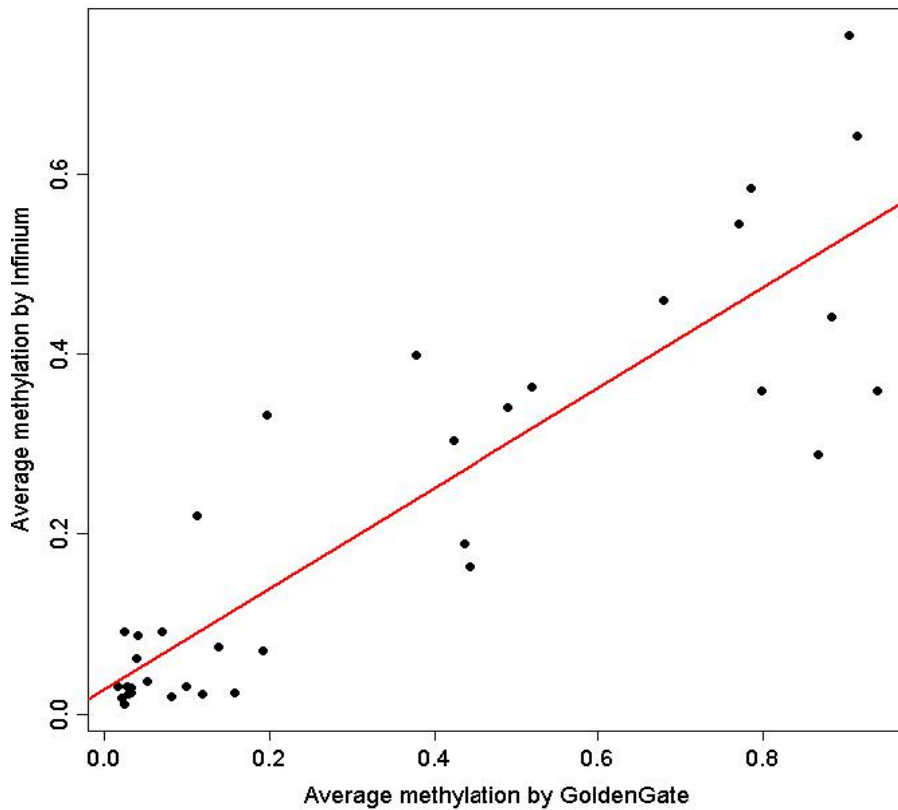


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**Supplemental Data**

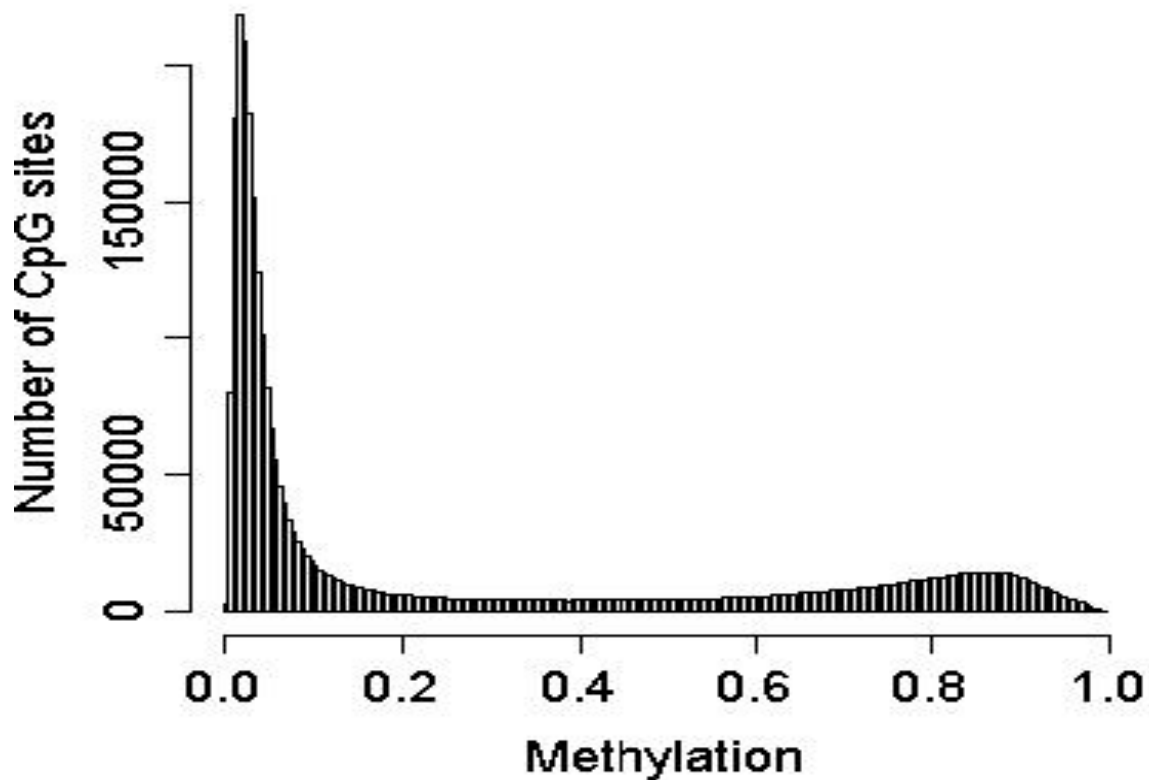
**DNA Methylation Signatures in Development  
and Aging of the Human Prefrontal Cortex**

**Shusuke Numata, Tianzhang Ye, Thomas M. Hyde, Xavier Guitart-Navarro, Ran Tao, Michael Winger, Carlo Colantuoni, Daniel R. Weinberger, Joel E. Kleinman, and Barbara K. Lipska**



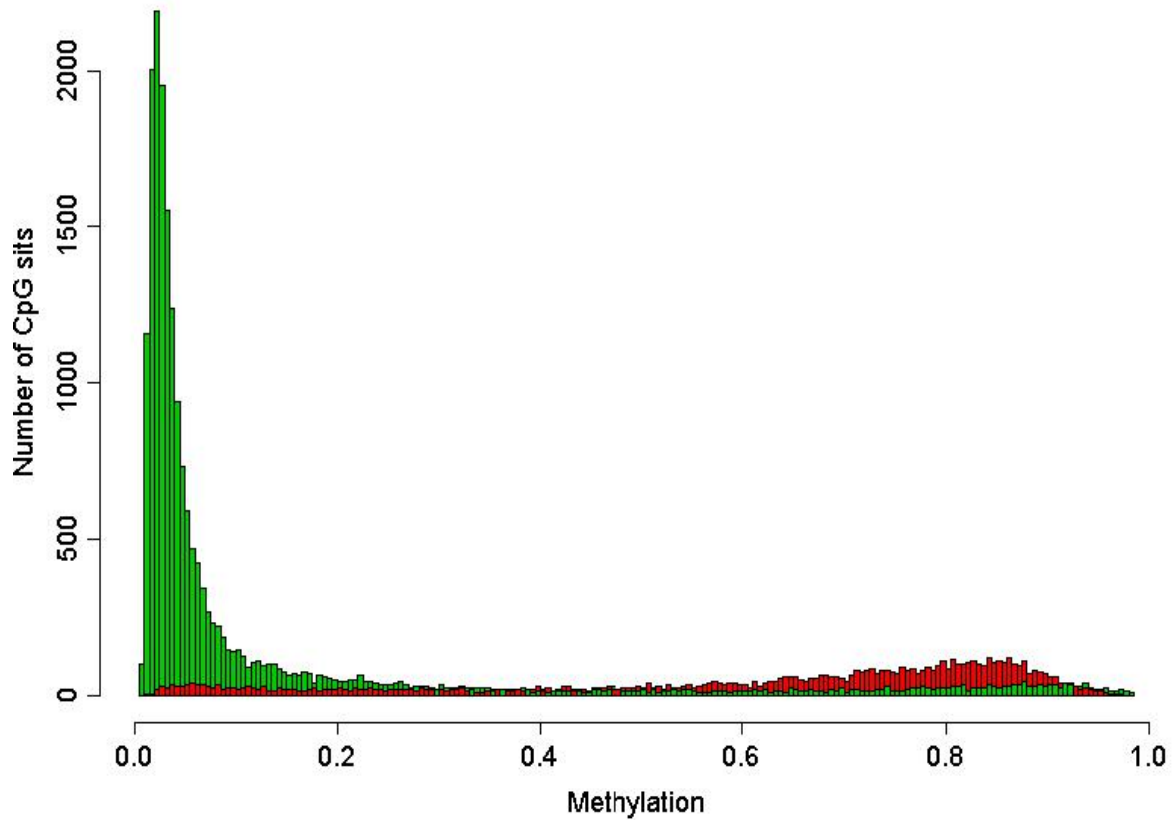
**Figure S1. Validation of DNA Methylation by Illumina GoldenGate Assay**

The x axis represents the mean methylation levels of 92 samples at 34 CpG sites using Illumina GoldenGate assay. The y axis represents the mean DNA methylation levels of the same samples at the same CpG sites using Illumina Infinium assay. A high correlation between the two platforms ( $r^2=0.79$ ) was observed.



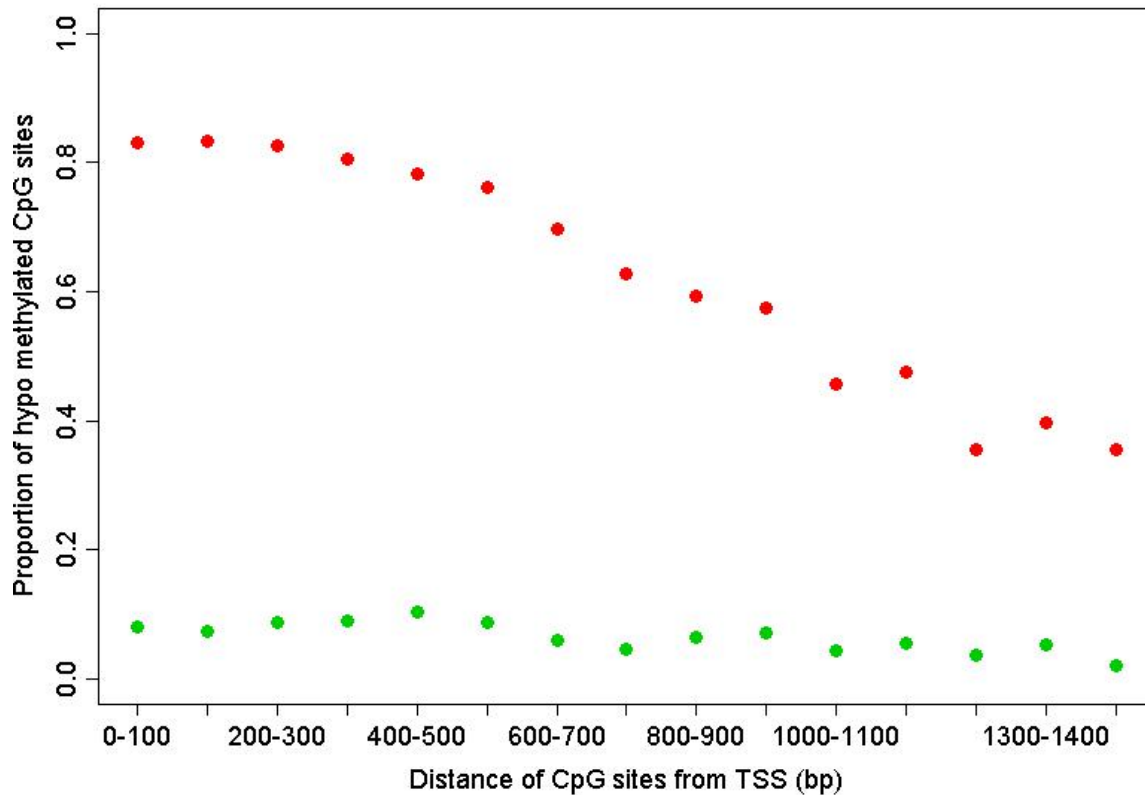
**Figure S2. DNA Methylation Levels across All Samples and all CpG Sites**

The x axis of the histogram represents the methylation levels (beta values = the ratios of signal from a methylated probe relative to the sum of both methylated and unmethylated probes). The y axis represents the number of CpG sites. The DNA methylation levels across all samples (N = 108) and all the methylation sites (N = 27,578) showed a bimodal distribution with 63.3% of loci hypomethylated ( $\beta < 0.2$ ), 13% of loci hypermethylated ( $\beta > 0.8$ ).



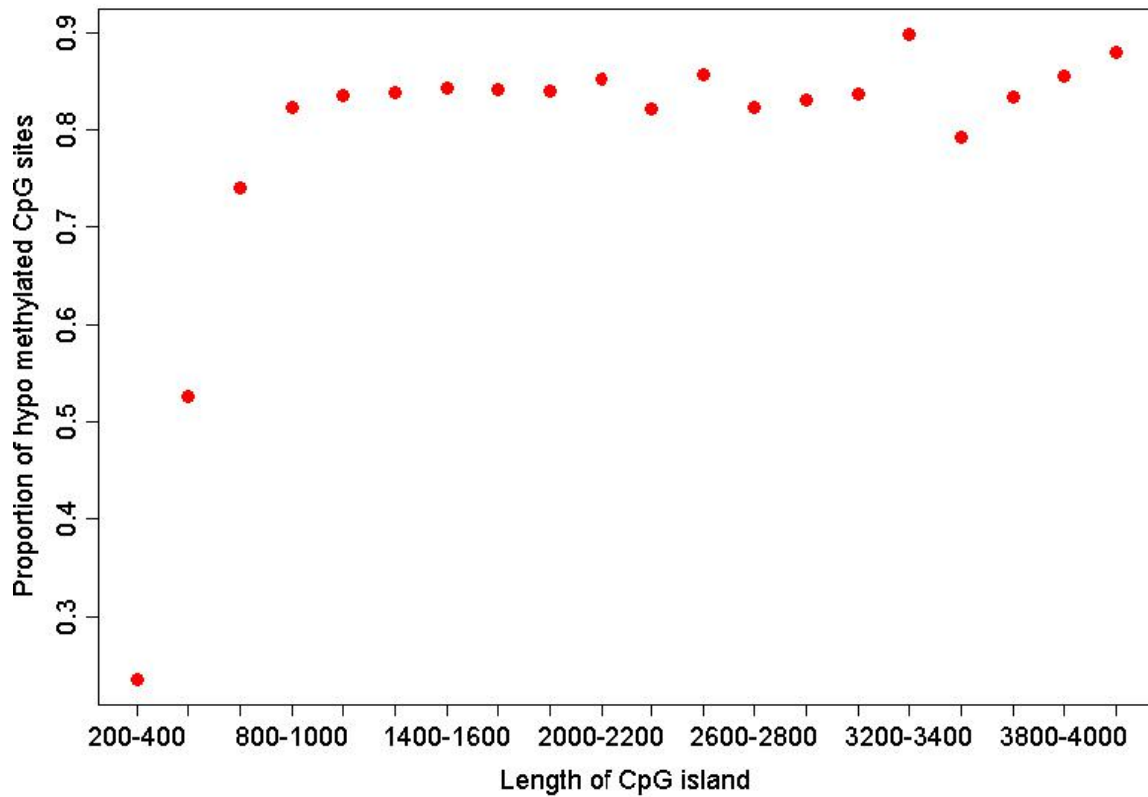
**Figure S3. DNA Methylation in CpG Islands (CGIs) and Non-CpG Islands**

The x axis represents the mean methylation levels of 108 samples. The y axis represents the number of CpG sites (total 27,578 CpG sites). CpG sites in CGIs are colored green and CpG sites in non-CGIs are colored red. The mean methylation levels of sites in non-CGIs were significantly higher than the sites in CGIs.



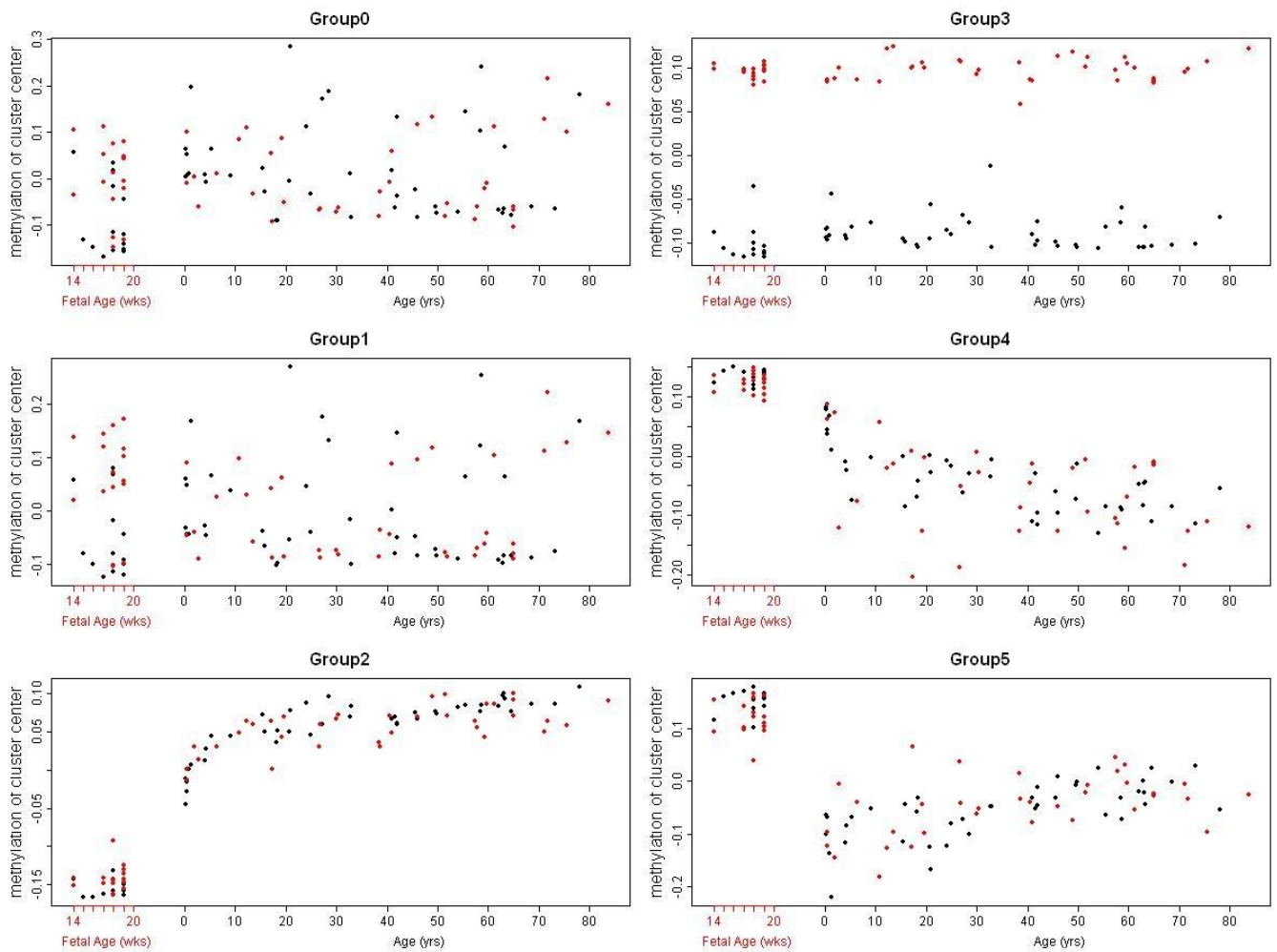
**Figure S4. Relationship between Methylation and the Distance from Transcription Start Sites (TSS)**

The x axis represents the distance of CpG site (in base pairs) from TSS. The y axis represents the proportion of hypomethylated CpG sites ( $\beta < 0.2$ ). CpG sites in CpG islands (CGIs) are colored red and CpG sites in non-CGIs are colored green. The longer the distance the higher was the proportion of hyper-methylated CpG sites located in CGIs. No such relationship was observed for the CpG sites in non-CGIs.



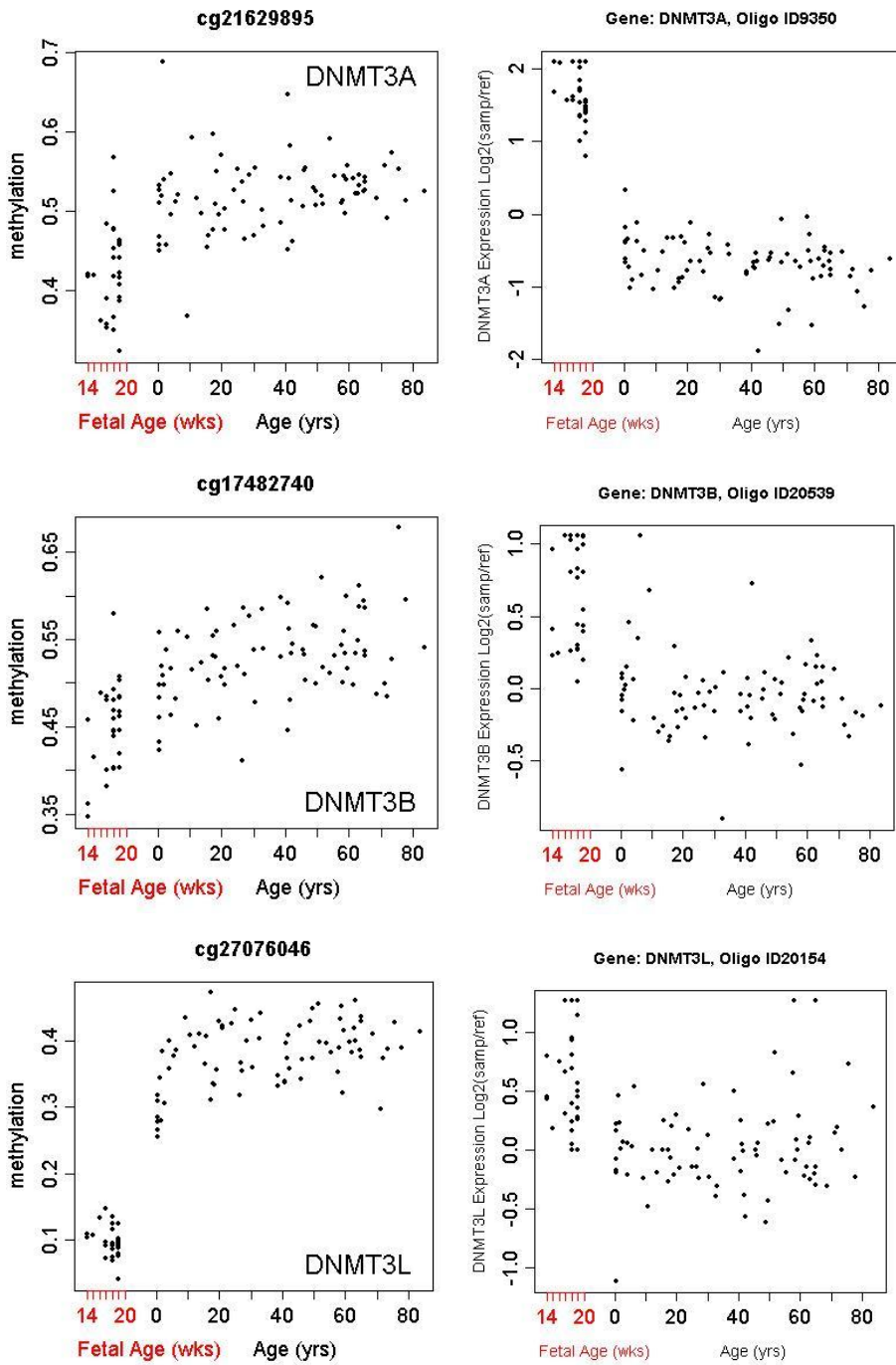
**Figure S5. Relationship between Methylation and the Length of CpG Islands**

The x axis represents the length of CpG islands (CGIs) in base pairs. The y axis represents the proportion of hypomethylated CpG sites ( $\beta < 0.2$ ). A relatively higher proportion of hypo-methylated CpG sites were observed in larger CGIs as compared to small CGIs (< 1,000 bp).



**Figure S6. Module-Specific Patterns of DNA Methylation during the Lifespan**

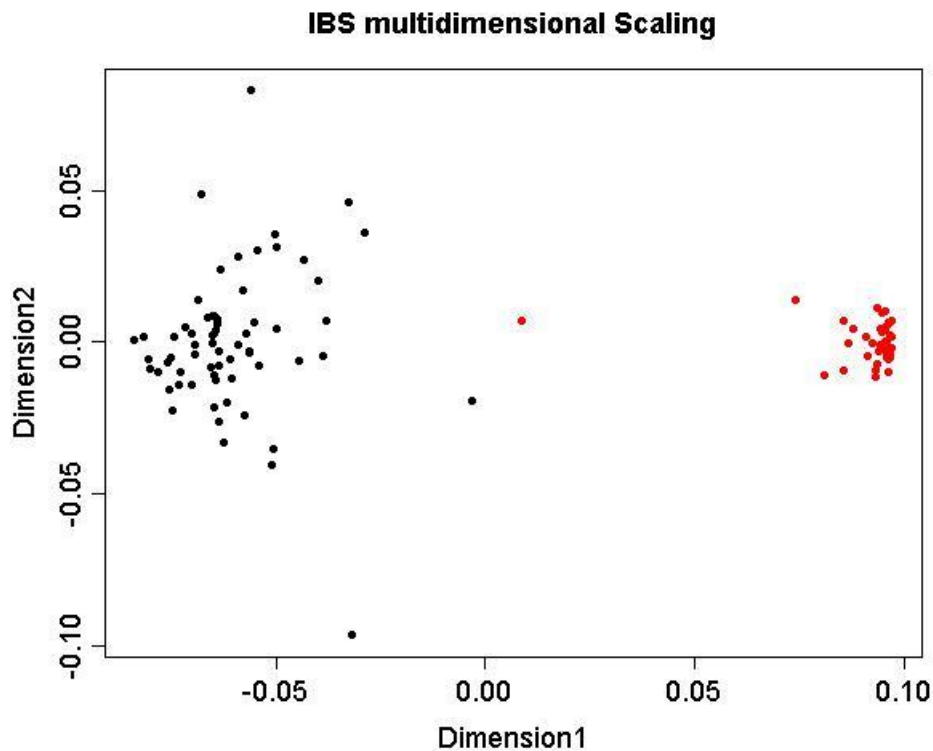
Group 0 contains all unclassified loci. Groups 1-5 contain loci classified according to weighted correlation network analysis (WGCNA). X axis represents age (fetal age in gestational weeks, postnatal age in years), Y axis represents methylation in the arbitrary units with 0 corresponding to the methylation status of the module center.



**Figure S7. DNA Methylation (Panels on the Left Side) and Expression (Right Side) Patterns of DNMT3 Genes**



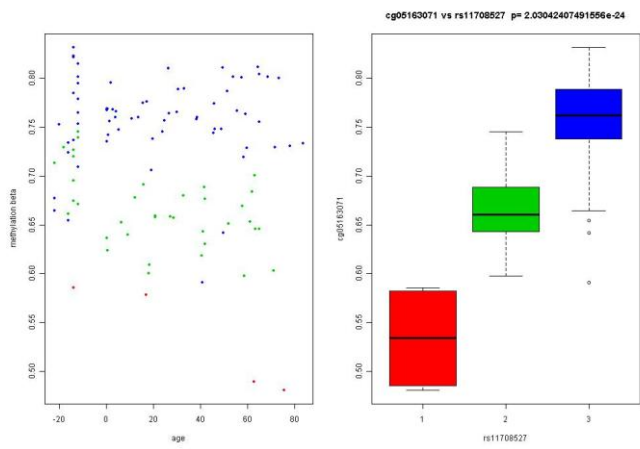
Expression levels of DNMT3A, DNMT3B and DNMT3L are high in fetal samples and drop by birth, whereas DNA methylation increases from the fetal period to postnatal life. There is a significant inverse correlation between expression and methylation for all three genes ( $p < 10^{-6}$ ).



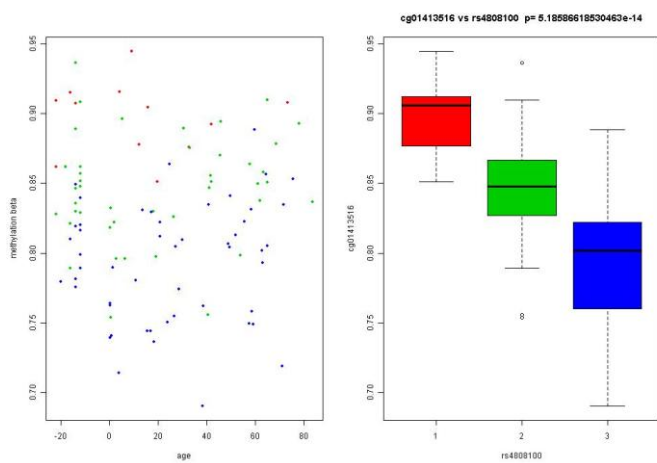
**Figure S8. Multidimensional Scaling Plot Visualizing Genetic Structure of the Cohort**

In the Identity-by-state plot in PLINK using 605,371 genotypic markers in all 108 subjects included in the study, two distinct clusters were identified, corresponding to Caucasians (red dots) and African Americans (black dots). One outlier (a red dot in the center of the graph) was removed from mQTL analysis.

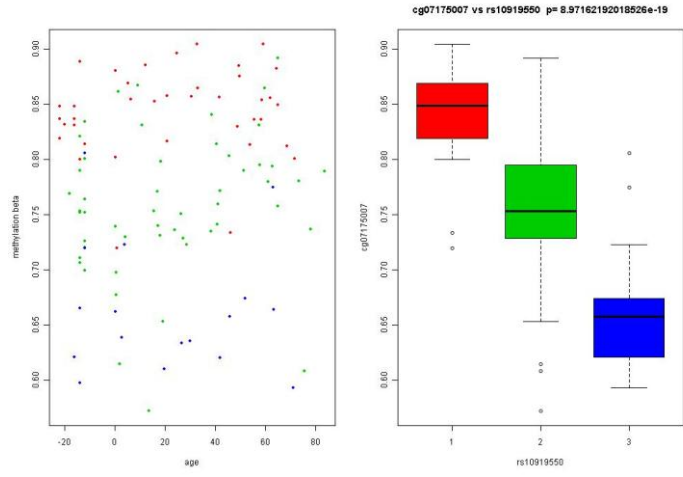
A.



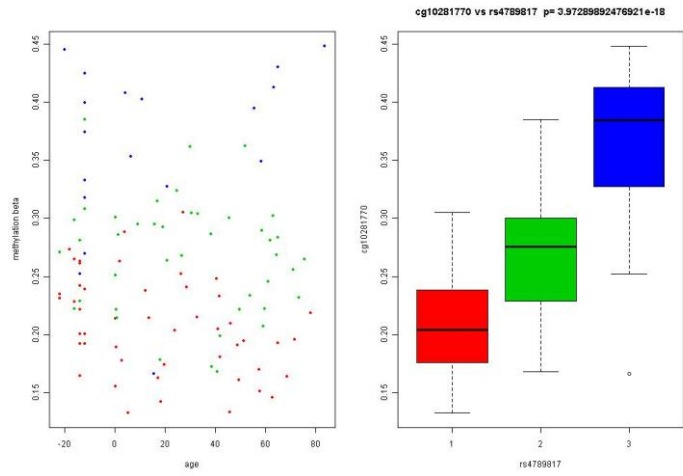
B.



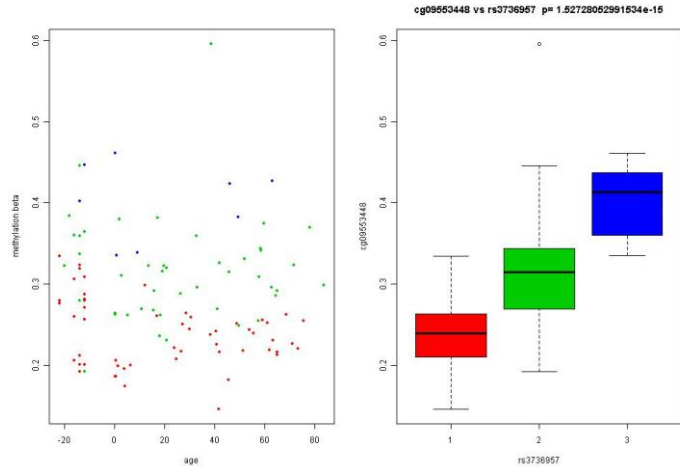
C.



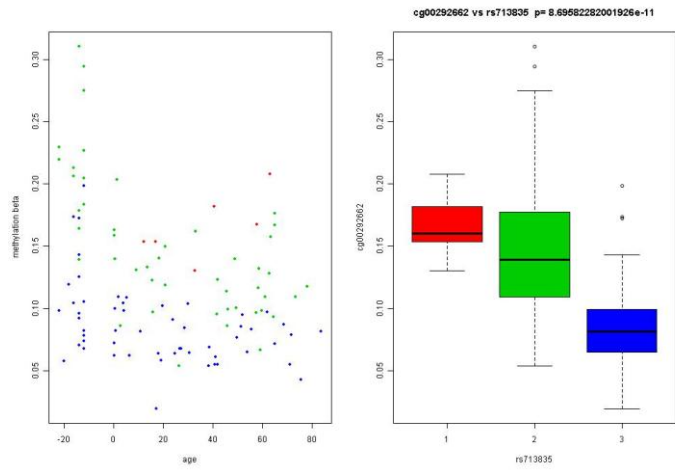
D.



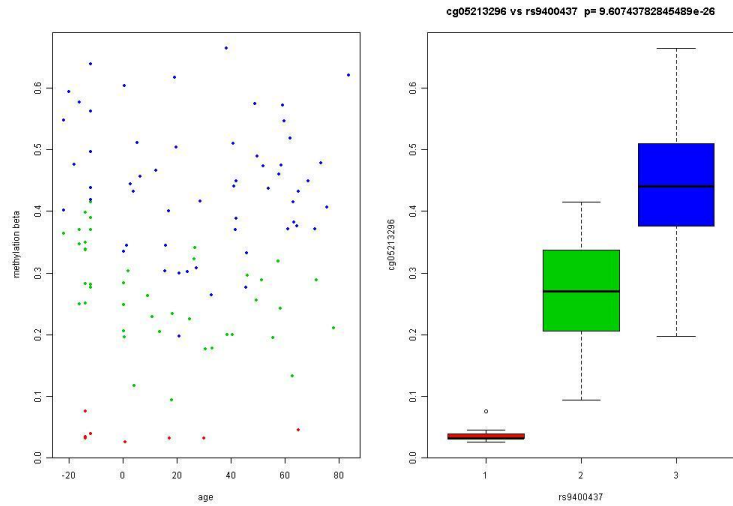
E.



F.



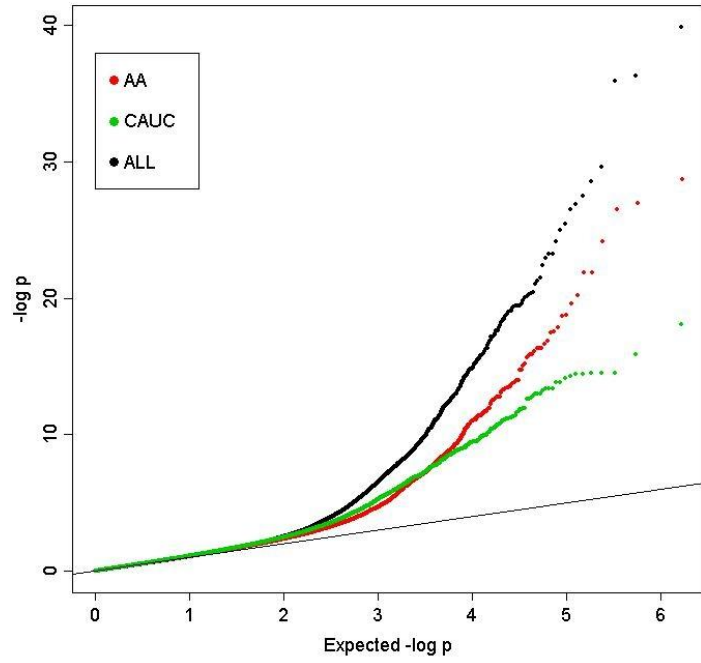
G.



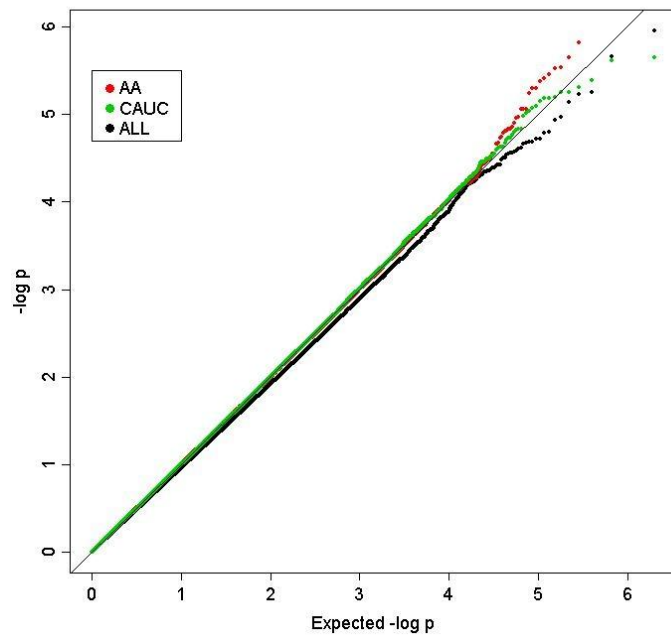
**Figure S9. Examples of SNP-DNA Methylation Associations across the Lifespan**

The differences in DNA methylation between the genotypic groups are consistent and apparent across the entire lifespan as shown in the scatterplots. Associations between A) *RETNLB* (cg05163071) and rs11708527 in *RETNLB*; B) *INSL3* (cg01413516) and rs4808100 in *INSL3*; C) *UHMK1* (cg07175007) and rs10919550 in *UHMK1*; D) *WDR45L* (cg10281770) and rs4789817 in *WDR45L*; E) *NUP214* (cg09553448) and rs3736957 in *NUP214*; F) *LGALS1* (cg00292662) and rs713835 in *CRYBB3* (located on the same chromosome as *LGALS1*); G) *BXDC1* (cg05213296) and rs9400437 in *GTF3C6* (located in the proximity of *BXDC1*).

A.



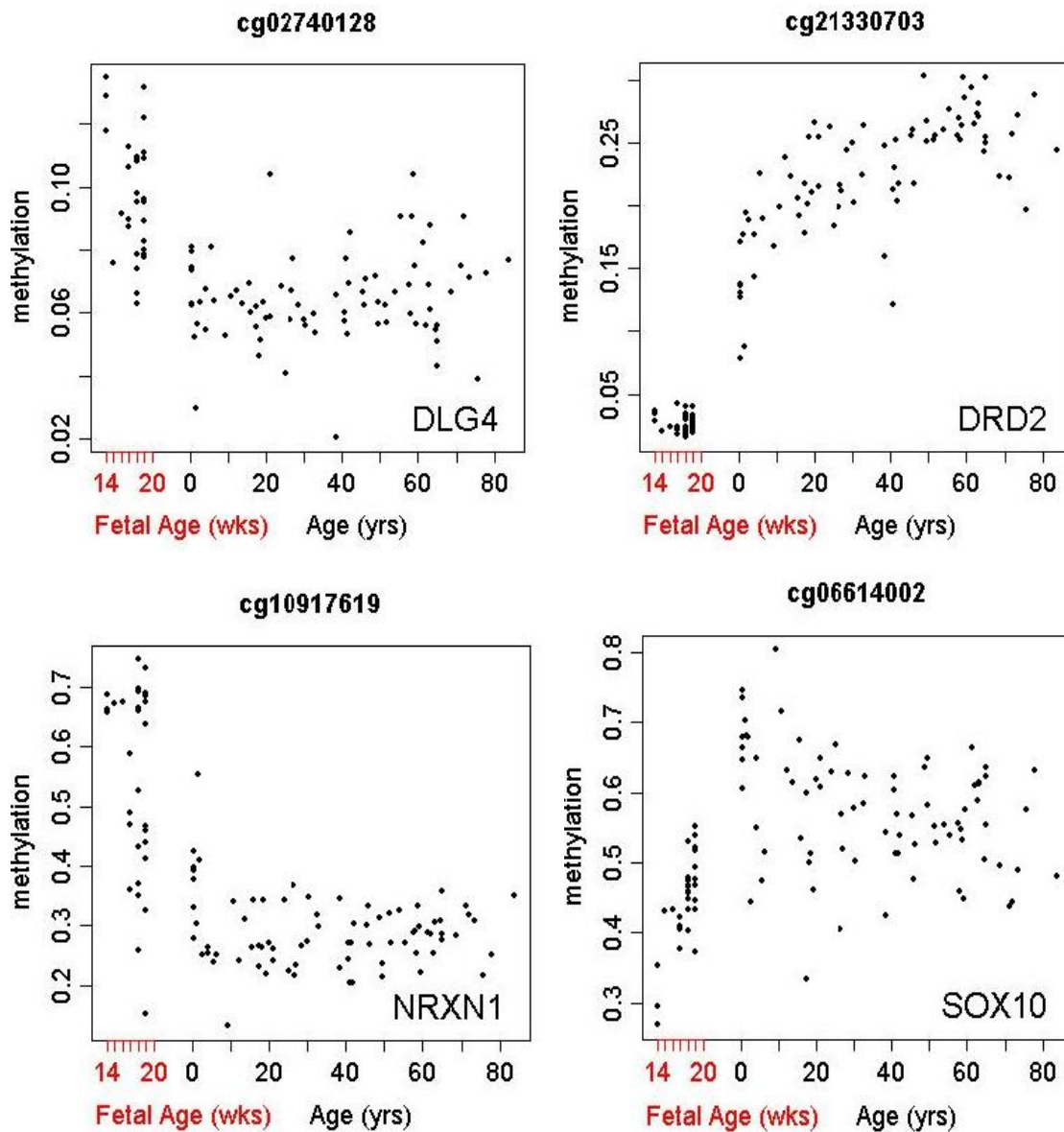
B.



### Figure S10. Q-Q Plots of Observed versus Expected Association Strength

(A) All *cis*-associations (1.07 million). Both plots show analysis of associations across all samples (black), as well as within African American (red) and Caucasian (green) samples separately. (B) One million randomly selected associations across all possible associations (*cis*- and *trans*-). The expected  $-\log p$  was calculated as:  $-\log_{10}[(i-0.5)/n]$  where  $i$  takes on values from 1 –  $n$ ; creating a uniform distribution of expected  $p$  values. Vertical departure of the fits from the black identity line indicates abundances of extreme  $p$  values among the observed associations.





**Figure S11. Age-Related Methylation Changes in DLG4, DRD2, NRXN1, and SOX10**

The x axis represents age, and the y axis represents DNA methylation levels. The CpG site in DLG4 (cg02740128) showed a significant age-related decrease during

the fetal period ( $p = 3.6 \times 10^{-4}$ ). The CpG site in DRD2 (cg21330703) showed significant age-related increases during childhood and in older ages ( $p = 2.4 \times 10^{-4}$  and  $p = 2.2 \times 10^{-5}$ , respectively). The CpG site in NRXN1 (cg10917619) showed significant age-related decreases during the fetal period and childhood ( $p = 4.2 \times 10^{-4}$  and  $p = 1.0 \times 10^{-3}$ , respectively). The CpG site in SOX10 (cg06614002) showed a significant age-related increase during the fetal period ( $p = 1.2 \times 10^{-6}$ ) and decreases during childhood and in older ages ( $p = 1.3 \times 10^{-5}$  and  $p = 1.1 \times 10^{-4}$ , respectively).

**Table S1. Demographic Data**

Subject	PMI	Sex	Race	Nicotine	pH	MannerOfDeath	Age (years)
1	33.5	F	CAUC	No	6.49	Accident	83.64
2	21.5	M	CAUC	No	6.87	Natural	77.99
3	50	F	CAUC	No	6.26	Natural	75.57
4	68.5	M	AA	Yes	6.41	Natural	73.28
5	25	F	AA	No	6.47	Natural	71.82
6	23.5	F	CAUC	No	6.16	Natural	71.11
7	58	M	AA	No	6.72	Natural	68.59
8	57.5	F	AA	No	6.57	Natural	65.04
9	28.5	F	AA	Yes	6.65	Natural	64.96
10	52.5	F	AA	No	6.83	Natural	64.91
11	53.5	M	AA	No	6.57	Natural	64.56
12	26	M	CAUC	No	6.74	Natural	63.24
13	45.5	M	CAUC	No	6.2	Accident	63.00
14	37	M	AA	No	6.79	Natural	62.78
15	19.5	M	CAUC	Yes	6.27	Natural	61.96
16	24.5	F	CAUC	No	5.73	Natural	61.19
17	37	F	AA	Yes	6.64	Natural	59.62
18	22	F	CAUC	No	6.31	Natural	59.26
19	64	M	CAUC	Yes	6.87	Natural	58.61
20	50	M	AA	No	5.96	Natural	58.44
21	45.5	F	AA	No	6	Natural	57.87
22	29	F	CAUC	No	6.1	Natural	57.48
23	29.5	M	CAUC	No	6.69	Natural	55.44
24	32.5	M	AA	No	6.76	Natural	53.96
25	51.5	F	CAUC	No	6.53	Natural	51.94
26	24	F	AA	No	6.79	Natural	51.48
27	51	M	AA	No	6.83	Natural	49.76
28	18.5	M	CAUC	No	6.57	Natural	49.56
29	36	F	CAUC	No	6.47	Natural	49.02
30	13	F	AA	No	7.1	Natural	46.10
31	38.5	M	AA	No	6.66	Homicide	45.94
32	43.5	M	CAUC	No	6.26	Natural	45.68
33	24.5	M	CAUC	No	6.34	Natural	42.07
34	24.5	M	AA	No	7.08	Natural	42.02
35	14.5	M	AA	No	6.12	Natural	41.58
36	18	M	CAUC	Yes	6.82	Natural	41.04
37	40	F	AA	Yes	6.17	Natural	40.85

38	28.5	F	CAUC	No	6.1	Natural	40.61
39	38.5	F	AA	Yes	6.58	Natural	38.61
40	41	F	CAUC	No	6.76	Homicide	38.41
41	43	M	AA	No	6.62	Natural	33.00
42	22.5	M	CAUC	No	6.38	Natural	32.70
43	32.5	F	AA	No	6.37	Accident	30.50
44	9.5	F	CAUC	No	6.92	Natural	30.04
45	7.5	M	CAUC	No	6.85	Natural	28.59
46	14	M	AA	No	6.37	Homicide	27.22
47	25	F	AA	No	5.99	Homicide	26.78
48	40	F	CAUC	No	6.94	Homicide	26.53
49	14.5	M	AA	No	6.6	Homicide	24.85
50	20.5	M	CAUC	Yes	6.98	Accident	24.04
51	32	M	CAUC	No	6.73	Natural	20.86
52	25.5	M	AA	No	6.46	Homicide	20.79
53	19	F	AA	No	6.98	Natural	19.71
54	9.5	F	CAUC	No	5.91	Natural	19.27
55	43.5	M	CAUC	No	6.84	Natural	18.42
56	36.5	M	AA	No	6.7	Homicide	18.16
57	15.5	F	AA	Yes	6.77	Homicide	17.28
58	12	F	CAUC	No	6.79	Accident	17.09
59	12	M	CAUC	Yes	6.52	Accident	15.80
60	14.5	M	AA	Yes	6.93	Homicide	15.49
61	19.5	F	AA	No	6.34	Homicide	13.49
62	67.5	F	CAUC	No	6.38	Accident	12.28
63	22	F	AA	No	N/A	Accident	10.73
64	67.5	M	CAUC	No	6.39	Accident	9.16
65	20	F	CAUC	No	6.9	Accident	6.34
66	18	M	CAUC	No	6.67	Accident	5.35
67	20	M	AA	No	6.52	Natural	4.21
68	37	M	CAUC	No	6.24	Homicide	3.98
69	44	F	CAUC	No	6.06	Accident	2.72
70	21	F	AA	No	6.73	Accident	2.02
71	19	M	CAUC	No	6.72	Accident	1.34
72	37.5	M	AA	No	6.57	Natural	0.97
73	26	F	CAUC	No	6.26	Accident	0.52
74	31.5	F	AA	No	6.77	Natural	0.48
75	59.5	M	AA	No	6.27	Accident	0.41
76	27	M	CAUC	No	6.51	Natural	0.35
77	22	M	CAUC	No	6.21	Natural	0.33

78	61	M	AA	No	6.48	Natural	0.22
79	3	F	AA	No	N/A	N/A	-0.40
80	1	M	CAUC	Yes	N/A	N/A	-0.40
81	1	F	AA	Yes	N/A	N/A	-0.40
82	1	M	AA	No	N/A	N/A	-0.40
83	3	M	AA	No	N/A	N/A	-0.40
84	2	M	AA	No	N/A	N/A	-0.40
85	2	F	AA	No	N/A	N/A	-0.40
86	2	F	AA	No	N/A	N/A	-0.40
87	2	M	CAUC	No	N/A	N/A	-0.40
88	8	F	AA	Yes	N/A	N/A	-0.40
89	3	F	CAUC	No	N/A	N/A	-0.40
90	1	F	AA	Yes	N/A	N/A	-0.42
91	1	F	AA	No	N/A	N/A	-0.42
92	2	F	AA	Yes	N/A	N/A	-0.42
93	12	M	AA	No	N/A	N/A	-0.42
94	4	M	AA	No	N/A	N/A	-0.42
95	4	M	AA	No	N/A	N/A	-0.42
96	3	F	AA	Yes	N/A	N/A	-0.42
97	6	M	AA	Yes	N/A	N/A	-0.42
98	1	F	AA	Yes	N/A	N/A	-0.42
99	1	M	AA	No	N/A	N/A	-0.42
100	1	F	AA	No	N/A	N/A	-0.44
101	2	M	AA	No	N/A	N/A	-0.44
102	1	F	AA	No	N/A	N/A	-0.44
103	4	F	AA	No	N/A	N/A	-0.44
104	1	M	AA	Yes	N/A	N/A	-0.46
105	4	M	AA	No	N/A	N/A	-0.48
106	1	M	AA	No	N/A	N/A	-0.50
107	3	F	AA	No	N/A	N/A	-0.50
108	1	F	AA	No	N/A	N/A	-0.50

**Table S2A. Top One Hundred Most Significant CpG Loci Showing Changes in DNA Methylation during the Fetal Period**

CpG locus	Chr	Gene Symbol	CPG_ISLAND (1 denotes in CGIs and 0 denotes in non-CGIs)	beta regression coefficient	p value
cg09398185	10	IFIT2	0	3.6309342	8.62E-30
cg08399444	12	GSG1	0	3.6906079	7.73E-28
cg06353720	10	IFIT3	0	3.5812806	5.21E-21
cg06476606	10	IFIT2	0	1.9048426	2.27E-20
cg16692277	13	GUCY1B2	1	3.7688943	1.24E-17
cg09494546	1	SLC16A4	0	3.2890392	2.88E-16
cg00075967	15	STRA6	0	2.9868582	6.32E-16
cg06426831	1	SLC35A3	1	1.2661272	8.70E-16
cg22740835	1	DDR2	0	2.2377317	6.08E-15
cg25599242	11	RARRES3	0	1.6785498	1.09E-14
cg18201077	2	RSAD2	0	1.9317723	1.60E-14
cg04761824	9	1-Dec	0	-2.907676	8.13E-14
cg06142324	11	FLJ25530	1	3.1366541	1.30E-13
cg21048669	16	CLEC3A	0	1.7707384	1.69E-13
cg02456292	19	FLJ90805	1	0.6820287	3.15E-13
cg19530885	5	SCGB3A2	0	2.3974417	4.54E-13
cg17749384	10	MPP7	0	0.9687017	5.20E-13
cg19447496	13	RB1	1	0.8377441	9.12E-13
cg17204557	2	FLJ14816	1	1.4735331	3.01E-12
cg07823755	2	UGT1A1	0	2.8095304	6.20E-12

cg09195271	1	RNF186	0	0.8365116	7.39E-12
cg18003231	22	SLC25A18	1	3.3141259	1.94E-11
cg12697789	4	TLR3	0	0.9629027	2.09E-11
cg19620294	8	TNFRSF11B	1	1.0010442	2.14E-11
cg03622431	1	DNASE2B	0	2.2920245	2.44E-11
cg13112511	5	PDE4D	0	1.9857987	4.52E-11
cg03296929	4	IBSP	0	1.6303843	6.12E-11
cg24646513	12	MTERFD3	1	0.5250633	1.99E-10
cg09425611	16	CES1	0	1.9217543	2.53E-10
cg24389347	3	C3orf22	0	1.5673401	3.05E-10
cg01446692	9	CER1	0	1.4583827	4.31E-10
cg01636591	17	CCL8	0	2.1040586	4.90E-10
cg01305421	12	IGF1	0	2.2779757	5.95E-10
cg04999691	7	C7orf29	0	1.9076787	6.00E-10
cg17238009	10	C10orf11	1	2.5257245	6.68E-10
cg16948369	X	KLHL4	0	1.2928321	6.73E-10
cg24471894	9	KIAA0020	0	1.5217802	8.49E-10
cg02774160	22	GGT1	0	1.6007604	1.06E-09
cg22168676	6	OFCC1	0	1.8867206	1.50E-09
cg12108912	2	MGC10993	1	1.4671126	2.40E-09
cg03330678	17	9-Sep	1	-1.935966	2.48E-09
cg16698623	10	MGMT	1	0.8695482	2.48E-09
cg01511567	11	SSRP1	1	1.1744267	2.86E-09
cg21825364	Y	VCY	1	0.1954877	3.19E-09

cg11484576	11	LGALS12	0	2.0747302	3.37E-09
cg07412254	2	FLJ14816	1	1.203986	4.01E-09
cg01041367	8	TMEM70	1	0.5521116	4.29E-09
cg24216701	5	CDX1	1	0.9922836	5.09E-09
cg17398283	1	CCDC76	0	0.7091409	6.40E-09
cg25140571	3	OXTR	1	0.7987879	6.95E-09
cg10313675	1	C1orf74	1	0.0976426	8.41E-09
cg03891319	3	ACY1	1	-0.75828	9.14E-09
cg04394967	14	RDH12	0	0.8971498	9.77E-09
cg17489451	12	DKFZP779L1558	0	1.5324891	9.85E-09
cg11787522	15	STRA6	0	1.2983386	9.99E-09
cg23286660	1	PLOD1	1	0.3979566	1.08E-08
cg20955688	8	TMEM71	0	-1.747684	1.30E-08
cg13668129	19	HNRPUL1	1	0.7594149	1.37E-08
cg17751569	5	CD180	0	1.0961425	1.44E-08
cg13277939	14	CTAGE5	0	1.3446617	1.56E-08
cg00729275	18	C18orf16	0	1.9322543	1.57E-08
cg27217148	10	PCGF6	1	-1.031381	1.70E-08
cg23047271	3	PRICKLE2	0	0.4828295	2.04E-08
cg24391122	19	SNAPC2	1	0.5914802	2.72E-08
cg03112433	7	PFTK1	0	0.9491788	3.07E-08
cg01161611	2	GALNT13	0	1.4967455	3.72E-08
cg04106785	17	CDK5R1	1	2.0207243	3.86E-08
cg12428447	11	SLC22A6	0	1.9190744	4.01E-08
cg21974766	7	NBLA04196	1	0.3092393	4.43E-08



cg08108641	9	NTNG2	1	1.12111	5.05E-08
cg08970446	1	SLC1A7	0	0.9503666	5.13E-08
cg22150335	10	ANK3	0	1.8634168	5.32E-08
cg12623088	15	MGC4562	1	1.0256772	5.48E-08
cg10148280	3	HPS3	0	1.2674274	6.09E-08
cg21457147	13	KCTD4	0	1.5963143	6.36E-08
cg25003924	15	ARPP-19	0	0.6701577	9.67E-08
cg27015931	16	MGC50721	1	0.4065638	9.71E-08
cg12611860	11	PIK3C2A	0	1.2139528	1.04E-07
cg24624841	19	RPS9	1	0.5675865	1.11E-07
cg15534366	20	CDH4	0	1.4396748	1.14E-07
cg08109646	1	ZNF683	0	1.0541842	1.36E-07
cg16986720	11	DLG2	0	1.3527417	1.39E-07
cg16215361	11	MUC15	0	1.4282414	1.46E-07
cg02332073	7	TSGA13	0	1.0652523	1.51E-07
cg01137065	17	FOXK2	1	0.5638921	1.69E-07
cg21120249	9	FLJ36268	0	-1.209997	1.74E-07
cg10447080	6	FILIP1	0	1.2542217	1.76E-07
cg13802966	11	CASP1	0	1.1502967	1.86E-07
cg03431064	9	TUBB2C	1	0.2418145	1.94E-07
cg17777592	13	CAB39L	0	1.3411312	2.26E-07
cg19357849	19	ELAVL1	1	0.5101581	2.33E-07
cg04457051	4	SCOC	0	1.2566917	2.36E-07
cg22726338	1	C1orf62	0	1.5868851	2.45E-07
cg12532500	13	STARD13	0	1.0280815	2.56E-07

cg13415850	2	C2orf7	0	0.5880546	2.78E-07
cg21643191	7	ABCB5	0	1.0268644	2.83E-07
cg22807700	1	DNTTIP2	1	1.3457144	3.46E-07
cg00986320	5	CYFIP2	1	1.8689455	3.60E-07
cg15661409	14	C14orf105	0	1.249462	3.88E-07

**Table S2B. Top One Hundred Most Significant CpG Loci Showing Changes in DNA Methylation Loci during Childhood (0–10 years).**

CpG locus	Chr	Gene Symbol	CPG_ISLAND (1 denotes in CGIs and 0 denotes in non-CGIs)	beta regression coefficient	p value
cg08300860	10	LDB3	0	-0.066	2.38E-29
cg27258399	8	HTRA4	1	0.0507	7.71E-28
cg13406950	1	GBP1	0	-0.053	4.62E-26
cg14467840	1	S100A1	0	-0.04	2.54E-24
cg26218269	4	MAB21L2	1	0.0497	1.37E-23
cg14634319	12	BAZ2A	0	-0.014	3.25E-22
cg06456031	7	FLJ11000	0	-0.051	4.01E-22
cg26790059	5	MGC27121	0	0.0454	4.06E-22
cg02717866	11	FLJ32771	0	0.038	2.35E-21
cg03245641	11	GPHA2	0	0.0503	2.88E-21
cg19464252	16	FBS1	0	-0.046	3.60E-21
cg04033774	1	GPSM2	1	-0.059	1.63E-20
cg07888040	15	GLDN	0	-0.063	1.65E-20
cg25683012	12	BAZ2A	0	-0.016	2.68E-20
cg25203980	1	CENTB5	1	-0.055	4.59E-20
cg12535715	8	HTRA4	1	0.055	5.87E-20
cg14818279	5	SH3TC2	0	-0.051	6.32E-20
cg16555388	3	TNFSF10	0	-0.031	1.12E-19
cg08290628	15	CORO2B	0	-0.052	1.89E-19
cg09432376	22	APOL6	0	-0.057	3.86E-19
cg08446111	16	ABCC11	0	-0.037	4.23E-19
cg27117399	18	CNDP1	1	-0.074	6.03E-19
cg09573795	4	MSX1	1	0.0551	1.09E-18
cg15227610	11	CRYAB	0	-0.071	1.47E-18
cg24938727	3	GUP1	0	-0.04	3.05E-18
cg20334738	4	MAB21L2	0	0.0475	3.93E-18
cg00237010	12	NINJ2	0	-0.065	4.67E-18
cg11719283	19	ZNF574	0	0.0411	4.97E-18
cg13060154	9	DAB2IP	1	0.0437	5.88E-18
cg16504798	19	MYO1F	0	-0.035	6.70E-18
cg05125838	3	UCN2	0	-0.058	1.21E-17
cg20028470	2	UCN	1	0.032	1.47E-17
cg02228185	17	ASPA	0	-0.052	1.49E-17

cg13576290	2	LOC165186	0	-0.042	1.94E-17
cg21129531	7	LRR4	1	0.0594	2.23E-17
cg19154438	19	CKM	0	0.0313	2.28E-17
cg16463460	11	WT1	1	0.0444	2.49E-17
cg13210534	11	HSPB2	0	-0.032	2.94E-17
cg16393207	11	GDPD5	1	0.0549	3.20E-17
cg27089714	8	KIAA0196	0	-0.039	3.69E-17
cg19481686	9	CDKN2B	1	0.0601	4.55E-17
cg13718960	14	RNASE1	0	-0.07	7.31E-17
cg14448116	1	ADAMTS4	0	-0.05	8.58E-17
cg12862537	20	NNAT	1	0.0387	1.62E-16
cg12467090	1	PIK3C2B	0	-0.038	1.72E-16
cg04716261	1	ARPM2	0	0.0335	2.00E-16
cg18669381	1	ARHGEF19	0	0.0446	2.21E-16
cg21402071	15	CHRNA4	0	0.0339	2.45E-16
cg18665384	1	FLJ43505	0	0.0382	2.73E-16
cg05624196	3	APOD	1	-0.035	3.28E-16
cg03733371	3	LIPH	0	-0.04	3.52E-16
cg16744741	4	PRKG2	0	-0.04	3.99E-16
cg17034109	1	CYB561D1	1	0.0317	4.22E-16
cg05766474	17	CCL16	0	-0.04	5.91E-16
cg27038439	4	MSX1	1	0.0417	5.92E-16
cg15820955	12	HDAC7A	0	-0.044	6.54E-16
cg14679230	19	LIPE	0	-0.057	6.77E-16
cg01656750	16	KATNB1	0	-0.053	8.78E-16
cg18565510	1	CENTB5	1	-0.036	1.60E-15
cg05781767	3	PODXL2	0	0.0388	1.70E-15
cg20956314	3	XYLB	0	0.0149	1.85E-15
cg18204685	3	BTD	0	-0.032	1.92E-15
cg20847746	1	S100A1	0	-0.05	2.14E-15
cg25799986	20	WFDC2	1	0.0349	2.65E-15
cg22449114	20	TCF15	1	0.029	2.78E-15
cg25162301	3	AHSG	0	-0.045	3.50E-15
cg23902550	8	TIGD5	1	0.0482	3.71E-15
cg12008118	10	LDB3	0	-0.047	4.15E-15
cg12813797	6	TAAR6	1	-0.045	5.13E-15
cg20125091	1	GF11	1	0.0296	5.73E-15
cg22630748	12	INHBE	0	0.0247	5.85E-15
cg18219418	15	PARP6	0	-0.03	6.29E-15
cg18555555	6	FABP7	0	0.0359	8.72E-15

cg05078019	4	PDE6B	1	0.0348	9.03E-15
cg08946332	17	ALOX12	1	0.0431	1.16E-14
cg15238200	17	TRIM65	1	0.0378	1.36E-14
cg18680834	19	ZNF536	0	-0.049	1.62E-14
cg02789485	12	MGC39497	0	-0.045	1.63E-14
cg12188416	3	TP73L	0	-0.048	1.65E-14
cg01269795	6	BTN3A3	0	-0.034	1.83E-14
cg13492227	17	FGF11	1	0.0406	1.90E-14
cg27371741	3	TDGF1	1	0.043	2.05E-14
cg05958352	14	RNASE1	0	-0.056	2.07E-14
cg14959707	16	ZC3H7A	1	-0.038	2.24E-14
cg04377282	10	NODAL	1	0.0381	2.33E-14
cg04527918	2	UCN	1	0.0365	2.63E-14
cg02218324	19	RSHL1	1	0.0364	2.98E-14
cg10732834	18	KIAA1632	0	-0.043	3.33E-14
cg22609784	4	MSX1	1	0.0349	3.55E-14
cg12953249	9	CRB2	1	0.0333	4.20E-14
cg07180649	1	WNT4	1	0.0248	4.30E-14
cg10934032	14	RNASE6	0	0.045	5.28E-14
cg25533774	7	SOSTDC1	0	0.033	5.88E-14
cg26279025	19	IL11	1	0.0209	8.19E-14
cg19921353	6	HLA-DPB1	0	-0.034	8.26E-14
cg26770882	17	AIPL1	0	0.0286	8.28E-14
cg15538820	9	OBP2B	0	-0.058	1.04E-13
cg05890484	5	BHMT	1	0.0417	1.18E-13
cg02497428	16	IGSF6	0	-0.018	1.32E-13

**Table S2C. Top One Hundred Most Significant CpG Loci Showing Changes in DNA Methylation Loci during the Age of >10 Years**

CpG locus	Chr	Gene Symbol	CPG_ISLAND (1 denotes in CGIs and 0 denotes in non-CGIs)	beta regression coefficient	p value
cg22736354	6	NHLRC1	1	0.00253	3.15E-39
cg10301967	6	RPS18	1	0.001678	6.10E-36
cg12448933	17	RAB37	1	0.001241	5.19E-34
cg01644850	19	ZNF551	1	0.001757	1.88E-32
cg19996355	19	PBX4	1	0.001379	3.07E-31
cg06156376	3	SHOX2	1	0.001552	6.29E-31
cg15201877	1	PTGER3	1	0.001358	1.22E-30
cg25136310	19	RPL36	1	0.00197	2.06E-30
cg17050972	6	HIST1H2AJ	1	0.001416	3.40E-30
cg26005082	19	C19orf30	1	0.000724	1.03E-29
cg06458239	19	ZNF549	1	0.003847	1.36E-29
cg21053323	21	SUMO3	1	0.003246	1.62E-29
cg08211967	15	AKAP13	1	0.000747	6.79E-29
cg00164898	22	MAPK11	1	0.001593	7.86E-29
cg02512860	7	CLDN15	0	-0.005083	1.91E-28
cg08370996	15	NR2F2	1	0.000971	3.76E-28
cg06291867	10	HTR7	1	0.001446	5.45E-28
cg05266781	16	IRX5	1	0.001373	6.76E-28
cg10792326	12	DNCL1	1	0.002236	1.43E-27
cg02331561	16	ABCA3	1	0.000556	2.12E-27
cg00548268	7	NPTX2	1	0.0023	2.41E-27
cg06336792	10	CREM	1	0.000825	6.53E-27
cg02409351	12	CART1	1	0.000652	8.81E-27
cg02479575	19	C19orf30	1	0.000452	1.56E-25
cg04084157	7	VGFB	1	0.000987	3.71E-25
cg26780333	14	ACOT4	1	0.000833	8.03E-25
cg14228238	3	EVI1	1	0.001113	8.63E-25
cg06220235	16	SOCS1	1	0.001226	9.14E-25
cg23854009	19	ZNF530	1	0.000916	1.03E-24
cg06493386	8	TRPA1	1	0.000865	1.81E-24
cg21589115	19	DKKL1	1	0.000858	2.13E-24
cg22815110	1	FOXD3	1	0.000844	3.90E-24
cg10947146	8	XKR6	1	0.000654	4.52E-24
cg03664992	1	BMP8A	1	0.001335	6.09E-24

cg03160135	6	VGLL2	1	0.001144	8.95E-24
cg04033774	1	GPSM2	1	-0.003499	1.17E-23
cg06490988	3	GATA2	1	0.002167	4.63E-23
cg15658426	5	MGC39633	1	0.002783	5.05E-23
cg01288598	6	CD83	1	0.000817	1.26E-22
cg23748737	22	SCARF2	1	0.000494	1.74E-22
cg01947224	19	ZNF416	1	0.000504	3.97E-22
cg03794550	11	FANCF	1	0.000683	5.59E-22
cg16652063	17	SLC13A5	1	0.000677	6.37E-22
cg13929328	10	FLJ46831	1	0.000758	6.48E-22
cg18809289	10	ALOX5	1	0.0022	8.16E-22
cg04676561	6	HIST1H1B	1	0.000755	1.66E-21
cg03562120	20	WISP2	1	-0.004415	3.56E-21
cg06462291	12	NT5DC3	0	0.000926	3.86E-21
cg10225525	14	FUT8	0	-0.002881	5.02E-21
cg04970352	11	ALX4	1	0.000923	5.43E-21
cg22809047	2	RPL31	1	0.003409	8.29E-21
cg13744194	5	OCLN	1	0.001043	1.40E-20
cg04133652	17	MLLT6	1	0.001187	1.66E-20
cg14407667	1	EPS15	1	0.00157	1.71E-20
cg13854874	21	CHAF1B	1	0.001435	1.76E-20
cg18108623	17	FLJ34922	1	0.000652	1.78E-20
cg09298289	5	CENPH	1	0.00051	1.84E-20
cg02599464	6	HIST1H4I	1	0.001685	1.85E-20
cg05421555	15	AKAP13	1	0.000384	1.96E-20
cg00453193	7	TES	1	0.000513	2.14E-20
cg25943276	11	C11orf39	1	-0.00333	2.24E-20
cg04498511	1	ZC3H11A	0	-0.002753	2.27E-20
cg16313343	14	BRF1	1	0.002358	2.49E-20
cg21208104	4	PRSS12	1	0.000826	2.97E-20
cg08300860	10	LDB3	0	-0.003167	4.00E-20
cg08460435	1	C1orf59	1	0.001239	4.06E-20
cg00282347	1	CHD5	1	0.000986	4.35E-20
cg15599064	6	HIST1H4H	1	0.001356	5.74E-20
cg12447832	2	TTC15	1	0.003646	5.84E-20
cg10608333	6	HIST1H4K	1	0.000741	7.40E-20
cg03890877	3	PTK9L	1	0.002116	9.56E-20
cg23941599	5	FEM1C	1	0.001951	9.58E-20
cg18943383	6	HIST1H3H	1	0.001288	9.93E-20
cg07888040	15	GLDN	0	-0.004078	1.09E-19
cg00563932	9	PTGDS	0	-0.003533	1.18E-19
cg03688818	3	APEH	1	0.000835	1.21E-19

cg03975694	19	ZNF540	1	0.001166	1.58E-19
cg27529628	12	GAS2L3	1	0.000768	1.60E-19
cg21421701	1	SNFT	1	0.000408	1.78E-19
cg21269897	6	HIST1H4I	1	0.002093	1.80E-19
cg24903376	1	STIL	1	0.000744	2.38E-19
cg20797766	16	PRSS27	1	0.000954	2.63E-19
cg24587268	20	OSBPL2	1	0.001312	2.68E-19
cg25186143	17	FAM57A	1	0.000841	3.05E-19
cg00059225	5	GLRA1	1	0.001239	3.15E-19
cg13749822	4	HHIP	1	0.000881	4.07E-19
cg26677448	10	PAX2	1	0.000861	4.25E-19
cg27650434	1	MYCL1	1	0.000726	4.32E-19
cg06821120	3	RASSF1	1	0.002082	4.53E-19
cg12815841	10	LHPP	1	0.000786	5.18E-19
cg20979799	6	RFXDC1	1	0.000742	5.63E-19
cg22647018	1	AGT	0	-0.003567	5.64E-19
cg26149678	11	IL18BP	0	0.001826	7.24E-19
cg20692569	7	FZD9	1	0.001912	7.42E-19
cg07109287	9	LHX2	1	0.000388	7.74E-19
cg21380294	15	ZSCAN2	1	0.001441	8.00E-19
cg19224837	14	GSC	1	0.000535	8.58E-19
cg14121103	3	ABHD5	1	0.000585	8.81E-19
cg02613386	17	FBXO39	1	0.000535	1.03E-18



**Table S3. Cancer-Related Genes that Showed Significant Age-Related Changes during Both Childhood and in Subjects Older than 10 Years (FDR < 0.05)**

Gene Symbol	Location	CpG island	beta regression coefficient for Age		beta regression coefficient for Age		CpG locus
			term (childhood)	p value (childhood)	term (adulthood)	p values (adulthood)	
PRDM1	6q21-q22.1	1	0.0039	0.000432	0.0007	7.34E-16	cg19464016
LOX	5q23.2	1	0.0017	0.002367	0.0003	1.27E-13	cg02548238
MRVI1	11p15	0	-0.0150	0.000285	-0.0024	2.90E-13	cg24541550
BAP1	3p21.31-p21.2	1	0.0053	1.56E-05	0.0005	4.24E-13	cg24747396
PAWR	12q21	1	0.0026	0.002869	0.0003	2.27E-12	cg00864867
STEAP3	2q14.2	0	0.0173	1.53E-08	0.0012	2.91E-12	cg06872331
SMO	7q32.3	1	0.0113	2.98E-07	0.0008	1.01E-11	cg04478795
ERBB3	12q13	1	-0.0118	4.48E-05	-0.0013	3.01E-09	cg19258882
APC	5q21-q22	1	0.0034	0.0004	0.0004	3.03E-09	cg16970232
TP53	17p13.1	1	0.0027	0.001039	0.0003	1.23E-08	cg11519508
LCK	1p34.3	0	-0.0385	1.81E-08	-0.0019	1.70E-08	cg01525376
PDLIM4	5q31.1	1	0.0275	3.28E-09	0.0012	2.66E-08	cg20512303
COL4A3	2q36-q37	1	0.0057	0.000271	0.0005	3.02E-08	cg16640096
NBL1	1p36.13-p36.11	1	0.0159	6.98E-05	0.0011	5.69E-08	cg21057046
CHEK2	22q11 22q12.1	1	0.0061	0.00901	0.0007	8.25E-08	cg22585269
BRCA1	17q21	1	0.0069	0.001098	0.0006	1.71E-07	cg08993267
FABP3	1p33-p32	1	0.0017	0.001995	0.0002	3.69E-07	cg03484533
BAI3	6q12	0	0.0021	0.002917	0.0002	5.16E-07	cg10244047
PTCH	9q22.3	1	0.0022	0.000122	0.0002	6.68E-07	cg21526212
DAB2	5p13	0	0.0130	0.000207	0.0010	9.15E-07	cg17491456
LOH11CR2A	11q23	1	-0.0094	0.003816	-0.0011	1.00E-06	cg09109996
MPL	1p34	0	-0.0072	0.000799	-0.0005	6.12E-06	cg19337279
MEN1	11q13	1	0.0059	4.25E-05	0.0005	1.13E-05	cg16668394
CDH13	16q24.2-q24.3	1	0.0233	2.61E-06	0.0012	1.63E-05	cg01880569
RARB	3p24	1	0.0046	0.001015	0.0004	2.80E-05	cg10712623
ROS1	6q22	0	-0.0309	1.75E-10	-0.0010	3.18E-05	cg21166999
MAPK8	10q11.22	0	-0.0284	0.002386	-0.0021	3.22E-05	cg19612574
BCL10	1p22	0	-0.0042	0.000145	-0.0003	4.68E-05	cg05475904
IGSF4	11q23.2	0	0.0080	1.77E-05	0.0004	7.38E-05	cg08654655
CUL1	7q36.1	1	0.0038	6.15E-05	0.0003	8.94E-05	cg12592716
LGI1	10q24	0	0.0182	9.51E-05	0.0010	0.0001132	cg00532335
TFE3	Xp11.22	1	0.0102	0.003802	0.0010	0.0001139	cg02004156

TTC4	1p31.3	1	0.0084	0.003198	0.0006	0.0001457	cg02255609
ZNF146	19q13.1	0	-0.0242	0.000105	-0.0015	0.0001984	cg02275359
COL18A1	21q22.3	0	0.0103	0.000631	0.0007	0.0002088	cg02066681
MLH1	3p21.3	0	0.0184	2.63E-07	0.0009	0.0002551	cg10990993
SMARCB1	22q11.23 22q11	1	-0.0017	0.003287	-0.0001	0.0006012	cg19906397
FGFR3	4p16.3	1	-0.0015	0.003116	-0.0001	0.0007362	cg17269277
DLEC1	3p22-p21.3	1	0.0209	9.30E-05	0.0009	0.001141	cg23881725
CDKN2A	9p21	1	0.0090	6.06E-08	0.0003	0.0019241	cg07752420
NEURL	10q25.1	1	0.0164	7.25E-07	0.0007	0.0020264	cg02324920
BRCA2	13q12.3	1	-0.0120	1.24E-06	-0.0004	0.0022151	cg12836863
EXTL1	1p36.1	0	0.0118	0.000131	0.0005	0.0042412	cg04629204
RUNX3	1p36	1	-0.0040	0.008871	-0.0003	0.004737	cg24019564
CDKN2B	9p21	1	0.0306	6.69E-11	0.0007	0.0047883	cg06421800
ST13	22q13.2	1	0.0257	1.89E-07	0.0009	0.0049285	cg18291690
SLC26A3	7q31	0	0.0048	0.000105	0.0002	0.0082885	cg22294577
MYBBP1A	17p13.3	1	0.0046	0.003215	0.0002	0.0091711	cg21000021

**Table S4. Top One Hundred CpG loci Showing Sexually Dimorphic DNA Methylation**

<b>CpG locus</b>	<b>Chr</b>	<b>Gene Symbol</b>	<b>CPG_ISLAND (1 denotes in CGIs and 0 denotes in non-CGIs)</b>	<b>beta regression coefficient</b>	<b>p value</b>
cg04493740	X	SLC25A14	1	-0.4054	1.61E-91
cg13286902	X	CXorf34	1	-0.4758	2.36E-91
cg02148711	X	ATRX	1	-0.4821	4.11E-91
cg25591670	X	CXorf26	1	-0.3763	2.36E-88
cg00618396	X	VBP1	1	-0.4835	2.48E-88
cg20514061	X	MID2	1	-0.5040	1.92E-87
cg20816612	X	PHKA1	1	-0.3928	3.23E-87
cg10818284	X	SYP	1	-0.5846	3.75E-87
cg18799866	X	SLC9A7	1	-0.4836	8.82E-87
cg26955512	X	HDAC8	1	-0.4138	1.47E-86
cg14506668	X	FHL1	1	-0.3255	3.45E-86
cg13928116	X	AFF2	1	-0.4161	1.83E-85
cg02649608	X	ZBTB33	1	-0.4440	3.21E-85
cg23545272	X	EFNB1	1	-0.4845	3.23E-85
cg26606552	X	CCDC22	1	-0.3466	1.05E-84
cg03057808	X	FLJ10178	1	-0.3593	1.51E-84
cg01079126	X	MTMR1	1	-0.3997	8.64E-84
cg09928375	X	OTUD5	1	-0.5256	3.01E-83
cg21365235	X	OCRL	1	-0.4789	3.95E-83
cg02973971	X	CXorf40B	1	-0.3491	4.61E-83
cg11653864	X	ELK1	1	-0.5193	7.48E-83
cg12650780	X	SH3BGR1	0	-0.3678	8.79E-83
cg23947872	X	MTMR1	1	-0.4659	3.42E-82
cg21509846	X	BEX1	1	-0.4362	3.65E-82
cg12687215	X	FAM50A	1	-0.4752	5.42E-82
cg11291200	X	MAGEB2	1	0.3130	5.91E-82
cg04238548	X	FLJ20298	1	-0.4002	7.77E-82
cg23936476	X	BEX1	1	-0.5579	8.18E-82
cg07137581	X	FLJ39827	1	-0.2946	1.47E-81
cg05254049	X	SYN1	1	-0.4528	1.62E-81
cg19949137	X	HTATSF1	1	-0.3879	2.28E-81
cg17552650	X	WDR45	1	-0.4240	2.29E-81
cg21860846	X	ELK1	1	-0.5337	3.35E-81
cg25317260	X	PDCD8	1	-0.3440	3.70E-81

cg18923230	X	RPL10	1	-0.4987	4.52E-81
cg21030483	X	FAM11A	1	-0.3840	4.59E-81
cg18256128	X	PDK3	1	-0.4478	5.30E-81
		RP11-			
cg19011603	X	311P8.3	1	-0.4027	7.39E-81
cg19696622	X	RPS6KA3	1	-0.3392	9.74E-81
cg21966410	X	AR	1	-0.4325	1.24E-80
cg06162422	X	GLA	1	-0.3495	2.10E-80
cg02804166	X	PHF6	1	-0.2692	2.63E-80
cg24054653	X	C1GALT1C1	1	-0.3917	2.66E-80
cg11371160	X	UBL4A	1	-0.4823	3.26E-80
cg01080862	X	IL13RA1	1	-0.5153	4.21E-80
cg14854487	X	LAMP2	1	-0.4401	4.39E-80
cg17843048	X	PHF16	1	-0.4090	4.71E-80
cg15895359	X	EFNB1	1	-0.2996	5.51E-80
cg04872051	X	CHST7	1	-0.6251	5.97E-80
cg16243644	X	STAG2	1	-0.3305	6.19E-80
cg18507125	X	RPL36A	1	-0.5161	9.38E-80
cg03936963	X	TMEM29	1	-0.4460	9.59E-80
cg24779040	X	TSPYL2	1	-0.6085	1.14E-79
cg12431196	X	MAGEE1	1	-0.3463	1.27E-79
cg26738912	X	MAGED4	1	-0.3954	1.28E-79
cg04455999	X	FAM70A	1	-0.4721	2.08E-79
		RP1-			
cg20504202	X	112K5.2	1	-0.4732	6.09E-79
cg05019001	X	AR	1	-0.4470	6.25E-79
cg15231886	X	UTP14A	1	-0.4216	7.82E-79
cg09202373	X	DNASE1L1	1	-0.4103	8.64E-79
cg19392138	X	ZNF449	1	-0.3133	9.44E-79
cg16343842	X	CD99L2	1	-0.3392	1.01E-78
cg19410841	X	NKAP	1	-0.3496	1.18E-78
cg20085077	X	ARMCX4	1	-0.4882	1.41E-78
cg13771629	X	EBP	1	-0.3044	1.43E-78
cg09347151	X	MGC39606	1	-0.3725	1.62E-78
cg14642832	X	RBMX	1	-0.4065	1.97E-78
cg18414950	X	PDK3	1	-0.4920	2.31E-78
cg00029931	X	RPL36A	1	-0.3555	2.77E-78
cg05782975	X	NGFRAP1	1	-0.4913	5.03E-78
cg09229960	X	EMD	1	-0.6356	5.33E-78
cg06277838	X	SLC16A2	0	-0.4120	5.65E-78
cg11291009	X	ARHGEF9	1	-0.5205	6.07E-78
cg08496601	X	EBP	1	-0.5091	6.21E-78

cg12536534	X	G6PD	1	-0.3572	7.38E-78
cg01718602	X	DACH2	1	-0.3764	7.52E-78
cg18307604	X	LAMP2	1	-0.4392	1.00E-77
cg08798116	X	GPC4	1	-0.4827	1.89E-77
cg09018810	X	IDS	1	-0.4297	2.08E-77
cg01241836	X	TFE3	1	-0.3645	2.18E-77
cg18049750	X	SCML1	1	-0.3653	2.83E-77
cg21697779	X	FUNDC2	1	-0.4024	3.77E-77
cg02205962	X	BCAP31	1	-0.5273	5.12E-77
cg17231524	X	MGC39606	1	-0.4559	5.61E-77
cg18503052	X	PLP2	1	-0.3882	5.81E-77
cg15636587	X	GK	1	-0.4069	6.45E-77
cg14520892	X	POLA	1	-0.3947	6.78E-77
cg19421044	X	DNASE1L1	1	-0.4118	7.34E-77
cg14345281	X	NHS	1	-0.3969	1.14E-76
cg15977272	X	EFNB1	1	-0.5988	1.21E-76
cg08695223	X	SLC9A6	1	-0.5836	1.39E-76
cg25813820	X	MPP1	1	-0.4916	1.39E-76
cg23750556	X	SRPX	1	-0.3823	1.63E-76
cg07473550	X	TSC22D3	1	-0.4185	1.79E-76
cg20622056	X	SLC7A3	1	-0.2629	1.82E-76
cg09950034	X	BIRC4	1	-0.3513	2.38E-76
cg01353347	X	IRAK1	1	-0.5745	2.65E-76
cg13613682	X	ZIC3	1	-0.4650	3.02E-76
cg26810336	X	IL1RAPL1	0	-0.3392	3.73E-76

Negative beta regression coefficients indicate higher levels of methylation in females vs males.

**Table S5. Top One Hundred Negative Correlations between Gene Expression and CpG Methylation**

Expression_Probe_ID	CpG locus	Gene Symbol	Chr	CpGI (0-outside, 1-in)	Correlation coefficient (r)	p value
6428	cg13759778	OMG	17	0	-0.943	2.76E-52
38869	cg21588305	NNAT	20	1	-0.922	1.30E-45
12803	cg02066887	POLD4	11	0	-0.921	3.36E-45
17240	cg15227610	CRYAB	11	0	-0.905	3.89E-41
22927	cg08477744	MFAP2	1	0	-0.902	2.24E-40
23208	cg19853760	LGALS1	22	0	-0.901	3.78E-40
38869	cg12862537	NNAT	20	1	-0.891	3.08E-38
6121	cg19096475	ASAM	11	1	-0.891	4.70E-38
18618	cg19111262	IGSF9	1	0	-0.887	2.24E-37
21257	cg08191854	TRPM2	21	0	-0.886	3.97E-37
12868	cg12045829	TNFSF12	17	1	-0.883	1.10E-36
27540	cg21588305	NNAT	20	1	-0.879	8.25E-36
15244	cg13796218	C1orf187	1	1	-0.877	1.43E-35
10652	cg00476577	ZNF217	20	0	-0.876	2.68E-35
21420	cg07685786	S100B	21	0	-0.876	2.79E-35
13585	cg05798712	FABP7	6	0	-0.875	3.80E-35
17306	cg21038229	HMOX2	16	1	-0.873	7.17E-35
15536	cg19921353	HLA-DPB1	6	0	-0.872	1.21E-34
36867	cg04337944	FBLN1	22	1	-0.872	1.31E-34

34423	cg20648149	SYNE2	14	1	-0.871	1.61E-34
27540	cg12862537	NNAT	20	1	-0.863	3.16E-33
9994	cg12144803	KALRN	3	1	-0.861	5.82E-33
17458	cg01484156	NCALD	8	0	-0.860	8.16E-33
24882	cg03991512	LDHD	16	0	-0.859	1.26E-32
38458	cg20544605	SORBS2	4	1	-0.858	1.86E-32
12523	cg00221494	FARP1	13	1	-0.858	1.89E-32
38869	cg22298088	NNAT	20	1	-0.857	2.36E-32
31358	cg10942056	DISP1	1	0	-0.856	4.46E-32
6390	cg05624196	APOD	3	1	-0.855	4.96E-32
23481	cg23801057	P2RX7	12	0	-0.854	7.42E-32
14022	cg08880153	MAP1A	15	0	-0.853	1.10E-31
13862	cg09158314	TNFSF13B	13	0	-0.851	2.19E-31
15351	cg13718960	RNASE1	14	0	-0.850	2.45E-31
38367	cg20544605	SORBS2	4	1	-0.850	2.58E-31
7705	cg27117399	CNDP1	18	1	-0.849	4.16E-31
12807	cg25599242	RARRES3	11	0	-0.842	3.87E-30
8729	cg15021292	PIK3R1	5	0	-0.840	6.61E-30
27540	cg22298088	NNAT	20	1	-0.836	2.18E-29
19162	cg03364781	ALPK1	4	0	-0.834	3.58E-29
35517	cg05598246	MOG	6	0	-0.833	4.90E-29
8090	cg19118077	AKR1C3	10	0	-0.833	4.96E-29
4309	cg15021292	PIK3R1	5	0	-0.832	7.92E-29

							29
						1.16E-	28
7963	cg15021292	PIK3R1	5	0	-0.830		
						1.92E-	28
35959	cg20648149	SYNE2	14	1	-0.828		
						2.35E-	28
11645	cg12360736	MBNL1	3	0	-0.828		
						2.59E-	28
40633	cg24127874	HES6	2	1	-0.827		
						2.74E-	28
13714	cg05598246	MOG	6	0	-0.827		
						3.24E-	28
12312	cg13210534	HSPB2	11	0	-0.827		
						3.34E-	28
35597	cg19007731	RUNX1T1	8	0	-0.826		
						3.91E-	28
15991	cg21068030	LSMD1	17	0	-0.826		
						4.80E-	28
9994	cg10430690	KALRN	3	1	-0.825		
						1.14E-	27
6810	cg22252999	ART3	4	0	-0.822		
						1.34E-	27
19402	cg02939139	RASAL1	12	1	-0.821		
						1.47E-	27
28950	cg21091679	ELL2	5	1	-0.821		
						1.95E-	27
6910	cg18204685	BTD	3	0	-0.820		
						2.57E-	27
18835	cg03633120	NDUFA7	19	1	-0.819		
						2.99E-	27
17071	cg00431549	MGP	12	0	-0.818		
						3.93E-	27
38869	cg18433380	NNAT	20	1	-0.817		
						4.05E-	27
18987	cg22215728	FHIT	3	1	-0.817		
						7.36E-	27
8026	cg11787522	STRA6	15	0	-0.815		
						1.15E-	26
8715	cg21588305	NNAT	20	1	-0.813		
						1.37E-	26
10994	cg20131968	CCDC47	17	0	-0.812		
						1.69E-	26
19484	cg23732024	LY96	8	0	-0.812		
						3.14E-	26
35314	cg19007731	RUNX1T1	8	0	-0.809		



34905	cg20648149	SYNE2	14	1	-0.809	3.37E-26
9583	cg17095731	LRP8	1	1	-0.809	3.70E-26
9971	cg17701886	B3GNT5	3	1	-0.808	4.59E-26
2019	cg08816023	FGF1	5	0	-0.807	5.46E-26
8715	cg12862537	NNAT	20	1	-0.807	5.58E-26
22785	cg13796218	C1orf187	1	1	-0.806	7.13E-26
14581	cg17099569	GLI2	2	0	-0.804	1.08E-25
28966	cg14467840	S100A1	1	0	-0.804	1.17E-25
26118	cg04337944	FBLN1	22	1	-0.803	1.31E-25
27540	cg18433380	NNAT	20	1	-0.803	1.33E-25
15351	cg05958352	RNASE1	14	0	-0.803	1.34E-25
14555	cg21091679	ELL2	5	1	-0.803	1.35E-25
34306	cg20648149	SYNE2	14	1	-0.802	1.87E-25
9071	cg07888040	GLDN	15	0	-0.801	2.33E-25
36968	cg20648149	SYNE2	14	1	-0.800	2.64E-25
25124	cg05949660	MICAL1	6	1	-0.800	3.29E-25
17468	cg20011134	DDO	6	0	-0.799	3.44E-25
16780	cg23801057	P2RX7	12	0	-0.797	5.51E-25
4978	cg24127874	HES6	2	1	-0.797	5.58E-25
31448	cg10942056	DISP1	1	0	-0.796	7.23E-25
6933	cg11318251	BAALC	8	1	-0.796	7.48E-25
34422	cg20648149	SYNE2	14	1	-0.796	8.16E-25
275	cg10584819	HPRT1	23	1	-0.795	8.48E-25

							25
2468	cg23352695	EVI2A	17	0	-0.795	8.63E-	25
32811	cg08477744	MFAP2	1	0	-0.794	1.22E-	24
16869	cg17701886	B3GNT5	3	1	-0.794	1.24E-	24
17472	cg11225410	SOCS2	12	1	-0.793	1.36E-	24
4530	cg10150813	KIAA0746	4	1	-0.792	2.02E-	24
464	cg10584819	HPRT1	23	1	-0.792	2.02E-	24
10734	cg07085271	MMP24	20	0	-0.791	2.16E-	24
367	cg10584819	HPRT1	23	1	-0.790	2.72E-	24
224	cg10584819	HPRT1	23	1	-0.790	2.87E-	24
8026	cg00075967	STRA6	15	0	-0.790	3.17E-	24
24933	cg00221494	FARP1	13	1	-0.789	3.76E-	24
23081	cg07294734	ATP5D	19	1	-0.788	4.20E-	24

**Table S6. Top One Hundred Significant Cis-mQTLs**

<b>CpG locus</b>	<b>SNP Symbol</b>	<b>CpG Gene Symbol</b>	<b>CpG Chr</b>	<b>SNP Gene Symbol</b>	<b>SNP Chr</b>	<b>P value (-log)</b>
cg17749961	rs1662955	LYCAT	2	LYCAT	2	39.91
cg17749961	rs1723167	LYCAT	2	LYCAT	2	36.36
cg19766460	rs1571737	C21orf128	21	UMODL1	21	36.11
cg17749961	rs1612616	LYCAT	2	LYCAT	2	35.83
cg01889448	rs1063355	HLA-DQB1	6	HLA-DQB1	6	29.41
cg12339802	rs11264091	C1orf109	1	EPHA10	1	28.71
cg06665322	rs2281962	GPA33	1	GPA33	1	28.30
cg14129786	rs7076950	MGMT	10	MGMT	10	27.05
cg06509940	rs4330287	CD80	3	ADPRH	3	26.89
cg08679985	rs663818	KLF17	1	KLF17	1	26.78
cg26063872	rs17090740	DEFB123	20	DEFB121	20	25.87
cg26981881	rs10982549		9	TNC	9	25.18
cg08679985	rs1291051	KLF17	1	LOC644743	1	25.00
cg08679985	rs600450	KLF17	1	KLF17	1	24.42
cg25427638	rs10409701	CYP2A7	19	CYP2B6	19	23.65
cg14893161	rs708727	FLJ32569	1	SLC41A1	1	23.30
cg14159672	rs708727	FLJ32569	1	SLC41A1	1	23.27
cg14141399	rs11672222	HAS1	19	HAS1	19	23.24
cg05213296	rs3862838	BXDC1	6	BXDC1	6	22.91
cg05213296	rs9400437	BXDC1	6	GTF3C6	6	22.91
cg08424423	rs3095320	CDSN	6	CDSN	6	21.94
cg15028436	rs1470719	TXNDC3	7	TXNDC3	7	21.45
cg11003133	rs1935067	AIM2	1	AIM2	1	21.32
cg14162076	rs7298236	CLEC4D	12	CLEC4D	12	21.17
cg22680812	rs16957292	EPB42	15	UBR1	15	20.98
cg25040282	rs1220841	HTN3	4	CSN1S1	4	20.91
cg16354207	rs10167355	UBE2F	2	UBE2F	2	20.38
cg13782134	rs7196925	UNQ2446	16	PSKH1	16	20.35
cg00849368	rs17084916	ARSK	5	ARSK	5	20.34
cg00799727	rs916016	MAGEA11	23	MAGEA11	23	20.18
cg13131015	rs2099015	GUCY2C	12	GUCY2C	12	20.14
cg20022541	rs971618	C14orf152	14	C14orf152	14	20.05
cg20389709	rs7632	KLF11	2	KLF11	2	20.03
cg13284426	rs7731035	RAB24	5	NSD1	5	19.74
cg06210526	rs12460494	CYP2F1	19	CYP2A13	19	19.60
cg05163071	rs11708527	RETNLB	3	RETNLB	3	19.59
cg22373097	rs2833073	KRTAP21-1	21	KRTAP21-2	21	19.52

cg07175007	rs2050907	UHMK1	1	UHMK1	1	19.45
cg07175007	rs4657201	UHMK1	1	UHMK1	1	19.45
cg25677688	rs2010481	TAS2R48	12	TAS2R44	12	19.43
cg25677688	rs10772420	TAS2R48	12	TAS2R48	12	19.43
cg25677688	rs1376250	TAS2R48	12	TAS2R48	12	19.43
cg25677688	rs4763602	TAS2R48	12	TAS2R50	12	19.43
cg25677688	rs2708389	TAS2R48	12	TAS2R46	12	19.33
cg07175007	rs6427680	UHMK1	1	UHMK1	1	19.31
cg23183296	rs2088092	UGT2B28	4	UGT2B4	4	19.29
cg23183296	rs2101793	UGT2B28	4	UGT2B4	4	19.29
cg14129786	rs7080548	MGMT	10	MGMT	10	19.08
cg19109431	rs2233434	NFKBIE	6	NFKBIE	6	19.05
cg25677688	rs2900554	TAS2R48	12	TAS2R50	12	19.00
cg06617418	rs7887044	RGAG1	23	RGAG1	23	18.94
cg08424423	rs3094211	CDSN	6	CDSN	6	18.84
cg17571291	rs10215155	BLVRA	7	BLVRA	7	18.81
cg17385448	rs11580170	AGMAT	1	AGMAT	1	18.72
cg00849368	rs3909479	ARSK	5	FAM81B	5	18.65
cg07175007	rs10919550	UHMK1	1	UHMK1	1	18.64
cg14129786	rs11016838	MGMT	10	MGMT	10	18.48
cg06509940	rs12496520	CD80	3	ADPRH	3	18.47
cg06509940	rs12487334	CD80	3	ADPRH	3	18.47
cg06509940	rs6438537	CD80	3	CD80	3	18.26
cg12308275	rs471122	TGM5	15	TGM5	15	18.22
cg13877915	rs1465789	ZNF132	19	ZNF132	19	18.04
cg25677688	rs7486717	TAS2R48	12	TAS2R42	12	17.94
cg25677688	rs2600359	TAS2R48	12	NULL	12	17.94
cg22680812	rs9972367	EPB42	15	TUBGCP4	15	17.93
cg19234089	rs7926657	SART1	11	TSGA10IP	11	17.90
cg12454167	rs3821815	KNG1	3	KNG1	3	17.80
cg23183296	rs12501393	UGT2B28	4	LOC642496	4	17.77
cg10735607	rs7107068	TMEM109	11	PRPF19	11	17.65
cg17267907	rs10503362	DEFA1	8	DEFA1	8	17.62
cg09553448	rs3736957	NUP214	9	NUP214	9	17.62
cg14332079	rs9644041	CDCA2	8	CDCA2	8	17.56
cg23183296	rs12506196	UGT2B28	4	LOC642496	4	17.46
cg07175007	rs6665354	UHMK1	1	UHMK1	1	17.34
cg23855989	rs3759129	AQP5	12	AQP5	12	17.32
cg00750606	rs1890005	CDA	1	CDA	1	17.32
cg25427638	rs3745275	CYP2A7	19	CYP2B6	19	17.25
cg10281770	rs4789817	WDR45L	17	WDR45L	17	17.20
cg20203395	rs2441132	MGC33648	5	MIER3	5	17.20

cg14751914	rs2337146	SMAD7	18	SMAD7	18	17.19
cg14633704	rs4743713	HSD17B3	9	HSD17B3	9	17.18
cg10237469	rs10402677	CEACAM4	19	CEACAM1	19	17.17
cg14893161	rs708724	FLJ32569	1	RAB7L1	1	17.13
cg24920358	rs7547787	PPIE	1	PPIE	1	16.92
cg14633704	rs9299367	HSD17B3	9	HSD17B3	9	16.90
cg10115873	rs5758108	DNAJB7	22	ST13	22	16.81
cg10237469	rs11666835	CEACAM4	19	CEACAM1	19	16.75
cg25427638	rs3745277	CYP2A7	19	CYP2B6	19	16.67
cg05467918	rs4949874	ACADM	1	LOC646425	1	16.62
cg08634464	rs8100809	LOC126295	19	ZNF57	19	16.56
cg14893161	rs823130	FLJ32569	1	NUCKS1	1	16.36
cg10001720	rs3762296	LAPTM5	1	LAPTM5	1	16.36
cg21298523	rs7673763	NUDT9	4	NUDT9	4	16.35
cg10237469	rs16975865	CEACAM4	19	CEACAM1	19	16.34
cg10237469	rs1859341	CEACAM4	19	CEACAM8	19	16.28
cg25172835	rs7182756	PUNC	15	PUNC	15	16.26
cg21717724	rs10760117	PSMD5	9	PSMD5	9	16.23
cg24150528	rs12110174	FLJ10246	5	ZNF131	5	16.22
cg02579736	rs7615646	FANCD2	3	FANCD2	3	16.22

**Table S7. Top One Hundred Significant Trans-mQTLs**

CpG locus	SNP Symbol	CpG Gene Symbol	CpG Chr	SNP Gene Symbol	SNP Chr	P value (-log)
cg18984499	rs11847580	RPL26	17	C14orf72	14	24.16
cg17704839	rs733675	UBL5	19	RHOT1	17	23.55
cg18634211	rs2288322	LIN28	1	FKBP7	2	21.51
cg18634211	rs10207436	LIN28	1	PRKRA	2	21.38
cg25299176	rs4281963	YWHAE	17	LOC647002	2	19.66
cg03923277	rs326387	TDG	12	TMEM132B	12	19.52
cg25299176	rs6716175	YWHAE	17	LOC440917	2	18.85
cg18984499	rs4906142	RPL26	17	PPP2R5C	14	18.48
cg13514129	rs12130070	MACF1	1	SMYD3	1	18.38
cg13514129	rs2878079	MACF1	1	SMYD3	1	18.38
cg13514129	rs1361409	MACF1	1	SMYD3	1	18.38
cg13514129	rs1770011	MACF1	1	SMYD3	1	18.38
cg10052190	rs2891924	C16orf52	16	LOC389199	4	18.32
cg18540325	rs2855983	PRSS3	9	PRSS2	7	17.53
cg18634211	rs3752689	LIN28	1	PRKRA	2	17.15
cg13055278	rs1508399	ID2	2	ID2B	3	16.73
cg27059238	rs162344	HIST1H2BI	6	HSF2BP	21	14.91
cg18634211	rs4894020	LIN28	1	PRKRA	2	14.80
cg13055278	rs886556	ID2	2	PTPRG	3	14.19
cg05294455	rs16833894	MYL4	17	RGS18	1	13.94
cg27059238	rs8131020	HIST1H2BI	6	H2BFS	21	13.72
cg02367951	rs8131020	HIST1H2AK	6	H2BFS	21	13.58
cg02367951	rs162344	HIST1H2AK	6	HSF2BP	21	13.49
cg13514129	rs2878076	MACF1	1	SMYD3	1	13.33
cg13514129	rs4654096	MACF1	1	SMYD3	1	13.07
cg13514129	rs10924574	MACF1	1	SMYD3	1	13.07
cg25136926	rs10843881	DDX12	12	DDX11	12	12.97
cg04482110	rs17110725	TMEM106A	17	NOVA1	14	12.87
cg13735697	rs11958487	MYOG	1	H2AFY	5	12.82
cg27050763	rs3849350	AHCTF1	1	TBR1	2	12.77
cg23698956	rs2423515	FAM3A	23	JAG1	20	12.76
cg16791686	rs17635194	GLTSCR2	19	LOC440311	15	12.60
cg18121684	rs17073456	SERPINB13	18	KIAA0774	13	12.34
cg05294455	rs11963169	MYL4	17	LOC643623	6	12.32
cg25136926	rs4031375	DDX12	12	DDX11	12	12.27
cg10066332	rs1733161	PPP1R13B	14	PTPRN2	7	12.10
cg08081407	rs16853445	ARF4	3	LIMCH1	4	12.01
cg24457403	rs13405816	KRT16	17	ZNF385B	2	11.98

cg20530056	rs16968827	IKBKE	1	HMG20A	15	11.96
cg16639637	rs1541352	TUBGCP5	15	HS3ST3A1	17	11.92
cg11159299	rs7247364	GZMM	19	ATP8B3	19	11.84
cg13043862	rs16878308	EYA1	8	RBPJ	4	11.83
cg07296772	rs12361631	CHMP4A	14	C11orf39	11	11.72
cg05294455	rs4924379	MYL4	17	FSIP1	15	11.66
cg05294455	rs16952186	MYL4	17	FSIP1	15	11.66
cg12623088	rs12062445	MGC4562	15	PLD5	1	11.64
cg26970800	rs10053496	GIF	11	WWC1	5	11.58
cg05749792	rs9504822	DGAT2L6	23	RP3- 398D13.1	6	11.55
cg10237469	rs10424276	CEACAM4	19	CEACAM8	19	11.54
cg10237469	rs10413014	CEACAM4	19	CEACAM8	19	11.54
cg25007250	rs10803607	NOS3	7	LOC729958	2	11.43
cg13547237	rs9593567	Bles03	11	LOC647313	13	11.41
cg18806365	rs2062235	FABP5	8	AKAP13	15	11.38
cg02921257	rs226591	CMYA1	3	ACTRT1	23	11.38
cg05294455	rs7557971	MYL4	17	COL4A4	2	11.38
cg04756629	rs2910948	LOC400696	19	DAB2	5	11.38
cg26594488	rs5999501	LOC54103	7	LOC646677	22	11.35
cg13514129	rs12033048	MACF1	1	SMYD3	1	11.26
cg01144251	rs11106707	KLK9	19	NAV3	12	11.24
cg03000846	rs9681990	RAC3	17	FLNB	3	11.23
cg26155617	rs12261706	DDO	6	ADARB2	10	11.22
cg24784109	rs8131020	HIST1H3D	6	H2BFS	21	11.21
cg22909609	rs10509870	ITGBL1	13	SORCS1	10	11.14
cg07806164	rs8124998	UBE2E2	3	APCDD1L	20	11.07
cg23698956	rs12361631	FAM3A	23	C11orf39	11	11.03
cg09988116	rs11190327	MGC52423	1	DNMBP	10	11.01
cg07755653	rs3093032	STX11	6	ICAM1	19	11.00
cg07440877	rs16875123	FLJ46358	13	ADAMTS16	5	10.96
cg10115873	rs16978267	DNAJB7	22	SETBP1	18	10.96
cg25299176	rs4328686	YWHAE	17	LOC647002	2	10.95
cg00592315	rs17060350	C14orf152	14	FBXO8	4	10.95
cg24789869	rs6487735	DDX11	12	LOC642846	12	10.93
cg03065661	rs234798	CRSP6	11	PSAT1	9	10.91
cg01228667	rs2304955	GPR101	23	GOLGA1	9	10.91
cg00974864	rs4673130	FCGR3B	1	DOCK10	2	10.88
cg20530056	rs904874	IKBKE	1	ARHGEF3	3	10.88
cg27050763	rs768835	AHCTF1	1	TBR1	2	10.88
cg18806365	rs1828482	FABP5	8	LOC642935	15	10.86
cg26907889	rs10509870	NONO	23	SORCS1	10	10.79

cg21824213	rs6935954	CASC5	15	HIST1H2BH	6	10.77
cg23940655	rs11748623	C14orf43	14	FLJ43080	5	10.76
cg13547237	rs13395406	Bles03	11	LOC284998	2	10.74
cg27303882	rs1003301	PAGE2	23	NULL	12	10.72
cg21353232	rs12456242	SEZ6L	22	LOC728864	18	10.71
cg23698956	rs6087073	FAM3A	23	PSMF1	20	10.70
cg20833786	rs17035639	MRGPRX3	11	SLC5A7	2	10.70
cg24457403	rs13360221	KRT16	17	MGC23985	5	10.68
cg03704031	rs11569726	INGX	23	SULT1B1	4	10.68
cg00658007	rs11000153	C1orf36	1	SPOCK2	10	10.67
cg14850026	rs11728293	ECAT11	1	CENTD1	4	10.67
cg13806135	rs6826708	PCDH17	13	GABRB1	4	10.65
cg26594488	rs16944749	LOC54103	7	LOC390419	13	10.65
cg05294455	rs6882215	MYL4	17	RAB3C	5	10.64
cg05294455	rs17077508	MYL4	17	TMEM158	3	10.61
cg15521097	rs10509870	ITIH5L	23	SORCS1	10	10.57
cg21824213	rs9393692	CASC5	15	HIST1H2BI	6	10.56
cg25942450	rs12694755	TLX3	5	LOC729968	2	10.55
cg26390526	rs13029721	FLG	1	PMS1	2	10.53
cg02275359	rs4771834	ZNF146	19	GPC5	13	10.52



**Table S9A. Top One Hundred mQTLs in African American Subjects**

CpG locus	CpG Gene Symbol	CpG Chr	SNP Symbol	SNP Gene Symbol	SNP Chr	P value (-log)
cg17749961	LYCAT	2	rs1662955	LYCAT	2	28.70
cg14129786	MGMT	10	rs7076950	MGMT	10	26.98
cg17749961	LYCAT	2	rs1612616	LYCAT	2	26.48
cg17749961	LYCAT	2	rs1723167	LYCAT	2	24.19
cg05213296	BXDC1	6	rs3862838	BXDC1	6	21.85
cg05213296	BXDC1	6	rs9400437	GTF3C6	6	21.85
cg22373097	KRTAP21-1	21	rs2833073	KRTAP21-2	21	21.48
cg14159672	FLJ32569	1	rs708727	SLC41A1	1	20.21
cg06617418	RGAG1	23	rs7887044	RGAG1	23	19.63
cg06665322	GPA33	1	rs2281962	GPA33	1	18.80
cg01889448	HLA-DQB1	6	rs1063355	HLA-DQB1	6	18.65
cg12339802	C1orf109	1	rs11264091	EPHA10	1	17.82
cg13131015	GUCY2C	12	rs2099015	GUCY2C	12	17.53
cg06509940	CD80	3	rs4330287	ADPRH	3	17.50
cg08679985	KLF17	1	rs663818	KLF17	1	16.87
cg00849368	ARSK	5	rs17084916	ARSK	5	16.66
cg13284426	RAB24	5	rs7731035	NSD1	5	16.46
cg14159672	FLJ32569	1	rs1172198	SLC45A3	1	16.43
cg14159672	FLJ32569	1	rs823105	SLC45A3	1	16.43
cg14751914	SMAD7	18	rs2337146	SMAD7	18	16.36
cg21717724	PSMD5	9	rs4837796	PSMD5	9	16.35
cg21717724	PSMD5	9	rs10760117	PSMD5	9	16.35
cg19584733	DENND4C	9	rs7851902	DENND4C	9	16.13
cg27398547	C14orf39	14	rs1955700	SIX1	14	16.09
cg09419670	PSMD5	9	rs4837796	PSMD5	9	15.90
cg09419670	PSMD5	9	rs10760117	PSMD5	9	15.90
cg08679985	KLF17	1	rs1291051	LOC644743	1	15.74
cg01119135	C1orf116	1	rs2629676	C1orf116	1	15.62
cg00849368	ARSK	5	rs3909479	FAM81B	5	15.50
cg27398547	C14orf39	14	rs12436632	SIX6	14	15.36
cg12308275	TGM5	15	rs471122	TGM5	15	15.17
cg22680812	EPB42	15	rs9972367	TUBGCP4	15	15.14
cg27398547	C14orf39	14	rs2224410	SIX6	14	15.05
cg13798376	DSPG3	12	rs10859103	KERA	12	14.71
cg13798376	DSPG3	12	rs2735333	KERA	12	14.71
cg14893161	FLJ32569	1	rs708727	SLC41A1	1	14.71
cg17385448	AGMAT	1	rs11580170	AGMAT	1	14.01
cg08679985	KLF17	1	rs600450	KLF17	1	13.98

cg12454167	KNG1	3	rs1621816	KNG1	3	13.94
cg14129786	MGMT	10	rs11016838	MGMT	10	13.84
cg08424423	CDSN	6	rs3094211	CDSN	6	13.73
cg08424423	CDSN	6	rs3095320	CDSN	6	13.71
cg25427638	CYP2A7	19	rs10409701	CYP2B6	19	13.61
cg10237469	CEACAM4	19	rs10402677	CEACAM1	19	13.60
cg27398547	C14orf39	14	rs10873125	SIX6	14	13.59
cg10237469	CEACAM4	19	rs1859341	CEACAM8	19	13.59
cg04001333	C14orf58	14	rs2287015	FLVCR2	14	13.56
cg04001333	C14orf58	14	rs4903329	FLVCR2	14	13.56
cg12454167	KNG1	3	rs3821815	KNG1	3	13.46
cg27398547	C14orf39	14	rs1268621	C14orf39	14	13.44
cg14074641	ABCC12	16	rs16945883	ABCC12	16	13.40
cg02254407	PLEKHB1	11	rs652229	PLEKHB1	11	13.32
cg15028436	TXNDC3	7	rs1470719	TXNDC3	7	13.29
cg23183296	UGT2B28	4	rs2088092	UGT2B4	4	13.29
cg23183296	UGT2B28	4	rs2101793	UGT2B4	4	13.29
cg23183296	UGT2B28	4	rs12501393	LOC642496	4	13.22
cg13798376	DSPG3	12	rs4842515	KERA	12	13.22
cg13877915	ZNF132	19	rs1465789	ZNF132	19	13.17
cg10237469	CEACAM4	19	rs11666835	CEACAM1	19	13.16
cg08634464	LOC126295	19	rs8100809	ZNF57	19	13.09
cg23183296	UGT2B28	4	rs12506196	LOC642496	4	12.98
cg20051177	TCF20	22	rs5996130	TCF20	22	12.95
cg05163071	RETNLB	3	rs11708527	RETNLB	3	12.76
cg13410437	OR5P2	11	rs11500784	OR5P3	11	12.75
cg14386312	ZNF544	19	rs260428	ZNF544	19	12.74
cg13798376	DSPG3	12	rs734722	KERA	12	12.73
cg18081313	ULK1	12	rs11246867	ULK1	12	12.68
cg00406188	LCE2C	1	rs12096806	LCE2C	1	12.64
cg14141399	HAS1	19	rs11672222	HAS1	19	12.61
cg10708675	NQO1	16	rs8047010	WWP2	16	12.53
cg02579736	FANCD2	3	rs7615646	FANCD2	3	12.53
cg10708675	NQO1	16	rs11861500	NFAT5	16	12.53
cg10237469	CEACAM4	19	rs16975865	CEACAM1	19	12.52
cg24655310	CYP4F11	19	rs3810427	CYP4F11	19	12.45
cg02254407	PLEKHB1	11	rs1723846	MRPL48	11	12.30
cg02254407	PLEKHB1	11	rs1723849	RAB6A	11	12.30
cg02254407	PLEKHB1	11	rs4944859	RAB6A	11	12.30
cg02254407	PLEKHB1	11	rs2515095	PAAF1	11	12.27
cg02254407	PLEKHB1	11	rs1670561	PAAF1	11	12.27
cg02254407	PLEKHB1	11	rs2511262	MRPL48	11	12.27

cg22825487	VNN3	6	rs6942306	VNN3	6	12.25
cg05213296	BXDC1	6	rs3763195	BXDC1	6	11.92
cg05149586	SDSL	12	rs12823432	SDSL	12	11.90
cg14332079	CDCA2	8	rs9644041	CDCA2	8	11.89
cg00799727	MAGEA11	23	rs916016	MAGEA11	23	11.85
cg27398547	C14orf39	14	rs1010053	SIX6	14	11.85
cg13055001	PPP1CA	11	rs3781941	CLCF1	11	11.74
cg13055001	PPP1CA	11	rs1790740	CLCF1	11	11.74
cg13055001	PPP1CA	11	rs1638567	POLD4	11	11.74
cg02579736	FANCD2	3	rs3732966	TMEM111	3	11.67
cg10001720	LAPTM5	1	rs3762296	LAPTM5	1	11.65
cg05213296	BXDC1	6	rs1704721	LOC442244	6	11.59
cg23183296	UGT2B28	4	rs12513058	LOC642496	4	11.58
cg07175007	UHMK1	1	rs10919550	UHMK1	1	11.58
cg20203395	MGC33648	5	rs2662027	MIER3	5	11.51
cg13055001	PPP1CA	11	rs1638566	POLD4	11	11.47
cg00292662	LGALS1	22	rs929039	LGALS1	22	11.43
cg00292662	LGALS1	22	rs4820294	LGALS1	22	11.43
cg00292662	LGALS1	22	rs713835	PDXP	22	11.43

**Table S9B. Top One Hundred mQTLs in Caucasian Subjects**

<b>CpG locus</b>	<b>CpG Gene Symbol</b>	<b>CpG Chr</b>	<b>SNP Symbol</b>	<b>SNP Gene Symbol</b>	<b>SNP Chr</b>	<b>P value (-log)</b>
cg19766460	C21orf128	21	rs1571737	UMODL1	21	18.11
cg14893161	FLJ32569	1	rs708727	SLC41A1	1	15.87
cg21717724	PSMD5	9	rs12343516	PSMD5	9	14.52
cg06210526	CYP2F1	19	rs1709112	CYP2F1	19	14.51
cg06210526	CYP2F1	19	rs1709084	CYP2A13	19	14.51
cg21717724	PSMD5	9	rs10760117	PSMD5	9	14.46
cg05740244	LDHC	11	rs4757662	LDHC	11	14.40
cg23855392	MTHFS	15	rs7167420	C15orf37	15	14.30
cg14633704	HSD17B3	9	rs4742910	HSD17B3	9	14.16
cg14893161	FLJ32569	1	rs708724	RAB7L1	1	13.81
cg06210526	CYP2F1	19	rs12460494	CYP2A13	19	13.79
cg14633704	HSD17B3	9	rs9299367	HSD17B3	9	13.38
cg14633704	HSD17B3	9	rs4743713	HSD17B3	9	13.38
cg14159672	FLJ32569	1	rs708727	SLC41A1	1	13.36
cg17749961	LYCAT	2	rs829689	LYCAT	2	13.20
cg12339802	C1orf109	1	rs11264091	EPHA10	1	13.01
cg17749961	LYCAT	2	rs1723167	LYCAT	2	13.00
cg17749961	LYCAT	2	rs1662955	LYCAT	2	13.00
cg21717724	PSMD5	9	rs4837796	PSMD5	9	12.80
cg19767249	DCPS	11	rs1893352	TIRAP	11	12.72
cg25729068	MTAC2D1	14	rs1884841	TC2N	14	12.58
cg25729068	MTAC2D1	14	rs2402074	TC2N	14	12.58
cg10237469	CEACAM4	19	rs10410147	CEACAM8	19	12.07
cg09553448	NUP214	9	rs353512	C9orf58	9	11.94
cg09553448	NUP214	9	rs353513	C9orf58	9	11.94
cg18885346	PKHD1	6	rs9357723	PKHD1	6	11.88
cg14159672	FLJ32569	1	rs708724	RAB7L1	1	11.86
cg02196730	MTHFS	15	rs7167420	C15orf37	15	11.83
cg25427638	CYP2A7	19	rs10409701	CYP2B6	19	11.82
cg10237469	CEACAM4	19	rs11671846	CXCL17	19	11.79
cg14141399	HAS1	19	rs11672222	HAS1	19	11.71
cg18885346	PKHD1	6	rs2184460	PKHD1	6	11.66
cg21832243	TTC3	21	rs1015549	TTC3	21	11.63
cg08679985	KLF17	1	rs1291051	LOC644743	1	11.42
cg05089968	MGC35308	6	rs10946158	SFT2D1	6	11.35
cg19766460	C21orf128	21	rs11203184	C21orf128	21	11.33
cg25729068	MTAC2D1	14	rs3783829	TC2N	14	11.28
cg27519424	HLCS	21	rs8132470	DSCR6	21	11.28

cg24857721	RHD	1	rs873308	TMEM57	1	11.28
cg25729068	MTAC2D1	14	rs4904818	TC2N	14	11.24
cg17749961	LYCAT	2	rs1612616	LYCAT	2	11.17
cg05089968	MGC35308	6	rs4144886	SFT2D1	6	11.16
cg14893161	FLJ32569	1	rs823130	NUCKS1	1	11.15
cg04616566	THSD4	15	rs8041918	THSD4	15	11.13
cg14893161	FLJ32569	1	rs823105	SLC45A3	1	11.13
cg10281770	WDR45L	17	rs4789817	WDR45L	17	11.12
cg23855989	AQP5	12	rs3759129	AQP5	12	11.10
cg24857721	RHD	1	rs10903129	TMEM57	1	11.05
cg20389709	KLF11	2	rs3885668	KLF11	2	11.03
cg21717724	PSMD5	9	rs10760112	MEGF9	9	11.02
cg00750606	CDA	1	rs1890005	CDA	1	10.98
cg01889448	HLA-DQB1	6	rs1063355	HLA-DQB1	6	10.89
cg08679985	KLF17	1	rs600450	KLF17	1	10.80
cg08679985	KLF17	1	rs663818	KLF17	1	10.80
cg10237469	CEACAM4	19	rs11666835	CEACAM1	19	10.78
cg10237469	CEACAM4	19	rs10402677	CEACAM1	19	10.78
cg10237469	CEACAM4	19	rs16975865	CEACAM1	19	10.78
cg14893161	FLJ32569	1	rs823096	NUCKS1	1	10.78
cg10237469	CEACAM4	19	rs1859341	CEACAM8	19	10.78
cg10281770	WDR45L	17	rs11655621	WDR45L	17	10.72
cg21167159	H19	11	rs2067051	H19	11	10.69
cg13798376	DSPG3	12	rs4842515	KERA	12	10.59
cg21298523	NUDT9	4	rs7673763	NUDT9	4	10.53
cg14893161	FLJ32569	1	rs1172198	SLC45A3	1	10.49
cg25729068	MTAC2D1	14	rs11160029	FBLN5	14	10.49
cg07455279	NDUFA3	19	rs11670086	PRPF31	19	10.47
cg19767249	DCPS	11	rs4420285	RPUSD4	11	10.44
cg06665322	GPA33	1	rs2281962	GPA33	1	10.41
cg17571291	BLVRA	7	rs10215155	BLVRA	7	10.39
cg13771579	TCL1B	14	rs1748952	TCL1B	14	10.34
cg25427638	CYP2A7	19	rs3745277	CYP2B6	19	10.34
cg00186954	ST5	11	rs2653601	C11orf16	11	10.23
cg08380539	CTBS	1	rs11164005	SPATA1	1	10.21
cg13877915	ZNF132	19	rs1465789	ZNF132	19	10.20
cg04616566	THSD4	15	rs1501422	THSD4	15	10.15
cg12339802	C1orf109	1	rs768659	CDCA8	1	10.12
cg18151487	ARL3	10	rs10786705	SFXN2	10	10.11
cg04616566	THSD4	15	rs17737742	THSD4	15	10.03
cg21832243	TTC3	21	rs1003719	TTC3	21	9.95
cg20022541	C14orf152	14	rs971618	C14orf152	14	9.95

cg20203395	MGC33648	5	rs1573998	MIER3	5	9.94
cg20203395	MGC33648	5	rs2441132	MIER3	5	9.94
cg20389709	KLF11	2	rs7632	KLF11	2	9.92
cg08380539	CTBS	1	rs15911	CTBS	1	9.91
cg00799727	MAGEA11	23	rs916016	MAGEA11	23	9.89
cg21167159	H19	11	rs4930103	H19	11	9.85
cg27535305	SCP2	1	rs11206043	SCP2	1	9.81
cg06509940	CD80	3	rs4330287	ADPRH	3	9.81
cg06873352	LYK5	17	rs2665833	PSMC5	17	9.76
cg06873352	LYK5	17	rs2584624	FTSJ3	17	9.76
cg13798376	DSPG3	12	rs10859103	KERA	12	9.71
cg13798376	DSPG3	12	rs2735333	KERA	12	9.71
cg22825487	VNN3	6	rs6942306	VNN3	6	9.68
cg14159672	FLJ32569	1	rs823105	SLC45A3	1	9.66
cg10281770	WDR45L	17	rs3826310	WDR45L	17	9.63
cg10735607	TMEM109	11	rs7107068	PRPF19	11	9.58
cg17829936	TAAR5	6	rs7765655	TAAR6	6	9.54
cg15028436	TXNDC3	7	rs2722333	TXNDC3	7	9.51
cg15028436	TXNDC3	7	rs2598053	TXNDC3	7	9.51