

King's Research Portal

DOI:

[10.1080/15592294.2015.1099797](https://doi.org/10.1080/15592294.2015.1099797)

Document Version

Peer reviewed version

[Link to publication record in King's Research Portal](#)

Citation for published version (APA):

Fisher, H., Murphy, T., Arseneault, L., Caspi, A., Moffitt, T. E., Viana, J., Hannon, E., Pidsley, R., Burrage, J., Dempster, E. L., Wong, C. C. Y., Parante, C. M., & Mill, J. (2015). Methylyomic analysis of monozygotic twins discordant for childhood psychotic symptoms. *Epigenetics, 10*(11), 1014-1023.
<https://doi.org/10.1080/15592294.2015.1099797>

Citing this paper

Please note that where the full-text provided on King's Research Portal is the Author Accepted Manuscript or Post-Print version this may differ from the final Published version. If citing, it is advised that you check and use the publisher's definitive version for pagination, volume/issue, and date of publication details. And where the final published version is provided on the Research Portal, if citing you are again advised to check the publisher's website for any subsequent corrections.

General rights

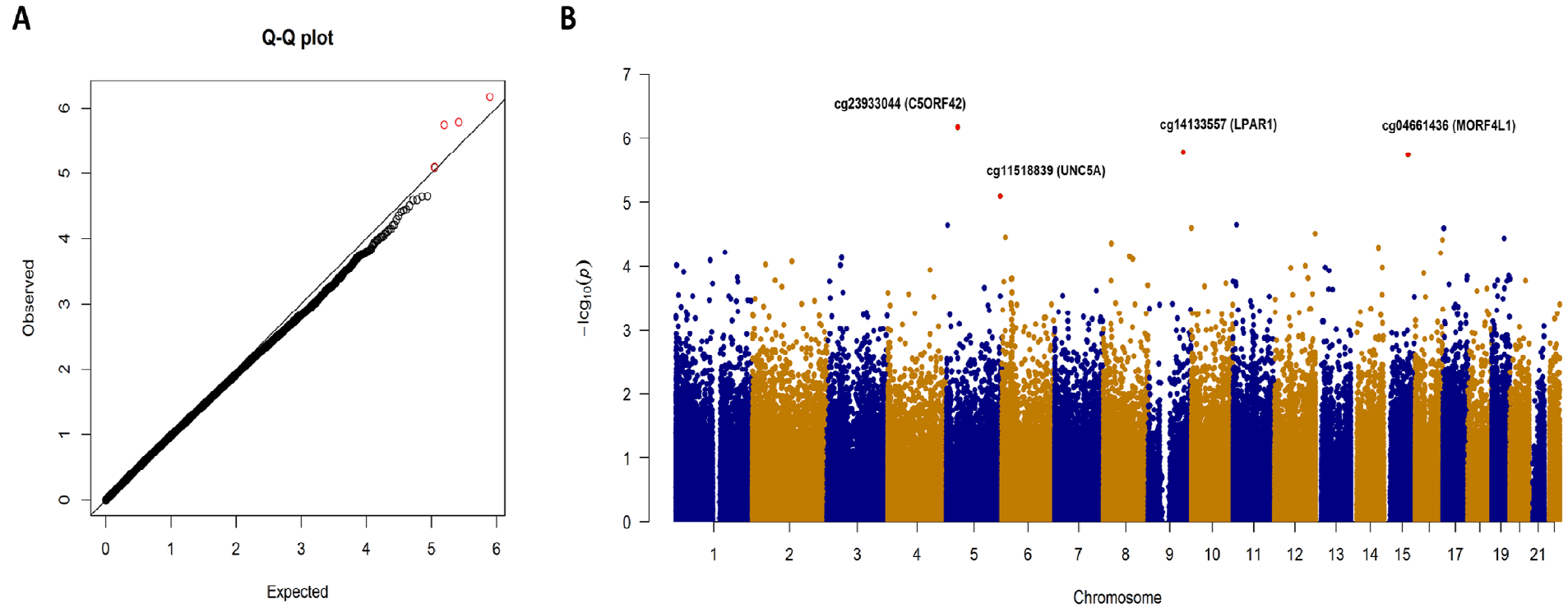
Copyright and moral rights for the publications made accessible in the Research Portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognize and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the Research Portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the Research Portal

Take down policy

If you believe that this document breaches copyright please contact librarypure@kcl.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.

Supplementary Material



Supplementary Figure 1. A, Quantile-quantile (QQ) plot illustrating the $-\log_{10}(\text{observed } p \text{ value})$ (Observed) to the $-\log_{10}(\text{expected } p \text{ value})$ (Expected). **B**, Manhattan plot showing the distribution of p values from the paired comparison of 24 monozygotic twin pairs at age 10 who were discordant for psychotic symptoms at age 12, with the top 4 ranked differentially methylated positions (DMPs) shown in red and identified in the plot.

Supplementary Table 1. The top 100 ranked DMPs at age 10 in monozygotic twin pairs discordant for psychotic symptoms at age 12

Probe ID	Affected Twin Mean	Co-Twin Mean	Mean $\Delta\beta$	P value	Hg19	Relation to CpG Island	Gene region feature category (UCSC)	SNPs in probe (+/- 10bp SBE)	Illumina Gene Annotation	Probe Type	Gene Annotation from GREAT (Distance from TSS)
cg23933044	0.315	0.349	-0.034	6.76E-07	Chr5:37249909	S_Shore	TSS1500		C5ORF42	II	C5ORF42 (-380)
cg14133557	0.796	0.742	0.055	1.65E-06	Chr9:113802005	S_Shore			LPAR1 (-1641)	II	LPAR1 (-1641)
cg04661436	0.795	0.751	0.044	1.81E-06	Chr15:79169207	S_Shelf	Body		MORF4L1	II	MORF4L1 (+4036), CTSH (+68212)
cg11518839	0.378	0.428	-0.051	8.11E-06	Chr5:176216711					II	UNC5A (-20848), TSPAN17 (+142324)
cg16508913	0.766	0.698	0.068	2.25E-05	Chr11:11609419		Body		GALNTL4	II	CSNK2A1 (-234516), GALNTL4 (+34141)
cg19115205	0.899	0.873	0.026	2.28E-05	Chr5:5062128		Body	rs75560907	LOC340094	I	ADAMTS16 (-78314)
cg05764011	0.880	0.907	-0.027	2.55E-05	Chr10:409541	S_Shore	Body		DIP2C	II	ZMYND11 (+183608), DIP2C (+326066)
cg26403608	0.308	0.396	-0.088	2.58E-05	Chr17:2319719		TSS1500;3'UTR		LOC284009;METT10D	II	MNT (-15462), METTL16 (+95480)
cg04576398	0.747	0.700	0.047	3.10E-05	Chr12:132262872	N_Shore	Body		SFRS8	II	MMP17 (-50068), SFSWAP (+67238)
cg16991886	0.903	0.888	0.015	3.58E-05	Chr6:11832079					I	HIVEP1 (-180644), C6orf105 (-52800)
cg08061902	0.848	0.818	0.030	3.71E-05	Chr19:40169418		TSS1500		LOC400696	II	LGALS14 (-25527), LGALS16 (+22861)
cg27418099	0.744	0.690	0.054	3.92E-05	Chr16:88941395	N_Shelf	3'UTR		CBFA2T3	II	PABPN1L (-8328), CBFA2T3 (+102108)
cg20546928	0.068	0.057	0.011	4.47E-05	Chr8:27167985	N_Shore	TSS1500;Body		PTK2B;TRIM35	II	TRIM35 (+848)
cg06889165	0.604	0.556	0.048	5.18E-05	Chr14:90042580		Body;5'UTR		PRO1768;FOXN3	II	FOXN3 (+42913), TTC8 (+751663)
cg12754671	0.366	0.391	-0.025	6.12E-05	Chr1:161171876	Island	5'UTR;TSS200		NDUFS2	I	ADAMTS4 (-3032), NDUFS2 (-60)
cg03804206	0.855	0.825	0.031	6.21E-05	Chr16:82191819		Body		MPHOSPH6	I	MPHOSPH6 (+12009), HSD17B2 (+122962)
cg21211020	0.047	0.061	-0.014	7.15E-05	Chr8:86132685	Island	TSS200		C8orf59	II	CA13 (-25030), E2F5 (+43067)
cg04602043	0.866	0.831	0.034	7.35E-05	Chr3:47827617	S_Shelf				II	SMARCC1 (-4213)
cg13160891	0.738	0.790	-0.052	7.77E-05	Chr8:96768366					II	GDF6 (+404653), PLEKHF2 (+622418)
cg21304211	0.262	0.275	-0.014	8.12E-05	Chr1:112281877	Island	Body;1stExon;5'UTR		C1orf183	I	DDX20 (-16312), RAP1A (+119473)
cg21875839	0.850	0.815	0.035	8.39E-05	Chr2:129308196					II	HS6ST1 (-232026)
cg03181376	0.132	0.147	-0.015	9.34E-05	Chr2:43454447	Island	TSS1500;Body		ZFP36L2;LOC100129726	I	ZFP36L2 (-703)
cg25512936	0.173	0.198	-0.025	9.57E-05	Chr3:44041103	Island				II	C3orf23 (-338840), ABHD5 (+308729)
cg12857678	0.785	0.725	0.060	9.60E-05	Chr1:3549732		Body		WDR8	II	TPRG1L (+8177), WRAP73 (+16938)
cg14893473	0.649	0.593	0.056	9.88E-05	Chr12:100041071		Body;TSS1500		ANKS1B	II	ANKS1B (+337360)
cg23470196	0.873	0.842	0.031	0.00010	Chr14:102695671	Island	Body		RAGE	II	HSP90AA1 (-89586), MOK (+75859)
cg06770877	0.823	0.788	0.035	0.00011	Chr13:31897247		Body		B3GALT1	II	RXFP2 (-416431), B3GALT1 (+123136)
cg10227191	0.059	0.067	-0.008	0.00011	Chr12:53342746	N_Shore	TSS200;5'UTR		KRT18	II	KRT18 (-96)
cg13443950	0.686	0.736	-0.050	0.00011	Chr4:138584567					II	PCDH18 (-130939), SLC7A11 (+578935)
cg08261525	0.221	0.281	-0.060	0.00012	Chr13:44239135		5'UTR		ENOX1	II	SERP2 (-708842), ENOX1 (-35523)
cg03987192	0.352	0.395	-0.043	0.00012	Chr1:26373407	S_Shore	TSS1500		SLC30A2	II	SLC30A2 (-804)
cg14431699	0.101	0.079	0.021	0.00013	Chr16:27121094	Island				II	JMJD5 (-94201)
cg08199563	0.803	0.763	0.041	0.00014	Chr19:55816212	Island	Body		BRSK1	II	TMEM150B (+20495), BRSK1 (+20679)
cg06919800	0.890	0.909	-0.019	0.00014	Chr17:78803320		Body		RPTOR	II	CHMP6 (-162320), RPTOR (+284696)
cg16028336	0.880	0.852	0.028	0.00015	Chr1:200194941					II	FAM58BP (+12286), ZNF281 (+184224)
cg00095930	0.287	0.335	-0.048	0.00015	Chr12:109569116					II	ACACB (-8085), UNG (+33718)
cg07025169	0.884	0.858	0.026	0.00016	Chr6:33236905	N_Shelf	Body		VPS52	II	RPS18 (-2946), VPS52 (+2756)
cg07061692	0.073	0.084	-0.011	0.00016	Chr19:59010811	Island	Body		SLC27A5	II	SLC27A5 (+12620), ZNF446 (+23017)
cg16880210	0.771	0.741	0.030	0.00016	Chr6:31130290	S_Shelf	Body	rs77870954	TCF19	I	CCHCR1 (-4725), TCF19 (+3988)
cg07428200	0.922	0.888	0.034	0.00016	Chr17:78046742		Body		CCDC40	I	GAA (-28612), CCDC40 (+36312)
cg24836583	0.157	0.130	0.027	0.00017	Chr19:19051747	Island	TSS1500;5'UTR		HOMER3	I	HOMER3 (+293)

cg03820024	0.077	0.091	-0.015	0.00017	Chr2:74649460	S_Shore	Body	WDR54	II	C2orf81 (-4617)
cg11903133	0.144	0.163	-0.019	0.00017	Chr20:50722613	S_Shore	Body	WFP64	I	SALL4 (-303566), ZFP64 (+85910)
cg12252412	0.908	0.886	0.021	0.00017	Chr8:26513782		3'UTR	DPYSL2	II	DPYSL2 (+142074), ADRA1A (+209139)
cg00419186	0.105	0.096	0.010	0.00017	Chr19:48825265	Island			I	EMP3 (-3363)
cg17114283	0.083	0.071	0.012	0.00017	Chr11:696207	Island	Body;TSS1500	TMEM80;DEAF1	II	DEAF1 (-468), TMEM80 (+592)
cg12353927	0.851	0.825	0.026	0.00017	Chr3:9814514	S_Shelf			II	CAMK1 (-2847)
cg07915528	0.123	0.141	-0.019	0.00018	Chr1:202936986	S_Shore	TSS1500	CYB5R1	I	CYB5R1 (-583)
cg13323047	0.097	0.107	-0.011	0.00018	Chr6:7261517	S_Shore			II	SSR1 (+52023), RREB1 (+153432)
cg00186954	0.802	0.751	0.051	0.00018	Chr11:8933980	S_Shore	TSS1500;Body	ST5;C11orf17	II	AKIP1 (+1280), ASCL3 (+30599)
cg05318275	0.811	0.772	0.039	0.00019	Chr10:112794609			rs58174822	II	ADRA2A (-42180), SHOC2 (+115309)
cg26791905	0.060	0.071	-0.010	0.00019	Chr1:120254664	N_Shore	1stExon	PHGDH	II	PHGDH (+246)
cg25819816	0.737	0.673	0.064	0.00019	Chr17:20076850		Body	CYTSB	II	SPECC1 (+164202), LGALS9B (+293997)
cg21310731	0.978	0.974	0.004	0.00020	Chr8:145618932	Island	Body	CPSF1	I	CPSF1 (+15800), ADCK5 (+21202)
cg21949229	0.768	0.722	0.045	0.00020	Chr11:9529385		Body	ZNF143	I	WEE1 (-65842), ZNF143 (+46874)
cg06622468	0.237	0.254	-0.017	0.00020	Chr19:10491460	Island	TSS1500	TYK2	I	TYK2 (-213)
cg01291590	0.634	0.590	0.044	0.00021	Chr10:42646111	Island		rs34948030	II	ZNF33B (+487880)
cg01310600	0.090	0.099	-0.009	0.00021	Chr2:96987238	Island			I	ITPRIPL1 (-4706)
cg18368265	0.919	0.900	0.018	0.00022	Chr5:123968247				II	ZNF608 (+112617)
cg25237016	0.125	0.151	-0.026	0.00022	Chr19:41018757	Island	Body	SPTBN4	II	SHKBP1 (-63999), SPTBN4 (+45632)
cg21266547	0.853	0.873	-0.020	0.00022	Chr18:61654618		3'UTR;3'UTR	SERPINB8	II	SERPINB8 (+17356), LINC00305 (+111255)
cg00131557	0.834	0.796	0.038	0.00023	Chr13:43596656	N_Shore	TSS1500	DNAJC15	II	DNAJC15 (-705)
cg20621674	0.698	0.645	0.053	0.00023	Chr13:56188634				II	NONE
cg08263941	0.715	0.660	0.054	0.00024	Chr7:136401170				II	MTPN (-738967), CHR2 (-152661)
cg14482684	0.043	0.038	0.005	0.00024	Chr18:30051176	Island	TSS1500	FAM59A	I	MEP1B (+281190), KLHL14 (+301797)
cg20729846	0.090	0.104	-0.013	0.00025	Chr6:32822182	Island	Body;TSS1500	rs4148878	II	PSMB9;TAP1
cg12365107	0.026	0.021	0.005	0.00026	Chr3:52720035	Island	1stExon;5'UTR;TSS200	GNL3;PBRM1	I	TAP1 (-435), PSMB9 (+245)
cg18657303	0.885	0.857	0.028	0.00026	Chr4:1051139	S_Shore			II	GNL3 (+100)
cg05826626	0.091	0.102	-0.011	0.00026	Chr6:32820862	Island	TSS1500;1stExon	PSMB9;TAP1	I	FGFRL1 (+45380), RNF212 (+56212)
cg23822643	0.845	0.863	-0.018	0.00027	Chr12:123341665		Body	HIP1R	II	PSMB9 (-1075), TAP1 (+885)
cg17780992	0.052	0.059	-0.007	0.00028	Chr4:69215675	Island	1stExon;5'UTR	YTHDC1	I	HIP1R (+21627), VPS37B (+39046)
cg06835156	0.873	0.835	0.038	0.00028	Chr14:101131459		Body	C14orf70	II	TMPPRSS11B (-104264), TMPPRSS11E (-97491)
cg11871280	0.864	0.828	0.036	0.00028	Chr12:60082038		TSS1500	SLC16A7	II	BEGAIN (-97053), DLK1 (-61742)
cg22711777	0.065	0.072	-0.007	0.00029	Chr1:9352663		TSS1500	SPSB1	I	SLC16A7 (-1087)
cg08093568	0.849	0.810	0.038	0.00029	Chr7:27626595		Body	HIBADH	II	SPSB1 (-277)
cg00394844	0.411	0.447	-0.037	0.00030	Chr19:18343302	N_Shore	Body	PDE4C	II	HIBADH (+76024), EVX1 (+344432)
cg02624704	0.337	0.373	-0.035	0.00030	Chr1:173446429	Island	TSS200	PRDX6	I	RAB3A (-28429), PDE4C (+15707)
cg04554817	0.645	0.582	0.062	0.00030	Chr1:55508184	S_Shelf	Body	PCSK9	II	PRDX6 (-56)
cg11097675	0.646	0.702	-0.056	0.00030	Chr5:175612438				II	PCSK9 (+3036), USP24 (+172854)
cg07315693	0.061	0.076	-0.015	0.00030	Chr11:118135203		TSS200	MPZL2;MPZL2	II	THOC3 (-216894), KIAA1191 (+176370)
cg11058916	0.683	0.745	-0.062	0.00031	Chr16:34257749	Island			II	MPZL2 (+47)
cg23709782	0.820	0.777	0.043	0.00031	Chr15:99386939		Body	IGF1R	II	BC068290 (+473239)
cg22396878	0.882	0.858	0.025	0.00031	Chr4:151097199		Body	DCLK2	II	PGPEP1L (+161945), IGF1R (+194179)
cg23405575	0.207	0.186	0.021	0.00032	Chr3:11034281	N_Shore	TSS200	SLC6A1	I	MAB21L2 (-405877), DCLK2 (+97774)
cg05925971	0.087	0.096	-0.010	0.00033	Chr19:36485966	Island	TSS200	SDHAF1	I	SLC6A1 (-138)
cg20273697	0.094	0.107	-0.013	0.00033	Chr2:8977583	Island	5'UTR	KIDINS220	I	SDHAF1 (-123)
cg02567344	0.944	0.936	0.009	0.00033	Chr1:179010239		5'UTR	FAM20B	I	KIDINS220 (+171)
cg03402805	0.060	0.066	-0.006	0.00033	Chr12:2921865	Island	1stExon;5'UTR	ITFG2	I	TOR3A (-40872), FAM20B (+15166)
cg08455719	0.772	0.735	0.037	0.00034	Chr1:234351342	S_Shore	Body	SLC35F3	II	FKBP4 (+17758), NRIP2 (+22355)
									II	C1orf31 (-158086), SLC35F3 (+310664)

Fisher, Murphy et al.

cg18792689	0.639	0.602	0.037	0.00035	Chr1:109254098		TSS1500	rs61797272	FNDC7	II	FNDC7 (-1457)
cg03345454	0.582	0.495	0.087	0.00035	Chr2:202901428	S_Shore	1stExon;3'UTR		FZD7;FZD7	II	FZD7 (+2119), SUMO1 (+201893)
cg08708599	0.098	0.107	-0.010	0.00035	Chr1:244893918	Island				I	FAM36A (-104720), C1orf101 (+269246)
cg08831369	0.805	0.766	0.040	0.00036	Chr1:197511177		Body		DENND1B	II	DENND1B (+233445), CRB1 (+273844)
cg01890712	0.551	0.615	-0.064	0.00036	Chr11:57790918		TSS1500		OR9Q1	II	OR9Q1 (-434)
cg17546147	0.774	0.755	0.019	0.00038	Chr6:29710109		Body		LOC285830	II	LOC554223 (-49573), HLA-F (+18993)
cg00000321	0.381	0.434	-0.053	0.00038	Chr8:41167802	S_Shore	TSS1500		SFRP1	II	SFRP1 (-813)
cg02494549	0.894	0.868	0.025	0.00039	Chr2:161798364					II	RBMS1 (-448047), TANK (-195101)
cg13482432	0.173	0.156	0.017	0.00039	Chr9:79633350	Island	TSS1500		FOXB2	I	FOXB2 (-1220)
cg03883640	0.860	0.816	0.044	0.00039	Chr22:50727014	N_Shore	Body		PLXNB2	II	MAPK11 (-18236), PLXNB2 (+18986)
cg02017892	0.835	0.796	0.038	0.00040	Chr8:103550807					II	UBR5 (-125891), ODF1 (-13040)
cg10182151	0.878	0.836	0.042	0.00040	Chr6:161575294		Body		AGPAT4	II	AGPAT4 (+119812), MAP3K4 (+162473)
cg14827481	0.731	0.687	0.045	0.00040	Chr10:134361889	S_Shore	Body	rs57835447	INPP5A	II	INPP5A (+10537), NKX6-2 (+237647)
cg09375907	0.868	0.830	0.038	0.00040	Chr6:49706534		5'UTR		CRISP3	II	CRISP2 (-25236), CRISP3 (+5633)
cg08077354	0.924	0.907	0.017	0.00040	Chr17:40437010	N_Shelf				II	STAT5A (-2554)
cg14293614	0.308	0.264	0.043	0.00040	Chr9:37593003	S_Shore	TSS1500		TOMM5	II	TOMM5 (-368)
cg12044213	0.230	0.263	-0.033	0.00041	Chr6:31124978	N_Shore	Body;TSS1500;5'UTR		CCHCR1;TCF19	II	TCF19 (-1324), CCHCR1 (+587)
cg17332705	0.815	0.842	-0.027	0.00041	Chr4:7768162		Body		AFAP1;LOC84740	II	PSAPL1 (-331463), AFAP1 (+173490)
cg09867322	0.847	0.818	0.029	0.00041	Chr5:135329478			rs73294763		II	LECT2 (-38756), TGFBI (-35105)
cg18507032	0.773	0.712	0.060	0.00042	Chr11:61382092		TSS1500		RPLP0P2	II	DAGLA (-65812), SYT7 (-33749)
cg10105699	0.898	0.881	0.017	0.00043	Chr2:37869895					II	CDC42EP3 (+29430), QPCT (+298143)
cg07224918	0.913	0.882	0.031	0.00043	Chr1:17944423		Body		ARHGEF10L	II	ACTL8 (-137384), ARHGEF10L (+78094)
cg27214721	0.082	0.094	-0.012	0.00043	Chr17:49337257	Island	1stExon;TSS1500;5'UTR		MBTD1;UTP18	II	UTP18 (-639), MBTD1 (+169)
cg00994583	0.667	0.701	-0.033	0.00044	Chr17:36613498	S_Shelf	TSS200		ARHGAP23	II	ARHGAP23 (+28779), SRCIN1 (+148684)
cg01409207	0.539	0.578	-0.039	0.00046	Chr12:117538129	S_Shore	TSS1500		TESC	II	TESC (-879)
cg14480858	0.041	0.045	-0.004	0.00046	Chr9:4666499	S_Shelf	1stExon;5'UTR		C9orf68	I	CDC37L1 (-13066), PPAPDC2 (+4202)
cg02997817	0.886	0.868	0.018	0.00046	Chr14:64929012	N_Shelf				II	AKAP5 (-3204)
cg13697735	0.453	0.509	-0.056	0.00046	Chr14:65172103	S_Shore	5'UTR		PLEKHG3	II	PLEKHG3 (-22207), HSPA2 (+164918)
cg22456479	0.758	0.706	0.051	0.00048	Chr12:113793985	N_Shelf				II	PLBD2 (-2385)
cg15669092	0.090	0.113	-0.023	0.00048	Chr16:89989024	Island	TSS1500		TUBB3	II	TUBB3 (-662)
cg13883063	0.891	0.874	0.018	0.00048	Chr9:138836839		Body		UBAC1	II	CAMSAP1 (-37835), UBAC1 (+16386)
cg25569234	0.047	0.057	-0.010	0.00048	Chr6:33257790	S_Shore	Body;TSS1500		PFDN6;WDR46	I	WDR46 (-487), PFDN6 (+413)
cg19745903	0.749	0.684	0.065	0.00049	Chr6:3129401		Body		BPHL	II	BPHL (+10476), TUBB2A (+28381)
cg01236849	0.092	0.102	-0.010	0.00049	Chr11:16760157	Island	1stExon;5'UTR	rs34623871	C11orf58	II	C11orf58 (+10)
cg15340582	0.080	0.069	0.011	0.00050	Chr5:139780509	Island	TSS1500		ANKHD1;EIF4EBP3	II	ANKHD1-EIF4EBP3 (-889)
cg18602913	0.314	0.263	0.052	0.00050	Chr19:16022934	Island				II	CYP4F2 (-14051), CYP4F11 (+22741)
cg15340582	0.069	0.080	0.011	0.00050	Chr5:139780509	Island	TSS1500		ANKHD1;ANKHD1-EIF4EBP3	II	ANKHD1-EIF4EBP3 (-889)
cg18602913	0.263	0.314	0.052	0.00050	Chr19:16022934	Island				II	CYP4F2 (-14051), CYP4F11 (+22741)
cg00615915	0.063	0.073	0.010	0.00051	Chr18:61637299	N_Shore	5'UTR;1stExon		SERPINB8	II	SERPINB8 (+37)
cg15050310	0.875	0.844	-0.032	0.00051	Chr11:86617582	Island				II	FZD4 (+48857), PRSS23 (+106092)
cg04462209	0.078	0.068	-0.009	0.00051	Chr1:202896493	Island	TSS200		KLHL12	II	KLHL12 (-123)
cg15885786	0.693	0.743	0.050	0.00051	Chr10:54054127		3'UTR		PRKG1;PRKG1	II	CSTF2T (-594773), DKK1 (-19913)
cg20060394	0.813	0.837	0.024	0.00052	Chr1:34328648		5'UTR;Body;TSS1500		HMGB4;CSMD2	II	HMGB4 (+2573), CSMD2 (+302226)
cg11855409	0.776	0.810	0.034	0.00052	Chr7:14380781		Body		DGKB	II	ETV1 (-351140), DGKB (+500293)
cg05409419	0.548	0.608	0.060	0.00052	Chr14:30953702					II	PRKD1 (-556804), G2E3 (-74626)
cg03310242	0.239	0.207	-0.033	0.00052	Chr12:2903563	Island	TSS1500		FKBP4	I	FKBP4 (-544)
cg09361958	0.819	0.851	0.032	0.00053	Chr3:128947790					II	CNBP (-44981), COPG (-20662)
cg21126707	0.774	0.708	-0.066	0.00054	Chr12:81111012	Island	1stExon		MYF5	II	MYF5 (+305)

cg14303948	0.130	0.120	-0.010	0.00054	Chr7:43878684				I	MRPS24 (+30460), BLVRA (+80413)
cg23631932	0.549	0.507	-0.043	0.00054	Chr8:52322341	S_Shore	Body	PXDNL	II	PXDNL (+399663)
cg03715152	0.067	0.061	-0.006	0.00055	Chr17:46969953	Island	TSS200	ATP5G1	I	ATP5G1 (-194)
cg16519433	0.956	0.962	0.006	0.00055	Chr10:3143596	N_Shelf	Body	PFKP	I	PFKP (+33885), PITRM1 (+71436)
cg19533294	0.459	0.394	-0.066	0.00055	Chr4:87857667	S_Shore	5'UTR	AFF1	II	AFF1 (+1514), HSD17B13 (+386388)
cg02377690	0.487	0.455	-0.032	0.00055	Chr6:37400392	N_Shore	TSS1500	FTSJ2	II	FTSJ2 (-514)
cg04692538	0.570	0.602	0.031	0.00055	Chr22:43586097	S_Shelf			II	TLL12 (-2961)
cg07551054	0.977	0.982	0.005	0.00056	Chr8:140744200	Island	Body	TRAPPC9	I	KCNK9 (-28902), TRAPPC9 (+724477)
cg07050192	0.877	0.898	0.021	0.00056	Chr10:22038263				II	MLLT10 (+214690), DNAJC1 (+254386)
cg03097111	0.087	0.102	0.015	0.00057	Chr10:99078896	Island	TSS200	FRAT1	I	FRAT1 (-125)
cg23138461	0.060	0.048	-0.012	0.00057	Chr10:17685950	N_Shore	TSS200	STAM	II	STAM (-173)
cg15975890	0.354	0.313	-0.041	0.00058	Chr5:11903145	N_Shore	Body	CTNND2	II	CTNND2 (+964)
cg25450121	0.235	0.222	-0.014	0.00058	Chr17:46970175	S_Shore	1stExon;5'UTR	ATP5G1	II	ATP5G1 (+28)
cg06954520	0.735	0.781	0.046	0.00058	Chr18:68095624	N_Shelf			II	SOCS6 (+139488)
cg10700334	0.123	0.109	-0.014	0.00058	Chr3:118753610	Island	5'UTR;1stExon;Body	IGSF11	II	IGSF11 (+65)
cg14523898	0.449	0.380	-0.069	0.00058	Chr1:38220138	S_Shore	Body	EPHA10	II	EPHA10 (+10685), CDCA8 (+61980)
cg17926940	0.097	0.074	-0.023	0.00059	Chr14:97685060	Island			II	VRK1 (+421377)
cg20786876	0.712	0.753	0.041	0.00059	Chr2:1938415	N_Shelf	Body	MYT1L	II	PXDN (-190125), MYT1L (+396629)
cg16960573	0.889	0.910	0.021	0.00060	Chr10:131200784				I	MGMT (-64669)
cg08940097	0.979	0.983	0.004	0.00060	Chr17:74094040		Body	EXOC7	I	EXOC7 (+5827), ZACN (+18778)
cg18196374	0.818	0.853	0.035	0.00060	Chr3:196243502		TSS1500	C3orf43	II	C3orf43 (-1266)
cg13956932	0.835	0.880	0.045	0.00060	Chr2:3493521				II	ADI1 (+29828), TRAPPC12 (+110076)
cg08107701	0.121	0.111	-0.010	0.00060	Chr2:218933668		TSS200	RUFY4	II	RUFY4 (-69)
cg01447322	0.076	0.092	0.016	0.00062	Chr11:66035600	N_Shore	TSS1500	RAB1B	II	RAB1B (-455)
cg06805253	0.070	0.080	0.010	0.00062	Chr3:15900513	Island	Body	ANKRD28	I	ANKRD28 (+539)
cg12658052	0.692	0.743	0.051	0.00062	Chr1:1078295				II	TLL10 (-30990), C1orf159 (-26560)
cg25488160	0.822	0.860	0.038	0.00062	Chr3:133097868		Body	TMEM108	II	BFSP2 (-20921), TMEM108 (+340698)
cg03393769	0.891	0.909	0.018	0.00062	Chr2:54611906				I	TSPYL6 (-128498), SPTBN1 (-71547)
cg03716590	0.738	0.781	0.043	0.00062	Chr7:95435309		Body	DYNC111	II	DYNC111 (+33492), SLC25A13 (+516149)
cg08591761	0.172	0.156	-0.016	0.00063	Chr19:57922319	N_Shore	TSS1500	ZNF17	I	ZNF17 (-209)
cg19004134	0.078	0.069	-0.009	0.00064	Chr6:142468346	Island	TSS200	VTA1	I	VTA1 (-63)
cg21503582	0.133	0.122	-0.011	0.00064	Chr7:151001017	Island			I	SMARCD3 (-55269), NUB1 (-37829)
cg21843272	0.807	0.845	0.038	0.00065	Chr12:48235729		3'UTR	VDR	II	HDAC7 (-21967), VDR (+63084)
cg13347970	0.160	0.113	-0.047	0.00065	Chr6:137809630	Island			II	IFNGR1 (-269064), OLIG3 (+5900)
cg23394673	0.476	0.402	-0.074	0.00065	Chr1:1149211	Island	Body	TNFRSF4	I	TNFRSF4 (+336)
cg07203817	0.818	0.845	0.027	0.00066	Chr1:64300033		Body	ROR1	II	UBE2U (-369456), ROR1 (+60344)
cg08439468	0.075	0.065	-0.010	0.00066	Chr9:95526812	Island	1stExon	BICD2	II	BICD2 (+270)
cg06407434	0.685	0.626	-0.059	0.00067	Chr22:34046529	Island	Body	LARGE	II	SYN3 (-643721), LARGE (+269886)
cg15444081	0.707	0.766	0.059	0.00068	Chr7:123406500				II	HYAL4 (-78722), WASL (-17385)
cg01780585	0.505	0.476	-0.029	0.00068	Chr1:36348359	N_Shore	TSS1500	EIF2C1	I	EIF2C1 (-450)
cg15398152	0.267	0.322	0.055	0.00069	Chr6:32016535		Body	TNXB	II	CYP21A2 (+10443), TNXB (+60615)
cg14711016	0.112	0.100	-0.012	0.00070	Chr16:790766	Island	Body	NARFL	II	NARFL (+230)
cg07887753	0.770	0.805	0.036	0.00071	Chr8:57817338				II	PENK (-458746), IMPAD1 (+89091)
cg24250374	0.822	0.854	0.032	0.00071	Chr1:184591081		3'UTR	C1orf21	I	EDEM3 (+132959), TSEN15 (+570271)
cg22765829	0.620	0.665	0.045	0.00071	Chr6:168216358				II	TCP10 (-418361), MLLT4 (-11312)
cg04569202	0.855	0.819	-0.036	0.00072	Chr7:157444423	S_Shore	Body	PTPRN2	II	DNAJB6 (+314714), PTPRN2 (+936058)
cg14368406	0.720	0.756	0.035	0.00072	Chr7:148923027	Island	3'UTR	ZNF282	II	ZNF212 (-13714), ZNF282 (+30451)
cg01776691	0.809	0.845	0.037	0.00072	Chr7:44279727	S_Shore	Body	CAMK2B	I	YKT6 (+39150), CAMK2B (+85502)

cg20529923	0.250	0.208	-0.042	0.00072	Chr11:32110187	N_Shelf			II	RCN1 (-2289)
cg19478105	0.786	0.836	0.050	0.00072	Chr10:98946943	S_Shore	TSS1500	SLIT1	II	SLIT1 (-1261)
cg20121258	0.859	0.880	0.021	0.00072	Chr11:119652442				II	PVRL1 (-53008), TRIM29 (+356420)
cg16876823	0.699	0.747	0.048	0.00072	Chr19:2987082		Body	TLE6	II	TLE6 (+9547), TLE2 (+42082)
cg12900467	0.075	0.065	-0.010	0.00073	Chr13:21635665	Island	5'UTR;1stExon	LATS2	II	LATS2 (+56)
cg27492102	0.622	0.676	0.054	0.00073	Chr13:26759970	N_Shore			II	SHISA2 (-134773), RNF6 (+36537)
cg16953064	0.075	0.067	-0.009	0.00074	Chr16:72127243	Island	5'UTR;TSS1500	DHX38;TXNL4B	II	DHX38 (-371), TXNL4B (+524)
cg04290835	0.821	0.857	0.036	0.00075	Chr17:5350284	S_Shelf	Body	DHX33	II	C1QBP (-7814), DHX33 (+22095)
cg21396956	0.735	0.779	0.044	0.00075	Chr18:56340167	S_Shore	Body	MALT	II	ZNF532 (-189893), MALT1 (+1550)
cg16561957	0.917	0.934	0.017	0.00076	Chr14:103430940	S_Shore	Body	CDC42BPB	I	AMN (+41948), CDC42BPB (+92801)
cg05419798	0.677	0.719	0.042	0.00077	Chr17:74928552	N_Shore	Body	MGAT5B	II	SEC14L1 (-208452), MGAT5B (+63755)
cg16139011	0.095	0.086	-0.010	0.00078	Chr11:9596224	Island	TSS200;Body	WEE1	II	WEE1 (+997)
cg20202881	0.096	0.085	-0.011	0.00078	Chr17:57784779	Island	TSS200;5'UTR;1stExon	TMEM49;PTRH2	I	VMP1 (-83), PTRH2 (+76)
cg18630756	0.632	0.595	-0.038	0.00079	Chr10:107460450				II	NONE
cg21068030	0.749	0.811	0.063	0.00079	Chr17:7762413	S_Shore	Body;TSS1500	CYB5D1;LSMD1	II	LSMD1 (-1242)
cg14987769	0.248	0.213	-0.035	0.00079	Chr2:220197576	S_Shore	Body	RESP18	II	RESP18 (+322)
cg08234149	0.690	0.648	-0.042	0.00079	Chr14:22925659				II	TCRDV2 (-2429)
cg24449706	0.669	0.709	0.040	0.00079	Chr8:25229721		Body	DOCK5	II	GNRH1 (+52834), DOCK5 (+187435)
cg14711428	0.081	0.069	-0.012	0.00080	Chr7:112090348	Island	TSS200;5'UTR	IFRD1	I	C7orf53 (-30559), IFRD1 (+27150)
cg07237214	0.082	0.074	-0.008	0.00080	Chr5:42424604	Island	5'UTR	GHR	I	GHR (+728)
cg15445958	0.687	0.656	-0.031	0.00080	Chr6:110266125				II	GPR6 (-34172), FIG4 (+253702)
cg18415382	0.838	0.895	0.057	0.00081	Chr10:135012575	N_Shelf	Body	KNDC1	I	UTF1 (-31202), KNDC1 (+38605)
cg25484904	0.252	0.212	-0.040	0.00081	Chr4:48988015	Island	TSS1500	CWH43	II	CWH43 (-249)
cg09100988	0.088	0.103	0.015	0.00082	Chr11:66725961	Island	TSS200	PC	I	SYT12 (-64854), PC (-50622)
cg01969473	0.772	0.813	0.041	0.00083	Chr2:102978461		TSS1500	IL18R1	II	IL18R1 (-631)
cg00742472	0.343	0.360	0.017	0.00083	Chr14:31889912	Island			I	HEATR5A (-125)
cg11998425	0.159	0.141	-0.017	0.00083	Chr19:8213583	N_Shore	TSS1500	FBN3	II	FBN3 (-1203)
cg14256643	0.809	0.830	0.020	0.00084	Chr2:224896241		TSS200;5'UTR;Body	SERPINE2	II	SERPINE2 (+7794), MRPL44 (+74121)
cg20103018	0.790	0.825	0.034	0.00084	Chr6:33996522	S_Shore	Body	GRM4	II	MLN (-224730), GRM4 (+105113)
cg11923627	0.054	0.048	-0.005	0.00085	Chr18:55470401	Island			I	ATP8B1 (-75)
cg19170009	0.636	0.681	0.045	0.00085	Chr10:17277756		Body	VIM	II	VIM (+7499), ST8SIA6 (+218497)
cg12333210	0.839	0.865	0.025	0.00085	Chr6:136685884	S_Shelf	Body	MAP7	II	BCLAF1 (-74896), MAP7 (+161466)
cg02060434	0.845	0.869	0.024	0.00085	Chr12:52473014	N_Shore			II	C12orf44 (+9257), KRT80 (+112769)
cg08156927	0.873	0.896	0.022	0.00086	Chr16:963866	S_Shore	Body	LMF1	II	GNG13 (-113134), LMF1 (+57117)
cg07385577	0.063	0.059	-0.005	0.00086	Chr21:47394015	Island			I	COL6A1 (-7647), PCBP3 (+124141)
cg12606891	0.729	0.770	0.040	0.00087	Chr1:7913872		TSS1500	UTS2;UTS2	II	UTS2 (-308)
cg27607283	0.797	0.755	-0.042	0.00087	Chr5:15385796				II	ANKH (-513910), FBXL7 (-114508)
cg08650251	0.872	0.892	0.020	0.00088	Chr4:166030097	N_Shelf	Body	TMEM192	II	TMEM192 (+3926), TRIM60 (+76947)
cg24627332	0.202	0.165	-0.037	0.00088	Chr6:76059450		Body	FILIP1	I	SENPG6 (-252171), TMEM30A (-64819)
cg08578568	0.721	0.677	-0.044	0.00089	Chr16:86492943				II	FOXF1 (-51189), IRF8 (+560170)
cg14320358	0.887	0.863	-0.024	0.00089	Chr20:31397044		3'UTR	DNMT3B	II	MAPRE1 (-10654), DNMT3B (+46854)
cg22736280	0.075	0.067	-0.008	0.00089	Chr8:95565249	N_Shore	Body	KIAA1429	I	KIAA1429 (+496)
cg26883033	0.430	0.499	0.069	0.00090	Chr10:80027004				II	ZMIZ1 (-801787), RPS24 (+233487)
cg08254399	0.764	0.794	0.031	0.00092	Chr6:45671659				II	SUPT3H (-325990), CLIC5 (+376425)
cg05573737	0.882	0.897	0.016	0.00092	Chr10:134684065	S_Shore			II	NKX6-2 (-84529), TTC40 (+72023)
cg11081580	0.121	0.105	-0.017	0.00094	Chr7:1286650	Island			II	UNCX (+13997), MICALL2 (+212458)
cg11009335	0.114	0.095	-0.020	0.00094	Chr2:166651299	S_Shore	TSS1500	GALNT3	I	GALNT3 (-497)
cg01359962	0.489	0.428	-0.061	0.00095	Chr3:43148002	S_Shore	TSS1500	C3orf39	II	C3orf39 (-438)

Fisher, Murphy et al.

cg08808677	0.853	0.822	-0.031	0.00095	Chr2:6911141					II	CMPK2 (+94794)
cg03165383	0.780	0.810	0.030	0.00095	Chr18:74981431		3'UTR		GALR1	II	GALR1 (+19424)
cg17283347	0.072	0.066	-0.006	0.00095	Chr17:56736571	N_Shore	5'UTR		TEX14	II	SEPT4 (-129794), TEX14 (+32844)
cg08118412	0.835	0.861	0.027	0.00095	Chr3:64113418		Body		PRICKLE2	II	PSMD6 (-104299), PRICKLE2 (+97712)
cg22288011	0.711	0.749	0.038	0.00095	Chr3:182881613	S_Shore	TSS1500	rs34992803	LAMP3	II	LAMP3 (-947)
cg10690515	0.803	0.838	0.035	0.00096	Chr3:44751120	N_Shelf				II	ZNF502 (-3014)
cg01914743	0.845	0.860	0.015	0.00096	Chr19:9270907	Island	Body		ZNF317	II	OR7D2 (-25362), ZNF317 (+19852)
cg22557029	0.082	0.073	-0.009	0.00096	Chr7:45026411	Island	TSS1500		SNORA9;C7orf40	II	CCM2 (-13375), MYO1G (-7708)
cg03854796	0.157	0.121	-0.036	0.00096	Chr11:31819162	N_Shore	Body		PAX6	II	PAX6 (+20346), ELP4 (+287866)
cg02483043	0.863	0.837	-0.025	0.00097	Chr10:134536498	S_Shore	Body		INPP5A	II	NKX6-2 (+63038), INPP5A (+185146)
cg08285446	0.553	0.503	-0.050	0.00097	Chr8:1273856					II	C8orf42 (-778526), DLGAP2 (-175712)
cg20084184	0.863	0.837	-0.027	0.00097	Chr4:1148524					II	RNF212 (-41173), SPON2 (+18132)
cg13473086	0.787	0.817	0.030	0.00097	Chr13:67676107		Body		PCDH9	II	PCDH9 (+128360)
cg15558616	0.604	0.659	0.055	0.00098	Chr3:173630182		Body		NLGN1	II	NAALADL2 (-946928), NLGN1 (+513939)
cg19355190	0.175	0.132	-0.042	0.00098	Chr10:64575798	Island	5'UTR;1stExon		EGR2	II	EGR2 (+327)
cg07594674	0.167	0.111	-0.056	0.00099	Chr2:47499812	Island				II	EPCAM (-96474), CALM2 (-96073)
cg09784168	0.616	0.669	0.053	0.00099	Chr7:111843174	N_Shelf	Body		DOCK4	II	ZNF277 (-3468), DOCK4 (+3287)
cg13948230	0.037	0.041	0.005	0.00099	Chr10:126106957	Island	5'UTR		OAT	II	OAT (+587)
cg11046502	0.080	0.088	0.009	0.00100	Chr8:27491495	Island	TSS200		SCARA3	I	SCARA3 (-81)

Note. Ranked by p value ($p < 5e^{-4}$). $\Delta\beta$, difference in DNA methylation; DMPs, differentially methylated positions; GREAT, Genomic Regions Enrichment of Annotations Tool; Hg19, Human Genome build 19; SBE, single-base extension; SNP, single nucleotide polymorphism; TSS, transcription start site.

Supplementary Table 2. Top ten ranked DMPs at age 10 adjusted for internalizing and externalizing problems at age 10 and depressive symptoms at age 12.

Probe ID	Mean $\Delta\beta$	P value
cg23933044	-0.037	1.74E-06
cg14133557	0.051	2.22E-06
cg04661436	0.042	6.47E-06
cg11518839	-0.047	7.48E-05
cg16508913	0.065	4.72E-05
cg19115205	0.027	4.90E-05
cg05764011	-0.024	0.00011
cg26403608	-0.082	6.80E-05
cg04576398	0.045	6.55E-05
cg16991886	0.014	0.00015

Note. $\Delta\beta$, difference in DNA methylation; DMP, differentially methylated position.

Supplementary Table 3. Gene Ontology (GO) enrichment analysis of top ranked age 10 DMPs.

GO Accession ID	GO Function	Ontology	P value
GO:0002335	mature B cell differentiation	BP	0.0002
GO:0051966	regulation of synaptic transmission, glutamatergic	BP	0.0034
GO:0017147	Wnt-protein binding	MF	0.0037
GO:0042976	activation of Janus kinase activity	BP	0.0037
GO:0071305	cellular response to vitamin D	BP	0.0043
GO:0007163	establishment or maintenance of cell polarity	BP	0.0045
GO:0051649	establishment of localization in cell	BP	0.0050
GO:0016310	phosphorylation	BP	0.0054
GO:0071295	cellular response to vitamin	BP	0.0055
GO:0016773	phosphotransferase activity, alcohol group as acceptor	MF	0.0058
GO:0031175	neuron projection development	BP	0.0064
GO:0050804	regulation of synaptic transmission	BP	0.0064
GO:0051168	nuclear export	BP	0.0067
GO:0042220	response to cocaine	BP	0.0068
GO:0017046	peptide hormone binding	MF	0.0069
GO:0030165	PDZ domain binding	MF	0.0073
GO:0016226	iron-sulfur cluster assembly	BP	0.0074
GO:0031163	metallo-sulfur cluster assembly	BP	0.0074
GO:0006107	oxaloacetate metabolic process	BP	0.0075
GO:0033209	tumor necrosis factor-mediated signaling pathway	BP	0.0092
GO:0016301	kinase activity	MF	0.0094
GO:0004715	non-membrane spanning protein tyrosine kinase activity	MF	0.0116
GO:0046907	intracellular transport	BP	0.0121
GO:0032892	positive regulation of organic acid transport	BP	0.0125
GO:0009081	branched-chain amino acid metabolic process	BP	0.0129
GO:0004713	protein tyrosine kinase activity	MF	0.0134
GO:0045664	regulation of neuron differentiation	BP	0.0136
GO:0071356	cellular response to tumor necrosis factor	BP	0.0142
GO:0051955	regulation of amino acid transport	BP	0.0143
GO:0006641	triglyceride metabolic process	BP	0.0146

GO:0007215	glutamate receptor signaling pathway	BP	0.0146
GO:0051287	NAD binding	MF	0.0147
GO:0004672	protein kinase activity	MF	0.0150
GO:0071229	cellular response to acid chemical	BP	0.0150
GO:0030098	lymphocyte differentiation	BP	0.0150
GO:0006468	protein phosphorylation	BP	0.0157
GO:0010975	regulation of neuron projection development	BP	0.0159
GO:0007216	G-protein coupled glutamate receptor signaling pathway	BP	0.0167
GO:0031503	protein complex localization	BP	0.0170
GO:0045822	negative regulation of heart contraction	BP	0.0178
GO:0033280	response to vitamin D	BP	0.0180
GO:0090330	regulation of platelet aggregation	BP	0.0181
GO:0031670	cellular response to nutrient	BP	0.0183
GO:0017146	N-methyl-D-aspartate selective glutamate receptor complex	CC	0.0185
GO:0008028	monocarboxylic acid transmembrane transporter activity	MF	0.0188
GO:0006639	acylglycerol metabolic process	BP	0.0189
GO:0006638	neutral lipid metabolic process	BP	0.0193
GO:0034451	centriolar satellite	CC	0.0194
GO:0016482	cytoplasmic transport	BP	0.0200
GO:0048505	regulation of timing of cell differentiation	BP	0.0219
GO:0042813	Wnt-activated receptor activity	MF	0.0222
GO:0007271	synaptic transmission, cholinergic	BP	0.0222
GO:1902582	single-organism intracellular transport	BP	0.0224
GO:0048666	neuron development	BP	0.0229
GO:0051954	positive regulation of amine transport	BP	0.0229
GO:0040034	regulation of development, heterochronic	BP	0.0230
GO:2000310	regulation of N-methyl-D-aspartate selective glutamate receptor activity	BP	0.0234
GO:0035249	synaptic transmission, glutamatergic	BP	0.0236
GO:0038083	peptidyl-tyrosine autophosphorylation	BP	0.0237
GO:1901135	carbohydrate derivative metabolic process	BP	0.0240
GO:0050767	regulation of neurogenesis	BP	0.0241
GO:0050806	positive regulation of synaptic transmission	BP	0.0247
GO:0033036	macromolecule localization	BP	0.0254

GO:0005085	guanyl-nucleotide exchange factor activity	MF	0.0255
GO:0034612	response to tumor necrosis factor	BP	0.0260
GO:0051960	regulation of nervous system development	BP	0.0264
GO:0042562	hormone binding	MF	0.0270
GO:0042744	hydrogen peroxide catabolic process	BP	0.0272
GO:0051968	positive regulation of synaptic transmission, glutamatergic	BP	0.0282
GO:0006888	ER to Golgi vesicle-mediated transport	BP	0.0282
GO:0030426	growth cone	CC	0.0284
GO:0060999	positive regulation of dendritic spine development	BP	0.0294
GO:0016772	transferase activity, transferring phosphorus-containing groups	MF	0.0297
GO:0018108	peptidyl-tyrosine phosphorylation	BP	0.0298
GO:0048103	somatic stem cell division	BP	0.0307
GO:0018212	peptidyl-tyrosine modification	BP	0.0309
GO:0030427	site of polarized growth	CC	0.0312
GO:0060284	regulation of cell development	BP	0.0314
GO:0030183	B cell differentiation	BP	0.0317
GO:0008104	protein localization	BP	0.0320
GO:0021683	cerebellar granular layer morphogenesis	BP	0.0333
GO:0002028	regulation of sodium ion transport	BP	0.0335
GO:0042659	regulation of cell fate specification	BP	0.0337
GO:0031669	cellular response to nutrient levels	BP	0.0339
GO:0002521	leukocyte differentiation	BP	0.0340
GO:0034110	regulation of homotypic cell-cell adhesion	BP	0.0342
GO:0032855	positive regulation of Rac GTPase activity	BP	0.0346
GO:0006369	termination of RNA polymerase II transcription	BP	0.0347
GO:0007270	neuron-neuron synaptic transmission	BP	0.0352
GO:0030850	prostate gland development	BP	0.0358
GO:1901605	alpha-amino acid metabolic process	BP	0.0359
GO:0060359	response to ammonium ion	BP	0.0364
GO:0009118	regulation of nucleoside metabolic process	BP	0.0364
GO:0048708	astrocyte differentiation	BP	0.0370
GO:0004683	calmodulin-dependent protein kinase activity	MF	0.0375
GO:0021681	cerebellar granular layer development	BP	0.0393

GO:0033218	amide binding	MF	0.0394
GO:0071837	HMG box domain binding	MF	0.0395
GO:0017112	Rab guanyl-nucleotide exchange factor activity	MF	0.0408
GO:0022904	respiratory electron transport chain	BP	0.0418
GO:0032526	response to retinoic acid	BP	0.0419
GO:0042063	gliogenesis	BP	0.0425
GO:0019637	organophosphate metabolic process	BP	0.0429
GO:0048167	regulation of synaptic plasticity	BP	0.0436
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	BP	0.0447
GO:0071300	cellular response to retinoic acid	BP	0.0451
GO:0007398	ectoderm development	BP	0.0453
GO:0046128	purine ribonucleoside metabolic process	BP	0.0453
GO:0021510	spinal cord development	BP	0.0453
GO:0022900	electron transport chain	BP	0.0454
GO:0010656	negative regulation of muscle cell apoptotic process	BP	0.0455
GO:0006968	cellular defense response	BP	0.0457
GO:0009950	dorsal/ventral axis specification	BP	0.0460
GO:0007622	rhythmic behavior	BP	0.0461
GO:0019221	cytokine-mediated signaling pathway	BP	0.0467
GO:0030279	negative regulation of ossification	BP	0.0467
GO:0006903	vesicle targeting	BP	0.0471
GO:0042278	purine nucleoside metabolic process	BP	0.0473
GO:0043087	regulation of GTPase activity	BP	0.0474
GO:0032319	regulation of Rho GTPase activity	BP	0.0479
GO:0030010	establishment of cell polarity	BP	0.0479
GO:0033124	regulation of GTP catabolic process	BP	0.0481
GO:0051539	4 iron, 4 sulfur cluster binding	MF	0.0485
GO:0009205	purine ribonucleoside triphosphate metabolic process	BP	0.0485
GO:0042113	B cell activation	BP	0.0486
GO:0009119	ribonucleoside metabolic process	BP	0.0490
GO:0009199	ribonucleoside triphosphate metabolic process	BP	0.0495
GO:0001101	response to acid chemical	BP	0.0496

Note. BP, Biological Processes; CC, Cellular; DMPs, differentially methylated positions; MF, Molecular Function.

Supplementary Table 4. Details of post-mortem prefrontal cortex brain samples.

Sample	SZ	Control	Total	P value
LBBND				
Number	20	23	43	
Sex (male:female)	11:09	17:06	28:15	0.19
Age at death (years)	62.1 ± 15.87	62 ± 18.74	62.05 ± 17.26	0.99
Total brain weight (g)	1359 ± 150	1465 ± 197.8	1420 ± 182	0.07
pH	6.64 ± 0.28	6.49 ± 0.33	6.56 ± 0.31	0.13
DBCBB				
Number	18	15	33	
Sex (male:female)	15:03	13:02	28:05	0.79
Age at death (years)	45.5 ± 16.6	42.3 ± 14.8	44.0 ± 15.7	0.28
Total brain weight (g)	1432 ± 188	1463 ± 175	1447 ± 179	0.32
pH	6.6 ± 0.28	6.48 ± 0.33	6.54 ± 0.31	0.13

Note. Schizophrenia (SZ) cases and controls are matched (Chi-Squared test [for sex] or t-test P value > 0.05) for all variables. DBCBB, Douglas Bell-Canada Brain Bank; g, grams; LBBND, London Brain Bank for Neurodegenerative Disorders.

Supplementary Table 5. The top 100 ranked DMPs at age 5 for monozygotic twins discordant for psychotic symptoms at age 12

Probe ID	Affected Twin Mean	Co-Twin Mean	Mean $\Delta\beta$	P value	Hg19	Relation to CpG Island	Gene region feature category (UCSC)	SNPs in probe (+/- 10bp SBE)	Illumina Gene Annotation	Probe Type	Gene Annotation from GREAT (Distance from TSS)
cg15031661	0.150	0.130	0.020	1.26E-05	Chr1:238323226	Island	1stExon		FMN2	I	FMN2 (+1419), GREM2 (+518858)
cg26432347	0.082	0.063	0.018	1.87E-05	Chr6:30818615	Island	TSS200		FLOT1	I	FLOT1 (-184)
cg11356706	0.070	0.061	0.010	1.95E-05	Chr20:604240	Island	1stExon		SCRT2	I	SCRT2 (+582)
cg16011679	0.116	0.094	0.022	2.59E-05	Chr1:85497983	Island	TSS200		C1orf52	I	SYDE2 (-58668), BCL10 (+17191)
cg21480740	0.899	0.883	0.016	2.64E-05	Chr7:158511954	S_Shore				II	ESYT2 (-196875), VIPR2 (+118455)
cg10377582	0.443	0.520	-0.077	3.03E-05	Chr12:49899061	S_Shore	TSS1500		POU6F1	I	POU6F1 (-20845), DAZAP2 (-19713)
cg24085426	0.863	0.839	0.024	3.05E-05	Chr12:45869545					II	AMIGO2 (-109545), FAM113B (-26726)
cg03044239	0.072	0.080	-0.008	3.15E-05	Chr3:139549743	Island	5'UTR;TSS1500;1stExon		MRAS	II	MRAS (-454)
cg06547771	0.044	0.052	-0.008	3.34E-05	Chr11:43336969	Island	TSS200		TTC17	I	TTC17 (-41)
cg14659771	0.138	0.114	0.024	3.59E-05	Chr2:231625606	Island				I	PSMD1 (-4215)
cg24391460	0.525	0.462	0.062	4.12E-05	Chr7:78922102	S_Shore	TSS1500		MAGI2	I	MAGI2 (-1277)
cg24106824	0.927	0.918	0.009	5.24E-05	Chr17:77284720	Island	3'UTR		MRPL12	I	SLC25A10 (-5055), HGS (+23354)
cg21155461	0.048	0.042	0.006	5.57E-05	Chr19:63432065	Island	5'UTR;1stExon		ZNF544	I	ZNF544 (+184)
cg09501025	0.760	0.718	0.043	5.59E-05	Chr10:72982961		Body		CDH23	II	CDH23 (+156265), C10orf105 (+166622)
cg12730562	0.779	0.727	0.052	6.27E-05	Chr11:44884452		5'UTR;TSS200		TSPAN18	II	TP53I11 (+44731), TSPAN18 (+141901)
cg15648026	0.100	0.084	0.016	7.32E-05	Chr11:106967008	Island	TSS200;TSS1500		ELMOD1	I	ELMOD1 (-18)
cg08370347	0.799	0.841	-0.041	8.64E-05	Chr5:171504398		Body		STK10	II	FBXW11 (-137917), STK10 (+43552)
cg08307030	0.381	0.294	0.087	8.85E-05	Chr15:74421435	Island	3'UTR		ISL2	II	ISL2 (+5234), SCAPER (+541836)
cg10624784	0.166	0.179	-0.012	9.08E-05	Chr7:77265849	Island	TSS200		PHTF2;TMEM60	I	PHTF2 (-195), TMEM60 (-167)
cg01353538	0.872	0.847	0.025	9.66E-05	Chr6:43860500		3'UTR		VEGFA	II	VEGFA (+14577), MRPL14 (+342668)
cg00802617	0.938	0.927	0.012	9.77E-05	Chr15:97489121		Body		SYNM	II	SYNM (+26313), TTC23 (+118216)
cg17397135	0.082	0.073	0.009	0.00011	Chr2:28643320	Island	Body		PLB1	I	PPP1CB (-184797), PLB1 (+70879)
cg13382000	0.047	0.040	0.007	0.00011	Chr4:71772749	Island	TSS1500		UTP3	I	UTP3 (-310)
cg04262465	0.733	0.778	-0.045	0.00012	Chr14:100475446		TSS200		SNORD113-6	II	DIO3 (-621994), RTL1 (-54510)
cg11556416	0.308	0.262	0.046	0.00013	Chr2:191587497	Island	TSS1500		STAT1	I	STAT1 (-277)
cg10970392	0.884	0.910	-0.026	0.00015	Chr1:152809742	N_Shore	Body		CHRN2	II	CHRN2 (+2862), ADAR (+37605), CDC42EP3 (-219646), FAM82A1 (-58624)
cg25523261	0.849	0.882	-0.033	0.00016	Chr2:37972475					II	
cg12493050	0.042	0.037	0.005	0.00016	Chr6:31234065	Island	TSS1500		CCHCR1;TCF19	I	CCHCR1 (-521), TCF19 (-216)
cg17806717	0.798	0.831	-0.033	0.00017	Chr6:32135497		Body		TNXB	II	CYP21A2 (+21427), TNXB (+49631)
cg14344261	0.081	0.065	0.016	0.00018	Chr9:36976380	Island	Body		PAX5	I	PAX5 (+48095), MELK (+413476)
cg12928619	0.040	0.049	-0.009	0.00018	Chr2:74502262	Island	TSS200		WDR54	I	C2orf81 (-3911)
cg14014964	0.914	0.867	0.046	0.00019	Chr9:93483513					I	NFIL3 (-257549), ROR2 (+268751)
cg10113467	0.084	0.074	0.011	0.00019	Chr13:74954491	Island	TSS1500		TBC1D4	I	TBC1D4 (-241)
cg17025730	0.162	0.136	0.026	0.00019	Chr5:133887697	N_Shore				I	PHF15 (-1999)

Fisher, Murphy et al.

cg01314143	0.059	0.049	0.010	0.00019	Chr5:1852486	Island	5'UTR		MRPL36	I	NDUFS6 (-2009), MRPL36 (+469)
cg00422638	0.272	0.211	0.061	0.00020	Chr10:25506033	S_Shore	TSS1500;Body		GPR158	II	MYO3A (-756974), GPR158 (+1738)
cg10539936	0.894	0.862	0.032	0.00020	Chr14:69569738					II	SMOC1 (+153872), SLC8A3 (+155801)
cg12667002	0.727	0.780	-0.053	0.00020	Chr13:113830404	N_Shore	Body		RASA3	II	GAS6 (-245257), RASA3 (+85792)
cg14837825	0.905	0.881	0.024	0.00021	Chr2:96281294		3'UTR		TMEM127	II	STARD7 (-42995), TMEM127 (+14183)
cg08550421	0.087	0.123	-0.036	0.00021	Chr5:140286131	Island	Body;TSS1500		PCDHA1-12	II	PCDHAC2 (-39799), ZMAT2 (+225916)
cg01964795	0.901	0.874	0.027	0.00022	Chr16:2182897	N_Shelf	Body		CASKIN1	II	CASKIN1 (+3568), TRAF7 (+37098)
cg24324984	0.626	0.676	-0.050	0.00022	Chr19:51110894	S_Shore	TSS1500		NANOS2	II	NANOS2 (-1019)
cg03357540	0.062	0.054	0.008	0.00022	Chr18:17434821	Island	TSS200		ESCO1	I	ESCO1 (-131)
cg01684006	0.892	0.870	0.022	0.00022	Chr11:129518567		Body;3'UTR		APLP2	II	ST14 (-16324), APLP2 (+72895)
cg25053907	0.120	0.099	0.022	0.00023	Chr4:482859	Island	5'UTR;TSS200;TSS200;1stExon		ZNF721;PIGG	I	PIGG (-129), ZNF721 (+582)
cg17802633	0.734	0.676	0.059	0.00023	Chr2:68724972	S_Shore	TSS1500		PROKR1	I	PROKR1 (-1325)
cg04881131	0.224	0.263	-0.039	0.00023	Chr20:21633834	N_Shore	TSS1500		PAX1	I	PAX1 (-462)
cg25333216	0.071	0.056	0.015	0.00023	Chr17:72245033	Island	TSS1500;TSS200		MIR636;SFRS2;MFSD11	I	MFSD11 (-144), SRSF2 (+54)
cg11913790	0.194	0.165	0.029	0.00024	Chr5:154116329	Island	Body		LARP1	II	LARP1 (+43675), C5orf4 (+94076)
cg26169156	0.521	0.566	-0.045	0.00025	Chr8:128909061		Body		PVT1	II	MYC (+91565)
cg14297332	0.893	0.876	0.017	0.00025	Chr2:241828117	Island	Body		HDLBP	II	HDLBP (+32801), ANO7 (+51521)
cg00155429	0.066	0.050	0.016	0.00026	Chr1:152422321	Island	1stExon;5'UTR;Body		TPM3	I	NUP210L (-28106), TPM3 (+8911)
cg10673740	0.138	0.154	-0.016	0.00027	Chr10:121401816	Island	Body		BAG3	II	BAG3 (+945)
cg14883916	0.098	0.129	-0.031	0.00028	Chr11:6904117	Island	TSS200		ZNF215	I	ZNF215 (-112)
cg11214889	0.043	0.066	-0.023	0.00028	Chr18:587111		5'UTR;1stExon		CLUL1	II	CLUL1 (-19588), CETN1 (+16743)
cg05617732	0.918	0.896	0.023	0.00029	Chr6:47361869		Body		TNFRSF21	II	GPR110 (-243829), TNFRSF21 (+23769)
cg06740963	0.050	0.055	-0.005	0.00030	Chr16:2767349	Island	TSS200		TCEB2	I	TCEB2 (-52)
cg07154861	0.034	0.039	-0.005	0.00030	Chr2:121210284	Island				I	GLI2 (-61052), INHBB (+390096)
cg11550971	0.317	0.345	-0.028	0.00030	Chr18:11971317	Island	TSS200		IMPA2	I	IMPA2 (-109)
cg09691810	0.052	0.060	-0.008	0.00030	Chr5:34951393	Island	1stExon;Body;TSS200;5'UTR		RAD1;;BRX1	II	BRX1 (-183), RAD1 (+143)
cg01925594	0.870	0.833	0.037	0.00030	Chr8:1308193	N_Shore				II	C8orf42 (-825456), DLGAP2 (-128782)
cg22690046	0.030	0.026	0.003	0.00030	Chr1:36636250	S_Shore	TSS200	rs60673492	LSM10	I	LSM10 (-171)
cg10409248	0.049	0.042	0.007	0.00032	Chr17:75389668	Island				I	CBX8 (-4159)
cg02434121	0.562	0.492	0.070	0.00032	Chr7:4868324	S_Shore	TSS200;Body		PAPOLB;RADIL	I	PAPOLB (-174)
cg23016766	0.030	0.034	-0.004	0.00032	Chr1:32889284	Island	TSS200;TSS1500		RBBP4;ZBTB8OS	I	RBBP4 (-51)
cg24419324	0.136	0.109	0.027	0.00033	Chr2:222880573	S_Shore				I	SGPP2 (-116992), PAX3 (-8615)
cg16347279	0.091	0.120	-0.029	0.00033	Chr17:70179304	Island	5'UTR;1stExon		RAB37	II	CD300E (-47813), CD300LF (+41398)
cg26616283	0.071	0.062	0.008	0.00033	Chr7:11838060		1stExon		THSD7A	I	THSD7A (+288)
cg19706795	0.379	0.316	0.063	0.00033	Chr7:24764364	S_Shore	TSS1500		DFNA5	II	DFNA5 (-757)
cg05716350	0.885	0.857	0.028	0.00034	Chr4:79811906					II	BMP2K (-104649), ANXA3 (+120141)
cg10092691	0.884	0.909	-0.025	0.00034	Chr1:203658419		TSS1500		LEMD1	II	LEMD1 (-583)
cg10307119	0.875	0.854	0.021	0.00035	Chr10:103979244	N_Shore	3'UTR		ELOVL3	II	ELOVL3 (+3112), PITX3 (+11976)
cg10590925	0.401	0.467	-0.066	0.00035	Chr11:1420196	N_Shore	Body		BRSK2	II	MOB2 (+38494), BRSK2 (+52492)
cg16706629	0.079	0.089	-0.010	0.00035	Chr5:93980117	Island	TSS200		ANKRD32;C5orf36	II	ANKRD32 (-29)
cg22641058	0.872	0.839	0.033	0.00037	Chr2:130867352	S_Shore				II	CFC1 (-127784), PTPN18 (+37303)

cg21907579	0.122	0.074	0.048	0.00038	Chr12:113330251	Island	1stExon;5'UTR		TBX5	II	TBX5 (-1980)
cg16123090	0.246	0.196	0.050	0.00038	Chr2:3677085	Island				II	ALLC (-6575), COLEC11 (+56574)
cg02335306	0.901	0.920	-0.019	0.00039	Chr11:2516456		Body		KCNQ1	I	KCNQ1 (+93660), CDKN1C (+347114)
cg01725864	0.897	0.881	0.016	0.00039	Chr13:97627558	S_Shore	5'UTR;TSS200;5'UTR		FARP1;RNF113B	II	RNF113B (-37)
cg10593713	0.720	0.658	0.062	0.00039	Chr10:3779788					II	PITRM1 (-574756), KLF6 (+37684)
cg05869173	0.052	0.058	-0.005	0.00039	Chr7:99451128	Island	TSS200		ZKSCAN1	I	ZKSCAN1 (-26)
cg24459409	0.338	0.298	0.040	0.00040	Chr19:51196252	S_Shore	Body		CCDC61	II	CCDC61 (+6074), PGLYRP1 (+22143)
cg02002960	0.894	0.872	0.022	0.00041	Chr19:5406386	N_Shore	TSS200	rs17271813	ZNRF4	II	ZNRF4 (-39)
cg25867726	0.042	0.049	-0.007	0.00041	Chr19:10057726	Island	TSS200		C19orf66	I	ANGPTL6 (+16698), RDH8 (+72802)
cg21158737	0.769	0.808	-0.040	0.00042	Chr9:139463438	Island	3'UTR		NELF	I	ENTPD8 (-7717), NELF (+10168)
cg03184243	0.168	0.131	0.037	0.00042	Chr8:28403881	N_Shelf	TSS200		FBXO16	II	FZD3 (-3759)
cg17516330	0.632	0.675	-0.043	0.00042	Chr15:72281834		5'UTR		STRA6	II	STRA6 (+438)
cg04064828	0.862	0.902	-0.040	0.00042	Chr10:133852741	S_Shore	Body		DPYSL4	I	DPYSL4 (+2338), STK32C (+118725)
cg20416037	0.083	0.111	-0.028	0.00042	Chr12:56270979	N_Shore	TSS1500		PIP4K2C	II	PIP4K2C (-229)
cg07321536	0.419	0.373	0.046	0.00042	Chr4:39136292	N_Shore	TSS1500;Body		LIAS;RPL9	II	LIAS (-767), RPL9 (+309)
cg11985680	0.074	0.054	0.020	0.00042	Chr1:76024455		TSS1500;TSS200		SNORD45C;RABGGTB	II	RABGGTB (-18)
cg24025255	0.298	0.354	-0.056	0.00043	Chr14:68687527	N_Shore	Body		DCAF5	II	ACTN1 (-171692), DCAF5 (+2139)
cg21963436	0.115	0.100	0.015	0.00044	Chr13:27439142	Island	Body		CDX2	I	CDX2 (+2174), PDX1 (+46975)
cg11021661	0.847	0.872	-0.026	0.00044	Chr11:76430237	S_Shore	3'UTR		B3GNT6	II	CAPN5 (-25402), B3GNT6 (+7155)
cg03441257	0.075	0.064	0.010	0.00044	Chr1:148305713	N_Shore	TSS1500		VPS45	I	VPS45 (-252)
cg21879791	0.451	0.493	-0.042	0.00044	Chr6:29702809	N_Shore	Body		GABBR1	II	GABBR1 (+6131), OR2H2 (+39148)
cg04958124	0.075	0.087	-0.013	0.00045	Chr7:148454795	Island	5'UTR;TSS1500		ZNF398;ZNF425	I	ZNF425 (-425)
cg02335804	0.085	0.113	-0.028	0.00045	Chr17:33179352	N_Shore	TSS200		HNF1B	II	HNF1B (-144)
cg16442298	0.809	0.767	0.042	0.00045	Chr8:1390457	N_Shore				II	C8orf42 (-907720), DLGAP2 (-46518)
cg25810178	0.508	0.547	-0.039	0.00046	Chr19:60569183	N_Shelf	3'UTR		IL11	II	COX6B2 (-10909), IL11 (+4442)
cg18516946	0.890	0.860	0.030	0.00046	Chr11:94774414	S_Shelf				I	SRSF8 (-25641), KDM4DL (+15993)
cg23208152	0.037	0.030	0.007	0.00047	Chr3:50383134	Island	1stExon;5'UTR		ZMYND10	I	RASSF1 (-4768), ZMYND10 (+21)
cg27603283	0.101	0.094	0.007	0.00047	Chr7:4998649	Island	1stExon;5'UTR		MMD2	I	MMD2 (+194)
cg26841013	0.281	0.234	0.048	0.00047	Chr1:228248013	S_Shore	3'UTR		WNT3A	I	ARF1 (-22347), WNT3A (+53291)
cg23327070	0.134	0.147	-0.013	0.00047	Chr14:93214896		1stExon;5'UTR		LGMN	I	LGMN (+150)
cg23842941	0.665	0.694	-0.028	0.00048	Chr20:33762631	Island	Body		PROCR	I	MMP24 (-51907), PROCR (+2858)
cg10728960	0.904	0.889	0.015	0.00048	Chr3:78079111					I	ROBO2 (+989818)
cg17993148	0.894	0.914	-0.020	0.00048	Chr6:169717551					II	C6orf120 (-384705), THBS2 (-63415)
cg21937169	0.129	0.101	0.029	0.00049	Chr7:65541137	S_Shore	Body		ASL	II	ASL (+362)
cg15166583	0.652	0.708	-0.056	0.00049	Chr11:86208322		Body		ME3	II	ME3 (+174917), C11orf73 (+195070)
cg23715749	0.464	0.419	-0.045	0.00050	Chr1:37413867		Body		GRIK3	II	CSF3R (-464953), GRIK3 (+85976)
cg18170076	0.609	0.562	-0.047	0.00050	Chr7:76240583		3'UTR;Body;Body		POMZP3;LOC100133091	II	POMZP3 (+16036), UPK3B (+100839)
cg09571345	0.673	0.711	0.037	0.00050	Chr10:26931926		TSS200		LOC731789	I	PDSS1 (-54668), APBB1IP (+204661)
cg07059157	0.667	0.697	0.030	0.00051	Chr12:54519802	Island	TSS200		LOC400043	I	SMUG1 (+62975), HOXC4 (+72142)
cg25140501	0.058	0.074	0.016	0.00051	Chr14:23564641	Island	5'UTR;1stExon;TSS200		ACIN1;C14orf119	II	ACIN1 (+181)
cg22220310	0.959	0.967	0.008	0.00051	Chr1:1168541	Island	TSS1500;1stExon		SDF4;B3GALT6	I	SDF4 (-1095), B3GALT6 (+913)
cg13279019	0.962	0.947	-0.015	0.00051	Chr7:5266987	Island	Body		WIPI2	I	SLC29A4 (-55573), WIPI2 (+37153)

cg10455412	0.920	0.899	-0.021	0.00053	Chr12:67919042				II	DYRK2 (-123469), CAND1 (+255982)
cg01751341	0.057	0.048	-0.009	0.00053	Chr16:85045118	Island	5'UTR;1stExon;5'UTR;1stExon	ZDHHC7	II	ZDHHC7 (+22)
cg27380218	0.072	0.088	0.016	0.00053	Chr15:99602811	Island			I	PGPEP1L (-53927), SYNM (-42474)
cg10113589	0.756	0.710	-0.046	0.00053	Chr10:98118853		1stExon;5'UTR	OPALIN	II	OPALIN (+238)
cg00441301	0.815	0.845	0.031	0.00056	Chr8:33458593	S_Shore	TSS1500	DUSP26	II	DUSP26 (-1155)
cg22468497	0.651	0.618	-0.033	0.00056	Chr19:54241421		TSS1500	MIR518A2	II	NLRP12 (+86226), DPRX (+106112)
cg22081003	0.734	0.773	0.039	0.00056	Chr1:55416790				II	DHCR24 (-63870), TMEM61 (-29674)
cg10556999	0.831	0.866	0.036	0.00057	Chr1:158088745				II	CD1D (-60991), KIRREL (+125683)
cg02977752	0.086	0.100	0.014	0.00058	Chr7:86689099	Island	TSS200	KIAA1324L	I	KIAA1324L (-86)
cg05987564	0.878	0.901	0.023	0.00059	Chr2:156981620				II	NR4A2 (+207666)
cg12746717	0.093	0.108	0.015	0.00059	Chr2:240323484	Island	TSS1500	HDAC4	I	HDAC4 (-842)
cg04499015	0.580	0.534	-0.046	0.00059	Chr6:33141696		Body	COL11A2	II	COL11A2 (+18548), HLA-DPB1 (+97994)
cg07234439	0.859	0.880	0.021	0.00059	Chr9:110479374	Island			I	KLF4 (-227328)
cg17830308	0.133	0.181	0.049	0.00060	Chr5:134872124	S_Shore	TSS1500	NEUROG1	II	NEUROG1 (-486)
cg11050988	0.713	0.763	0.050	0.00060	Chr7:1952600	S_Shelf	Body	MAD1L1	I	ELFN1 (+203803), MAD1L1 (+319982)
cg00627347	0.878	0.825	-0.053	0.00060	Chr17:915265	N_Shore	Body	ABR	I	TIMM22 (+14909), ABR (+167865)
cg07145229	0.938	0.951	0.013	0.00062	Chr8:99422528				I	NIPAL2 (-115908), KCNS2 (-16721)
cg07086918	0.118	0.145	0.027	0.00062	Chr5:176784688		TSS200	RGS14	II	RGS14 (-155)
cg10929213	0.070	0.064	-0.006	0.00062	Chr11:66056787	Island	TSS200	YIF1A	I	TMEM151A (-2585), YIF1A (-150)
cg14791747	0.233	0.255	0.022	0.00062	Chr16:20752902	Island	1stExon	THUMPDP1	II	ACSM1 (-50325), ACSM3 (-22409)
cg17196805	0.887	0.866	-0.020	0.00063	Chr17:37796442	S_Shelf	5'UTR	STARD3	II	TCAP (-25156), STARD3 (+3110)
cg21045000	0.071	0.093	0.022	0.00063	Chr12:118811074	S_Shore	TSS1500	TAOK3	II	SUDS3 (-3283), TAOK3 (-325)
cg12363545	0.049	0.059	0.010	0.00063	Chr3:107809973	Island	TSS200	CD47	I	CD47 (-39)
cg27162392	0.765	0.708	-0.057	0.00063	Chr7:2208908		Body	MAD1L1	II	MAD1L1 (+63674), ELFN1 (+460111)
cg15847198	0.059	0.071	0.012	0.00064	Chr11:106889318	Island	TSS200	GUCY1A2	I	GUCY1A2 (-148)
cg22980293	0.635	0.592	-0.043	0.00064	Chr10:126158010		Body	LHPP	II	LHPP (+7670), FAM53B (+274919)
cg18730023	0.154	0.201	0.047	0.00064	Chr12:44199730	Island	Body	TWF1	II	TWF1 (+447)
cg20562220	0.933	0.918	-0.015	0.00065	Chr14:106068824	S_Shore			I	TMEM121 (+75872), IGHE (+260637)
cg08917121	0.746	0.710	-0.037	0.00066	Chr5:176097773				II	UNC5A (-139786), TSPAN17 (+23386)
cg16539675	0.084	0.104	0.019	0.00066	Chr5:31532179	Island	5'UTR;1stExon;TSS200	RNASEN;C5orf22	I	DROSHA (+102)
cg06890152	0.862	0.887	0.025	0.00066	Chr8:19800242	S_Shelf	Body	LPL	II	LPL (+3661), SLC18A1 (+240474)
cg06293099	0.639	0.620	-0.019	0.00067	Chr11:67745999				II	ALDH3B2 (-297315), UNC93B1 (+25593)
cg19984355	0.837	0.871	0.033	0.00067	Chr5:1794232				II	LPCAT1 (-270157), MRPL36 (+5723)
cg22827324	0.791	0.813	0.022	0.00067	Chr2:33612876		Body	LTBP1	II	RASGRP3 (-126065), LTBP1 (+440508)
cg18766170	0.059	0.051	-0.008	0.00068	Chr6:30421655	S_Shelf			I	HLA-E (-35527), TRIM39-RPP21 (+124568)
cg02824202	0.049	0.044	-0.006	0.00068	Chr18:6729810	Island			I	L3MBTL4 (-314901), ARHGAP28 (-104621)
cg10583297	0.066	0.075	0.008	0.00069	Chr15:45422095	Island	TSS200	DUOX1	I	DUOX1 (-96), DUOX1A1 (-39)
cg25719439	0.041	0.038	-0.003	0.00070	Chr16:89788035	Island	TSS1500;5'UTR;1stExon	C16orf7;ZNF276	I	C16orf7 (-642), ZNF276 (+84)
cg16073236	0.786	0.821	0.035	0.00070	Chr7:107789943		3'UTR	NRCAM	II	LAMB4 (-19143), NRCAM (+90670)
cg02794434	0.582	0.522	-0.060	0.00071	Chr4:2341196	Island	Body	ZFYVE28	II	MXD4 (-77458), ZFYVE28 (+79173)

cg13519194	0.734	0.704	-0.030	0.00073	Chr10:43539572				I	RET (-32944), BMS1 (+261619)
cg11609366	0.060	0.083	0.023	0.00074	Chr8:146018277	Island	TSS1500	RPL8	II	RPL8 (-473)
cg19919692	0.121	0.147	0.027	0.00074	Chr13:32421462	S_Shore	Body	EEF1DP3	II	FRY (-183974), RXFP2 (+107784)
cg16041550	0.788	0.819	0.031	0.00075	Chr19:47633739	N_Shore	TSS1500	SAE1	II	SAE1 (-340)
cg09901342	0.863	0.883	0.021	0.00075	Chr13:64418337	N_Shore			I	NONE
cg00844950	0.122	0.086	-0.036	0.00075	Chr19:1789060	N_Shore	Body	ATP8B3	II	ATP8B3 (+23138), ONECUT3 (+35399)
cg09172752	0.069	0.084	0.016	0.00076	Chr15:77197536	Island			I	RCN2 (-26425), SCAPER (-21320)
cg21294616	0.696	0.615	-0.082	0.00076	Chr7:143093848		Body	EPHA1	II	EPHA1 (+12136), ZYX (+15489)
cg18959169	0.885	0.855	-0.030	0.00077	Chr2:240239988		Body	HDAC4	II	HDAC4 (+82654), TWIST2 (+483316)
cg17780413	0.873	0.851	-0.022	0.00077	Chr17:703938		3'UTR	NXN	II	GLOD4 (-18368), NXN (+179059)
cg24974729	0.783	0.698	-0.085	0.00077	Chr11:67764320	N_Shore	Body	UNC93B1	I	ALDH3B2 (-315636), UNC93B1 (+7272)
cg11652597	0.831	0.861	0.030	0.00079	Chr20:48521725	N_Shore	3'UTR	SPATA2	II	SPATA2 (+10354), SLC9A8 (+92476)
cg23530850	0.078	0.064	-0.014	0.00079	Chr16:85647010	Island	5'UTR;Body	KIAA0182	II	KIAA0182 (+87)
cg18976765	0.053	0.042	-0.012	0.00079	Chr13:101240690	Island			II	A2LD1 (-54635), TMTC4 (+86412)
cg02286091	0.091	0.070	-0.021	0.00079	Chr5:78407678		5'UTR;1stExon	BHMT	I	BHMT (+75)
cg11534574	0.857	0.825	-0.031	0.00079	Chr22:41739529	N_Shelf	Body	ZC3H7B	II	TEF (-38433), ZC3H7B (+41963)
cg19807694	0.863	0.888	0.025	0.00080	Chr1:223835369		Body	CAPN8	II	SUSD4 (-297826), CAPN8 (+18066)
cg06353069	0.729	0.789	0.060	0.00081	Chr2:238500081		TSS1500	RAB17	II	RAB17 (-313)
cg09778229	0.162	0.145	-0.017	0.00082	Chr10:48354530	Island	TSS1500	ZNF488	I	ZNF488 (-558)
cg14150280	0.074	0.088	0.014	0.00083	Chr10:70660547	Island	TSS1500	DDX50	I	DDX50 (-486)
cg11165357	0.095	0.108	0.013	0.00083	Chr1:38274375	Island	Body;TSS1500	C1orf122;YRDC	II	YRDC (-511)
cg10140728	0.321	0.272	-0.049	0.00083	Chr15:63569646	Island	TSS200	APH1B	I	APH1B (-102)
cg14483771	0.821	0.866	0.046	0.00083	Chr10:134998463	N_Shore	Body	KNDC1	II	UTF1 (-45314), KNDC1 (+24493)
cg22846582	0.775	0.812	0.037	0.00084	Chr12:52848214				II	KRT6B (-2305)
cg21514529	0.544	0.484	-0.060	0.00084	Chr5:168885285				II	SLIT3 (-157153), CCDC99 (-125352)
cg20408147	0.089	0.111	0.023	0.00085	Chr1:239551249	Island			II	CHRM3 (-241123)
cg11828180	0.282	0.340	0.058	0.00085	Chr1:41848985	Island			I	SCMH1 (-141171), EDN2 (+101358)
cg18878150	0.564	0.503	-0.060	0.00085	Chr19:11594384	Island	3'UTR	ZNF653	II	ELAVL3 (-2582)
cg19607983	0.077	0.071	-0.006	0.00085	Chr4:39528789	Island	5'UTR	UGDH	I	UGDH (+428)
cg21417399	0.068	0.075	0.008	0.00085	Chr8:145598329	Island	Body	ADCK5	I	ADCK5 (+599)
cg01760475	0.067	0.079	0.012	0.00085	Chr8:145104359	Island			I	OPLAH (+11224), SPATC1 (+17778)
cg12585158	0.098	0.075	-0.023	0.00086	Chr3:121265726	S_Shore	TSS1500	POLQ	II	POLQ (-874) GLT1D1 (+452252), TMEM132D (+597879)
cg05479657	0.773	0.817	0.044	0.00088	Chr12:129790332	S_Shelf	Body	TMEM132D	II	
cg26790372	0.102	0.126	0.023	0.00089	Chr18:5542879	Island	5'UTR	EPB41L3	II	ZFP161 (-246686), EPB41L3 (+1106)
cg14287512	0.111	0.092	-0.018	0.00090	Chr1:228074806	N_Shore			II	WNT9A (+60869), PRSS38 (+71389)
cg08080038	0.845	0.815	-0.030	0.00090	Chr3:61655044		Body	PTPRG	II	PTPRG (+107802), FEZF2 (+704145)
cg14716734	0.725	0.691	-0.035	0.00091	Chr10:18549397		TSS200;Body	CACNB2	II	CACNB2 (+119792), NSUNG (+391152)
cg07750914	0.106	0.093	-0.013	0.00091	Chr2:60983838	Island	Body	PAPOLG	I	PAPOLG (+474)
cg15797527	0.543	0.494	-0.049	0.00091	Chr6:135814781	N_Shelf	5'UTR	AHI1	II	AHI1 (+4121), MYB (+312329)
cg09197112	0.220	0.252	0.032	0.00091	Chr10:46992448	Island	TSS1500	GPRIN2	II	PPYR1 (-91085), SYT15 (-21848)
cg21894762	0.868	0.898	0.029	0.00092	Chr14:73731131		Body	PAPLN	II	PAPLN (+26927), NUMB (+194154)

Fisher, Murphy et al.

cg02524205	0.476	0.539	0.063	0.00092	Chr6:167559851				I	GPR31 (+11467), CCR6 (+34557)
cg03801179	0.046	0.056	0.009	0.00093	Chr2:20212423	Island	5'UTR;1stExon	MATN3	I	MATN3 (+31)

Note. Ranked by p value ($p < 0.001$). $\Delta\beta$, difference in DNA methylation; DMPs, differentially methylated positions; GREAT, Genomic Regions Enrichment of Annotations Tool; Hg19, Human Genome build 19; SBE, single-base extension; SNP, single nucleotide polymorphism; TSS, transcription start site.

Supplementary Table 6. The top 100 ranked CpG sites which show changes in DNA methylation levels between age 5 and age 10 in the monozygotic twins discordant for age-12 psychotic symptoms

Probe ID	Affected Twin Mean	Co-Twin Mean	Mean $\Delta\beta$	P value	Relation to CpG Island	Gene region feature category (UCSC)	SNPs in probe (+/- 10bp SBE)	Hg19	Illumina Gene Annotation	Probe Type	Gene Annotation from GREAT (Distance from TSS)
cg15797527	0.044	-0.040	0.084	4.30E-06	N_Shelf	5'UTR		Chr6:135814781	AHI1	II	AHI1 (+4121), MYB (+312329)
cg10052038	0.040	-0.036	0.076	7.91E-06	N_Shore	5'UTR		Chr3:196293939	WDR53	II	FBXO45 (-1785)
cg27403609	-0.016	0.028	-0.044	1.14E-05	Island			Chr2:11101403		I	PQLC3 (-194136), KCNF1 (+49341)
cg11556416	-0.034	0.041	-0.074	1.35E-05	Island	TSS1500		Chr2:191879252	STAT1	I	STAT1 (-277)
cg13567282	0.023	-0.043	0.066	1.40E-05		5'UTR		Chr6:149653214	MAP3K7IP2	II	TAB2 (+13779), ZC3H12D (+152933)
cg19599395	0.066	-0.007	0.073	1.40E-05	N_Shore	Body	rs72972973	Chr19:3837031	ZFR2	II	MATK (-50617), ZFR2 (+31995)
cg26998693	-0.024	0.013	-0.036	1.54E-05	S_Shore	TSS1500		Chr6:132834590	STX7	II	STX7 (-254)
cg19050351	0.037	-0.052	0.089	1.76E-05		Body		Chr2:113820090	IL1F5	II	IL1F10 (-5456), IL36RN (+3406)
cg18260625	-0.011	0.015	-0.027	1.87E-05	Island			Chr5:42951192		I	SEPP1 (-139169), C5orf39 (+89254)
cg14297966	-0.003	-0.057	0.055	2.40E-05	N_Shore	Body		Chr9:35101708	STOML2	II	PIGO (-5163), STOML2 (+1445)
cg02524205	-0.038	0.054	-0.091	2.51E-05				Chr6:167559851		I	GPR31 (+11467), CCR6 (+34557)
cg12730562	-0.025	0.041	-0.067	2.87E-05		5'UTR;TSS200		Chr11:44927876	TSPAN18	II	TP53I11 (+44731), TSPAN18 (+141901)
cg22827324	-0.017	0.022	-0.039	3.31E-05		Body		Chr2:33612876	LTBP1	II	RASGRP3 (-126065), LTBP1 (+440508)
cg26613742	0.015	-0.053	0.068	3.42E-05	N_Shelf	TSS200;Body		Chr19:14225000	PRKACA	II	SAMD1 (-23769), PRKACA (+3558)
cg03359468	0.014	-0.008	0.023	3.62E-05	Island	TSS200		Chr8:26240463	BNIP3L	I	BNIP3L (-59)
cg25367206	0.038	-0.020	0.059	3.82E-05	S_Shore	TSS1500		Chr8:142239055	SLC45A4	I	SLC45A4 (-383)
cg03916630	0.053	-0.040	0.092	4.01E-05				Chr10:45065415		II	TMEM72 (-341348), CXCL12 (-184871)
cg00496455	0.004	-0.011	0.016	5.25E-05	Island	TSS200;Body		Chr2:220118770	TUBA4A	I	TUBA4A (-133), TUBA4B (+806)
cg03964515	0.014	-0.027	0.041	5.27E-05		Body		Chr8:21588527	GFRA2	I	GFRA2 (+57818)
cg08862148	0.001	0.029	-0.028	5.68E-05	Island	Body;1stExon;Body		Chr6:29595315	GABBR1	II	GABBR1 (+5646), OR2H2 (+39633)
cg10656871	0.031	-0.027	0.058	5.84E-05				Chr11:45765692		I	CHST1 (-78487), SLC35C1 (-59930)
cg23417011	-0.032	0.030	-0.062	5.95E-05		Body;TSS200		Chr5:93077375	FAM172A;POU5F2	I	POU5F2 (-67)
cg06888554	-0.007	0.009	-0.015	6.01E-05	Island	TSS200		Chr19:42580220	ZNF574	I	ZNF574 (-69)
cg03464229	0.054	-0.055	0.109	6.56E-05		Body;Body		Chr7:120646878	C7orf58	II	WNT16 (-322211), C7orf58 (+18128)
cg26403608	-0.045	0.084	-0.129	6.75E-05		TSS1500;3'UTR		Chr17:2319719	LOC284009;METT10D	II	MNT (-15462), METTL16 (+95480)
cg08548315	0.044	-0.032	0.076	6.89E-05				Chr1:81609992		II	LPHN2 (-656089)
cg08359347	-0.011	0.004	-0.015	7.11E-05	Island	TSS1500		Chr11:86667175	FZD4	I	FZD4 (-736)
cg22327778	0.051	-0.014	0.066	7.23E-05		TSS1500;TSS200		Chr11:1860218	TNNI2	II	TNNI2 (-1213)
cg13839439	0.025	-0.030	0.055	7.28E-05	N_Shore			Chr12:54144521		II	HOXC13 (-188054), CALCOCO1 (-23215)
cg08838610	-0.020	0.006	-0.026	7.31E-05	Island	TSS200		Chr17:5322907	RPAIN	I	RPAIN (-53), NUP88 (+151)
cg01084257	-0.028	0.021	-0.049	7.89E-05		Body;TSS1500		Chr8:129020419	PVT1;MIR1206	II	MYC (+272105)
cg09696939	-0.020	0.017	-0.037	7.94E-05	N_Shore	TSS1500		Chr10:60272079	BICC1	I	BICC1 (-824)
cg21211020	-0.014	0.010	-0.024	8.02E-05	Island	TSS200		Chr8:86132685	C8orf59	II	CA13 (-25030), E2F5 (+43067)

cg06992486	0.094	-0.027	0.120	8.05E-05				Chr15:96855353	II	NR2F2 (-18757)
cg00947686	0.031	-0.017	0.048	8.16E-05	S_Shore		rs35684285	Chr1:5774259	II	NPHP4 (+278273)
cg18500286	-0.010	0.005	-0.015	8.62E-05	Island	TSS1500		Chr4:87855942	I	AFF1 (-211)
cg04274199	0.043	-0.045	0.088	9.09E-05	Island	Body		Chr21:47334057	I	COL6A1 (-67605), PCBP3 (+64183)
cg24153044	0.003	-0.006	0.009	9.34E-05	Island	1stExon		Chr1:6485201	I	ESPN (+354)
cg24438749	-0.022	0.014	-0.036	9.35E-05		Body		Chr13:110929101	II	IRS2 (-490188), COL4A1 (+30394)
cg24557917	0.014	-0.031	0.046	0.0001013		TSS200		Chr4:165980112	II	TRIM60 (+26962), TMEM192 (+53911)
cg13800209	-0.024	0.007	-0.031	0.0001029	Island	1stExon;Body;5'UTR		Chr15:37390284	I	MEIS2
cg13858054	0.002	-0.016	0.017	0.0001049	Island	5'UTR;TSS1500		Chr9:86595264	I	MEIS2 (+2456)
cg01370541	-0.032	0.015	-0.047	0.0001069	Island			Chr4:41882812	II	RMI1 (-372), HNRNPk (-81)
cg18247223	-0.023	0.036	-0.059	0.0001076		5'UTR		Chr11:44908673	II	PHOX2B (-131826), TMEM33 (-54324)
cg15425527	0.037	-0.034	0.071	0.0001093	N_Shelf			Chr19:47849437	II	TP53I11 (+63934), TSPAN18 (+122698)
cg27356115	0.051	-0.013	0.064	0.000111				Chr15:53422311	II	DHX34 (-3100)
cg18837542	0.011	-0.025	0.036	0.000113				Chr4:139610152	I	UNC13C (-882789), ONECUT1 (-340103)
cg18014842	0.034	-0.022	0.056	0.000115		Body		Chr11:126355874	II	SLC7A11 (-446650), CCRN4L (-326790)
cg06352924	-0.025	0.029	-0.055	0.0001185	Island	Body		Chr3:150321728	I	ST3GAL4 (+130335), KIRREL3 (+514891)
cg24912419	-0.032	0.016	-0.048	0.0001206	Island	Body		Chr9:130922817	II	SELT (+663)
cg08732623	-0.018	0.009	-0.027	0.0001229	Island	1stExon;5'UTR		Chr10:127408269	I	C9orf16 (+279)
cg07322688	0.009	-0.003	0.012	0.0001274	Island	Body		Chr7:122526033	I	C10orf137 (+186)
cg22380353	-0.034	0.025	-0.059	0.0001302	S_Shelf			Chr13:42537904	II	CADPS2 (+779)
cg26281728	0.001	-0.010	0.011	0.0001321	Island	1stExon;5'UTR		Chr15:85923949	I	KIAA0564 (-2684)
cg23666536	0.036	-0.047	0.083	0.0001348		3'UTR		Chr1:114240177	II	AKAP13 (+79)
cg13145644	0.053	-0.050	0.103	0.0001353		TSS1500		Chr1:114240177	II	PHTF1 (+61599), MAGI3 (+306703)
cg26327442	-0.019	0.017	-0.036	0.0001354	S_Shelf			Chr3:39324326	II	CX3CR1 (-1101)
cg23079217	-0.034	0.022	-0.057	0.0001363		TSS200;TSS1500		Chr11:82447767	II	PRCP (+163789)
cg05134426	0.059	-0.030	0.089	0.0001389		1stExon		Chr12:79257730	I	SYT1 (-181702)
cg24748771	0.021	-0.017	0.039	0.0001516		TSS1500		Chr5:124080479	II	SYT1 (+385)
cg23395165	0.007	-0.010	0.017	0.0001526	Island	Body;Body		Chr21:43300770	II	ZNF608 (+385)
cg12715136	0.054	-0.041	0.095	0.0001642		3'UTR		Chr19:4483111	I	PRDM15 (-1180)
cg07144713	0.030	-0.041	0.071	0.0001657		3'UTR		Chr10:100004513	II	HDGFRP2 (+10857), PLIN4 (+34604)
cg04064828	0.052	-0.003	0.055	0.0001673	S_Shore	Body		Chr16:85009145	II	LOXL4 (+23493), C10orf28 (+110133)
cg14827481	0.031	-0.033	0.064	0.0001674	S_Shore	Body		Chr10:134002751	I	ZDHHC7 (+35995), CRISPLD2 (+155559)
cg02925268	0.020	-0.024	0.044	0.000172				Chr10:134361889	II	DPYSL4 (+2338), STK32C (+118725)
cg05462570	-0.024	0.022	-0.046	0.0001753	N_Shore	Body		Chr12:132301999	II	INPP5A (+10537), NKX6-2 (+237647)
cg09956924	0.024	-0.036	0.060	0.0001771		Body		Chr8:143596713	I	MMP17 (-10941), SFSWAP (+106365)
cg02770097	0.036	-0.041	0.077	0.0001821		Body		Chr11:64814948	II	SAC3D1 (+6573), NAALADL1 (+11060)
cg09786257	-0.036	0.029	-0.065	0.0001834	N_Shore	1stExon		Chr8:143596713	I	BAI1 (+51337), ARC (+99119)
cg02720566	-0.032	0.015	-0.047	0.0001839	S_Shore	Body		Chr10:88445317	II	BMP1R1A (-71078), LDB3 (+16892)
cg27162392	0.045	-0.043	0.088	0.0001841		Body		Chr5:95768695	II	PCSK1 (+289)
cg12920882	-0.006	0.011	-0.017	0.0001853	Island	Body;5'UTR		Chr19:18230196	II	PIK3R2 (-33819), MAST3 (+21594)
cg21793452	0.041	-0.034	0.075	0.0001861	N_Shore			Chr7:2208908	II	MAD1L1 (+63674), ELFN1 (+460111)
cg26670245	-0.005	0.003	-0.008	0.0001892	Island	5'UTR;5'UTR;TSS1500		Chr2:69664317	II	NFU1 (+442)
								Chr3:197182658	II	DLG1 (-157212), BDH1 (+100199)
								Chr2:170551352	I	PHOSPHO2 (+389)

cg06895675	0.026	-0.034	0.060	0.0001907	S_Shore		Chr10:88137553		II	GRID1 (-11304), WAPAL (+143987)
cg27533472	0.023	-0.010	0.033	0.0001963		1stExon;5'UTR	Chr11:59856225	MS4A2	II	MS4A2 (+89)
cg18333694	0.028	-0.015	0.042	0.0001977	S_Shore		Chr11:357882		II	IFITM3 (-36969), B4GALNT4 (-11912)
cg23497569	0.054	-0.062	0.115	0.0002004			Chr7:19417585		II	FERD3L (-232542), TWISTNB (+331074)
cg14750743	0.018	-0.049	0.068	0.0002087	S_Shelf	Body	Chr6:32137294	AGPAT1	II	EGFL8 (+4939), AGPAT1 (+6621)
cg15907392	0.029	-0.024	0.053	0.0002104	Island		Chr12:34494852		II	ALG10 (+319637)
cg01917016	-0.017	0.013	-0.031	0.0002123	Island	Body;5'UTR;1stExon	Chr1:206730504	RASSF5	II	RASSF5 (+49626), EIF2D (+55399)
cg24885794	-0.026	0.062	-0.088	0.0002176	Island	TSS1500;5'UTR	Chr7:94286086	SGCE;PEG10	II	SGCE (-566), PEG10 (+405)
cg27425612	0.001	-0.006	0.008	0.0002184	Island	TSS200	Chr1:201368843	LAD1	I	LAD1 (-175)
cg20856064	-0.033	0.036	-0.069	0.0002287	Island	TSS200	Chr3:49027210	P4HTM	I	P4HTM (-130)
cg17025730	-0.022	0.027	-0.049	0.0002287	N_Shore		Chr5:133859798		I	PHF15 (-1999)
cg05790658	0.029	-0.047	0.076	0.0002291		5'UTR	Chr4:143748032	INPP4B	II	INPP4B (+19571)
cg24649269	-0.020	0.021	-0.041	0.0002316	S_Shore	Body	Chr6:7231857	RREB1	II	SSR1 (+81683), RREB1 (+123772)
cg05294300	0.036	-0.064	0.099	0.0002338	Island	Body	Chr19:17317009	MYO9B	II	USE1 (-9145), MYO9B (+130419)
cg27578734	-0.026	0.051	-0.076	0.0002343	N_Shore		Chr12:132972609		I	P2RX2 (-222793), GALNT9 (-66705)
cg12872560	-0.024	0.011	-0.035	0.0002382	Island	Body	Chr10:50340047	FAM170B	II	VSTM4 (-16489), C10orf128 (+56359)
cg15278386	0.017	-0.046	0.063	0.0002385	N_Shelf	5'UTR	Chr20:61924802	COL20A1	I	COL20A1 (+265)
cg15111554	0.014	-0.048	0.061	0.0002389		Body	Chr1:110172028	AMPD2	II	GSTM4 (-26669), AMPD2 (+8753)
cg13667739	-0.007	0.055	-0.062	0.0002518	Island	Body	Chr14:105944604	CRIP2	II	CRIP1 (-8652), CRIP2 (+3474)
cg24137511	-0.009	-0.081	0.072	0.0002519	Island	Body	Chr19:18260330	MAST3	I	PIK3R2 (-3685)
cg05982757	-0.053	0.030	-0.083	0.0002602	Island	5'UTR;Body	Chr12:54427528	HOXC4;HOXC5	II	HOXC5 (+697)
cg07066163	0.048	-0.026	0.074	0.0002602			Chr16:85635689		II	KIAA0182 (-11234), KIAA0513 (+574280)
cg13393580	0.020	-0.030	0.049	0.0002615	S_Shelf	TSS1500	Chr1:1295077	MXRA8	I	MXRA8 (-1163)
cg17692200	-0.003	0.009	-0.012	0.0002639	Island	TSS200	Chr7:35840513	SEPT7	I	SEPT7 (-82)
cg23466291	-0.016	0.011	-0.027	0.0002656	Island		Chr17:75243612		II	SEPT9 (-33879), SEC14L1 (+106608)
cg11251349	-0.013	0.005	-0.018	0.000267	Island	TSS1500	Chr1:33721607	ZNF362	I	ZNF362 (-566)
cg24811069	0.009	-0.046	0.055	0.0002673			Chr8:49049137		II	UBE2V2 (+128143), EFCAB1 (+598732)
cg07142668	-0.013	0.005	-0.018	0.0002764	Island	TSS1500	Chr1:32230251	BAI2	II	BAI2 (-604)
cg13644282	0.019	-0.039	0.058	0.0002781	N_Shelf		Chr12:132616666		I	DDX51 (+12213), EP400 (+182202)
cg20285609	0.023	-0.010	0.033	0.0002782		5'UTR;Body	Chr1:41622030	SCMH1	II	SLFNL1 (-134604), SCMH1 (+85784)
cg26771582	-0.025	0.026	-0.051	0.0002784	N_Shore	Body	Chr16:87415899	FBXO31	II	FBXO31 (+1494), FOXL1 (+803785)
cg02831037	0.060	-0.037	0.098	0.0002833	Island		Chr16:798278		II	MSLN (-12486), NARFL (-7282)
cg18887483	0.021	-0.013	0.034	0.0002851	Island	5'UTR;TSS1500;TSS200	Chr15:74422572	ISLR2;LOC283731	II	ISLR2 (-170)
cg21548940	0.023	-0.024	0.047	0.0002887			Chr5:162921557		II	MAT2B (-11027), HMMR (+34041)
cg10324825	-0.020	0.015	-0.035	0.0002911	S_Shore	Body	Chr1:158153227	CD1D	II	CD1A (-70699), CD1D (+3491)
cg26821579	-0.047	0.009	-0.056	0.0002949	S_Shore	TSS200	Chr11:22851416	SVIP	I	SVIP (-35)
cg17259741	-0.008	0.006	-0.014	0.0003002	Island	5'UTR	Chr4:4291994	ZNF509;LYAR	I	LYAR (-99), ZBTB49 (+71)
cg24552773	-0.018	0.033	-0.051	0.0003015	Island	Body	Chr1:9100506	SLC2A5;SLC2A5	II	SLC2A7 (-14103), SLC2A5 (+29380)
cg18126791	-0.017	0.007	-0.024	0.000302	Island	5'UTR;1stExon	Chr21:33031960	SOD1	I	SOD1 (+26)
cg26476156	0.038	-0.066	0.104	0.0003043	S_Shore	TSS1500	Chr10:46090807	MARCH8	II	MARCH8 (-59989), ZFAND4 (+77443)
cg00423675	0.016	-0.031	0.047	0.0003054	N_Shore		Chr9:138067680		II	PPP1R26 (-303967), OLFM1 (+100592)
cg04660577	0.044	-0.043	0.087	0.000306	S_Shore	TSS1500	Chr4:103267999	SLC39A8	II	SLC39A8 (-1345)

cg13523014	0.032	-0.081	0.114	0.0003061	N_Shelf	Body		Chr19:8618073	MYO1F	I	ZNF414 (-39026), MYO1F (+24257)
cg04217778	0.025	-0.023	0.048	0.0003125	Island	Body		Chr7:5111916	LOC389458	I	RBAK (+26364), ZNF890P (+60281)
cg01139526	-0.015	0.008	-0.022	0.0003181		TSS200		Chr5:139682850	PFDN1	II	PFDN1 (-162)
cg16711612	-0.020	-0.001	-0.019	0.0003222	Island	Body;TSS200		Chr14:79745592	NRXN3	I	NRXN3 (+875500), DIO2 (+932377)
cg06770877	0.023	-0.029	0.052	0.0003267		Body		Chr13:31897247	B3GALT1	II	RXFP2 (-416431), B3GALT1 (+123136)
cg27180315	0.005	-0.008	0.012	0.0003296	Island	TSS200		Chr7:75831194	SRRM3	I	HSPB1 (-100680), MDH2 (+153802)
cg06852824	0.033	-0.030	0.063	0.0003305	S_Shelf	5'UTR		Chr2:231582109	CAB39	I	ITM2C (-147511), CAB39 (+4553)
cg09446567	-0.024	0.016	-0.040	0.0003328				Chr4:179734204		II	NONE
cg08441633	0.029	-0.026	0.055	0.0003351	Island	Body	rs7201334	Chr16:88765295	RNF166	II	SNAI3 (-12414), RNF166 (+7533)
cg10856605	-0.007	0.005	-0.011	0.0003364		5'UTR	rs58290790	Chr6:28048756	ZNF165	I	ZNF165 (+275)
cg03799283	0.069	-0.016	0.085	0.0003407	Island			Chr15:96910011		I	NR2F2 (+35901)
cg20461912	-0.016	0.032	-0.048	0.000349	Island	1stExon;3'UTR		Chr3:138664350	FOXL2	II	PIK3CB (-186166), FOXL2 (+1631)
cg26564606	0.049	-0.066	0.114	0.0003506	N_Shelf	3'UTR		Chr5:660180	TPPP	II	TPPP (+33329), CEP72 (+47776)
cg00429402	0.014	0.000	0.014	0.0003592	Island	1stExon;5'UTR		Chr10:94833658	CYP26A1	I	CYP26A1 (+12)
cg20562220	0.009	-0.019	0.028	0.0003625	S_Shore			Chr14:106068824		I	TMEM121 (+75872), IGHE (+260637)
cg24347422	0.023	-0.024	0.048	0.0003629	N_Shelf	Body	rs73955766	Chr2:133400321	GPR39	II	LYPD1 (+28159), GPR39 (+226175)
cg11787218	0.024	-0.053	0.077	0.0003717		Body		Chr6:312105	DUSP22	I	IRF4 (-79633), DUSP22 (+20005)
cg15346359	0.074	-0.005	0.080	0.0003778		3'UTR		Chr11:47606064	NDUFS3	II	FAM180B (-2165)
cg24163575	0.023	-0.019	0.042	0.0003838	Island			Chr15:30261379		I	TJP1 (-146674), CHRFB7A (+424484)
cg17074213	-0.057	0.033	-0.090	0.000385	Island	1stExon;5'UTR		Chr1:92351695	TGFBR3	I	TGFBR3 (+140)
cg20126647	-0.019	0.018	-0.037	0.0003888	N_Shore	TSS200		Chr17:40714003	COASY	I	COASY (-88)
cg18342183	0.014	-0.047	0.061	0.0003899				Chr1:186732915		II	PTGS2 (-83357), PLA2G4A (-65116)
cg21659346	0.025	-0.007	0.032	0.000394			rs57186292	Chr11:72280409		II	CLPB (-134842), PDE2A (+105087)
cg20655369	0.044	-0.021	0.065	0.0003954	S_Shelf	Body		Chr15:89924975	LOC254559	II	POLG (-46950), RHCG (+114823)
cg14462686	0.019	-0.035	0.054	0.0003955		Body		Chr9:4226519	GLIS3	II	RFX3 (-700537), GLIS3 (+73515)
cg25485913	-0.051	0.034	-0.085	0.0003992				Chr19:49568962		II	NTF4 (-1844)
cg09055822	0.029	-0.033	0.063	0.0003993	N_Shelf	Body		Chr8:142180375	DENND3	II	PTK2 (-168964), SLC45A4 (+58297)
cg15447829	-0.044	0.022	-0.067	0.0004004	N_Shore	Body		Chr21:34960242	DONSON	II	DONSON (+1024), SON (+44893)
cg20113500	-0.023	0.014	-0.037	0.0004004	S_Shore	TSS200		Chr12:113773013	SLC24A6	I	SLC24A6 (-89)
cg15445958	-0.027	0.027	-0.054	0.0004065				Chr6:110266125		II	GPR6 (-34172), FIG4 (+253702)
cg20064122	-0.030	0.009	-0.039	0.0004107	Island	TSS200		Chr22:18593362	TUBA8	II	TUBA8 (-90)
cg07202054	-0.016	0.064	-0.080	0.0004124	S_Shelf			Chr1:48452740		II	LOC388630 (+9821), FOXD2 (+551052)
cg20162822	0.002	-0.016	0.018	0.0004141	S_Shore	3'UTR		Chr17:1658265	SERPINF2	I	SERPINF1 (-6993), SERPINF2 (+12136)
cg17926940	-0.026	0.012	-0.038	0.0004146	Island			Chr14:97685060		II	VRK1 (+421377)
cg12448989	-0.033	0.005	-0.038	0.0004167	Island	1stExon		Chr13:77459329	KCTD12	I	KCTD12 (+1210)
cg05002305	0.036	-0.040	0.076	0.0004174	Island	Body		Chr11:1273661	MUC5B	II	MUC5B (+29367), TOLLIP (+57230)
cg18736676	0.025	-0.057	0.082	0.0004182				Chr6:109053447		I	ARMC2 (-116171), FOXO3 (+171379)
cg02796790	0.015	-0.072	0.086	0.0004212	Island	Body		Chr19:10823761	QTRT1	II	DNM2 (-4967)
cg02210149	0.028	-0.032	0.060	0.0004219	N_Shore	TSS1500;Body		Chr6:32096599	ATF6B;FKBP1	II	ATF6B (-583)
cg00932808	0.005	-0.011	0.016	0.000422	Island		rs11757362	Chr6:14211322		I	CD83 (+93458)
cg19059495	0.025	-0.021	0.046	0.0004224	Island			Chr6:30095495		II	TRIM31 (-14629), TRIM40 (-9014)
cg17350432	0.032	-0.014	0.045	0.0004259	N_Shore			Chr4:841569		II	CPLX1 (-21625), GAK (+84604)

cg17882580	0.017	-0.014	0.030	0.0004261		3'UTR		Chr7:47315063	TNS3	II	TNS3 (+306678)
cg08141342	-0.018	0.005	-0.023	0.000428	Island	TSS1500		Chr1:45308976	PTCH2	I	PTCH2 (-361)
cg09706512	-0.003	0.005	-0.008	0.0004282	Island	TSS1500		Chr3:88108503	CGGBP1	I	CGGBP1 (-358)
cg24634810	-0.012	0.004	-0.016	0.0004288	Island	TSS200;TSS200		Chr17:40307043	RAB5C	II	RAB5C (+18)
cg13299436	0.013	-0.056	0.069	0.0004313		TSS1500		Chr6:29140622	OR2J2	II	OR14J1 (-133844), OR2B3 (-85533)
cg01149683	0.056	-0.028	0.084	0.0004344				Chr3:66705803		II	LRIG1 (-154959), SUCLG2 (+999234)
cg07675811	0.035	-0.028	0.063	0.0004352	N_Shore	Body		Chr7:5426831	TNRC18	II	TNRC18 (+36345), SLC29A4 (+104271)
cg07713135	-0.014	0.041	-0.055	0.0004372		Body		Chr13:99093756	FARP1	I	RNF113B (-264236), STK24 (+135639)
cg25635840	0.004	-0.008	0.012	0.0004402	N_Shore	Body		Chr17:26898051	PIGS	II	PIGS (+835)
cg03255741	0.005	-0.004	0.008	0.0004485	Island	1stExon;5'UTR		Chr18:48556964	SMAD4	I	SMAD4 (+382)
cg05241143	-0.025	0.013	-0.038	0.0004528	N_Shelf	Body		Chr7:157916636	PTPRN2	II	PTPRN2 (+463845), DNAJB6 (+786927)
cg13091883	0.007	-0.097	0.104	0.0004578	S_Shelf	Body	rs76135941	Chr1:111892655	C1orf88	II	C1orf88 (+3461), OVGP1 (+77743)
cg05754402	0.030	-0.031	0.061	0.0004603				Chr8:49063039		II	UBE2V2 (+142045), EFCAB1 (+584830)
cg04416981	-0.033	0.042	-0.074	0.0004629		TSS1500		Chr16:89043707	CBFA2T3	II	CBFA2T3 (-204)
cg27314324	0.032	-0.021	0.053	0.0004641		Body		Chr1:112476724	KCND3	I	KCND3 (+55052), DDX20 (+178535)
cg07307994	-0.032	0.008	-0.040	0.0004828			rs35938927	Chr2:3828216		II	ALLC (+122431)
cg14338234	-0.019	0.010	-0.029	0.0004853	S_Shore	Body;TSS1500		Chr3:93782253	NSUN3;DHFRL1	II	DHFRL1 (-187), NSUN3 (+399)
cg11214889	0.008	-0.013	0.020	0.0004863		5'UTR;1stExon		Chr18:597111	CLUL1	II	CLUL1 (-19588), CETN1 (+16743)
cg08418841	0.002	-0.003	0.005	0.0004883	Island			Chr19:1725758		I	TCF3 (-75473), ONECUT3 (-27903)
cg09123773	0.003	-0.002	0.006	0.0004892	Island	TSS1500		Chr16:48419537	SIAH1	I	SIAH1 (-309)
cg21688288	0.027	-0.026	0.053	0.0004912		Body		Chr21:44181258	PDE9A	II	PDE9A (+107397), WDR4 (+118419)
cg21294812	-0.015	0.019	-0.035	0.0004917	Island	TSS200		Chr6:132722770	MOXD1	I	MOXD1 (-107)
cg16048517	0.004	-0.002	0.007	0.0004949	Island	TSS1500		Chr5:11904442	CTNND2	I	CTNND2 (-333)
cg18389933	-0.022	0.034	-0.057	0.0004961	N_Shore			Chr14:57263993		II	OTX2 (+13190), C14orf101 (+217483)
cg18414618	0.008	-0.015	-0.023	0.000505	Island	TSS1500;TSS200		Chr14:50999710	MAP4K5;ATL1	I	MAP4K5 (-335), ATL1 (-89)
cg11998425	0.013	-0.017	-0.030	0.0005069	N_Shore	TSS1500	rs3813771	Chr19:8213583	FBN3	II	FBN3 (-1203)
cg02939090	0.004	-0.005	-0.009	0.0005169	Island	1stExon		Chr11:77348733	CLNS1A	I	CLNS1A (+117)
cg14719352	-0.040	0.004	0.045	0.0005182	S_Shore	TSS1500;5'UTR		Chr19:49258131	FGF21;FUT1	II	FGF21 (-1016), FUT1 (+515)
cg02602601	0.005	-0.019	-0.024	0.0005215	Island	TSS200		Chr12:56618057	OBFC2B	I	RNF41 (-2305), OBFC2B (-67)
cg21386099	-0.041	0.027	0.068	0.0005281		3'UTR		Chr3:37476831	C3orf35	II	ITGA9 (-16981), C3orf35 (+35864)
cg15770125	-0.014	0.042	0.056	0.0005289		TSS200		Chr3:8693781	C3orf32	II	CAV3 (-81704), LMCD1 (+150271)
cg15699623	0.035	-0.012	-0.046	0.0005365	N_Shelf	Body		Chr19:42633695	POU2F2	II	POU2F2 (+2929), ZNF574 (+53406)
cg09236819	0.018	-0.033	-0.051	0.0005394	Island	Body		Chr11:64876055	C11orf2	II	TM7SF2 (-3285)
cg07080946	-0.008	0.044	0.051	0.0005399	N_Shore	TSS1500		Chr16:280046	LUC7L	II	ITFG3 (-4754), LUC7L (-598)
cg00658394	0.005	-0.020	-0.025	0.0005402	S_Shore	Body;TSS200		Chr3:11685410	VGLL4	II	VGLL4 (-13)
cg23889013	0.029	-0.024	-0.053	0.0005408	S_Shelf			Chr19:48710006		II	C19orf68 (+36058), CARD8 (+43097)
cg01852049	-0.023	0.035	0.058	0.0005408	N_Shore	TSS1500		Chr15:91072061	CRTC3	II	CRTC3 (-1136)
cg04928875	0.010	-0.005	-0.015	0.0005409	Island	TSS200		Chr2:128568924	WDR33	I	WDR33 (-164)
cg21199659	-0.025	0.038	0.062	0.0005413		Body		Chr9:133366752	ASS1;ASS1	II	FUBP3 (-88207), ASS1 (+46659)
cg07023791	-0.012	0.009	0.021	0.0005428	Island	TSS1500		Chr10:83633980	NRG3	II	NRG3 (-1089)
cg05230854	-0.061	0.014	0.075	0.0005447				Chr8:8162989		II	SGK223 (+76267), LOC100132396 (+379131)

cg14791747	0.035	-0.006	-0.041	0.0005464	Island	1stExon		Chr16:20752902	THUMPD1	II	ACSM1 (-50325), ACSM3 (-22409)
cg06614044	-0.029	0.028	0.057	0.0005528	Island	Body		Chr18:42324631	SETBP1	II	SLC14A2 (-468315), SETBP1 (+63769)
cg09648702	0.024	-0.039	-0.063	0.0005534	Island			Chr11:20184779		II	DBX1 (-2910)
cg06621900	0.016	-0.016	-0.031	0.0005553		Body		Chr2:240239815	HDAC4	II	HDAC4 (+82827), TWIST2 (+483143)
cg14616584	0.031	-0.008	-0.040	0.0005639		Body		Chr1:37388124	GRIK3	II	CSF3R (-439210), GRIK3 (+111719)
cg19862235	-0.050	0.040	0.091	0.0005643		3'UTR		Chr20:7863971	HAO1	II	HAO1 (+57121)
cg15117681	-0.021	0.039	0.060	0.0005645	N_Shore	3'UTR		Chr17:80202426	CSNK1D	II	SLC16A3 (+16145), CSNK1D (+29167)
cg04387237	0.008	-0.015	-0.023	0.0005685	Island	Body		Chr19:14640867	TECR	II	TECR (+489)
cg21509821	0.015	-0.012	-0.028	0.0005696	N_Shore	TSS1500		Chr12:83079551	TMTC2	II	TMTC2 (-1382)
cg18016138	-0.041	0.022	0.063	0.0005699	N_Shore	TSS200		Chr11:278421	NLRP6	I	NLRP6 (-148)
cg24028798	0.040	-0.033	-0.073	0.0005712	S_Shelf	Body		Chr21:47322452	PCBP3	II	COL6A1 (-79210), PCBP3 (+52578)
cg16093537	-0.032	0.030	0.062	0.0005738		Body		Chr10:81924880	ANXA11	II	PLAC9 (+32623), ANXA11 (+40447)
cg08219700	0.064	-0.047	-0.111	0.0005755	Island			Chr8:58056026		II	FAM110B (-851086), IMPAD1 (-149597)
cg06781608	0.002	-0.069	-0.072	0.0005861	N_Shore	Body		Chr7:157361040	PTPRN2	II	DNAJB6 (+231331)
cg07551054	-0.003	0.003	0.007	0.0005924	Island	Body		Chr8:140744200	TRAPPC9	I	KCNK9 (-28902), TRAPPC9 (+724477)
cg05886537	0.021	-0.020	-0.040	0.000598	S_Shelf	Body		Chr11:132936428	OPCML	II	OPCML (-123392), SPATA19 (+778963)
cg13678939	0.006	-0.011	-0.017	0.0005986	Island	1stExon		Chr11:62414063	GANAB	I	GANAB (+40)
cg06549802	-0.026	0.014	0.040	0.0006073	N_Shore	5'UTR;TSS1500		Chr11:125756052	HYLS1	II	HYLS1 (+2544), PUS3 (+17063)
cg25725280	0.038	-0.008	-0.045	0.0006077	Island	Body		Chr1:33625382	TRIM62	I	TRIM62 (+22288), ADC (+78669)
cg09529871	-0.069	0.030	0.099	0.0006084		TSS200		Chr19:14911130	OR7C1	II	OR7C1 (-183)
cg22057372	-0.015	0.040	0.055	0.0006099		Body		Chr7:157711557	PTPRN2	II	DNAJB6 (+581848), PTPRN2 (+668924) BC068290 (-179325), TP53TG3B (+343066)
cg02056809	-0.034	0.022	0.055	0.0006112				Chr16:33605185		II	
cg14224452	-0.033	0.007	0.040	0.0006121		3'UTR		Chr10:103311489	BTRC	II	POLL (+36537), BTRC (+197665)
cg10763059	0.017	-0.024	-0.041	0.0006131	N_Shore	TSS1500		Chr7:77165728	PTPN12	I	PTPN12 (-1044)
cg14098470	-0.030	0.055	0.085	0.0006191		Body		Chr6:29573253	GABBR1	II	OR2H2 (+17571), GABBR1 (+27708)
cg15382568	0.046	-0.035	-0.081	0.0006193	N_Shore			Chr22:25800078		II	ADRBK2 (-160782), LRP5L (-22535)
cg13728604	-0.022	0.026	0.048	0.0006216	N_Shelf	Body	rs72757203	Chr9:132627095	USP20	II	USP20 (+29400), FNBP1 (+178377)
cg23687971	0.023	-0.041	-0.064	0.000629	N_Shore	TSS1500		Chr20:32262772	NECAB3	II	NECAB3 (-509)
cg11766468	0.036	0.113	0.077	0.0006307	N_Shelf	Body		Chr19:7923041	EVI5L	I	LRR8E (-30348), EVI5L (+11660)
cg20406374	0.006	-0.012	-0.018	0.0006308	Island	5'UTR;Body		Chr5:179248352	SQSTM1	II	SQSTM1 (+511)
cg14114804	0.021	-0.008	-0.029	0.0006318	Island	5'UTR		Chr14:77606990	ZDHHC22	II	IRF2BPL (-111957), ZDHHC22 (+1143)
cg04090412	0.073	-0.028	-0.101	0.0006333	Island	3'UTR		Chr4:183721565	ODZ3	II	DCTD (+117064), ODZ3 (+476467)
cg20534694	-0.039	0.032	0.071	0.0006334		Body;TSS1500		Chr7:151512686	PRKAG2	II	RHEB (-295677), PRKAG2 (+61629)
cg14674720	0.018	-0.024	-0.043	0.0006354	Island			Chr2:219827930		II	CDK5R2 (+3533), FEV (+22448)
cg09143221	-0.044	0.017	0.061	0.0006365	N_Shore	TSS1500;5'UTR		Chr17:3794657	CAMKK1	II	CAMKK1 (-621)
cg09670175	0.008	-0.023	-0.031	0.0006369	S_Shelf	3'UTR;1stExon		Chr12:4923468	KCNA6	II	KCNA1 (-95604), KCNA6 (+5127)
cg03323397	-0.034	0.013	0.047	0.0006399	N_Shelf	Body		Chr6:30519312	GNL1	II	PRR3 (-5173), HLA-E (+62130)
cg05193407	-0.025	0.025	0.050	0.0006399		TSS200		Chr4:57036298	KIAA1211	II	AASDH (+217339), CEP135 (+221262)
cg01988480	0.038	-0.025	-0.063	0.0006522	Island	TSS1500;5'UTR		Chr11:93474146	C11orf54;TAF1D	I	C11orf54 (-646), TAF1D (+556)
cg08711281	-0.039	0.023	0.062	0.0006554		TSS1500		Chr6:30908302	DPCR1	II	DPCR1 (-474)
cg16016036	-0.028	0.019	0.046	0.0006572		TSS200;TSS1500		Chr2:1417109	TPO	II	TPO (-123)

cg13650687	0.016	-0.026	-0.042	0.0006583		Body	Chr10:71655974	COL13A11	II	H2AFY2 (-156382), COL13A1 (+94331)
cg01832757	0.031	-0.041	-0.072	0.00066	N_Shelf		Chr6:159547894		II	TAGAP (-81711), FNDC1 (-42534)
cg19791379	-0.017	0.009	0.026	0.0006602		Body	Chr12:1555160	ERC1	II	FBXL14 (+148170), ERC1 (+454757)
cg04015907	-0.009	0.017	0.025	0.000664	Island	Body;1stExon	Chr20:825489	FAM110A	I	FAM110A (+11134), ANGPT4 (+71470)
cg21637015	-0.008	0.005	0.013	0.000667		Body	Chr3:129275285	PLXND1	I	H1FOO (+13229), PLXND1 (+50296)
cg06401614	-0.048	0.019	0.066	0.00067		Body;1stExon	Chr11:44927976	TSPAN18;TSPAN18	II	TP53I11 (+44631), TSPAN18 (+142001)
cg26335251	-0.032	0.035	0.067	0.0006707			Chr17:75539921		I	TNRC6C (-460396), SEPT9 (+262430)
cg21915639	0.021	-0.010	-0.031	0.0006715	S_Shore	TSS1500;TSS200	Chr1:46769308	LRRC41;UQCRH	I	UQCRH (-71)
cg25104124	0.013	-0.018	-0.031	0.0006719	Island		Chr10:74021022		II	ASCC1 (-45156), DDIT4 (-12654)
cg03152785	-0.014	0.010	0.024	0.0006747	Island	TSS1500	Chr1:110753723	KCNC4	I	KCNC4 (+388)
cg14987769	0.035	-0.009	-0.044	0.0006763	S_Shore	Body	Chr2:220197576	RESP18	II	RESP18 (+322)
cg19107120	-0.033	0.031	0.064	0.0006765	N_Shore	3'UTR	Chr17:42430376	GRN	II	GRN (+7886), FAM171A2 (+10858)
cg03368399	0.000	-0.020	-0.020	0.0006803	Island	TSS200	Chr8:22102556	POLR3D;MIR320A	I	POLR3D (-62)
cg07608033	-0.023	0.021	0.044	0.0006834	S_Shelf		Chr10:36056930		II	FZD8 (-126569)
cg27135125	0.024	-0.013	-0.037	0.0006834	S_Shore	TSS200	Chr7:23510082	IGF2BP3	I	IGF2BP3 (-88)
cg13484614	-0.031	0.031	0.062	0.0006848	S_Shore	TSS1500	Chr9:127178389	PSMB7	II	PSMB7 (-669)
cg07841529	0.024	-0.060	-0.084	0.0006893	N_Shore		Chr17:47269182		II	ABI3 (-18406), B4GALNT2 (+58854)
cg07717903	0.010	0.082	0.072	0.0006922	N_Shore	Body;TSS200	Chr5:140753536	PCDHGA4	II	PCDHGC5 (-115271), TAF7 (-53186)
cg00045190	0.005	-0.003	-0.007	0.0006928	Island		Chr6:33216612		I	VPS52 (+23049), RING1 (+40327)
cg00083262	0.013	-0.040	-0.054	0.0006952			Chr1:157125526		II	ETV3 (-17144), FCRL5 (+396783)
cg08495020	-0.031	0.024	0.055	0.0007023		TSS200	Chr19:17571888	NXNL1	II	NXNL1 (-164)
cg09859456	0.008	-0.014	-0.022	0.0007072	S_Shore	5'UTR;Body	Chr12:72234313	TBC1D15	I	TBC1D15 (+827)
cg22837512	-0.005	0.011	0.016	0.0007093	Island	TSS200	Chr11:108093386	ATM;NPAT	I	ATM (-172), NPAT (-22)
cg05730365	0.004	-0.038	-0.042	0.0007154	Island	5'UTR	Chr5:37838563	GDNF	II	GDNF (-2635)
cg09719850	-0.074	0.043	0.116	0.0007157			Chr12:6993936		II	LRRC23 (-19960), SPSB2 (-11488)
cg10859966	0.009	-0.011	-0.020	0.0007159	Island	TSS1500;TSS200	Chr14:24898992	CBLN3;KHNYN	I	CBLN3 (-262), KHNYN (-148)
cg25630594	-0.043	0.032	0.075	0.000718		TSS1500	Chr3:44914870	TGM4	I	TGM4 (-1227)
cg09730361	-0.008	0.005	0.013	0.0007183	S_Shore	TSS200	Chr9:20622599	MLLT3	II	MLLT3 (-86)
cg00123072	-0.045	0.017	0.062	0.0007183	N_Shore	TSS1500	Chr5:79330259	THBS4	II	THBS4 (-910)
cg10177795	0.041	-0.014	-0.055	0.0007221		Body	Chr2:242331545	FARP2	II	FARP2 (+35882), STK25 (+116488)
cg06402590	-0.023	0.037	0.061	0.0007272	S_Shelf	Body	Chr16:2820155	SRRM2	II	TCEB2 (+7141), SRRM2 (+17826)
cg26457569	-0.028	0.057	0.085	0.0007282	Island	Body	Chr19:11280837	KANK2	II	C19orf80 (-69457), SPC24 (-14354)
cg00940891	-0.005	0.004	0.008	0.0007374	Island	5'UTR;TSS1500	Chr4:1006016	FGFRL1	I	FGFRL1 (+257)
cg00175987	-0.030	0.027	0.057	0.0007377		TSS1500	Chr18:72342044	ZNF407	II	ZNF407 (-878)
cg19717216	-0.034	0.053	0.086	0.0007414	N_Shore	Body	Chr19:4171754	CREB3L3	I	SIRT6 (+10841), CREB3L3 (+18126)
cg06179039	-0.017	0.026	0.043	0.0007414	S_Shelf	3'UTR	Chr16:67263524	FHOD1	II	TMEM208 (+2509), FHOD1 (+17900)
cg19522185	-0.045	0.029	0.073	0.0007426	N_Shelf		Chr10:81103810		II	PIIF (-3409)
cg04291430	0.028	-0.016	-0.044	0.0007437	N_Shore	5'UTR	Chr17:48206283	SAMD14	II	PPP1R9B (+21593), PDK2 (+33645)
cg12927270	0.007	-0.008	-0.015	0.0007447	Island	TSS200	Chr3:94656950	LOC255025	I	DHFRL1 (-874884)
cg12658052	-0.062	0.005	0.067	0.0007473			Chr1:1078295		II	TLL10 (-30990), C1orf159 (-26560)
cg05045702	-0.027	0.026	0.054	0.0007488	Island	Body	Chr16:30616285	ZNF689	II	ZNF785 (-19194), ZNF689 (+5396)
cg05925971	0.004	-0.014	-0.019	0.0007514	Island	TSS200	Chr19:36485966	SDHAF1	I	SDHAF1 (-123)

cg07817400	0.012	-0.009	-0.022	0.000753	Island	Body		Chr6:33172817	HSD17B8	II	RXRΒ (-4386), RING1 (-3468)
cg05173373	0.003	-0.021	-0.023	0.0007533	S_Shore	TSS1500		Chr12:15942933	EPS8	II	EPS8 (-424)
cg00642468	-0.005	0.004	0.009	0.000761	Island	TSS1500;TSS200		Chr13:111364924	ING1	I	ING1 (-2434)
cg27659478	-0.016	0.004	0.020	0.0007665	N_Shore	Body		Chr17:73891062	TRIM65	I	TRIM47 (-16407), TRIM65 (+1991)
cg05769790	0.008	-0.005	-0.013	0.0007686	Island	TSS200		Chr6:126661238	C6orf173	II	CENPW (-14)
cg02567788	0.010	-0.013	-0.023	0.0007692	N_Shore	Body		Chr10:71992279	PPA1	II	PPA1 (+910)
cg21613693	-0.047	0.022	0.069	0.0007725	Island	Body		Chr17:73501181	CASKIN2	II	CASKIN2 (+10445), KIAA0195 (+48518)
cg04212651	-0.034	0.023	0.057	0.0007738		Body		Chr6:112671523	RFPL4B	II	RFPL4B (+2992)
cg22249386	-0.038	0.018	0.056	0.000779		Body		Chr17:10212450	MYH13	II	GAS7 (-110583), MYH13 (+63871)
cg27147114	-0.013	0.028	0.041	0.0007817		Body		Chr15:79358128	RASGRF1	II	CTSH (-120709), RASGRF1 (+25086)
cg07150629	-0.007	0.008	0.015	0.0007829	S_Shore	5'UTR;TSS1500		Chr4:40059484	N4BP2;LOC344967	II	LOC344967 (-666), N4BP2 (+961)
cg00817367	0.009	-0.020	-0.030	0.0007861	Island	Body		Chr12:52401214	GRASP	I	GRASP (+467)
cg01017689	0.040	-0.018	-0.058	0.0007871	S_Shelf	Body;5'UTR		Chr5:76376266	SNORA47;ZBED3	II	ZBED3 (+6763), AGGF1 (+50057)
cg21368481	-0.027	0.048	0.076	0.0007896		Body		Chr6:31747210	VARS	II	VWA7 (-2103)
cg04330884	0.039	-0.008	-0.047	0.0007916		Body		Chr10:126339578	FAM53B	I	FAM53B (+93351), LHPP (+189238)
cg25121621	0.017	-0.044	-0.060	0.0007918	N_Shore	TSS1500		Chr15:45926780	SQRDL	II	SQRDL (-475)
cg14496375	-0.025	0.027	0.053	0.0007971	S_Shore	TSS200		Chr19:51872365	CLDND2	II	CLDND2 (-109)
cg04106390	-0.018	0.011	0.028	0.0007997	N_Shelf	Body		Chr16:1224897	CACNA1H	I	CACNA1H (+21657), TPSG1 (+50356)
cg04535902	-0.065	0.095	0.160	0.0008055	Island	Body		Chr1:92947332	GFI1	II	GLMN (-182767), GFI1 (+4295)
cg10805039	0.024	-0.055	-0.079	0.0008071		Body		Chr17:750241	NXN	II	GLOD4 (-64671), NXN (+132756)
cg05550276	0.011	0.000	-0.011	0.0008104	Island	5'UTR;Body		Chr16:52580524	TOX3	I	TOX3 (+281)
cg26060667	0.027	-0.077	-0.103	0.0008105	N_Shore			Chr1:247681242		II	OR2C3 (+15898), OR2W5 (+26873)
cg27081107	-0.014	0.024	0.038	0.0008123		Body		Chr10:438661	DIP2C	I	ZMYND11 (+212728), DIP2C (+296946)
cg19192280	0.031	-0.074	-0.105	0.0008126	Island	3'UTR		Chr6:32116893	PRRT1	I	PPT2 (-4335), PRRT1 (+2826)
cg00387551	-0.061	0.037	0.098	0.0008128		Body		Chr1:3011304	PRDM16	II	ARHGEF16 (-359842), PRDM16 (+25563)
cg04554564	-0.053	0.037	0.090	0.0008173		TSS200		Chr17:19990302	CYTSB	II	SPECC1 (+77654), LGALS9B (+380545)
cg12643226	0.027	-0.015	-0.041	0.0008174		Body		Chr1:115829262	NGF	I	TSPAN2 (-197142), NGF (+51594)
cg27376437	0.005	-0.018	-0.023	0.0008187	N_Shore	Body		Chr17:56064565	VEZF1	II	MRPS23 (-137133), VEZF1 (+1049)
cg13676706	0.010	-0.018	-0.028	0.0008189	S_Shelf			Chr12:127944448		II	TMEM132C (-807499)
cg05982929	0.003	-0.018	-0.021	0.0008203	Island	TSS1500;Body		Chr6:32163523	GPSM3;NOTCH4	I	GPSM3 (-224)
cg21173803	0.042	-0.013	-0.054	0.0008215				Chr22:27299879		II	CRYBA4 (+281952), MN1 (+897606)
cg10202994	0.042	-0.021	-0.064	0.0008226	N_Shore	TSS1500		Chr2:220071050	ZFAND2B	II	ZFAND2B (-487)
cg00739667	-0.028	0.036	0.064	0.0008254		Body		Chr16:81731648	CMIP	I	PLCG2 (-81250), CMIP (+252874)
cg22823236	-0.045	0.057	0.101	0.0008272	N_Shelf	5'UTR		Chr14:70652710	SLC8A3	II	SLC8A3 (+3076), SMOC1 (+306597)
cg17330838	-0.056	0.031	0.087	0.0008353	Island	Body		Chr11:57267101	SLC43A1	I	SLC43A1 (+15256), RTN4RL2 (+38763)
cg01249202	-0.021	0.027	0.047	0.0008361				Chr13:78410079		II	EDNRB (+83823), SCEL (+300271)
cg19879479	0.007	-0.019	-0.027	0.0008447	N_Shore	5'UTR;5'UTR		Chr6:80246572	LCA5	I	LCA5 (+574)
cg23013958	0.043	-0.082	-0.125	0.0008456	N_Shore	TSS1500		Chr1:65612865	AK3L1	II	AK4 (-366)
cg02508664	0.040	-0.022	-0.061	0.0008465	N_Shore	TSS1500	rs828363	Chr6:87646738	HTR1E	II	HTR1E (-285)
cg14452650	0.007	-0.007	-0.013	0.0008499	N_Shore	TSS1500		Chr2:42396274	EML4	I	EML4 (-215)
cg25730717	0.015	-0.020	-0.035	0.0008512	Island	TSS1500		Chr7:148726076	PDIA4	I	PDIA4 (-295)
cg08313539	0.084	0.005	-0.079	0.0008512				Chr6:127094710		II	RSPO3 (-345337), CENPW (+433458)

cg09847284	0.005	-0.025	-0.030	0.000858	Island	TSS200		Chr11:45907071	MAPK8IP1	I	MAPK8IP1 (+25)
cg01112527	-0.027	0.045	0.072	0.0008585	N_Shore	Body		Chr2:1479810	TPO	II	TPO (+62578), PXDN (+268480)
cg06466917	-0.008	0.015	0.023	0.0008585	N_Shore	Body;TSS1500		Chr5:17216259	LOC285696;BASP1	II	BASP1 (-1490)
cg14964512	0.042	-0.033	-0.075	0.0008591	Island			Chr19:53832493		I	ZNF845 (-4508)
cg13842154	0.039	-0.023	-0.062	0.00086	Island	Body		Chr14:103390247	AMN	II	AMN (+1255), CDC42BPB (+133494)
cg08027943	-0.047	0.020	0.067	0.0008607				Chr14:53833982		II	DDHD1 (-213937), BMP4 (+587287)
cg12650685	-0.019	0.009	0.028	0.000863		Body		Chr6:3284109	SLC22A23	II	TUBB2B (-56142), SLC22A23 (+172683)
cg03004426	0.007	-0.011	-0.019	0.0008632	Island	TSS200		Chr16:53537293	AKTIP	II	AKTIP (-124)
cg18923635	-0.020	0.038	0.058	0.0008665	N_Shore			Chr18:48083994		II	MAPK4 (-2489)
cg24377285	-0.038	0.027	0.065	0.0008667	Island	Body		Chr19:38943724	RYR1;RYR1	I	RYR1 (+19385), MAP4K1 (+164918)
cg15589930	0.015	-0.011	-0.026	0.0008679	S_Shore	TSS1500		Chr1:94344944	DNTTIP2	II	DNTTIP2 (-183)
cg08169950	-0.028	0.072	0.101	0.0008722	N_Shelf			Chr1:247799571		II	OR2G3 (+30684), OR13G1 (+36771)
cg24789562	0.024	-0.019	-0.044	0.0008736				Chr11:27842648		II	BDNF (-120049), KIF18A (+287097)
cg01412524	0.003	-0.008	-0.011	0.0008749	Island	Body	rs72890727	Chr1:46860243	FAAH	I	FAAH (+305)
cg17474545	-0.019	0.046	0.066	0.0008775	S_Shore			Chr19:56061873		II	SGK110 (-4965)
cg04043957	-0.018	0.051	0.070	0.000879		TSS1500;TSS200		Chr11:1860215	TNNI2	I	TNNI2 (-1216)
cg24842354	-0.056	0.058	0.114	0.0008831	N_Shore	TSS1500;Body		Chr1:2004057	PRKCZ	II	SKI (-156076), PRKCZ (+22149)
cg05938623	0.019	0.000	-0.019	0.000884	Island			Chr1:223254899		II	TLR5 (+61724), DISP1 (+266469)
cg20053381	0.002	-0.014	-0.017	0.0008862	S_Shore	TSS200;TSS200		Chr2:220363572	GMPPA	I	GMPPA (-14)
cg13580027	-0.034	0.057	0.091	0.0008876	N_Shore			Chr10:134972063		II	KNDC1 (-1907)
cg14711428	0.015	-0.003	-0.018	0.000888	Island	TSS200;5'UTR		Chr7:112090348	IFRD1	I	C7orf53 (-30559), IFRD1 (+27150)
cg23399257	0.022	0.068	0.046	0.0008911				Chr2:394481		II	FAM150B (-106174), TMEM18 (+282957)
cg11832544	0.015	-0.021	-0.036	0.0008914		Body		Chr1:161094035	DEDD	II	PFDN2 (-6170), DEDD (+8220)
cg21937169	0.006	-0.025	-0.031	0.0008938	S_Shore	Body		Chr7:65541137	ASL	II	ASL (+362)
cg17623882	-0.019	0.009	0.028	0.0008952	N_Shore	Body		Chr6:41773611	USP49	I	TOMM6 (+19112), USP49 (+89487)
cg12293132	0.018	-0.012	-0.031	0.0008952	Island	Body		Chr7:23720668	C7orf46	II	STK31 (-29169), CCDC126 (+83671)
cg05658771	-0.040	0.032	0.072	0.0008988	S_Shore	TSS1500		Chr16:89884179	FANCA	I	FANCA (-1115)
cg16442298	0.028	-0.043	-0.071	0.0009015	N_Shore			Chr8:1403050		II	C8orf42 (-907720), DLGAP2 (-46518)
cg15975990	0.046	-0.038	-0.084	0.0009016	Island	TSS200		Chr2:180871849	CWC22	I	CWC22 (-70)
cg13890706	0.005	-0.018	-0.023	0.0009027	Island	1stExon;5'UTR;TSS1500		Chr10:118033115	GFRA1	II	GFRA1 (+10)
cg10281478	-0.030	0.028	0.058	0.0009069	S_Shore	5'UTR		Chr7:95402528	DYNC1I1	II	DYNC1I1 (+711)
cg01948724	-0.012	0.058	0.070	0.0009073				Chr16:3038035		II	CLDN9 (-24421), PKMYT1 (-7496)
cg17024952	0.002	-0.033	-0.035	0.0009092	S_Shore	Body		Chr6:116422486	NT5DC1	II	NT5DC1 (+488)
cg12231340	-0.026	0.052	0.078	0.0009107	Island	1stExon		Chr12:52685221	KRT81	II	KRT81 (+77)
cg07107628	-0.026	0.025	0.051	0.0009113				Chr6:27210934		II	PRSS16 (-4567)
cg07654559	0.021	-0.017	-0.039	0.0009125	S_Shore	Body;TSS1500		Chr2:74710618	TTC31;CCDC142;TTC31	I	CCDC142 (-262), TTC31 (+419)
cg24674304	0.035	-0.026	-0.061	0.0009177	Island	TSS1500		Chr3:44903063	MIR564;TMEM42	I	TMEM42 (-344)
cg22076495	0.009	-0.009	-0.019	0.0009237	Island	TSS1500		Chr5:32174716	GOLPH3	II	GOLPH3 (-292)
cg02101876	0.023	-0.026	-0.049	0.0009245				Chr13:40765110		II	FOXO1 (+475623), COG6 (+535347)
cg09186897	0.010	-0.006	-0.016	0.0009294	Island	5'UTR		Chr1:169862509	SCYL3	I	SCYL3 (+566)
cg25936902	0.013	-0.063	-0.076	0.0009307	S_Shore			Chr13:30982971		II	KATNAL1 (-101809), HMGB1 (+57109)
cg08532057	-0.041	0.029	0.070	0.0009356	Island	TSS1500		Chr13:25875436	NUPL1	II	NUPL1 (-229)

Fisher, Murphy et al.

cg25064029	-0.036	0.033	0.069	0.0009358		3'UTR	Chr4:113362371	ALPK1	II	NEUROG2 (+74956), ALPK1 (+143873)
cg09231514	0.006	-0.005	-0.011	0.0009436	Island	5'UTR;TSS1500	Chr19:5681323	HSD11B1L;C19orf70	I	C19orf70 (-413), HSD11B1L (+289)
cg14543966	0.014	-0.036	-0.051	0.0009472		Body	Chr9:123537218	FBXW2	II	MEGF9 (-60454), FBXW2 (+18521)
cg20668450	-0.045	0.026	0.070	0.0009483	N_Shelf	3'UTR	Chr11:64812208	SAC3D1	II	SAC3D1 (+3833), NAAALADL1 (+13800)
cg21594651	-0.027	0.034	0.061	0.0009501		Body	Chr4:79214428	FRAS1	II	ANXA3 (-258313), FRAS1 (+235705)
cg26250400	0.030	-0.066	-0.096	0.0009528	S_Shelf		Chr19:15921959		II	OR10H1 (-3024)
cg04998447	0.038	-0.022	-0.060	0.0009559	Island	Body	Chr15:90209223	PLIN1	II	KIF7 (-10542), PLIN1 (+13424)
cg12667002	-0.025	0.050	0.075	0.000958	N_Shore	Body	Chr13:114812302	RASA3	II	GAS6 (-245257), RASA3 (+85792)
cg02401132	0.007	-0.016	-0.022	0.0009594	S_Shore		Chr6:19805404		II	ID4 (-32212)
cg25058261	0.063	-0.082	-0.144	0.0009618	N_Shore	3'UTR	Chr12:115109452	TBX3	II	TBX5 (-265564), TBX3 (+12516)
cg16909783	-0.007	0.016	0.022	0.0009659	Island		Chr7:150869917		I	GBX1 (-5051), ASB10 (+15001)
cg08580032	-0.026	0.026	0.051	0.000969	Island		Chr18:77562500		II	KCNG2 (-61167), CTDP1 (+122700)
cg17614974	-0.016	0.008	0.024	0.0009716	Island		Chr3:44039919		II	C3orf23 (-340024), ABHD5 (+307545)
cg06719334	0.017	-0.023	-0.040	0.0009729		Body	Chr16:7501308	A2BP1	II	RBFOX1 (+118558)
cg14478589	0.035	-0.043	-0.078	0.0009799		Body	Chr9:124086862	GSN	II	GSN (+24784), STOM (+45682)
cg23334298	-0.041	0.024	0.064	0.0009807		Body	Chr4:78692537	CNOT6L	II	CNOT6L (+48006), CXCL13 (+259631)
cg06142142	-0.038	0.025	0.062	0.0009809	N_Shore	TSS1500	Chr10:115938512	TDRD1	II	TDRD1 (-516)
cg19526568	0.036	-0.009	-0.045	0.0009835	Island		Chr13:100643087		II	PCCA (-98181), ZIC2 (+9062)
cg25004270	-0.005	0.018	0.024	0.0009876	Island	TSS1500;1stExon	Chr1:1550864	MIB2	I	MIB2 (+70)
cg26665082	0.007	-0.011	-0.018	0.0009883	Island	TSS200	Chr1:78444860	FUBP1	I	FUBP1 (-84)
cg14060757	-0.043	0.007	0.050	0.0009887	Island	Body	Chr21:46715144	LOC642852	I	COL18A1 (-160279), POFUT2 (-7334)
cg02898665	-0.017	0.065	0.082	0.0009982	N_Shore		Chr8:55368762		II	SOX17 (-1732)
cg08886036	-0.014	0.008	0.022	0.0009986	S_Shelf	Body	Chr1:1118934	TTLL10	I	TTLL10 (+9649), TNFRSF18 (+23154)

Note. Ranked by p value. $\Delta\beta$, difference in DNA methylation; DMPs, differentially methylated positions; GREAT, Genomic Regions Enrichment of Annotations Tool; Hg19, Human Genome build 19; SBE, single-base extension; SNP, single nucleotide polymorphism; TSS, transcription start site.

Supplementary Table 7. Gene Ontology (GO) enrichment analysis of longitudinal DMPs between age 5 and age 10

GO Accession ID	GO Function	Ontology	P value
GO:0042734	presynaptic membrane	CC	0.00317
GO:0043204	perikaryon	CC	0.00347
GO:0060993	kidney morphogenesis	BP	0.00597
GO:0005783	endoplasmic reticulum	CC	0.00623
GO:0031941	filamentous actin	CC	0.00658
GO:0016525	negative regulation of angiogenesis	BP	0.00666
GO:0072075	metanephric mesenchyme development	BP	0.00732
GO:0003338	metanephros morphogenesis	BP	0.00897
GO:0072074	kidney mesenchyme development	BP	0.01068
GO:0042157	lipoprotein metabolic process	BP	0.01089
GO:0000050	urea cycle	BP	0.01104
GO:0060231	mesenchymal to epithelial transition	BP	0.01224
GO:0019627	urea metabolic process	BP	0.01226
GO:0045921	positive regulation of exocytosis	BP	0.01306
GO:0010870	positive regulation of receptor biosynthetic process	BP	0.01336
GO:0071941	nitrogen cycle metabolic process	BP	0.01397
GO:0051219	phosphoprotein binding	MF	0.01424
GO:0032799	low-density lipoprotein receptor particle metabolic process	BP	0.01456
GO:0035020	regulation of Rac protein signal transduction	BP	0.01675
GO:0010984	regulation of lipoprotein particle clearance	BP	0.01706
GO:0072215	regulation of metanephros development	BP	0.01725
GO:0032839	dendrite cytoplasm	CC	0.01985
GO:0006004	fucose metabolic process	BP	0.02103
GO:0006497	protein lipidation	BP	0.02146
GO:0009084	glutamine family amino acid biosynthetic process	BP	0.0218
GO:0071385	cellular response to glucocorticoid stimulus	BP	0.02222
GO:0016226	iron-sulfur cluster assembly	BP	0.02232
GO:0031163	metallo-sulfur cluster assembly	BP	0.02232
GO:0071384	cellular response to corticosteroid stimulus	BP	0.02246
GO:0051016	barbed-end actin filament capping	BP	0.02251
GO:0016601	Rac protein signal transduction	BP	0.026
GO:0042158	lipoprotein biosynthetic process	BP	0.02623

GO:0043604	amide biosynthetic process	BP	0.02646
GO:0065003	macromolecular complex assembly	BP	0.02702
GO:0031984	organelle subcompartment	CC	0.03066
GO:0045879	negative regulation of smoothened signaling pathway	BP	0.03228
GO:0003337	mesenchymal to epithelial transition involved in metanephros morphogenesis	BP	0.03284
GO:0006461	protein complex assembly	BP	0.0332
GO:0008083	growth factor activity	MF	0.03345
GO:0070271	protein complex biogenesis	BP	0.03374
GO:0034383	low-density lipoprotein particle clearance	BP	0.03382
GO:0010869	regulation of receptor biosynthetic process	BP	0.03463
GO:0009163	nucleoside biosynthetic process	BP	0.03466
GO:1901659	glycosyl compound biosynthetic process	BP	0.03466
GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	BP	0.03638
GO:0015758	glucose transport	BP	0.0365
GO:0061299	retina vasculature morphogenesis in camera-type eye	BP	0.03672
GO:0008645	hexose transport	BP	0.03712
GO:0051259	protein oligomerization	BP	0.03724
GO:0015749	monosaccharide transport	BP	0.03867
GO:0006525	arginine metabolic process	BP	0.0393
GO:0005758	mitochondrial intermembrane space	CC	0.03952
GO:0003382	epithelial cell morphogenesis	BP	0.04079
GO:0030857	negative regulation of epithelial cell differentiation	BP	0.04085
GO:0032314	regulation of Rac GTPase activity	BP	0.04242
GO:0071634	regulation of transforming growth factor beta production	BP	0.04323
GO:0007269	neurotransmitter secretion	BP	0.04344
GO:0004675	transmembrane receptor protein serine/threonine kinase activity	MF	0.04352
GO:0005024	transforming growth factor beta-activated receptor activity	MF	0.04352
GO:1902931	negative regulation of alcohol biosynthetic process	BP	0.0443
GO:0072088	nephron epithelium morphogenesis	BP	0.04443
GO:0010827	regulation of glucose transport	BP	0.04607
GO:0019433	triglyceride catabolic process	BP	0.04607
GO:0010894	negative regulation of steroid biosynthetic process	BP	0.04676
GO:0000578	embryonic axis specification	BP	0.04714
GO:0001895	retina homeostasis	BP	0.04838
GO:0032800	receptor biosynthetic process	BP	0.04924

Note. BP, Biological Processes; CC, Cellular; DMPs, differentially methylated positions; MF, Molecular Function.