0.66	0.116	0.185	0.53	0.68	-0.100	0.024	5.07E-05
cg08491066	1	156030669	0.101	0.019	1.11E-07	0.066	29.2	11201	951	464	7	-0.010	0.016	0.51	0.001	0.66	-0.104	0.153	0.50	0.66	-0.157	0.038	5.39E-05
cg15575356	11	47616757	0.137	0.032	1.70E-05	0.044	18.9	11864	1306	471	4	-0.020	0.032	0.52	0.001	0.68	-0.152	0.231	0.51	0.67	-0.201	0.047	2.78E-05
cg00078259	6	2656232	0.148	0.020	2.76E-13	0.121	57.0	16279	2501	1372	11	-0.008	0.012	0.53	0.001	0.68	-0.051	0.080	0.52	0.68	-0.105	0.027	1.50E-04
cg16140890	1	1082406	0.144	0.032	1.06E-05	0.046	19.9	16090	1384	843	5	0.010	0.017	0.56	0.001	0.72	0.068	0.122	0.58	0.72	-0.093	0.025	2.64E-04
cg21927431	9	134678366	0.173	0.028	2.39E-09	0.082	37.2	14813	1885	1114	6	-0.012	0.021	0.58	0.001	0.73	-0.076	0.136	0.58	0.72	-0.127	0.034	2.49E-04
cg20659588	1	237963267	0.262	0.054	1.77E-06	0.053	23.5	15158	2388	1277	3	-0.018	0.034	0.59	0.001	0.73	-0.073	0.132	0.58	0.72	-0.125	0.029	2.48E-05
cg13022891	9	5817706	0.054	0.006	2.68E-17	0.158	78.2	16090	1838	1205	38	-0.003	0.005	0.59	0.001	0.73	-0.054	0.098	0.58	0.72	-0.148	0.038	1.43E-04
cg25903144	7	131609806	0.086	0.017	3.43E-07	0.061	26.9	15819	2225	1281	10	-0.004	0.008	0.59	0.001	0.73	-0.052	0.095	0.59	0.72	-0.083	0.023	4.29E-04
cg27410679	17	43866278	0.068	0.010	3.00E-11	0.101	46.7	12078	2955	549	28	-0.003	0.006	0.61	0.001	0.73	-0.041	0.080	0.61	0.73	-0.108	0.026	5.00E-05
cg10883064	17	60757346	0.085	0.014	1.18E-09	0.085	38.8	12442	1144	568	20	-0.004	0.009	0.62	0.001	0.73	-0.050	0.098	0.61	0.73	-0.110	0.030	2.51E-04
cg11837181	1	3001002	0.101	0.026	0.00015292	0.034	14.6	17515	2132	1321	3	-0.009	0.018	0.62	0.001	0.73	-0.092	0.180	0.61	0.73	-0.127	0.033	1.51E-04
cg17985533	11	2019116	0.038	0.003	8.78E-38	0.328	202.9	17722	2867	1729	108	-0.001	0.003	0.62	0.001	0.73	-0.038	0.076	0.62	0.73	-0.175	0.043	5.97E-05
cg21778193	1	1098070	0.189	0.067	0.00483001	0.019	8.0	16295	1400	851	1	-0.018	0.040	0.66	0.000	0.77	-0.087	0.192	0.65	0.76	-0.119	0.029	4.25E-05
cg05851077	9	29802712	0.146	0.033	1.68E-05	0.044	19.0	16112	2731	1143	5	-0.006	0.013	0.67	0.000	0.77	-0.039	0.091	0.67	0.77	-0.084	0.019	1.04E-05
cg06981471	7	142982076	0.125	0.026	1.98E-06	0.053	23.3	10365	1303	535	5	0.008	0.020	0.67	0.000	0.77	0.064	0.155	0.68	0.77	-0.127	0.036	4.27E-04
cg12011250	1	30198037	0.065	0.008	3.19E-16	0.148	72.4	13795	2188	1217	29	-0.002	0.005	0.69	0.000	0.78	-0.033	0.080	0.68	0.77	-0.120	0.030	6.05E-05
cg07728373	2	229266790	0.077	0.016	1.82E-06	0.053	23.4	14340	2115	872	11	-0.003	0.007	0.69	0.000	0.78	-0.039	0.096	0.68	0.77	-0.108	0.021	5.53E-07
cg16608656	11	1082797	0.103	0.033	0.00173057	0.023	9.9	16848	2415	1343	2	-0.008	0.020	0.70	0.000	0.78	-0.072	0.184	0.69	0.78	-0.112	0.029	1.47E-04
cg13625403	11	120008510	0.057	0.012	3.76E-06	0.050	22.0	15102	2093	1233	9	0.003	0.007	0.71	0.000	0.79	0.047	0.129	0.71	0.79	-0.117	0.028	4.48E-05
cg00918900	1	1057335	0.087	0.012	1.22E-12	0.114	53.7	15892	1367	827	21	-0.003	0.007	0.71	0.000	0.79	-0.031	0.083	0.71	0.79	-0.124	0.029	1.83E-05
cg00403246	10	134794753	0.096	0.023	3.36E-05	0.041	17.6	18305	1964	1252	2	0.009	0.025	0.73	0.000	0.79	0.090	0.263	0.73	0.80	-0.188	0.051	2.46E-04
cg11138231	7	99475824	0.111	0.017	4.91E-11	0.099	45.6	12236	880	344	20	-0.003	0.008	0.76	0.000	0.83	-0.022	0.073	0.76	0.82	-0.095	0.023	4.48E-05
cg08474716	16	27079640	0.206	0.029	4.42E-12	0.109	50.9	16195	2472	1481	8	-0.004	0.016	0.78	0.000	0.84	-0.022	0.078	0.78	0.83	-0.092	0.025	2.08E-04
cg07203271	1	53926112	0.145	0.024	2.03E-09	0.083	37.6	14665	2120	967	9	-0.004	0.015	0.78	0.000	0.84	-0.028	0.101	0.78	0.83	-0.104	0.029	4.27E-04
cg25380707	15	86660946	0.252	0.080	0.00180737	0.023	9.9	17604	2562	1510	1	-0.010	0.040	0.81	0.000	0.85	-0.043	0.176	0.81	0.85	-0.086	0.024	2.83E-04
cg17905524	15	28305412	0.106	0.014	1.08E-12	0.115	54.0	11317	1447	661	17	-0.002	0.010	0.82	0.000	0.86	-0.021	0.094	0.82	0.86	-0.127	0.030	2.77E-05
cg18616558	7	158798592	0.080	0.014	1.49E-08	0.074	33.4	14247	1918	902	20	-0.001	0.006	0.92	0.000	0.95	-0.008	0.073	0.92	0.95	-0.071	0.020	4.52E-04
cg04140215	2	60540175	0.210	0.075	0.00563409	0.018	7.7	15077	1764	1102	1	0.004	0.050	0.94	0.000	0.96	0.021	0.265	0.94	0.97	-0.119	0.031	1.48E-04
cg26238771	19	592158	0.117	0.011	3.43E-23	0.211	111.2	17193	2642	2036	20	0.000	0.009	0.98	0.000	0.99	-0.002	0.080	0.98	0.99	-0.139	0.036	1.21E-04
cg05347757	15	51121020	0.103	0.034	0.00251697	0.022	9.2	13001	1995	637	3	0.000	0.018	0.98	0.000	0.99	-0.004	0.173	0.98	0.99	-0.083	0.025	1.10E-03
cg02688867	12	133019854	0.180	0.055	0.0012479	0.025	10.6	16623	2355	1394	2	-0.001	0.033	0.98	0.000	0.99	-0.004	0.179	0.98	0.99	-0.100	0.028	4.92E-04
cg15952840	8	11451312	0.159	0.035	5.66E-06	0.048	21.1	21931	3018	2084	3	0.000	0.022	0.99	0.000	0.99	0.003	0.145	0.99	0.99	-0.128	0.030	2.32E-05
cg00045690	6	32825897						19525	8434	2923	0										-0.086	0.022	1.12E-04
cg01216882	20	31804277						14128	1327	702	0										-0.137	0.031	9.94E-06
cg01530082	6	32784327						19703	8668	2934	0										-0.107	0.026	4.05E-05
cg01615861	16	85513978						21138	2881	2231	0										-0.283	0.080	4.45E-04
cg02831474	10	1783879						18860	3144	1828	0										-0.113	0.024	3.12E-06
cg03275961	9	90386329						15207	2428	1223	0										-0.161	0.040	5.57E-05
cg03710412	8	142938779						17500	2608	1446	0										-0.091	0.026	4.85E-04
cg04847540	1	182754070						13816	1976	812	0										-0.112	0.028	7.64E-05
cg04907218	12	132826672						16467	2098	1300	0										-0.118	0.030	9.09E-05
cg05444304	2	31442675						15973	2123	1458	0										0.133	0.039	6.39E-04
cg05790369	17	33202007						14788	2007	1086	0										-0.115	0.030	1.90E-04
cg06343669	12	132690782						16014	2044	1320	0										-0.117	0.028	2.72E-05
cg06495184	19	406256						13720	2023	1579	0										-0.142	0.035	5.34E-05
cg06830529	9	124960107						14549	1938	1035	0										-0.139	0.037	1.73E-04
cg07080246	13	63306618						13919	2164	705	0										-0.076	0.020	1.22E-04
cg07686906	1	3353825						18958	2698	1695	0										-0.150	0.037	5.70E-05
cg07865738	2	3649447						15986	2592	1436	0										-0.095	0.024	6.57E-05

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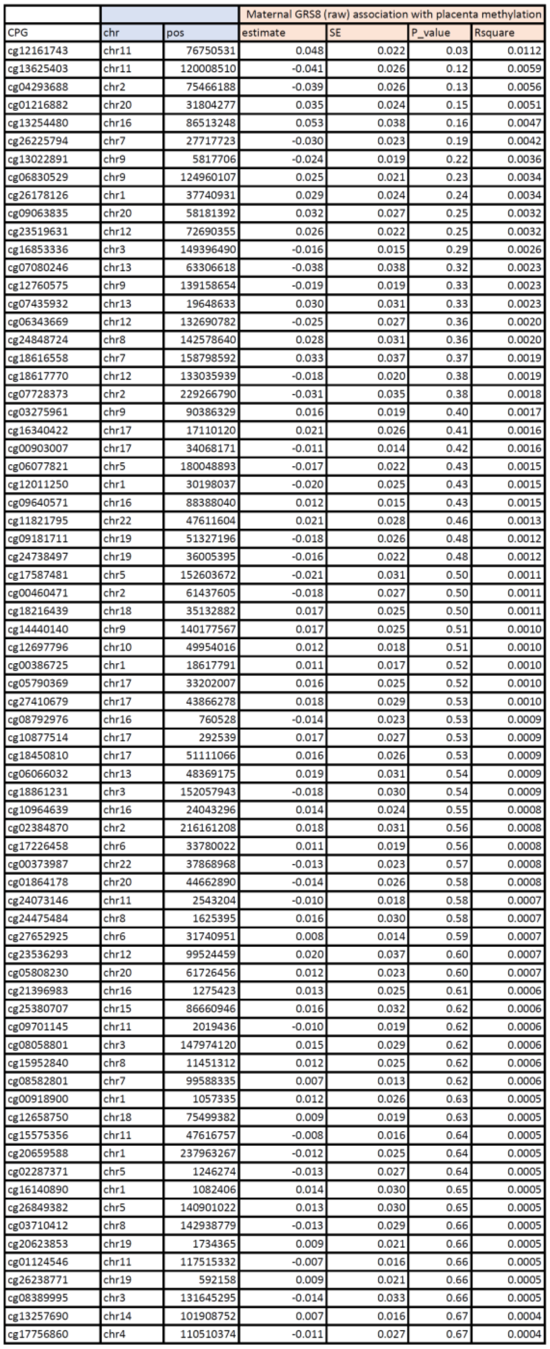
cg08058801	3	147974120						14142	1723	693	0										-0.114	0.026	1.13E-05
cg08357744	17	37559321						13259	1346	609	0										-0.084	0.023	2.31E-04
cg08372350	16	88943191						22238	2702	1867	0										-0.107	0.028	1.59E-04
cg08389995	3	131645295						14602	2835	1125	0										-0.083	0.023	3.49E-04
cg09181711	19	51327196						16264	2335	1602	0										-0.136	0.029	2.61E-06
cg09851596	8	143545214						18124	2792	1362	0										-0.177	0.044	7.97E-05
cg10877514	17	292539						12641	1872	1292	0										-0.105	0.028	1.79E-04
cg11086223	18	11487579						16274	2395	1276	0										-0.135	0.034	6.79E-05
cg11177743	20	21545361						13270	1160	444	0										-0.138	0.033	3.15E-05
cg11294782	3	10487409						15223	2264	1314	0										-0.152	0.040	1.69E-04
cg11416433	15	25429261						16557	1988	1141	0										-0.201	0.044	6.72E-06
cg11821795	22	47611604						19073	2440	1408	0										-0.109	0.027	4.59E-05
cg12697796	10	49954016						15686	2331	1086	0										-0.179	0.041	2.03E-05
cg13116906	12	119552989						14166	2319	1181	0										-0.105	0.027	1.44E-04
cg13254480	16	86513248						23316	3570	2722	0										-0.073	0.020	2.91E-04
cg13257690	14	101908752						15386	2170	1265	0										-0.178	0.046	1.17E-04
cg13480617	5	35230725						14639	2107	978	0										-0.121	0.038	1.49E-03
cg14494450	1	4190881						15856	2958	1567	0										-0.116	0.027	2.07E-05
cg14757962	5	2176287						19312	3591	2168	0										-0.108	0.030	3.06E-04
cg14759277	17	48674158						13790	1755	1128	0										-0.164	0.041	7.62E-05
cg14886500	6	23447204						17748	2646	1490	0										-0.080	0.023	7.30E-04
cg16513326	8	10877312						21573	3120	2033	0										-0.111	0.032	5.03E-04
cg16857113	3	1133865						18339	2963	1779	0										-0.114	0.029	1.12E-04
cg17224410	9	137852661						19804	2883	1965	0										-0.123	0.033	2.00E-04
cg17226458	6	33780022						16101	2493	1395	0										-0.145	0.039	2.71E-04
cg17587481	5	152603672						14222	2224	764	0										-0.103	0.024	1.78E-05
cg18108190	19	2727822						18307	2844	1847	0										-0.142	0.033	2.05E-05
cg18233010	10	114911413						14248	1705	1135	0										0.170	0.045	2.13E-04
cg18617770	12	133035939						16438	2356	1404	0										-0.160	0.037	2.04E-05
cg18650968	4	176340837						14564	1524	726	0										-0.100	0.028	4.36E-04
cg19450046	21	45712938						18589	2432	1382	0										-0.138	0.036	1.66E-04
cg20112984	10	1447183						18134	2767	1723	0										-0.103	0.027	2.03E-04
cg21307723	1	245215135						15619	2326	1412	0										0.143	0.038	2.22E-04
cg23016281	22	27616620						17311	3036	1986	0										-0.092	0.025	2.60E-04
cg23359229	13	29976597						15238	2418	1020	0										-0.110	0.026	2.82E-05
cg23536293	12	99524459						13533	1605	925	0										-0.071	0.021	6.41E-04
cg23561197	5	125852064						15210	2226	1108	0										-0.106	0.030	4.06E-04
cg25314607	5	2148308						19252	3620	2202	0										-0.122	0.030	6.85E-05
cg26178126	1	37740931						14242	2023	983	0										-0.125	0.031	6.10E-05
cg27332583	18	35150602						13359	1749	916	0										-0.175	0.041	2.12E-05

SUPPLEMENTARY DATA

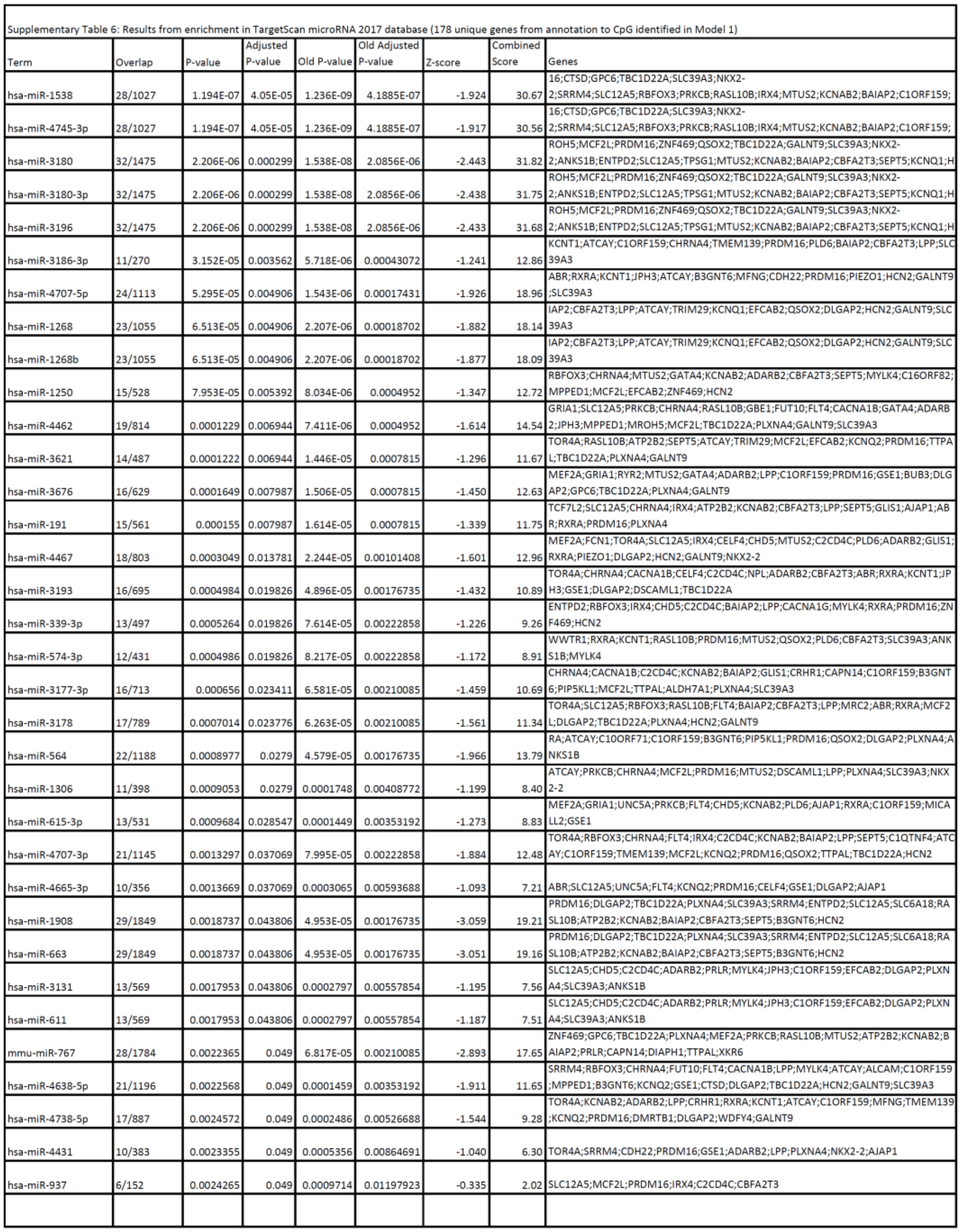
Supplementary Table 5. Results from Mendelian randomization analyses using GRS representing insulin sensitivity (8 SNPs) associations withmethylation levels at CpG sites identified in Model 1



			Maternal GRS8 (raw) association with placenta methylation			
CPG	chr	pos	estimate	SE	P_value	Rsquare
cg12161743	chr11	76750531	0.048	0.022	0.03	0.0112
cg13625403	chr11	120008510	-0.041	0.026	0.12	0.0059
cg04293688	chr2	75466188	-0.039	0.026	0.13	0.0056
cg01216882	chr20	31804277	0.035	0.024	0.15	0.0051
cg13254480	chr16	86513248	0.053	0.038	0.16	0.0047
cg26225794	chr7	27717723	-0.030	0.023	0.19	0.0042
cg13022891	chr9	5817706	-0.024	0.019	0.22	0.0036
cg06830529	chr9	124960107	0.025	0.021	0.23	0.0034
cg26178126	chr1	37740931	0.029	0.024	0.24	0.0034
cg09063835	chr20	58181392	0.032	0.027	0.25	0.0032
cg23519631	chr12	72690355	0.026	0.022	0.25	0.0032
cg16853336	chr3	149396490	-0.016	0.015	0.29	0.0026
cg07080246	chr13	63306618	-0.038	0.038	0.32	0.0023
cg12760575	chr9	139158654	-0.019	0.019	0.33	0.0023
cg07435932	chr13	19648633	0.030	0.031	0.33	0.0023
cg06343669	chr12	132690782	-0.025	0.027	0.36	0.0020
cg24848724	chr8	142578640	0.028	0.031	0.36	0.0020
cg18616558	chr7	158798592	0.033	0.037	0.37	0.0019
cg18617770	chr12	133035939	-0.018	0.020	0.38	0.0019
cg07728373	chr2	229266790	-0.031	0.035	0.38	0.0018
cg03275961	chr9	90386329	0.016	0.019	0.40	0.0017
cg16340422	chr17	17110120	0.021	0.026	0.41	0.0016
cg00903007	chr17	34068171	-0.011	0.014	0.42	0.0016
cg06077821	chr5	180048893	-0.017	0.022	0.43	0.0015
cg12011250	chr1	30198037	-0.020	0.025	0.43	0.0015
cg09640571	chr16	88388040	0.012	0.015	0.43	0.0015
cg11821795	chr22	47611604	0.021	0.028	0.46	0.0013
cg09181711	chr19	51327196	-0.018	0.026	0.48	0.0012
cg24738497	chr19	36005395	-0.016	0.022	0.48	0.0012
cg17587481	chr5	152603672	-0.021	0.031	0.50	0.0011
cg00460471	chr2	61437605	-0.018	0.027	0.50	0.0011
cg18216439	chr18	35132882	0.017	0.025	0.50	0.0011
cg14440140	chr9	140177567	0.017	0.025	0.51	0.0010
cg12697796	chr10	49954016	0.012	0.018	0.51	0.0010
cg00386725	chr1	18617791	0.011	0.017	0.52	0.0010
cg05790369	chr17	33202007	0.016	0.025	0.52	0.0010
cg27410679	chr17	43866278	0.018	0.029	0.53	0.0010
cg08792976	chr16	760528	-0.014	0.023	0.53	0.0009
cg10877514	chr17	292539	0.017	0.027	0.53	0.0009
cg18450810	chr17	51111066	0.016	0.026	0.53	0.0009
cg06066032	chr13	48369175	0.019	0.031	0.54	0.0009
cg18861231	chr3	152057943	-0.018	0.030	0.54	0.0009
cg10964639	chr16	24043296	0.014	0.024	0.55	0.0008
cg02384870	chr2	216161208	0.018	0.031	0.56	0.0008
cg17226458	chr6	33780022	0.011	0.019	0.56	0.0008
cg00373987	chr22	37868968	-0.013	0.023	0.57	0.0008
cg01864178	chr20	44662890	-0.014	0.026	0.58	0.0008
cg24073146	chr11	2543204	-0.010	0.018	0.58	0.0007
cg24475484	chr8	1625395	0.016	0.030	0.58	0.0007
cg27652925	chr6	31740951	0.008	0.014	0.59	0.0007
cg23536293	chr12	99524459	0.020	0.037	0.60	0.0007
cg05808230	chr20	61726456	0.012	0.023	0.60	0.0007
cg21396983	chr16	1275423	0.013	0.025	0.61	0.0006
cg25380707	chr15	86660946	0.016	0.032	0.62	0.0006
cg09701145	chr11	2019436	-0.010	0.019	0.62	0.0006
cg08058801	chr3	147974120	0.015	0.029	0.62	0.0006
cg15952840	chr8	11451312	0.012	0.025	0.62	0.0006
cg08582801	chr7	99588335	0.007	0.013	0.62	0.0006
cg00918900	chr1	1057335	0.012	0.026	0.63	0.0005
cg12658750	chr18	75499382	0.009	0.019	0.63	0.0005
cg15575356	chr11	47616757	-0.008	0.016	0.64	0.0005
cg20659588	chr1	237963267	-0.012	0.025	0.64	0.0005
cg02287371	chr5	1246274	-0.013	0.027	0.64	0.0005
cg16140890	chr1	1082406	0.014	0.030	0.65	0.0005
cg26849382	chr5	140901022	0.013	0.030	0.65	0.0005
cg03710412	chr8	142938779	-0.013	0.029	0.66	0.0005
cg20623853	chr19	1734365	0.009	0.021	0.66	0.0005
cg01124546	chr11	117515332	-0.007	0.016	0.66	0.0005
cg26238771	chr19	592158	0.009	0.021	0.66	0.0005
cg08389995	chr3	131645295	-0.014	0.033	0.66	0.0005
cg13257690	chr14	101908752	0.007	0.016	0.67	0.0004
cg17756860	chr4	110510374	-0.011	0.027	0.67	0.0004

cg01530082	chr6	32784327	-0.012	0.029	0.67	0.0004
cg00045690	chr6	32825897	0.014	0.034	0.67	0.0004
cg14839558	chr1	1874488	0.012	0.028	0.67	0.0004
cg25314607	chr5	2148308	0.011	0.025	0.67	0.0004
cg00781180	chr16	73984002	-0.011	0.026	0.67	0.0004
cg08474716	chr16	27079640	0.013	0.031	0.67	0.0004
cg13480617	chr5	35230725	0.008	0.020	0.67	0.0004
cg11416433	chr15	25429261	0.007	0.017	0.67	0.0004
cg17538538	chr6	106825021	0.009	0.020	0.67	0.0004
cg05775586	chr9	28889354	-0.012	0.029	0.68	0.0004
cg08737919	chr12	108840669	0.010	0.026	0.69	0.0004
cg01618245	chr20	61990279	0.012	0.030	0.69	0.0004
cg21307723	chr1	245215135	0.008	0.019	0.69	0.0004
cg20018106	chr4	21768009	-0.011	0.028	0.70	0.0004
cg02831474	chr10	1783879	0.012	0.031	0.70	0.0004
cg04535454	chr8	144035192	0.008	0.022	0.70	0.0004
cg08491066	chr1	156030669	0.007	0.019	0.70	0.0003
cg12673377	chr7	1388271	0.008	0.021	0.70	0.0003
cg07203271	chr1	53926112	-0.010	0.026	0.71	0.0003
cg09319487	chr20	56771178	0.009	0.025	0.71	0.0003
cg23359229	chr13	29976597	0.011	0.029	0.71	0.0003
cg23521973	chr10	125117429	0.009	0.024	0.72	0.0003
cg01948226	chr6	32829208	0.009	0.025	0.72	0.0003
cg18184975	chr20	3644192	0.008	0.023	0.72	0.0003
cg13116906	chr12	119552989	0.010	0.027	0.73	0.0003
cg04131502	chr1	2845583	0.008	0.023	0.73	0.0003
cg04907218	chr12	132826672	-0.009	0.025	0.74	0.0003
cg21778193	chr1	1098070	0.009	0.026	0.74	0.0003
cg11855710	chr19	29768180	-0.008	0.024	0.75	0.0002
cg26037026	chr7	1641922	-0.006	0.020	0.75	0.0002
cg25903144	chr7	131609806	0.010	0.033	0.76	0.0002
cg13377560	chr22	43860820	-0.006	0.021	0.76	0.0002
cg16444062	chr16	2770298	0.009	0.029	0.76	0.0002
cg27625886	chr20	62060443	-0.008	0.029	0.77	0.0002
cg01898225	chr15	99975141	-0.006	0.019	0.77	0.0002
cg07865738	chr2	3649447	-0.009	0.032	0.78	0.0002
cg23561197	chr5	125852064	-0.007	0.025	0.79	0.0002
cg14361947	chr9	140780551	0.004	0.015	0.79	0.0002
cg08099672	chr9	139944162	-0.005	0.021	0.79	0.0002
cg08357744	chr17	37559321	0.008	0.034	0.80	0.0002
cg03568769	chr11	1800837	0.006	0.023	0.80	0.0001
cg16857113	chr3	1133865	-0.006	0.026	0.81	0.0001
cg18682781	chr5	176277687	0.007	0.027	0.81	0.0001
cg25721832	chr3	81913557	-0.006	0.023	0.81	0.0001
cg27332583	chr18	35150602	-0.004	0.019	0.81	0.0001
cg11294782	chr3	10487409	0.004	0.019	0.82	0.0001
cg08511578	chr10	1403938	-0.007	0.030	0.82	0.0001
cg07686906	chr1	3353825	0.005	0.020	0.82	0.0001
cg23016281	chr22	27616620	-0.007	0.030	0.83	0.0001
cg08149223	chr10	50507130	-0.004	0.016	0.83	0.0001
cg24600306	chr20	61990671	0.004	0.016	0.83	0.0001
cg02688867	chr12	133019854	-0.006	0.026	0.83	0.0001
cg05444304	chr2	31442675	0.004	0.020	0.83	0.0001
cg05389237	chr9	125314173	0.006	0.031	0.84	0.0001
cg17985533	chr11	2019116	0.003	0.017	0.84	0.0001
cg00389386	chr1	6188136	0.003	0.017	0.84	0.0001
cg13827123	chr13	93971495	-0.006	0.031	0.85	0.0001
cg17905524	chr15	28305412	0.005	0.025	0.85	0.0001
cg11177743	chr20	21545361	0.004	0.023	0.86	0.0001
cg00046877	chr22	19702664	0.002	0.013	0.86	0.0001
cg11138231	chr7	99475824	0.006	0.033	0.86	0.0001
cg06981471	chr7	142982076	-0.004	0.021	0.86	0.0001
cg14757962	chr5	2176287	-0.004	0.025	0.87	0.0001
cg00078259	chr6	2656232	0.004	0.027	0.87	0.0001
cg00188627	chr3	159557779	0.004	0.025	0.88	0.0001
cg08372350	chr16	88943191	-0.004	0.027	0.88	0.0001
cg14886500	chr6	23447204	-0.005	0.032	0.88	0.0001
cg06751809	chr3	105047227	0.005	0.037	0.88	0.0001
cg17224410	chr9	137852661	-0.003	0.023	0.89	0.0000
cg13449257	chr9	137355128	0.003	0.022	0.89	0.0000
cg18650968	chr4	176340837	-0.004	0.027	0.89	0.0000
cg06429120	chr16	86309214	0.005	0.036	0.89	0.0000
cg24857040	chr13	113565214	-0.003	0.024	0.89	0.0000
cg16513326	chr8	10877312	-0.003	0.024	0.89	0.0000
cg20112984	chr10	1447183	-0.004	0.028	0.90	0.0000
cg16608656	chr11	1082797	-0.003	0.026	0.90	0.0000

cg19450046	chr21	45712938	-0.003	0.021	0.90	0.0000
cg09073467	chr1	6155515	-0.002	0.016	0.91	0.0000
cg08204714	chr16	87726461	-0.002	0.015	0.91	0.0000
cg14494450	chr1	4190881	-0.003	0.028	0.92	0.0000
cg00403246	chr10	134794753	0.002	0.015	0.92	0.0000
cg21927431	chr9	134678366	-0.002	0.022	0.92	0.0000
cg03510150	chr9	130690744	-0.002	0.015	0.92	0.0000
cg14204490	chr8	33330967	0.001	0.013	0.92	0.0000
cg11086223	chr18	11487579	0.002	0.022	0.93	0.0000
cg21347874	chr17	77122733	0.002	0.026	0.93	0.0000
cg20612875	chr17	1094308	0.001	0.015	0.94	0.0000
cg14759277	chr17	48674158	-0.001	0.018	0.94	0.0000
cg05851077	chr9	29802712	0.003	0.040	0.94	0.0000
cg05202700	chr8	38258250	-0.002	0.028	0.94	0.0000
cg11837181	chr1	3001002	-0.002	0.023	0.94	0.0000
cg04847540	chr1	182754070	-0.002	0.027	0.95	0.0000
cg08239663	chr16	52688569	-0.002	0.032	0.95	0.0000
cg13463516	chr9	138632121	-0.001	0.021	0.95	0.0000
cg22509138	chr20	44809026	-0.002	0.029	0.95	0.0000
cg04140215	chr2	60540175	0.001	0.024	0.96	0.0000
cg10883064	chr17	60757346	-0.001	0.025	0.96	0.0000
cg15867652	chr17	79011277	-0.002	0.029	0.96	0.0000
cg01095004	chr16	88454883	0.001	0.027	0.96	0.0000
cg09851596	chr8	143545214	0.001	0.017	0.97	0.0000
cg24064348	chr1	54181174	0.000	0.013	0.97	0.0000
cg18042910	chr13	19662609	0.001	0.029	0.98	0.0000
cg01615861	chr16	85513978	0.000	0.009	0.98	0.0000
cg00875983	chr11	3240213	0.000	0.016	0.98	0.0000
cg06495184	chr19	406256	-0.001	0.021	0.98	0.0000
cg18233010	chr10	114911413	0.000	0.017	0.98	0.0000
cg12193237	chr19	3907913	0.000	0.021	0.98	0.0000
cg16819051	chr2	229173235	0.000	0.025	0.99	0.0000
cg11765907	chr20	43103949	0.000	0.015	0.99	0.0000
cg25285919	chr3	188312215	0.000	0.024	0.99	0.0000
cg11586089	chr14	66644923	0.000	0.025	0.99	0.0000
cg03699074	chr16	88849875	0.000	0.030	0.99	0.0000
cg18108190	chr19	2727822	0.000	0.023	0.99	0.0000
cg05347757	chr15	51121020	0.000	0.030	1.00	0.0000
cg12954267	chr6	33093109	0.000	0.030	1.00	0.0000
cg02110836	chr17	71953083	0.000	0.013	1.00	0.0000



Supplementary Table 6: Results from enrichment in TargetScan microRNA 2017 database (178 unique genes from annotation to CpG identified in Model 1)

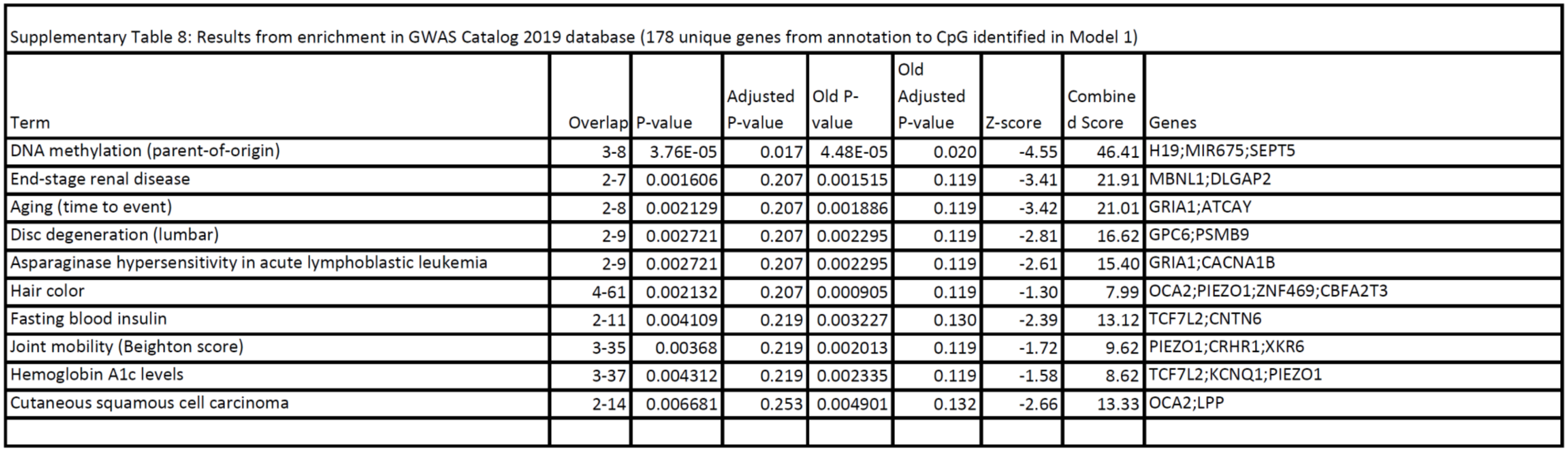
Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Z-score	Combined Score	Genes
hsa-miR-1538	28/1027	1.194E-07	4.05E-05	1.236E-09	4.1885E-07	-1.924	30.67	16;CTSD;GPC6;TBC1D22A;SLC39A3;NKX2-2;SRRM4;SLC12A5;RBFOX3;PRKCB;RASL10B;IRX4;MTUS2;KCNAB2;BAIAP2;C1ORF159;
hsa-miR-4745-3p	28/1027	1.194E-07	4.05E-05	1.236E-09	4.1885E-07	-1.917	30.56	16;CTSD;GPC6;TBC1D22A;SLC39A3;NKX2-2;SRRM4;SLC12A5;RBFOX3;PRKCB;RASL10B;IRX4;MTUS2;KCNAB2;BAIAP2;C1ORF159;
hsa-miR-3180	32/1475	2.206E-06	0.000299	1.538E-08	2.0856E-06	-2.443	31.82	ROH5;MCF2L;PRDM16;ZNF469;QSOX2;TBC1D22A;GALNT9;SLC39A3;NKX2-2;ANKS1B;ENTPD2;SLC12A5;TPSG1;MTUS2;KCNAB2;BAIAP2;CBFA2T3;SEPT5;KCNQ1;H
hsa-miR-3180-3p	32/1475	2.206E-06	0.000299	1.538E-08	2.0856E-06	-2.438	31.75	ROH5;MCF2L;PRDM16;ZNF469;QSOX2;TBC1D22A;GALNT9;SLC39A3;NKX2-2;ANKS1B;ENTPD2;SLC12A5;TPSG1;MTUS2;KCNAB2;BAIAP2;CBFA2T3;SEPT5;KCNQ1;H
hsa-miR-3196	32/1475	2.206E-06	0.000299	1.538E-08	2.0856E-06	-2.433	31.68	ROH5;MCF2L;PRDM16;ZNF469;QSOX2;TBC1D22A;GALNT9;SLC39A3;NKX2-2;ANKS1B;ENTPD2;SLC12A5;TPSG1;MTUS2;KCNAB2;BAIAP2;CBFA2T3;SEPT5;KCNQ1;H
hsa-miR-3186-3p	11/270	3.152E-05	0.003562	5.718E-06	0.00043072	-1.241	12.86	KCNT1;ATCAY;C1ORF159;CHRNA4;TMEM139;PRDM16;PLD6;BAIAP2;CBFA2T3;LPP;SLC39A3
hsa-miR-4707-5p	24/1113	5.295E-05	0.004906	1.543E-06	0.00017431	-1.926	18.96	ABR;RXRA;KCNT1;JPH3;ATCAY;B3GNT6;MFNG;CDH22;PRDM16;PIEZO1;HCN2;GALNT9;SLC39A3
hsa-miR-1268	23/1055	6.513E-05	0.004906	2.207E-06	0.00018702	-1.882	18.14	IAP2;CBFA2T3;LPP;ATCAY;TRIM29;KCNQ1;EFCAB2;QSOX2;DLGAP2;HCN2;GALNT9;SLC39A3
hsa-miR-1268b	23/1055	6.513E-05	0.004906	2.207E-06	0.00018702	-1.877	18.09	IAP2;CBFA2T3;LPP;ATCAY;TRIM29;KCNQ1;EFCAB2;QSOX2;DLGAP2;HCN2;GALNT9;SLC39A3
hsa-miR-1250	15/528	7.953E-05	0.005392	8.034E-06	0.0004952	-1.347	12.72	RBFOX3;CHRNA4;MTUS2;GATA4;KCNAB2;ADARB2;CBFA2T3;SEPT5;MYLK4;C16ORF82;MPPED1;MCF2L;EFCAB2;ZNF469;HCN2
hsa-miR-4462	19/814	0.0001229	0.006944	7.411E-06	0.0004952	-1.614	14.54	GRIA1;SLC12A5;PRKCB;CHRNA4;RASL10B;GBE1;FUT10;FLT4;CACNA1B;GATA4;ADARB2;JPH3;MPPED1;MROH5;MCF2L;TBC1D22A;PLXNA4;GALNT9;SLC39A3
hsa-miR-3621	14/487	0.0001222	0.006944	1.446E-05	0.0007815	-1.296	11.67	TOR4A;RASL10B;ATP2B2;SEPT5;ATCAY;TRIM29;MCF2L;EFCAB2;KCNQ2;PRDM16;TTPAL;TBC1D22A;PLXNA4;GALNT9
hsa-miR-3676	16/629	0.0001649	0.007987	1.506E-05	0.0007815	-1.450	12.63	MEF2A;GRIA1;RYR2;MTUS2;GATA4;ADARB2;LPP;C1ORF159;PRDM16;GSE1;BUB3;DLGAP2;GPC6;TBC1D22A;PLXNA4;GALNT9
hsa-miR-191	15/561	0.000155	0.007987	1.614E-05	0.0007815	-1.339	11.75	TCF7L2;SLC12A5;CHRNA4;IRX4;ATP2B2;KCNAB2;CBFA2T3;LPP;SEPT5;GLIS1;AJAP1;ABR;RXRA;PRDM16;PLXNA4
hsa-miR-4467	18/803	0.0003049	0.013781	2.244E-05	0.00101408	-1.601	12.96	MEF2A;FCN1;TOR4A;SLC12A5;IRX4;CELF4;CHD5;MTUS2;C2CD4C;PLD6;ADARB2;GLIS1;RXRA;PIEZO1;DLGAP2;HCN2;GALNT9;NKX2-2
hsa-miR-3193	16/695	0.0004984	0.019826	4.896E-05	0.00176735	-1.432	10.89	TOR4A;CHRNA4;CACNA1B;CELF4;C2CD4C;NPL;ADARB2;CBFA2T3;ABR;RXRA;KCNT1;JPH3;GSE1;DLGAP2;DSCAML1;TBC1D22A
hsa-miR-339-3p	13/497	0.0005264	0.019826	7.614E-05	0.00222858	-1.226	9.26	ENTPD2;RBFOX3;IRX4;CHD5;C2CD4C;BAIAP2;LPP;CACNA1G;MYLK4;RXRA;PRDM16;ZNF469;HCN2
hsa-miR-574-3p	12/431	0.0004986	0.019826	8.217E-05	0.00222858	-1.172	8.91	WWTR1;RXRA;KCNT1;RASL10B;PRDM16;MTUS2;QSOX2;PLD6;CBFA2T3;SLC39A3;ANKS1B;MYLK4
hsa-miR-3177-3p	16/713	0.000656	0.023411	6.581E-05	0.00210085	-1.459	10.69	CHRNA4;CACNA1B;C2CD4C;KCNAB2;BAIAP2;GLIS1;CRHR1;CAPN14;C1ORF159;B3GNT6;PIP5KL1;MCF2L;TTPAL;ALDH7A1;PLXNA4;SLC39A3
hsa-miR-3178	17/789	0.0007014	0.023776	6.263E-05	0.00210085	-1.561	11.34	TOR4A;SLC12A5;RBFOX3;RASL10B;FLT4;BAIAP2;CBFA2T3;LPP;MRC2;ABR;RXRA;MCF2L;DLGAP2;TBC1D22A;PLXNA4;HCN2;GALNT9
hsa-miR-564	22/1188	0.0008977	0.0279	4.579E-05	0.00176735	-1.966	13.79	RA;ATCAY;C10ORF71;C1ORF159;B3GNT6;PIP5KL1;PRDM16;QSOX2;DLGAP2;PLXNA4;ANKS1B
hsa-miR-1306	11/398	0.0009053	0.0279	0.0001748	0.00408772	-1.199	8.40	ATCAY;PRKCB;CHRNA4;MCF2L;PRDM16;MTUS2;DSCAML1;LPP;PLXNA4;SLC39A3;NKX2-2
hsa-miR-615-3p	13/531	0.0009684	0.028547	0.0001449	0.00353192	-1.273	8.83	MEF2A;GRIA1;UNC5A;PRKCB;FLT4;CHD5;KCNAB2;PLD6;AJAP1;RXRA;C1ORF159;MICALL2;GSE1
hsa-miR-4707-3p	21/1145	0.0013297	0.037069	7.995E-05	0.00222858	-1.884	12.48	TOR4A;RBFOX3;CHRNA4;FLT4;IRX4;C2CD4C;KCNAB2;BAIAP2;LPP;SEPT5;C1QTNF4;ATCAY;C1ORF159;TMEM139;MCF2L;KCNQ2;PRDM16;QSOX2;TTPAL;TBC1D22A;HCN2
hsa-miR-4665-3p	10/356	0.0013669	0.037069	0.0003065	0.00593688	-1.093	7.21	ABR;SLC12A5;UNC5A;FLT4;KCNQ2;PRDM16;CELF4;GSE1;DLGAP2;AJAP1
hsa-miR-1908	29/1849	0.0018737	0.043806	4.953E-05	0.00176735	-3.059	19.21	PRDM16;DLGAP2;TBC1D22A;PLXNA4;SLC39A3;SRRM4;ENTPD2;SLC12A5;SLC6A18;RASL10B;ATP2B2;KCNAB2;BAIAP2;CBFA2T3;SEPT5;B3GNT6;HCN2
hsa-miR-663	29/1849	0.0018737	0.043806	4.953E-05	0.00176735	-3.051	19.16	PRDM16;DLGAP2;TBC1D22A;PLXNA4;SLC39A3;SRRM4;ENTPD2;SLC12A5;SLC6A18;RASL10B;ATP2B2;KCNAB2;BAIAP2;CBFA2T3;SEPT5;B3GNT6;HCN2
hsa-miR-3131	13/569	0.0017953	0.043806	0.0002797	0.00557854	-1.195	7.56	SLC12A5;CHD5;C2CD4C;ADARB2;PRLR;MYLK4;JPH3;C1ORF159;EFCAB2;DLGAP2;PLXNA4;SLC39A3;ANKS1B
hsa-miR-611	13/569	0.0017953	0.043806	0.0002797	0.00557854	-1.187	7.51	SLC12A5;CHD5;C2CD4C;ADARB2;PRLR;MYLK4;JPH3;C1ORF159;EFCAB2;DLGAP2;PLXNA4;SLC39A3;ANKS1B
mmu-miR-767	28/1784	0.0022365	0.049	6.817E-05	0.00210085	-2.893	17.65	ZNF469;GPC6;TBC1D22A;PLXNA4;MEF2A;PRKCB;RASL10B;MTUS2;ATP2B2;KCNAB2;BAIAP2;PRLR;CAPN14;DIAPH1;TTPAL;XKR6
hsa-miR-4638-5p	21/1196	0.0022568	0.049	0.0001459	0.00353192	-1.911	11.65	SRRM4;RBFOX3;CHRNA4;FUT10;FLT4;CACNA1B;LPP;MYLK4;ATCAY;ALCAM;C1ORF159;MPPED1;B3GNT6;KCNQ2;GSE1;CTSD;DLGAP2;TBC1D22A;HCN2;GALNT9;SLC39A3
hsa-miR-4738-5p	17/887	0.0024572	0.049	0.0002486	0.00526688	-1.544	9.28	TOR4A;KCNAB2;ADARB2;LPP;CRHR1;RXRA;KCNT1;ATCAY;C1ORF159;MFNG;TMEM139;KCNQ2;PRDM16;DMRTB1;DLGAP2;WDFY4;GALNT9
hsa-miR-4431	10/383	0.0023355	0.049	0.0005356	0.00864691	-1.040	6.30	TOR4A;SRRM4;CDH22;PRDM16;GSE1;ADARB2;LPP;PLXNA4;NKX2-2;AJAP1
hsa-miR-937	6/152	0.0024265	0.049	0.0009714	0.01197923	-0.335	2.02	SLC12A5;MCF2L;PRDM16;IRX4;C2CD4C;CBFA2T3

SUPPLEMENTARY DATA

Supplementary Table 7: Results from enrichment in ENCODE Histone Modification 2015 database (178 unique genes from annotation to CpG identified in Model 1)

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Z-score	Combined Score	Genes
H3K27me3_ES-Bruce4_mm9	48/2000	9.6E-11	3.9E-08	9.34E-20	3.81E-17	-1.75	40.27	PTPRU;RYR2;CHRNA4;ONECUT3;CACNA1B;CELF4;CHD5;GATA4;ADARB2;TRHDE;GLIS1;CRHR1;CACNA1G;C1QTNF4;MRC2;IGSF21;RXRA;JPH3;ALCAM;MROH5;CDH22;PRDM16;DMRTB1;PHACTR3;MICALL2;DLGAP2;PLXNA4;NKX2-2; ANKS1B;DIO3OS;SLC12A5;UNC5A;RBFOX3;PRKCB;RASL10B;CCDC109B;IRX4;ATP2B2;TACR1;BAIAP2;SEPT5;AJAP1;FAM101B;MPPED1;KCNQ1;KCNQ2;DSCAML1;HCN2
H3K27me3_C2C12_mm9	34/1269	6.5E-09	1.3E-06	3.02E-15	6.16E-13	-1.75	33.09	PTPRU;RYR2;CHRNA4;ONECUT3;FLT4;CELF4;DMKN;CRHR1;CACNA1G;C1QTNF4;IGSF21;JPH3;MROH5;MCF2L;CDH22;DMRTB1;BAI1;DLGAP2;PLXNA4;GALNT9;SLC12A5;UNC5A;RBFOX3;RASL10B;ATP2B2;MIR200B;TACR1;CBFA2T3;GFRA4;PSMB9;MPPED1;KCNQ1;KCNQ2;HCN2
H3K27me3_myocyte_mm9	28/1183	2E-06	0.00027	2.12E-11	1.44E-09	-1.72	22.53	PTPRU;RYR2;CHRNA4;ONECUT3;C2CD4C;DMKN;GLIS1;CRHR1;CACNA1G;C1QTNF4;KCNT1;MUC2;JPH3;MROH5;MCF2L;CDH22;BAI1;DLGAP2;PLXNA4;GALNT9;NKX2-2;ENTPD2;RBFOX3;RASL10B;CBFA2T3;GFRA4;MPPED1;HCN2
H3K27me3_small intestine_mm9	38/2000	5.1E-06	0.00052	2E-12	1.81E-10	-1.61	19.67	PTPRU;RYR2;CHRNA4;ONECUT3;CACNA1B;CHD5;GATA4;C2CD4C;NPL;TRHDE;CRHR1;C1QTNF4;IGSF21;KCNT1;JPH3;MROH5;PRDM16;PHACTR3;BAI1;DLGAP2;PLXNA4;GALNT9;NKX2-2;ANKS1B;WWTR1;SLC12A5;UNC5A;RBFOX3;PRKCB;RASL10B; IRX4;ATP2B2;AJAP1;MPPED1;KCNQ2;ANKRD60;DSCAML1;HCN2
H3K27me3_kidney epithelial cell_hg19	40/2217	9.5E-06	0.00077	2.22E-12	1.81E-10	-1.65	19.08	GRIA1;OCA2;RYR2;CHRNA4;CPNE4;AIRE;FLT4;CACNA1B;CHD5;GATA4;C2CD4C;NPL;ADARB2;CACNA1G;C1QTNF4;IGSF21;KCNT1;JPH3;ATCAY;C10ORF71;MCF2L;PRDM16;PHACTR3;BAI1;PLXNA4;GALNT9;NKX2-2;ANKS1B;SRRM4;ENTPD2;SPHKAP;TPSG1; PRKCB;KCNIP4;IRX4;TACR1;GFRA4;AJAP1;C16ORF82;HAR1B
H3K27me3_kidney_mm9	32/1675	3E-05	0.00169	1.41E-10	7.19E-09	-1.68	17.54	PTPRU;RYR2;ONECUT3;SCHIP1;CACNA1B;CELF4;CHD5;GATA4;C2CD4C;TRHDE;CRHR1;CACNA1G;C1QTNF4;IGSF21;JPH3;CDH22;PRDM16;BAI1;DLGAP2;NKX2-2;DIO3OS;SRRM4;RBFOX3;PRKCB;CCDC109B;KCNIP4;MTUS2;GFRA4;KCNQ2;ANKRD60;DSCAML1;HCN2
H3K27me3_bronchial epithelial cell_hg19	37/2082	3.1E-05	0.00169	2.84E-11	1.66E-09	-1.61	16.67	GRIA1;OCA2;RYR2;CPNE4;ONECUT3;FLT4;CACNA1B;CELF4;CHD5;C2CD4C;ADARB2;TRHDE;CACNA1G;C1QTNF4;IGSF21;JPH3;ATCAY;C10ORF71;MCF2L;CDH22;PHACTR3;GPC6;PLXNA4;ANKS1B;SRRM4;SPHKAP;PRKCB;IRX4;ATP2B2;TACR1;PRLR;GFRA4;AJAP1;MPPED1;KCNQ2;GPR123;DSCAML1
H3K27me3_endothelial cell of umbilical vein_hg19	52/3393	3.3E-05	0.00169	1.98E-13	2.69E-11	-1.53	15.76	PTPRU;RYR2;ONECUT3;FLT4;CELF4;CHD5;DMKN;MYLK4;C1QTNF4;KCNT1;JPH3;ATCAY;OR2AE1;MCF2L;PHACTR3;BAI1;GALNT9;ANKS1B;SRRM4;ENTPD2;UNC5A;PRKCB;AZGP1P1;TACR1;PRLR;OR1N2;GFRA4;MPPED1;KCNQ1;KCNQ2;GPR123;DSCAML1;GRIA1;OCA2;CHRNA4;AIRE;CACNA1B;C2CD4C;NPL;TRHDE;GLIS1;IGSF21;CDH22;PRDM16;GPC6;NKX2-2;RASL10B;KCNIP4;IRX4 ;ATP2B2;HCN2;HAR1B
H3K27me3_spleen_mm9	34/2000	0.00016	0.00745	6.82E-10	3.09E-08	-1.57	13.66	PTPRU;CHRNA4;FUT10;GATA4;C2CD4C;NPL;PLD6;TRHDE;CRHR1;C1QTNF4;MRC2;IGSF21;KCNT1;ATCAY;ALCAM;MROH5;CDH22;MICALL2;GALNT9;NKX2-2;ANKS1B;WWTR1;ENTPD2;RBFOX3;RASL10B;MTUS2;ATP2B2;SEPT5;KCNQ1;KCNQ2; ANKRD60;DSCAML1;HCN2;XKR6
H3K27me3_BJ_hg19	34/2090	0.00037	0.01527	2.08E-09	8.47E-08	-1.53	12.09	OCA2;RYR2;CPNE4;FLT4;CELF4;CHD5;C2CD4C;CACNA1G;C1QTNF4;IGSF21;ABR;JPH3;ATCAY;MCF2L;CDH22;PRDM16;RPL38;PLXNA4;GALNT9;NKX2-2;ANKS1B;ENTPD2;UNC5A;PRKCB;KCNIP4;ATP2B2;TACR1;PRLR;GFRA4;AJAP1;MPPED1;KCNQ1;KCNQ2;GPR123

SUPPLEMENTARY DATA



Supplementary Table 8: Results from enrichment in GWAS Catalog 2019 database (178 unique genes from annotation to CpG identified in Model 1)

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Z-score	Combined Score	Genes
DNA methylation (parent-of-origin)	3-8	3.76E-05	0.017	4.48E-05	0.020	-4.55	46.41	H19;MIR675;SEPT5
End-stage renal disease	2-7	0.001606	0.207	0.001515	0.119	-3.41	21.91	MBNL1;DLGAP2
Aging (time to event)	2-8	0.002129	0.207	0.001886	0.119	-3.42	21.01	GRIA1;ATCAY
Disc degeneration (lumbar)	2-9	0.002721	0.207	0.002295	0.119	-2.81	16.62	GPC6;PSMB9
Asparaginase hypersensitivity in acute lymphoblastic leukemia	2-9	0.002721	0.207	0.002295	0.119	-2.61	15.40	GRIA1;CACNA1B
Hair color	4-61	0.002132	0.207	0.000905	0.119	-1.30	7.99	OCA2;PIEZO1;ZNF469;CBFA2T3
Fasting blood insulin	2-11	0.004109	0.219	0.003227	0.130	-2.39	13.12	TCF7L2;CNTN6
Joint mobility (Beighton score)	3-35	0.00368	0.219	0.002013	0.119	-1.72	9.62	PIEZO1;CRHR1;XKR6
Hemoglobin A1c levels	3-37	0.004312	0.219	0.002335	0.119	-1.58	8.62	TCF7L2;KCNQ1;PIEZO1
Cutaneous squamous cell carcinoma	2-14	0.006681	0.253	0.004901	0.132	-2.66	13.33	OCA2;LPP

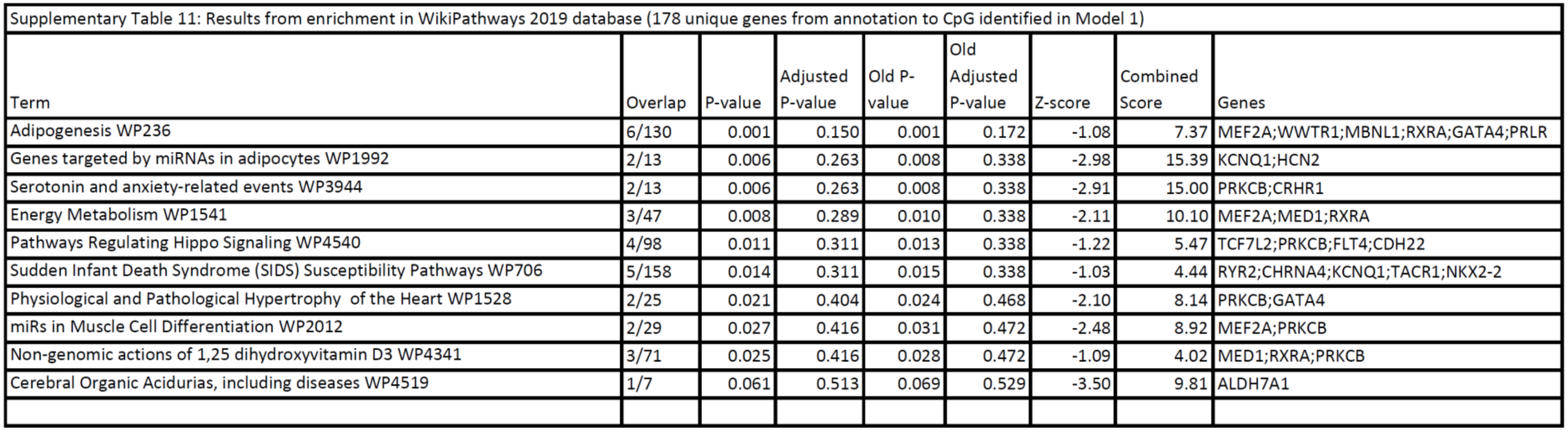
Supplementary Table 9: Results from enrichment in dbGAP (accessed 08/2019) database (178 unique genes from annotation to CpG identified in Model 1)

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Z-score	Combined Score	Genes
Body Height	14/385	9.49E-06	0.001	0.0002	0.02702	-2.36	27.29	GRIA1;RYR2;PRKCB;CACNA1B;TRHDE;IGSF21;ATIC;BPIFA3;WDR60;CDH22;BAI1;QSOX2;ANKRD60;XKR6
Body Mass Index	13/437	0.000153	0.008	0.0026	0.11918	-2.45	21.52	RYR2;MBNL1;RBFOX3;CPNE4;FUT10;USP34;KCNIP4;ADARB2;LPP;GLIS1;KCNT1;WDFY4;ANKS1B
Triglycerides	9/244	0.000348	0.013	0.0033	0.11918	-2.29	18.22	RBFOX3;CPNE4;AIRE;GBE1;KCNIP4;DLGAP2;DSCAML1;LPP;XKR6
Blood Pressure	12/454	0.000786	0.022	0.0095	0.14918	-2.30	16.44	RYR2;MPPED1;BPIFA3;CNTN6;KCNIP4;PHACTR3;MTUS2;ATP2B2;DSCAML1;GPC6;PRLR;PLXNA4
Electrocardiography	5/87	0.001082	0.024	0.005	0.13639	-1.96	13.37	RYR2;CPNE4;KCNQ1;ANKS1B;HLA-DPB2
Arthritis, Rheumatoid	4/59	0.001885	0.035	0.0069	0.14918	-1.80	11.28	PRKCB;AIRE;PHACTR3;TRHDE
Blood Pressure Determination	4/64	0.002543	0.040	0.009	0.14918	-1.88	11.24	TCF7L2;KCNIP4;ADARB2;PLXNA4
Echocardiography	8/273	0.003158	0.040	0.0197	0.19685	-1.97	11.36	CNTN6;CPNE4;SCHIP1;KCNIP4;ADARB2;GPC6;PLXNA4;GLIS1
Body Weight	7/216	0.003272	0.040	0.0178	0.19616	-1.97	11.25	RBFOX3;BPIFA3;CPNE4;WDR60;FUT10;USP34;LPP
Elbow	4/72	0.003898	0.043	0.0133	0.18237	-1.68	9.30	CCDC109B;PRDM16;KCNIP4;ADARB2

Supplementary Table 10: Results from enrichment in BioCarta 2016 database (178 unique genes from annotation to CpG identified in Model 1)

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Z-score	Combined Score	Genes
Role of PPAR-gamma Coactivators in Obesity and Thermogenesis_Homo sapiens_h_ppargPathway	2/9	0.003	0.158	0.004	0.256	-1.58	9.33	MED1;RXRA
Mechanism of Gene Regulation by Peroxisome Proliferators via PPARa_Homo sapiens_h_pparaPathway	3/52	0.011	0.285	0.013	0.314	-1.49	6.70	MED1;RXRA;PRKCB
Control of Gene Expression by Vitamin D Receptor_Homo sapiens_h_vdrPathway	2/27	0.024	0.285	0.030	0.314	-1.39	5.20	MED1;RXRA
VEGF, Hypoxia, and Angiogenesis_Homo sapiens_h_vegfPathway	2/30	0.029	0.285	0.036	0.314	-1.55	5.48	PRKCB;FLT4
Phospholipids as signalling intermediaries_Homo sapiens_h_edg1Pathway	2/33	0.035	0.285	0.042	0.314	-1.56	5.23	SPHKAP;PRKCB
Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling_Homo sapiens_h_At1rPathway	2/34	0.037	0.285	0.044	0.314	-1.69	5.58	MEF2A;PRKCB
Basic mechanism of action of PPARa, PPARb(d) and PPARg and effects on gene expression_Homo sapiens_h_pparPathway	1/5	0.044	0.285	0.056	0.314	1.76	-5.52	RXRA
Actions of Nitric Oxide in the Heart_Homo sapiens_h_no1Pathway	2/42	0.054	0.285	0.064	0.314	-1.14	3.33	RYR2;FLT4
Signal Dependent Regulation of Myogenesis by Corepressor MITR_Homo sapiens_h_MITRPathway	1/8	0.069	0.285	0.083	0.314	0.71	-1.89	MEF2A
CBL mediated ligand-induced downregulation of EGF receptors_Homo sapiens_h_cblPathway	1/8	0.069	0.285	0.083	0.314	0.77	-2.07	PRKCB

SUPPLEMENTARY DATA



Supplementary Table 11: Results from enrichment in WikiPathways 2019 database (178 unique genes from annotation to CpG identified in Model 1)

Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Z-score	Combined Score	Genes
Adipogenesis WP236	6/130	0.001	0.150	0.001	0.172	-1.08	7.37	MEF2A;WWTR1;MBNL1;RXRA;GATA4;PRLR
Genes targeted by miRNAs in adipocytes WP1992	2/13	0.006	0.263	0.008	0.338	-2.98	15.39	KCNQ1;HCN2
Serotonin and anxiety-related events WP3944	2/13	0.006	0.263	0.008	0.338	-2.91	15.00	PRKCB;CRHR1
Energy Metabolism WP1541	3/47	0.008	0.289	0.010	0.338	-2.11	10.10	MEF2A;MED1;RXRA
Pathways Regulating Hippo Signaling WP4540	4/98	0.011	0.311	0.013	0.338	-1.22	5.47	TCF7L2;PRKCB;FLT4;CDH22
Sudden Infant Death Syndrome (SIDS) Susceptibility Pathways WP706	5/158	0.014	0.311	0.015	0.338	-1.03	4.44	RYR2;CHRNA4;KCNQ1;TACR1;NKX2-2
Physiological and Pathological Hypertrophy of the Heart WP1528	2/25	0.021	0.404	0.024	0.468	-2.10	8.14	PRKCB;GATA4
miRs in Muscle Cell Differentiation WP2012	2/29	0.027	0.416	0.031	0.472	-2.48	8.92	MEF2A;PRKCB
Non-genomic actions of 1,25 dihydroxyvitamin D3 WP4341	3/71	0.025	0.416	0.028	0.472	-1.09	4.02	MED1;RXRA;PRKCB
Cerebral Organic Acidurias, including diseases WP4519	1/7	0.061	0.513	0.069	0.529	-3.50	9.81	ALDH7A1