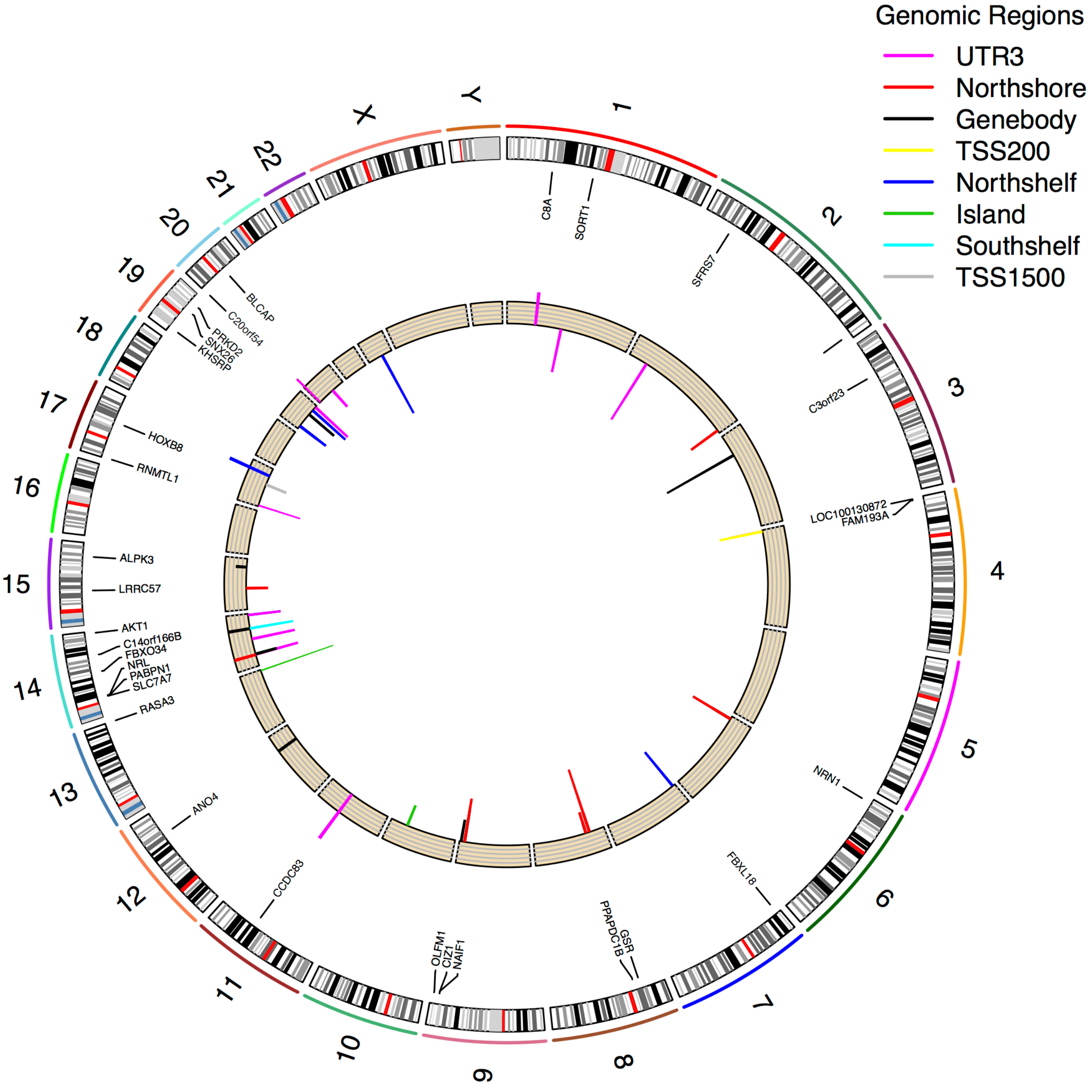
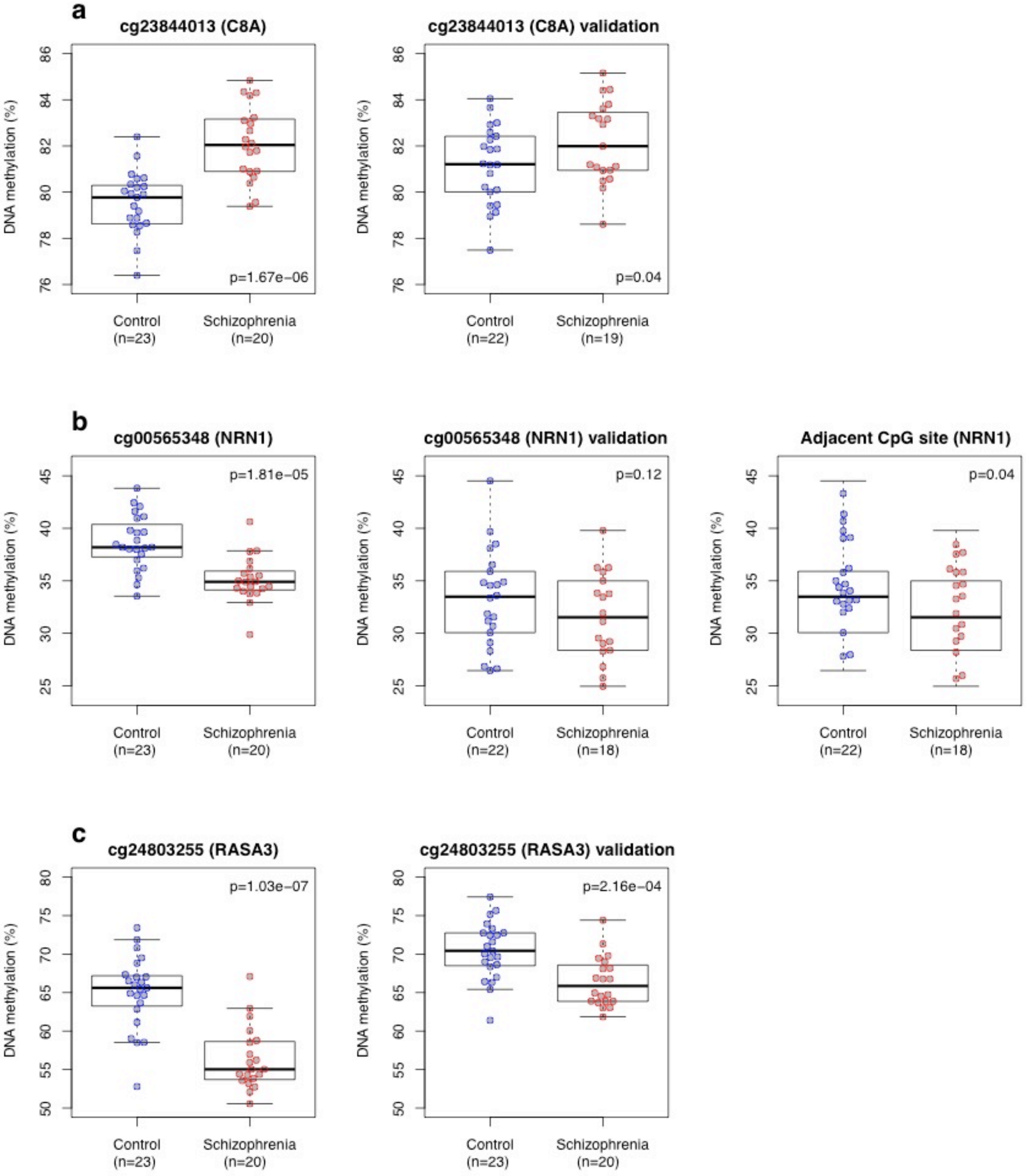
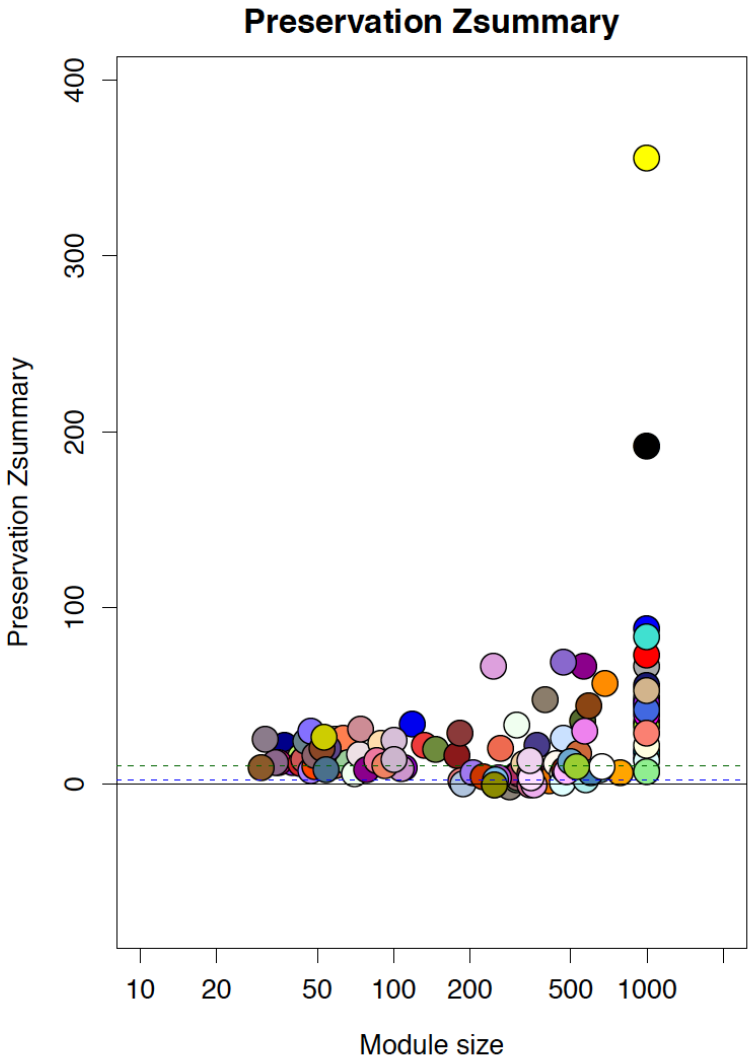
SUPPLEMENTARY FIGURE 1 – Circos plot of schizophrenia-associated differentially methylated regions (DMRs) in the prefrontal cortex. The outermost ring denotes chromosomal location (annotated with chromosomal number), with the pter-qter orientation in a clockwise direction. Small red lines represent the centromeres within each chromosome. The middle ring highlights the location of genes associated with schizophrenia-associated DMRs (FDR ≤ 0.05), with the magnitude and direction of DNA methylation difference for each region shown in the inner ring. Lines pointed inwards signify hypomethylated regions and outwards hypermethylated regions. Line colors indicate the genomic region or CpG island location of the probe. TSS=Transcription start site; UTR=Untranslated Region.



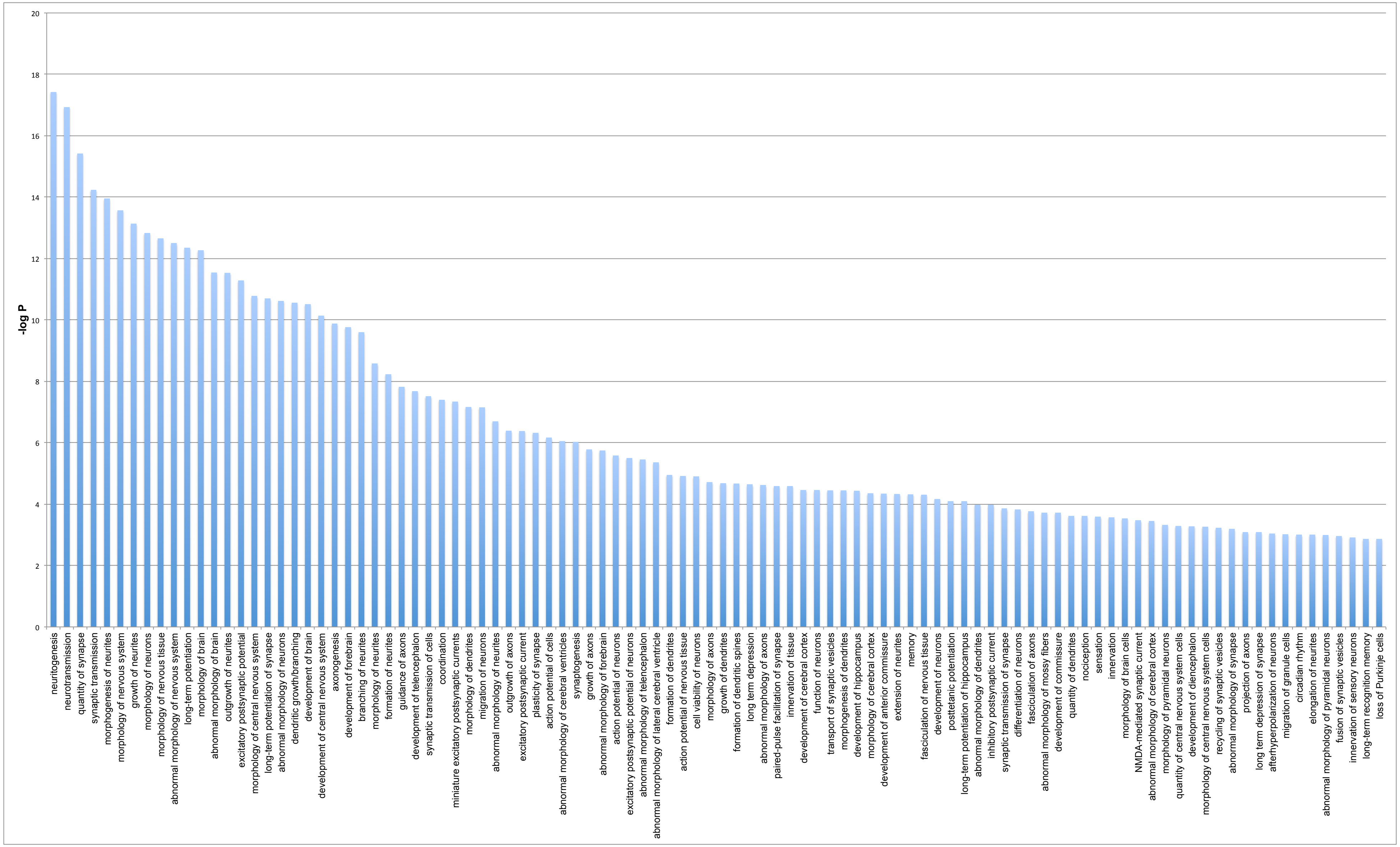
SUPPLEMENTARY FIGURE 2 - Validation of Illumina 450K array data using bisulfite-pyrosequencing. Shown is confirmation of schizophrenia-associated DNA methylation differences at a) cg23844013 *(C8A)*, b) cg00565348 *(NRN1)*, and c) cg24803255 *(RASA3)*. Additional validation data is presented in **Figure 1c**.



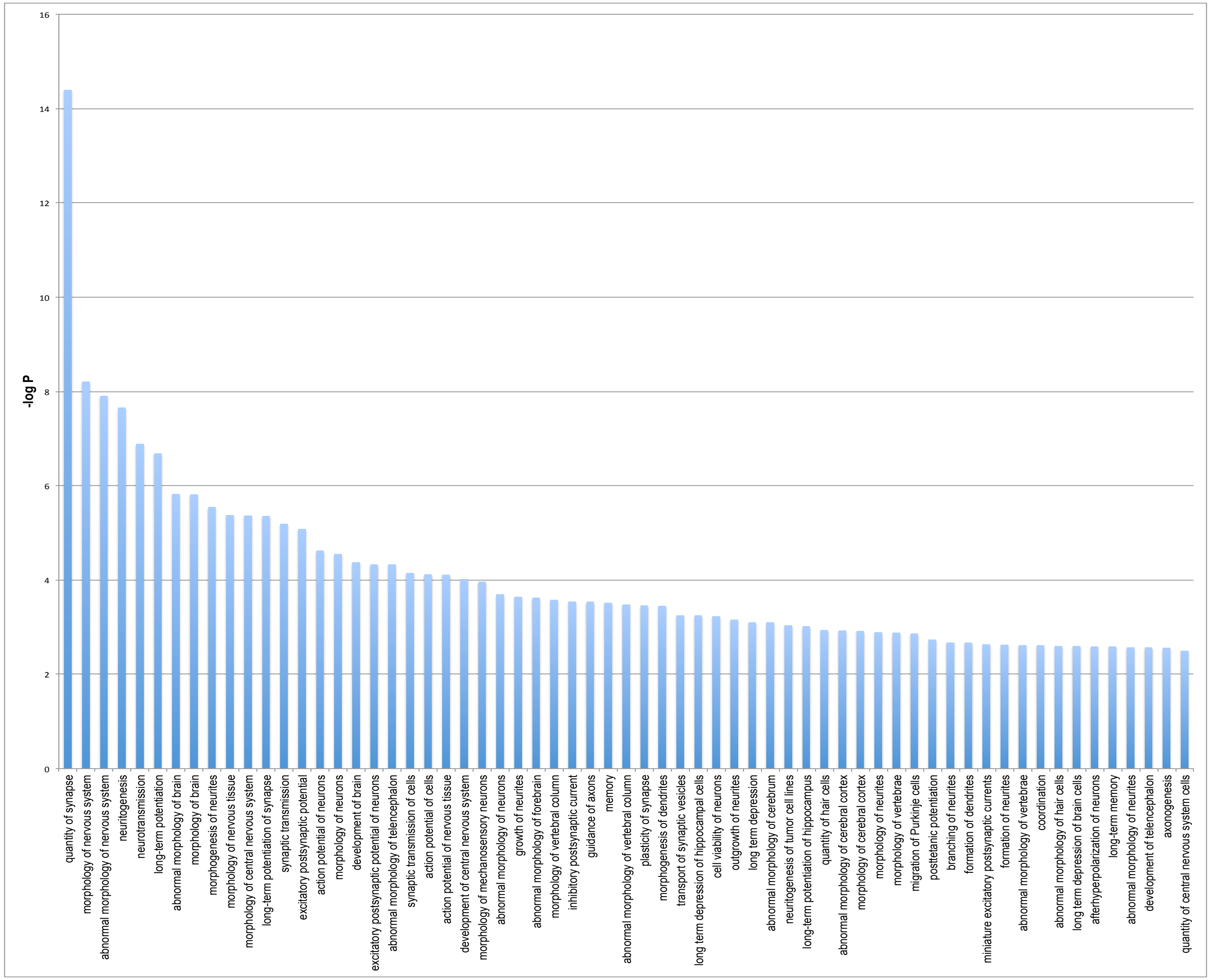
SUPPLEMENTARY FIGURE 3 – Modules of co-methylated loci identified in the 'discovery' PFC cohort by WGCNA are strongly preserved in the Montreal replication cohort. A Zsummary score > 10 is indicative of a strongly preserved module. Of note, the two modules associated with schizophrenia are highly conserved across datasets (black module: Zsummary score = 190; pink module: Zsummary score = 49).



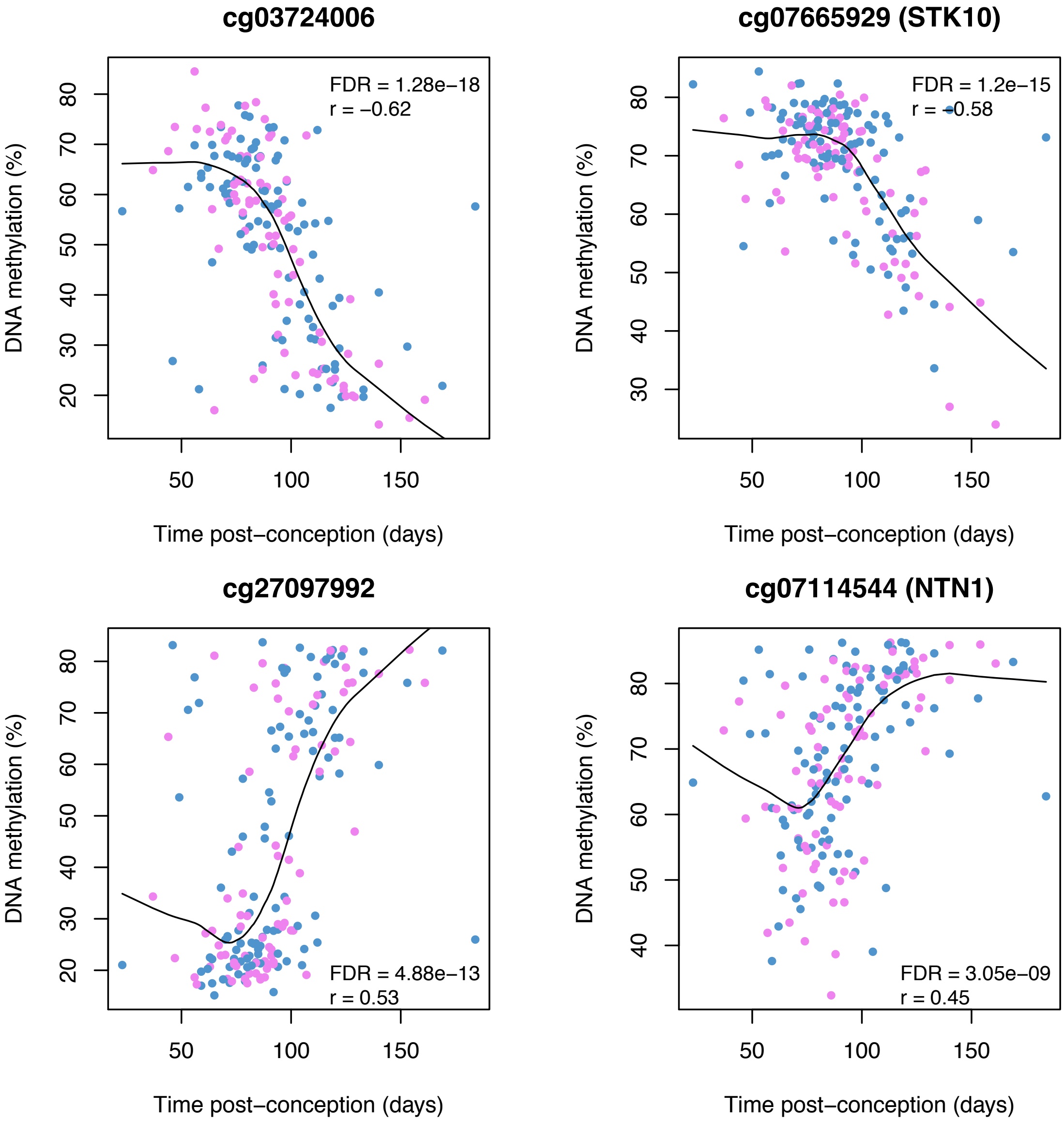
SUPPLEMENTARY FIGURE 4 - Ingenuity Pathway Analysis highlighted a highly significant (p=3.80E-18 to 1.37E-03) enrichment of pathways related to nervous system development and function in the black WGCNA module.

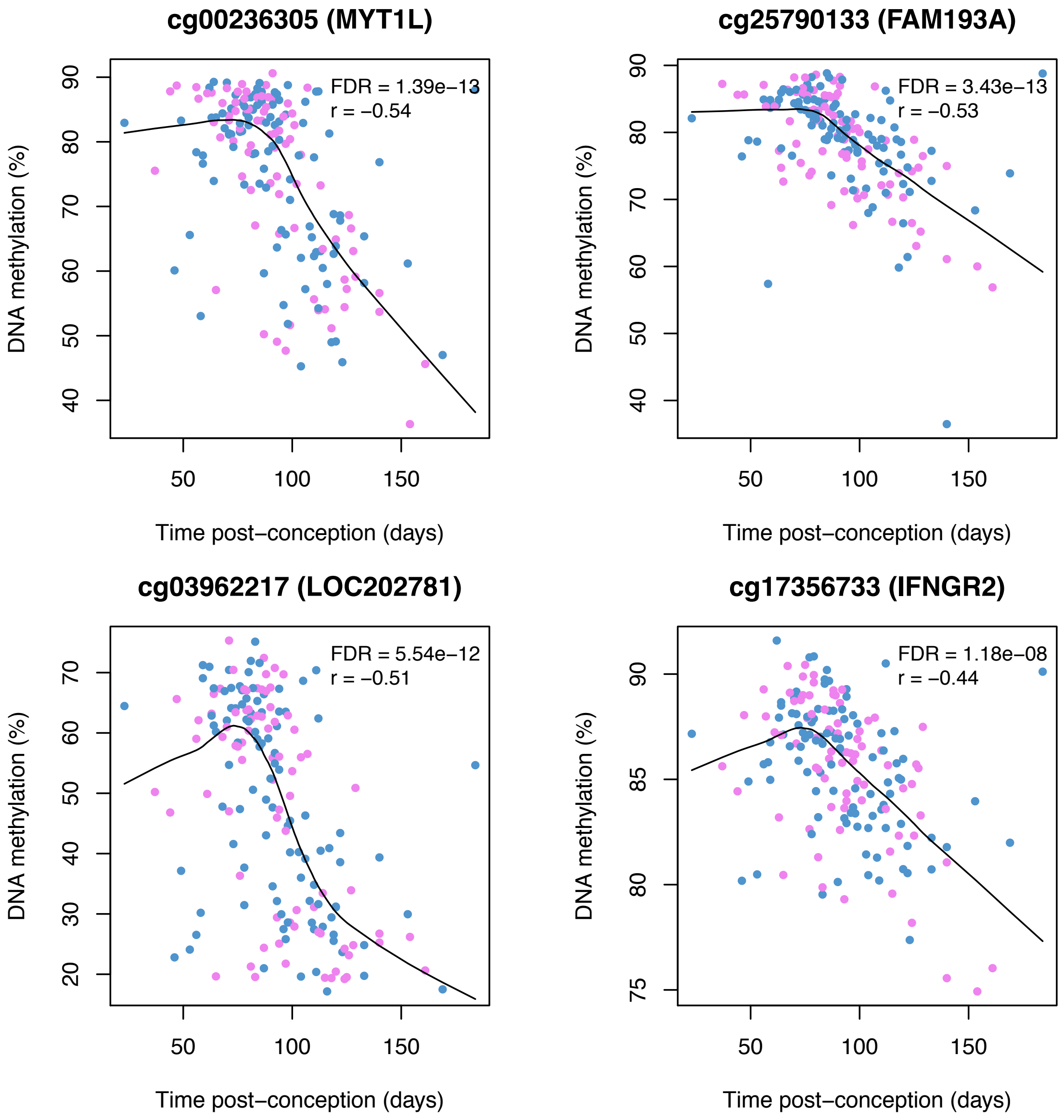


SUPPLEMENTARY FIGURE 5 - Ingenuity Pathway Analysis highlighted a highly significant ($p=4.04E-15$ to $3.16E-03$) enrichment of pathways related to nervous system development and function in the pink WGCNA module.



SUPPLEMENTARY FIGURE 6 - Schizophrenia-associated DMPs are enriched for loci showing dynamic changes in DNA methylation during human brain development. Correlation between DNA methylation and neurodevelopmental age (days post-conception) is shown for top-ranked schizophrenia-associated DMPs that are also associated with brain development (**Supplementary Table 13**).




cg00236305 (MYT1L)
FDR = 1.39e−13
r = −0.54
cg25790133 (FAM193A)
FDR = 3.43e−13
r = −0.53
cg03962217 (LOC202781)
FDR = 5.54e−12
r = −0.51
cg17356733 (IFNGR2)
FDR = 1.18e−08
r = −0.44
DNA methylation (%)
Time post−conception (days)
50
100
150
40
50
60
70
80
90
20
30
75
85

SUPPLEMENTARY TABLE 1 - Details of post-mortem brain samples from London Brain Bank of Neurodegenerative Disease. Schizophrenia cases and controls are matched (t-test p-value>0.05) for all variables except total brain weight. SZ=schizophrenia.

	SZ	Control	Total	p-value
Number	22	24	46	
Sex (male:female)	12:10	18:6	30:16	
Age at death (years)	61± 16.6	61.1 ± 18.9	61.1 ± 17.6	0.98
Total brain weight (g)	1354± 143	1465 ± 193	1416 ± 180	0.04**
Net brain weight (g)	1215± 132	1292 ± 173	1260 ± 160	0.11
Cerebellum weight (g)	164 ± 15.5	175 ± 28	171 ± 24	0.10
pH	6.60 ± 0.29	6.48 ± 0.33	6.54 ± 0.32	0.19

SUPPLEMENTARY TABLE 2 - Details of individual post-mortem brain samples from the London Brain Bank of Neurodegenerative Disease. NA=not available.

ID	Sex	Age at death (years)	Total brain weight (g)	Net brain weight (g)	Cerebellum weight (g)	pH
Schizophrenia						
ID1	M	67	1487	1313	174	6.36
ID2	M	79	NA	NA	NA	6.40
ID3	F	69	NA	NA	NA	6.80
ID4	F	76	1321	1143	178	6.25
ID5	F	84	1201	NA	NA	6.60
ID6	M	87	1126	993	133	6.19
ID7	F	32	1356	1185	171	6.30
ID8	F	70	1340	1193	147	6.17
ID9	F	49	1535	1354	181	6.90
ID10	M	46	1283	1117	166	7.00
ID11	M	62	1614	1439	175	7.00
ID12	M	31	1273	1273	NA	6.30
ID13	M	51	1663	1485	178	6.80
ID14	M	62	NA	NA	NA	7.10
ID15	F	34	1237	1092	145	6.20
ID16	F	75	1314	1141	173	6.60
ID17	M	64	1239	NA	NA	6.70
ID18	M	49	1263	1097	166	6.80
ID19	F	71	1283	1141	142	6.83
ID20	F	75	1310	1162	148	6.61
ID21	M	64	1375	1197	178	6.60
ID22	M	45	1499	1332	167	6.70
Control						
ID23	M	25	1731	1549	182	6.93
ID24	M	49	1411	1231	180	6.70
ID25	F	82	1376	1216	160	6.33
ID26	F	68	1196	1052	144	6.02
ID27	F	33	1503	1323	180	6.36
ID28	M	50	1857	1650	207	6.49
ID29	M	57	1287	1146	141	6.62
ID30	M	58	1364	1145	219	6.87
ID31	F	68	1305	1137	168	7.10
ID32	M	71	1606	1356	250	6.38
ID33	M	95	1310	1160	150	6.14
ID34	M	40	1458	1286	172	6.13
ID35	M	54	1487	1347	140	6.96
ID36	F	76	1329	1175	154	6.41
ID37	M	67	1505	1336	169	6.06
ID38	F	96	1263	1115	148	6.55
ID39	M	37	1389	1214	175	6.46
ID40	M	40	1670	1470	200	6.80
ID41	M	70	1175	1107	136	6.44
ID42	M	69	1943	1739	204	6.60
ID43	M	48	1450	1262	188	6.20
ID44	M	80	1488	1300	188	6.04
ID45	M	79	1598	1406	192	5.95
ID46	M	55	1452	1288	164	6.90

SUPPLEMENTARY TABLE 3 – Samples excluded during quality control (QC) for methylation assays. Pyro=Pyrosequencing, BC=Bisulfite Conversion, PFC=Prefrontal cortex, CER=Cerebellum, NA=not available.

ID	PFC 450K Barcode	PFC 450K QC	CER 450K Barcode	CER 450K QC	PFC NRN1 Pyro	PFC C8A Pyro	PFC RASA3 Pyro
Schizophrenia							
ID1	6055432012_R04C02		6042316042_R03C01				
ID2	6055432012_R06C01		6042316047_R02C01				
ID3	6055432012_R01C02		6042316024_R06C02				
ID4	6055432012_R01C01		6042316042_R05C01		Failed QC	Failed QC	
ID5	6055432066_R02C01		6042316024_R03C01				
ID6	6055432029_R02C02		6042316031_R03C02				
ID7	6055432060_R03C01		6042316024_R04C01				
ID8	6055432012_R04C01	Failed QC	6042316024_R04C02		NA on 450K	NA on 450K	NA on 450K
ID9	6055432066_R01C02		6042316031_R05C02				
ID10	6055432060_R04C02		6042316024_R02C02				
ID11	6055432066_R05C02		6042316024_R02C01				
ID12	6055432012_R02C01	Failed QC	6042316024_R01C01		NA on 450K	NA on 450K	NA on 450K
ID13	6055432060_R05C02		6042316042_R05C02				
ID14	6055432066_R03C02		6042316031_R01C01				
ID15	6055432060_R03C02		6042316047_R03C02				
ID16	6055432029_R05C01		6042316031_R06C01				
ID17	6055432029_R04C01		6042316042_R04C02				
ID18	6055432060_R04C01		6042316031_R02C01				
ID19	6055432029_R03C02		6042316031_R04C02				
ID20	6055432012_R03C01		6042316024_R05C02				
ID21	6055432066_R04C02		6042316031_R02C02				
ID22	6055432066_R01C01		6042316024_R03C02	Not CER	Failed QC		
Control							
ID23	6055432012_R06C02		6042316042_R01C02				
ID24	6055432012_R03C02		6042316031_R03C01				
ID25	6055432012_R05C01		6042316047_R06C01				
ID26	6055432060_R05C01		6042316024_R06C01				
ID27	6055432029_R02C01		6042316042_R06C02				
ID28	6055432066_R05C01		6042316047_R05C01				
ID29	6055432066_R04C01		6042316042_R02C02				
ID30	6055432012_R05C02		6042316031_R06C02				
ID31	6055432029_R03C01		6042316047_R05C02				
ID32	6055432012_R02C02		6042316024_R05C01		Failed QC	Failed QC	
ID33	6055432066_R02C02		6042316047_R04C02				
ID34	6055432066_R03C01	Failed QC	6042316031_R01C02		NA on 450K	NA on 450K	NA on 450K
ID35	6055432060_R02C02		6042316047_R04C01				
ID36	6055432060_R06C01		6042316042_R04C01				
ID37	6055432060_R01C01		6042316031_R05C01				
ID38	6055432060_R06C02		6042316031_R04C01				
ID39	6055432029_R01C02		6042316042_R03C02				
ID40	6055432029_R04C02		6042316042_R01C01				
ID41	6055432029_R05C02		6042316042_R02C01				
ID42	6055432060_R01C02		6042316024_R01C02				
ID43	6055432029_R06C01		6042316042_R06C01				
ID44	6055432060_R02C01		6042316047_R01C01				
ID45	6055432029_R06C02		6042316047_R02C02				
ID46	6055432029_R01C01		6042316047_R03C01	Failed BC			
Total included in analysis:		**43**		**44**	**40**	**41**	**43**

SUPPLEMENTARY TABLE 4 – 100 top-ranked schizophrenia-associated DMPs in the prefrontal cortex. P-value from linear model including age and sex as covariates. TSS=Transcription start site; UTR=Untranslated region, SZ=schizophrenia. The CETS algorithm[1] was used to correct for the potential effect of differential neuronal cell proportions across samples.

Probe ID	Genomic position (hg19)	Gene	Gene region	Probe type	*P*	FDR	CETS-adjusted *P*	Mean SZ	Mean Control	Beta difference
cg26173173	chr8:144642813*	GSDMD	Body	II	1.16E-07	0.03	2.76E-06	0.83	0.79	0.04
cg24803255	chr13:114807060	RASA3	Body	II	1.25E-07	0.03	1.09E-05	0.56	0.65	-0.09
cg00903099	chr7:154862441	HTR5A	TSS200	II	2.40E-07	0.03	1.95E-05	0.09	0.12	-0.02
cg08171022	chr11:70185278	PPFIA1	Body	II	2.85E-07	0.03	2.93E-05	0.48	0.53	-0.05
cg02857643	chr17:48696108	CACNA1G	Body	I	1.63E-06	0.1	5.88E-05	0.87	0.92	-0.05
cg00236305	chr2:1796076	MYT1L	Body	II	1.75E-06	0.1	1.95E-04	0.67	0.73	-0.06
cg14966346	chr14:104152124	KLC1	Body	II	2.51E-06	0.1	1.25E-04	0.72	0.77	-0.05
cg13079528	chr7:4027346	SDK1	Body	I	2.75E-06	0.1	3.07E-04	0.71	0.79	-0.08
cg14429765	chr8:6492531	MCPH1	Body	II	2.79E-06	0.1	2.94E-06	0.79	0.76	0.03
cg08602214	chr8:22864392	RHOBTB2	Body	II	2.87E-06	0.1	1.76E-04	0.69	0.75	-0.07
cg19735533	chr2:241196887	-	-	II	2.94E-06	0.1	2.22E-04	0.76	0.81	-0.06
cg09507608	chr22:29873338	-	-	II	2.95E-06	0.1	2.88E-04	0.56	0.62	-0.06
cg23844013	chr1:57383752	C8A	3'UTR	II	3.20E-06	0.1	4.07E-06	0.82	0.79	0.03
cg26578910	chr19:47204096	PRKD2	Body	I	3.47E-06	0.1	3.43E-04	0.67	0.71	-0.04
cg21847368	chr13:113744010	MCF2L	Body	II	3.70E-06	0.1	3.08E-05	0.80	0.84	-0.03
cg03607729	chr16:25138698	LCMT1	Body	II	4.19E-06	0.1	4.38E-04	0.70	0.75	-0.04
cg10248981	chr10:126157948	LHPP	Body	I	4.32E-06	0.1	4.81E-04	0.55	0.63	-0.07
cg03445663	chr2:242170236	HDLBP	Body	I	4.59E-06	0.1	4.11E-04	0.51	0.59	-0.08
cg15079231	chr3:42572745	VIPR1	Body	II	4.93E-06	0.1	4.18E-04	0.76	0.80	-0.04
cg21341878	chr4:2278462	ZFYVE28	Body	II	5.14E-06	0.1	2.71E-04	0.75	0.81	-0.05
cg04922803	chr12:104444418	GLT8D2	TSS1500	II	5.19E-06	0.1	1.36E-04	0.68	0.62	0.06
cg18857062	chr6:43276478	CRIP3	Body	I	5.29E-06	0.1	1.43E-04	0.21	0.26	-0.04
cg27138871	chr11:74950396	-	-	II	5.63E-06	0.11	6.10E-04	0.75	0.79	-0.05
cg27363226	chr19:6421747	KHSRP	Body	II	6.63E-06	0.12	7.06E-04	0.62	0.67	-0.05
cg02187259	chr2:16804452	FAM49A	5'UTR	II	6.72E-06	0.12	7.22E-04	0.74	0.79	-0.05

cg26182253	chr13:112236782	-	-	II	7.01E-06	0.12	7.68E-04	0.60	0.67	-0.06
cg14370653	chr9:137828210	-	-	II	7.18E-06	0.12	8.07E-04	0.75	0.80	-0.05
cg14527262	chr4:1202653	LOC100130 872-SPON2	TSS200	I	8.02E-06	0.12	8.77E-04	0.56	0.63	-0.07
cg16393877	chr17:65037838	-	-	II	8.07E-06	0.12	2.52E-04	0.78	0.74	0.04
cg26130533	chr4:1202700	LOC100130 872-SPON2	TSS200	II	8.92E-06	0.12	6.42E-04	0.57	0.63	-0.06
cg05860371	chr4:152931291	-	-	II	9.10E-06	0.12	1.02E-03	0.63	0.69	-0.06
cg03363012	chr20:741049	C20orf54	3'UTR	II	9.22E-06	0.12	4.94E-04	0.84	0.81	0.03
cg21609813	chr8:22004881	LGI3	3'UTR	I	9.89E-06	0.12	6.72E-04	0.77	0.73	0.04
cg27608031	chr16:77353824	ADAMTS18	Body	II	1.00E-05	0.12	1.46E-04	0.73	0.68	0.04
cg21390682	chr13:113743751	MCF2L	Body	II	1.01E-05	0.12	1.13E-03	0.68	0.73	-0.05
cg27654476	chr14:77503345	-	-	II	1.03E-05	0.12	3.98E-04	0.64	0.68	-0.04
cg20930320	chr1:109852598	SORT1	3'UTR	II	1.04E-05	0.12	3.86E-05	0.59	0.64	-0.04
cg12864185	chr1:240160972	-	-	II	1.07E-05	0.12	4.22E-05	0.17	0.22	-0.05
cg13119928	chr12:53228661	KRT79	TSS1500	II	1.13E-05	0.12	4.67E-04	0.81	0.78	0.03
cg20681783	chr5:8839868	-	-	I	1.14E-05	0.12	1.04E-03	0.38	0.33	0.05
cg07114544	chr17:9110369	NTN1	Body	II	1.15E-05	0.12	4.55E-04	0.73	0.69	0.04
cg09419102	chr11:65550444	-	-	II	1.15E-05	0.12	4.70E-04	0.70	0.66	0.04
cg25778661	chr19:56031373	-	-	II	1.20E-05	0.12	1.04E-03	0.79	0.84	-0.05
cg13280041	chr6:138866865	NHSL1	Body	I	1.22E-05	0.12	1.38E-03	0.31	0.26	0.05
cg14772639	chr2:128711564	SAP130	Body	II	1.28E-05	0.12	1.22E-03	0.79	0.74	0.04
cg09942424	chr17:74913419	MGAT5B	Body	II	1.35E-05	0.12	1.46E-03	0.78	0.82	-0.04
cg04691233	chr11:133989435	JAM3	Body	II	1.37E-05	0.12	1.46E-03	0.84	0.80	0.04
cg07500432	chr18:77918588	PARD6G	Body	II	1.37E-05	0.12	1.15E-05	0.81	0.71	0.11
cg03991188	chr7:98870835	MYH16	TSS200	II	1.41E-05	0.12	6.29E-05	0.82	0.78	0.04
cg21843517	chr12:123950174	SNRNP35	Body	II	1.41E-05	0.12	1.23E-04	0.83	0.79	0.04
cg12198176	chr22:23415316	RTDR1	Body	II	1.46E-05	0.12	1.58E-03	0.63	0.68	-0.05
cg19643441	chr19:19417142	SF4	Body	II	1.53E-05	0.12	2.85E-04	0.80	0.83	-0.03
cg07289133	chr16:85147146	FAM92B	TSS1500	II	1.54E-05	0.12	1.30E-03	0.74	0.69	0.05
cg11945824	chr6:32116963	PRRT1	3'UTR	I	1.54E-05	0.12	1.24E-03	0.58	0.64	-0.06

cg20011075	chr1:4008090	-	-	I	1.69E-05	0.13	1.92E-03	0.62	0.69	-0.07
cg14752965	chr17:17579346	-	-	II	1.72E-05	0.13	1.88E-03	0.75	0.80	-0.05
cg07421682	chr15:102030850	PCSK6	TSS1500	II	1.81E-05	0.13	1.94E-03	0.76	0.82	-0.05
cg22697364	chr5:32709859	-	-	II	1.85E-05	0.13	1.67E-03	0.26	0.22	0.04
cg25790133	chr4:2627014	FAM193A	TSS200	II	1.89E-05	0.13	2.06E-03	0.51	0.57	-0.06
cg10622536	chr1:36771021	C1orf113	TSS1500	II	1.90E-05	0.13	1.81E-03	0.77	0.81	-0.04
cg01936649	chr6:164062746	-	-	II	1.92E-05	0.13	1.85E-03	0.76	0.82	-0.06
cg07665929	chr5:171523225	STK10	Body	II	1.97E-05	0.13	2.23E-03	0.59	0.66	-0.07
cg21375204	chr7:73752935	CLIP2	Body	I	2.02E-05	0.13	2.19E-03	0.75	0.80	-0.05
cg23203234	chr8:103751623	-	-	II	2.02E-05	0.13	2.01E-03	0.71	0.76	-0.05
cg04215055	chr17:74911520	MGAT5B	Body	I	2.03E-05	0.13	2.12E-03	0.65	0.71	-0.06
cg06168875	chr19:13988438	NANOS3	1stExon	II	2.06E-05	0.13	4.21E-04	0.76	0.82	-0.06
cg24079702	chr2:106015771	FHL2	TSS200	I	2.08E-05	0.13	1.80E-03	0.17	0.21	-0.04
cg25900150	chr8:144601851	ZC3H3	Body	I	2.11E-05	0.13	1.84E-04	0.81	0.89	-0.07
cg27097992	chr14:104800950	-	-	I	2.15E-05	0.14	2.44E-03	0.66	0.54	0.12
cg22060153	chr2:101889653	SNORD89	TSS200	II	2.22E-05	0.14	4.21E-04	0.68	0.72	-0.04
cg23996071	chr1:60280809	HOOK1	1stExon	II	2.25E-05	0.14	4.48E-04	0.18	0.22	-0.04
cg07815131	chr6:99289733	-	-	II	2.27E-05	0.14	2.17E-04	0.39	0.44	-0.06
cg05583087	chr3:12894947	-	-	II	2.30E-05	0.14	2.65E-03	0.46	0.51	-0.06
cg03724006	chr11:62790783	-	-	II	2.36E-05	0.14	2.66E-03	0.48	0.54	-0.06
cg10535500	chr6:33398610	SYNGAP1	Body	II	2.39E-05	0.14	4.76E-04	0.43	0.47	-0.04
cg09235936	chr2:242170211	HDLBP	Body	I	2.41E-05	0.14	2.73E-03	0.68	0.74	-0.06
cg12473775	chr11:66824650	RHOD	Body	II	2.48E-05	0.14	3.09E-04	0.72	0.68	0.04
cg27252696	chr6:100912940	SIM1	TSS1500	I	2.51E-05	0.14	8.59E-05	0.07	0.09	-0.01
cg00172872	chr12:89461426	-	-	II	2.60E-05	0.14	2.42E-03	0.77	0.82	-0.04
cg07780199	chr19:18830892	CRTC1	Body	II	2.69E-05	0.14	3.06E-03	0.73	0.77	-0.05
cg19671331	chr8:143509438	-	-	I	2.70E-05	0.14	2.13E-03	0.72	0.80	-0.08
cg26925590	chr16:139752	C16orf35	Body	I	2.73E-05	0.14	1.43E-03	0.85	0.90	-0.05
cg02064366	chr17:79045526	BAIAP2	Body	I	2.79E-05	0.14	3.20E-03	0.62	0.67	-0.05
cg17244485	chr2:103443515	-	-	II	2.83E-05	0.14	1.58E-03	0.38	0.32	0.05

cg23236908	chr14:55819305	FBXO34	3'UTR	II	2.89E-05	0.14	3.26E-03	0.77	0.81	-0.04
cg03962217	chr7:154796431	LOC202781	Body	II	2.90E-05	0.14	1.64E-03	0.65	0.69	-0.05
cg17356733	chr21:34774627	IFNGR2	TSS1500	II	2.93E-05	0.14	3.33E-03	0.64	0.70	-0.06
cg16040341	chr15:83544284	HOMER2	Body	II	2.93E-05	0.14	2.13E-03	0.69	0.75	-0.05
cg24038762	chr1:87817476	-	-	II	2.95E-05	0.14	3.40E-03	0.73	0.77	-0.04
cg05529091	chr12:111475875	CUX2	Body	II	2.99E-05	0.14	3.25E-03	0.65	0.70	-0.05
cg05374733	chr12:42853791	PRICKLE1	Body	II	3.00E-05	0.14	7.73E-06	0.80	0.83	-0.03
cg06746318	chr7:101755186	CUX1	Body	I	3.04E-05	0.14	3.45E-03	0.70	0.76	-0.06
cg08404546	chr22:37910993	CARD10	Body	II	3.07E-05	0.14	5.98E-04	0.76	0.82	-0.05
cg14905600	chr10:134226361	PWWP2B	3'UTR	I	3.07E-05	0.14	1.13E-03	0.75	0.81	-0.06
cg10976478	chr2:241263838	-	-	II	3.20E-05	0.14	3.59E-06	0.84	0.80	0.04
cg21399807	chr2:54955581	EML6	Body	II	3.22E-05	0.14	2.58E-03	0.74	0.78	-0.04
cg21776682	chr8:1387801	-	-	II	3.22E-05	0.14	3.73E-03	0.68	0.73	-0.05
cg26593722	chr16:87376314	FBXO31	Body	I	3.28E-05	0.14	1.37E-03	0.80	0.85	-0.05
cg04543233	chr20:21689105	PAX1	Body	II	3.30E-05	0.14	6.38E-04	0.16	0.19	-0.04
cg06614697	chr1:3696285	-	-	II	3.32E-05	0.14	3.90E-04	0.62	0.67	-0.05

[1] Guintivano, J., Aryee, M. J. & Kaminsky, Z. A. *Epigenetics* 8, 290-302,(2013).

SUPPLEMENTARY TABLE 5 – 100 top-ranked schizophrenia-associated DMPs in the cerebellum. The CETS algorithm[1] was used to correct for the potential effect of differential neuronal cell proportions across samples.
TSS=Transcription start site; UTR=Untranslated region, SZ=schizophrenia.

Probe ID	Genomic position (hg19)	Gene	Gene region	Probe type	*P*	FDR	CETS-adjusted *P*	Mean SZ	Mean Control	Beta difference
cg05695876	chr1:201665422	NAV1	Body	II	1.87E-07	0.08	2.88E-07	0.12	0.17	-0.04
cg05388069	chr16:3284378	ZNF200	5'UTR	II	6.26E-06	0.97	9.91E-06	0.65	0.59	0.07
cg07208077	chr12:11081755	PRH2	TSS200	II	1.06E-05	0.97	2.18E-05	0.84	0.79	0.04
cg13941830	chr1:50891341	-	-	II	1.18E-05	0.97	1.81E-05	0.29	0.22	0.06
cg00560072	chr1:61750543	NFIA	Body	II	1.35E-05	0.97	3.72E-05	0.25	0.29	-0.04
cg13299148	chr1:32170433	COL16A1	TSS1500	II	1.72E-05	0.97	4.19E-05	0.84	0.77	0.07
cg05922563	chr17:40611593	ATP6V0A1	5'UTR	II	1.91E-05	0.97	5.83E-05	0.10	0.12	-0.02
cg01655427	chr4:109091059	LEF1	TSS1500	II	2.02E-05	0.97	2.35E-05	0.27	0.32	-0.05
cg07236939	chr6:110722253	DDO	Body	II	2.12E-05	0.97	5.19E-05	0.89	0.86	0.03
cg16487621	chr6:29395657	OR11A1	TSS200	II	2.26E-05	0.97	4.44E-05	0.89	0.86	0.04
cg15686782	chr7:2143886	MAD1L1	Body	II	2.65E-05	0.99	7.89E-05	0.83	0.78	0.05
cg00499539	chr2:113960266	PSD4	3'UTR	II	2.83E-05	0.99	8.32E-05	0.67	0.61	0.06
cg20863949	chr2:71213618	TEX261	3'UTR	II	3.10E-05	0.99	3.29E-05	0.82	0.75	0.06
cg19895047	chr8:19460197	CSGALNACT1	TSS200	II	3.37E-05	0.99	9.44E-05	0.24	0.28	-0.04
cg22240880	chr17:7466821	SENP3	Body	I	3.47E-05	0.99	9.64E-05	0.80	0.76	0.04
cg14213430	chr7:157190333	DNAJB6	Body	II	4.12E-05	1	1.06E-04	0.17	0.23	-0.06
cg18163452	chr1:63466707	-	-	II	4.24E-05	1	7.50E-05	0.69	0.76	-0.07
cg05187193	chr6:168397037	-	-	II	4.32E-05	1	9.33E-05	0.79	0.70	0.09
cg16239296	chr15:83736925	BTBD1	TSS1500	II	5.46E-05	1	3.31E-05	0.88	0.85	0.03
cg22849543	chr20:46997755	LOC284749	Body	II	5.46E-05	1	1.46E-04	0.12	0.15	-0.02
cg03506193	chr8:104033864	ATP6V1C1	5'UTR	II	5.52E-05	1	1.06E-04	0.31	0.38	-0.08
cg25836061	chr22:19939028	COMT	5'UTR	I	5.65E-05	1	1.51E-04	0.13	0.19	-0.06
cg19421752	chr5:1225224	SLC6A19	3'UTR	II	5.83E-05	1	1.42E-04	0.76	0.81	-0.05
cg02398342	chr17:80708632	TBCD	TSS1500	II	6.25E-05	1	4.25E-05	0.72	0.59	0.13
cg14044120	chr9:139949577	ENTPD2	TSS1500	II	6.56E-05	1	8.69E-05	0.82	0.79	0.03

cg02294302	chr1:47906276	FOXD2	3'UTR	II	7.23E-05	1	1.13E-04	0.76	0.71	0.05
cg23466059	chr18:56422682	-	-	II	7.27E-05	1	1.78E-04	0.11	0.15	-0.04
cg21196747	chr6:27521385	-	-	II	7.42E-05	1	2.05E-04	0.16	0.21	-0.05
cg12728623	chr22:19938992	COMT	5'UTR	II	7.79E-05	1	1.30E-04	0.13	0.19	-0.06
cg06855567	chr4:177117009	SPATA4	TSS200	II	8.29E-05	1	1.51E-04	0.12	0.15	-0.03
cg03812681	chr6:1397366	-	-	II	8.37E-05	1	1.85E-04	0.20	0.23	-0.03
cg03916014	chr16:1722352	CRAMP1L	Body	II	8.54E-05	1	9.53E-05	0.87	0.82	0.05
cg17381305	chr6:133226489	-	-	II	8.64E-05	1	1.29E-04	0.78	0.73	0.05
cg15384717	chr1:150294084	PRPF3	5'UTR	II	9.22E-05	1	1.31E-04	0.17	0.19	-0.02
cg16671988	chr7:148963796	ZNF783	Body	II	9.76E-05	1	8.23E-05	0.82	0.78	0.04
cg17468663	chr1:19048930	PAX7	Body	II	9.81E-05	1	1.43E-04	0.86	0.83	0.03
cg02048613	chr2:161343862	RBMS1	Body	II	1.01E-04	1	1.81E-04	0.73	0.78	-0.06
cg13137809	chr7:2768988	GNA12	3'UTR	I	1.02E-04	1	2.97E-04	0.82	0.78	0.04
cg09890930	chr12:56149396	SARNP	Body	II	1.03E-04	1	2.67E-04	0.68	0.74	-0.06
cg02283487	chr14:20904020	KLHL33	TSS1500	II	1.05E-04	1	3.03E-04	0.67	0.61	0.06
cg18951674	chr11:93641499	-	-	I	1.13E-04	1	2.63E-04	0.92	0.94	-0.02
cg01758993	chr20:44993436	SLC35C2	TSS1500	II	1.14E-04	1	7.03E-05	0.19	0.23	-0.04
cg18308233	chr11:120470179	-	-	II	1.19E-04	1	2.53E-04	0.87	0.83	0.04
cg03723001	chr12:117147681	-	-	II	1.21E-04	1	3.52E-04	0.22	0.28	-0.06
cg04162223	chr13:114164207	TMCO3	Body	II	1.23E-04	1	3.62E-04	0.68	0.65	0.03
cg11947857	chr19:1411919	DAZAP1	Body	II	1.24E-04	1	2.50E-04	0.09	0.11	-0.02
cg06841648	chr16:85479053	-	-	II	1.26E-04	1	2.15E-04	0.15	0.19	-0.04
cg23667707	chr7:152569949	-	-	I	1.27E-04	1	1.30E-04	0.87	0.90	-0.03
cg25240172	chr2:62435157	B3GNT2	5'UTR	II	1.28E-04	1	2.47E-04	0.84	0.83	0.02
cg26894575	chr1:153518054	S100A4	5'UTR	II	1.29E-04	1	5.40E-05	0.71	0.67	0.04
cg07438586	chr6:30509366	GNL1	3'UTR	II	1.29E-04	1	3.60E-04	0.15	0.19	-0.04
cg06637938	chr14:75390232	RPS6KL1	TSS1500	I	1.31E-04	1	5.27E-05	0.18	0.22	-0.04
cg26108046	chr3:183535040	MAP6D1	3'UTR	II	1.32E-04	1	2.04E-04	0.15	0.20	-0.05
cg02765496	chr9:71393662	FAM122A	TSS1500	II	1.42E-04	1	4.08E-04	0.68	0.64	0.04

cg23729107	chr17:6679264	FBXO39	TSS1500	I	1.44E-04	1	3.62E-04	0.06	0.05	0.01
cg17009978	chr3:183959000	VWA5B2	Body	II	1.48E-04	1	4.25E-04	0.75	0.71	0.04
cg19248564	chr22:43042879	CYB5R3	5'UTR	II	1.50E-04	1	2.52E-04	0.13	0.16	-0.03
cg16046505	chr1:246582116	SMYD3	Body	II	1.51E-04	1	4.11E-04	0.20	0.23	-0.04
cg20751795	chr19:58281019	ZNF586	TSS200	I	1.64E-04	1	2.59E-04	0.06	0.06	0.01
cg11481687	chr14:105499998	-	-	I	1.68E-04	1	4.46E-04	0.26	0.31	-0.05
cg00102266	chr1:121429834	-	-	II	1.68E-04	1	2.23E-04	0.85	0.82	0.03
cg07062338	chr10:123301036	FGFR2	Body	II	1.79E-04	1	7.14E-05	0.78	0.74	0.04
cg00390784	chr6:2682491	MYLK4	Body	II	1.81E-04	1	2.39E-04	0.86	0.89	-0.03
cg13600257	chr6:170449417	-	-	II	1.93E-04	1	1.83E-04	0.16	0.19	-0.03
cg18003751	chr8:1350552	-	-	II	1.93E-04	1	5.09E-04	0.81	0.84	-0.03
cg11571585	chr13:28365638	GSX1	TSS1500	II	1.95E-04	1	9.09E-05	0.08	0.10	-0.02
cg10380652	chr1:65612850	AK3L1	TSS1500	II	1.96E-04	1	2.66E-04	0.13	0.17	-0.04
cg15613100	chr5:72804620	-	-	II	1.96E-04	1	5.24E-04	0.78	0.73	0.05
cg26125384	chr2:70314274	PCBP1	TSS1500	I	1.96E-04	1	4.49E-04	0.14	0.17	-0.02
cg27650870	chr8:41583136	ANK1	Body	II	2.00E-04	1	3.44E-04	0.68	0.63	0.05
cg15827217	chr1:21833476	-	-	II	2.00E-04	1	3.58E-04	0.88	0.85	0.03
cg00688979	chr6:31113017	CCHCR1	Body	II	2.02E-04	1	5.73E-04	0.82	0.79	0.03
cg24744258	chr17:40939380	WNK4	Body	II	2.10E-04	1	2.13E-04	0.65	0.74	-0.09
cg00363312	chr7:139333296	HIPK2	Body	II	2.16E-04	1	4.58E-04	0.84	0.79	0.05
ch.16.725323R	chr16:23535908	EARS2	Body	II	2.20E-04	1	2.01E-04	0.16	0.20	-0.04
cg12304482	chr15:28377846	HERC2	Body	I	2.27E-04	1	2.67E-04	0.90	0.87	0.03
cg13917151	chr1:27730185	-	-	II	2.33E-04	1	5.55E-04	0.69	0.65	0.04
cg02997111	chr19:41698906	CYP2S1	TSS1500	II	2.38E-04	1	5.22E-05	0.08	0.10	-0.02
cg17089179	chr2:42990647	OXER1	1stExon	I	2.39E-04	1	8.39E-05	0.92	0.87	0.05
cg02288001	chr5:111496931	NCRNA00219	Body	II	2.39E-04	1	6.38E-04	0.12	0.14	-0.02
cg26020521	chr11:8680436	TRIM66	TSS200	II	2.47E-04	1	5.37E-04	0.16	0.22	-0.05
cg27033923	chr15:41106683	ZFYVE19	3'UTR	II	2.55E-04	1	5.42E-04	0.89	0.87	0.03
cg01169396	chr5:179372900	-	-	II	2.61E-04	1	4.14E-04	0.78	0.83	-0.05

cg07128326	chr7:973490	ADAP1	Body	II	2.62E-04	1	1.44E-04	0.81	0.84	-0.02
cg00310412	chr15:74724918	SEMA7A	Body	II	2.68E-04	1	7.61E-04	0.16	0.20	-0.05
cg23636406	chr17:12622228	MYOCD	Body	II	2.80E-04	1	6.56E-04	0.72	0.68	0.03
cg26999345	chr22:37584441	C1QTNF6	TSS200	II	2.81E-04	1	5.67E-04	0.64	0.58	0.07
cg01178486	chr5:68664852	TAF9	Body	II	2.81E-04	1	1.17E-04	0.12	0.15	-0.02
cg03290560	chr3:117774686	-	-	II	3.05E-04	1	1.27E-04	0.85	0.88	-0.03
cg05767562	chr17:76227422	LOC283999	5'UTR	II	3.06E-04	1	8.45E-04	0.64	0.59	0.05
cg21828899	chr17:79980823	LRRC45	TSS1500	I	3.10E-04	1	7.55E-04	0.07	0.08	-0.01
cg01000937	chr14:30730636	-	-	I	3.10E-04	1	6.41E-04	0.84	0.87	-0.03
cg01325465	chr16:85123554	KIAA0513	3'UTR	II	3.16E-04	1	7.66E-04	0.19	0.23	-0.05
cg10930101	chr17:62085466	ICAM2	TSS1500	II	3.18E-04	1	6.17E-04	0.87	0.85	0.02
cg11070176	chr11:70489806	SHANK2	Body	II	3.18E-04	1	2.46E-04	0.68	0.61	0.07
cg17170741	chr17:17942558	ATPAF2	TSS200	I	3.19E-04	1	6.20E-04	0.09	0.10	-0.01
cg14374521	chr10:124638874	FAM24B	5'UTR	I	3.21E-04	1	2.26E-04	0.24	0.16	0.08
cg21041329	chr8:56686126	TMEM68	TSS1500	I	3.22E-04	1	5.45E-04	0.09	0.10	-0.01
cg16818361	chr3:118792317	IGSF11	Body	II	3.24E-04	1	3.89E-04	0.90	0.88	0.02
cg15589582	chr3:5261136	EDEM1	3'UTR	II	3.25E-04	1	5.54E-04	0.41	0.50	-0.09

[1] Guintivano, J., Aryee, M. J. & Kaminsky, Z. A. *Epigenetics* 8, 290-302,(2013).

SUPPLEMENTARY TABLE 6 - List of differentially methylated regions (FDR<0.05) in the prefrontal cortex. Regions are annotated with genomic position (hg19, GRCh37), nearest gene and number of probes.

Genomic Region	Gene	Probes	Beta Difference	Mean SZ	Mean control	p-value	FDR
Gene body							
chr12:101342113-101480470	ANO4	8	0.02	0.65	0.63	3.92E-06	3.07E-02
chr6:5999266-6006917	NRN1	29	-0.02	0.24	0.26	8.28E-06	3.07E-02
chr8:38125449-38126556	PPAPDC1B	5	-0.01	0.16	0.17	2.65E-06	3.07E-02
chr9:130830948-130868874	NAIF1	9	-0.03	0.39	0.42	5.10E-06	3.07E-02
chr19:36266840-36269387	SNX26	2	-0.03	0.44	0.47	6.85E-06	3.07E-02
chr14:77296234-77335130	C14orf166B	6	0.02	0.68	0.66	1.23E-05	3.25E-02
chr19:6414982-6424217	KHSRP	7	-0.02	0.58	0.61	1.06E-05	3.25E-02
chr14:24550845-24551147	NRL	3	-0.02	0.23	0.25	1.40E-05	3.26E-02
chr15:85361858-85383124	ALPK3	6	0.01	0.74	0.73	1.88E-05	3.88E-02
chr3:44397397-44397397	C3orf23	1	-0.07	0.58	0.66	2.71E-05	4.19E-02
chr8:30556362-30583924	GSR	4	-0.02	0.71	0.73	2.49E-05	4.19E-02
chr9:137967652-138011814	OLFM1	24	-0.02	0.51	0.53	2.31E-05	4.19E-02
Island							
chr10:101287381-101287846		5	-0.02	0.16	0.18	3.61E-06	4.28E-02
chr13:114806955-114807060	RASA3	2	-0.07	0.62	0.69	2.80E-06	4.28E-02
chr14:24550395-24551147	NRL	4	-0.02	0.19	0.21	4.86E-06	4.28E-02
North Shelf							
chr19:47204096-47204096	PRKD2	1	-0.04	0.67	0.71	9.50E-07	9.35E-03
chr22:29873338-29873338		1	-0.06	0.56	0.62	1.13E-06	9.35E-03
chr14:105235891-105236654	AKT1	4	-0.03	0.53	0.56	2.90E-06	9.86E-03
chr17:65037838-65037838		1	0.04	0.78	0.74	2.97E-06	9.86E-03
chr19:6421149-6421747	KHSRP	2	-0.03	0.57	0.61	2.56E-06	9.86E-03
chr7:5518071-5518918	FBXL18	4	-0.04	0.54	0.58	1.48E-05	4.09E-02
North Shore							
chr6:6000601-6001842	NRN1	3	-0.04	0.66	0.7	9.90E-07	2.38E-02
chr20:741049-741049	C20orf54	1	0.03	0.84	0.81	4.30E-06	3.65E-02
chr4:1201492-1202930	LOC100130872	15	-0.03	0.54	0.57	6.08E-06	3.65E-02
chr8:38125449-38126029	PPAPDC1B	3	-0.02	0.21	0.24	4.59E-06	3.65E-02
chr14:23289114-23290798	SLC7A7	5	0.02	0.73	0.72	1.56E-05	4.16E-02
chr15:42839559-42840397	LRRC57	2	-0.02	0.45	0.46	1.29E-05	4.16E-02
chr2:237079122-237079967		5	-0.03	0.28	0.31	1.53E-05	4.16E-02
chr8:30583924-30583924	GSR	1	-0.06	0.62	0.68	1.18E-05	4.16E-02
chr9:130964374-130964374	CIZ1	1	-0.04	0.61	0.65	1.45E-05	4.16E-02

South Shelf							
chr14:77503345-77503345		1	-0.04	0.64	0.68	3.12E-06	4.86E-02
TSS1500							
chr17:46692534-46693336	HOXB8	4	-0.02	0.24	0.27	2.20E-06	4.41E-02
TSS200							
chr4:2627014-2627142	FAM193A	4	-0.04	0.5	0.53	1.17E-07	2.02E-03
UTR'3							
chr14:105235891-105236654	AKT1	4	-0.03	0.53	0.56	2.91E-06	1.17E-02
chr1:57383752-57383752	C8A	1	0.03	0.82	0.79	2.18E-06	1.17E-02
chr1:109852598-109852598	SORT1	1	-0.04	0.59	0.64	1.37E-06	1.17E-02
chr20:741049-741049	C20orf54	1	0.03	0.84	0.81	5.62E-06	1.69E-02
chr14:55819305-55819305	FBXO34	1	-0.04	0.77	0.81	7.46E-06	1.79E-02
chr17:695428-695661	RNMTL1	2	-0.04	0.64	0.69	9.13E-06	1.83E-02
chr19:55670288-55670288	C19orf51	1	-0.04	0.72	0.76	3.66E-05	4.65E-02
chr11:85630744-85630744	CCDC83	1	0.05	0.69	0.64	4.25E-05	4.65E-02
chr20:36151184-36151683	BLCAP	3	-0.02	0.61	0.63	4.22E-05	4.65E-02
chr14:23794739-23794739	PABPN1	1	-0.04	0.73	0.77	3.09E-05	4.65E-02
chr2:38970936-38970936	SFRS7	1	-0.06	0.7	0.76	3.17E-05	4.65E-02

SUPPLEMENTARY TABLE 7 – Bisulfite-pyrosequencing primers used in validation assays.

450K probe		**Gene**	**PCR Primers (5'-3')**	**Sequence analyzed (5'-3')**
Probe ID	**Genomic position (hg19)**			
cg00565348	chr6:6003303	*NRN1*	F: ATTGTTGGTGGTTTTTAGGGATTATAT R: Biot-ACACTTCCCCAACAAACCCTATCA S: GTTTATTTATTTAGTAGTGTTTG	TTGAGYGTTTATTAAGGATAGAGYGTTAAGTTTGAGGTTTATTTT
cg23844013	chr1:57383752	*C8A*	F: AGGGAGAATTTATAGGATGTTAGAG R: Biot-CAAAATATCTACTTACCCTACCAATTAA S: GAGATAAAATAAGTAGATATTTGAA	ATAATTAAYGTTTAATAAAATAAAGTAGGATGAAAATTTTTT
cg24803255	chr13:114807060	*RASA3*	F: TTGTTTTGGTGGTGTGTGAG R: Biot-ACTAACTACACCAAAACTCTAATCT S: TGGTGGTGTGTGAGG	TAYGGGGTGTTTATTTGTGAGATTAGAGT

SUPPLEMENTARY TABLE 8 – Technical validation of disease associated DNA methylation at CpG sites in the *C8A, NRN1* and *RASA3* genes. *T-test values from the pyrosequencing analysis are from a one-sided test. Pyro=pyrosequencing.

	C8A (cg23844013)		***NRN1* CpG1** (cg00565348)		***NRN1* CpG2**		***RASA3*** (cg24803255)	
	450K	***Pyro***	***450K***	***Pyro***	***450K***	***Pyro***	***450K***	***Pyro***
SZ DNA methylation (%) (mean±sd)	82.1±1.6	82.2±1.8	35.1 ±2.2	31.6±4.1	-	32.8±4.0	56.4±4.1	66.4±3.2
Control DNA methylation (%) (mean±sd)	79.4±1.6	81.2±1.7	38.7±2.6	33.3±4.6	-	35.0±4.1	65.1±4.7	70.5±3.7
Mean difference DNA methylation (%) (SZ - Control)	2.7	0.9	-3.5	-1.9	-	-2.7	-8.7	-4.0
T-test t-statistic	5.61	1.84	-4.85	-1.19	-	-1.74	-6.44	-3.83
T-test P-value*	1.67e-06	0.04	1.81e-05	0.12	-	0.04	1.03e-07	2.16e-04

SUPPLEMENTARY TABLE 9 – Details of post-mortem brain samples from Douglas Mental Health University Institute Research Centre. Schizophrenia cases and controls do not significantly differ for any of the available quality metrics (t-test p-value>0.05). SZ=schizophrenia.

	SZ	Control	Total	p-value
Number	18	15	33	
Sex (male:female)	15:3	13:2	28:5	
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

SUPPLEMENTARY TABLE 10 – Details of individual post-mortem brain samples samples from Douglas Mental Health University Institute Research Centre. NA=not available.

ID	Sex	Age at death (years)	Total brain weight (g)	pH
Schizophrenia				
MS01	M	70	1280	6.01
MS02	F	73	NA	6.16
MS03	M	30	1321	6.42
MS04	F	60	1175	6.23
MS05	F	51	1125	6.35
MS06	M	50	1615	6.55
MS07	M	29	1520	6.27
MS08	M	24	NA	6.01
MS09	M	69	1295	6.23
MS10	M	38	1550	6.32
MS11	M	39	1680	6.16
MS12	M	47	1516	5.76
MS13	M	65	1320	6.27
MS14	M	26	1430	6.44
MS15	M	29	NA	6.52
MS16	M	33	1812	5.92
MS17	M	32	1408	6.05
MS18	M	54	1430	6.47
Control				
MS19	F	57	1250	5.73
MS20	M	57	1400	5.72
MS21	F	50	1205	6.10
MS22	M	43	1343	6.25
MS23	M	44	1375	5.41
MS24	M	28	1565	6.59
MS25	M	26	1749	6.43
MS26	M	30	1517	6.22
MS27	M	37	1491	6.21
MS28	M	41	1430	5.89
MS29	M	33	1670	6.34
MS30	M	66	1260	6.09
MS31	M	21	1783	6.27
MS32	M	32	1516	6.49
MS33	M	69	1390	6.04

SUPPLEMENTARY TABLE 11 – DNA methylation data from the Montreal dataset matching the 100 top-ranked schizophrenia-associated DMPs from the LBBND prefrontal cortex dataset. DNA methylation differences at these loci are significantly correlated across datasets (r=0.54, p=6.8e-09, see **Figure 1c**).

Probe ID	Genomic position (hg19)	Gene	Gene region	London Mean SZ	London Mean Control	London Beta difference	Montreal Mean SZ	Montreal Mean Control	Montreal Beta difference
cg26173173	chr8:144642813	GSDMD	Body	0.83	0.79	0.04	0.79	0.77	0.02
cg24803255	chr13:114807060	RASA3	Body	0.56	0.65	-0.09	0.61	0.65	-0.04
cg00903099	chr7:154862441	HTR5A	TSS200	0.09	0.12	-0.02	0.09	0.09	0.00
cg08171022	chr11:70185278	PPFIA1	Body	0.48	0.53	-0.05	0.47	0.48	-0.01
cg02857643	chr17:48696108	CACNA1G	Body	0.87	0.92	-0.05	0.94	0.92	0.01
cg00236305	chr2:1796076	MYT1L	Body	0.67	0.73	-0.06	0.69	0.71	-0.02
cg14966346	chr14:104152124	KLC1	Body	0.72	0.77	-0.05	0.73	0.74	-0.01
cg13079528	chr7:4027346	SDK1	Body	0.71	0.79	-0.08	0.81	0.83	-0.02
cg14429765	chr8:6492531	MCPH1	Body	0.79	0.76	0.03	0.74	0.73	0.01
cg08602214	chr8:22864392	RHOBTB2	Body	0.69	0.75	-0.07	0.77	0.78	-0.01
cg19735533	chr2:241196887			0.76	0.81	-0.06	0.77	0.76	0.02
cg09507608	chr22:29873338			0.56	0.62	-0.06	0.56	0.58	-0.02
cg23844013	chr1:57383752	C8A	3'UTR	0.82	0.79	0.03	0.78	0.79	-0.01
cg26578910	chr19:47204096	PRKD2	Body	0.67	0.71	-0.04	0.73	0.75	-0.02
cg21847368	chr13:113744010	MCF2L	Body	0.80	0.84	-0.03	0.81	0.81	0.00
cg03607729	chr16:25138698	LCMT1	Body	0.70	0.75	-0.04	0.69	0.69	0.00
cg10248981	chr10:126157948	LHPP	Body	0.55	0.63	-0.07	0.61	0.64	-0.03
cg03445663	chr2:242170236	HDLBP	Body	0.51	0.59	-0.08	0.60	0.63	-0.03
cg15079231	chr3:42572745	VIPR1	Body	0.76	0.80	-0.04	0.74	0.76	-0.02
cg21341878	chr4:2278462	ZFYVE28	Body	0.75	0.81	-0.05	0.80	0.81	-0.01
cg04922803	chr12:104444418	GLT8D2	TSS1500	0.68	0.62	0.06	0.59	0.59	0.00
cg18857062	chr6:43276478	CRIP3	Body	0.21	0.26	-0.04	0.23	0.25	-0.02
cg27138871	chr11:74950396			0.75	0.79	-0.05	0.78	0.79	-0.02
cg27363226	chr19:6421747	KHSRP	Body	0.62	0.67	-0.05	0.65	0.66	-0.01
cg02187259	chr2:16804452	FAM49A	5'UTR	0.74	0.79	-0.05	0.75	0.77	-0.02
cg26182253	chr13:112236782			0.60	0.67	-0.06	0.65	0.68	-0.02

cg14370653	chr9:137828210			0.75	0.80	-0.05	0.77	0.77	0.01
cg14527262	chr4:1202653	LOC100130872-SPON2	TSS200	0.56	0.63	-0.07	0.68	0.72	-0.04
cg16393877	chr17:65037838			0.78	0.74	0.04	0.72	0.72	0.01
cg26130533	chr4:1202700	LOC100130872-SPON2	TSS200	0.57	0.63	-0.06	0.58	0.58	0.00
cg05860371	chr4:152931291			0.63	0.69	-0.06	0.65	0.67	-0.02
cg03363012	chr20:741049	C20orf54	3'UTR	0.84	0.81	0.03	0.79	0.77	0.02
cg21609813	chr8:22004881	LGI3	3'UTR	0.77	0.73	0.04	0.75	0.73	0.02
cg27608031	chr16:77353824	ADAMTS18	Body	0.73	0.68	0.04	0.64	0.62	0.02
cg21390682	chr13:113743751	MCF2L	Body	0.68	0.73	-0.05	0.65	0.65	0.00
cg27654476	chr14:77503345			0.64	0.68	-0.04	0.61	0.62	-0.01
cg20930320	chr1:109852598	SORT1	3'UTR	0.59	0.64	-0.04	0.57	0.58	-0.01
cg12864185	chr1:240160972			0.17	0.22	-0.05	0.15	0.16	-0.01
cg13119928	chr12:53228661	KRT79	TSS1500	0.81	0.78	0.03	0.76	0.76	0.00
cg20681783	chr5:8839868			0.38	0.33	0.05	0.32	0.33	-0.01
cg07114544	chr17:9110369	NTN1	Body	0.73	0.69	0.04	0.70	0.69	0.01
cg09419102	chr11:65550444			0.70	0.66	0.04	0.66	0.65	0.01
cg25778661	chr19:56031373			0.79	0.84	-0.05	0.79	0.80	-0.01
cg13280041	chr6:138866865	NHSL1	Body	0.31	0.26	0.05	0.27	0.25	0.03
cg14772639	chr2:128711564	SAP130	Body	0.79	0.74	0.04	0.74	0.72	0.02
cg09942424	chr17:74913419	MGAT5B	Body	0.78	0.82	-0.04	0.79	0.79	0.00
cg04691233	chr11:133989435	JAM3	Body	0.84	0.80	0.04	0.77	0.77	0.01
cg07500432	chr18:77918588	PARD6G	Body	0.81	0.71	0.11	0.82	0.80	0.02
cg03991188	chr7:98870835	MYH16	TSS200	0.82	0.78	0.04	0.79	0.78	0.02
cg21843517	chr12:123950174	SNRNP35	Body	0.83	0.79	0.04	0.79	0.76	0.02
cg12198176	chr22:23415316	RTDR1	Body	0.63	0.68	-0.05	0.67	0.67	0.00
cg19643441	chr19:19417142	SF4	Body	0.80	0.83	-0.03	0.81	0.82	-0.01
cg07289133	chr16:85147146	FAM92B	TSS1500	0.74	0.69	0.05	0.66	0.66	0.00
cg11945824	chr6:32116963	PRRT1	3'UTR	0.58	0.64	-0.06	0.69	0.70	0.00
cg20011075	chr1:4008090			0.62	0.69	-0.07	0.76	0.76	0.00
cg14752965	chr17:17579346			0.75	0.80	-0.05	0.79	0.77	0.01
cg07421682	chr15:102030850	PCSK6	TSS1500	0.76	0.82	-0.05	0.80	0.80	0.00

cg22697364	chr5:32709859			0.26	0.22	0.04	0.16	0.17	-0.01
cg25790133	chr4:2627014	FAM193A	TSS200	0.51	0.57	-0.06	0.53	0.56	-0.03
cg10622536	chr1:36771021	C1orf113	TSS1500	0.77	0.81	-0.04	0.77	0.80	-0.03
cg01936649	chr6:164062746			0.76	0.82	-0.06	0.81	0.81	0.00
cg07665929	chr5:171523225	STK10	Body	0.59	0.66	-0.07	0.63	0.64	-0.02
cg21375204	chr7:73752935	CLIP2	Body	0.75	0.80	-0.05	0.86	0.88	-0.02
cg23203234	chr8:103751623			0.71	0.76	-0.05	0.73	0.74	-0.01
cg04215055	chr17:74911520	MGAT5B	Body	0.65	0.71	-0.06	0.74	0.74	0.00
cg06168875	chr19:13988438	NANOS3	1stExon	0.76	0.82	-0.06	0.82	0.81	0.01
cg24079702	chr2:106015771	FHL2	TSS200	0.17	0.21	-0.04	0.12	0.10	0.01
cg25900150	chr8:144601851	ZC3H3	Body	0.81	0.89	-0.07	0.90	0.91	-0.01
cg27097992	chr14:104800950			0.66	0.54	0.12	0.61	0.61	0.00
cg22060153	chr2:101889653	SNORD89	TSS200	0.68	0.72	-0.04	0.65	0.66	-0.01
cg23996071	chr1:60280809	HOOK1	1stExon	0.18	0.22	-0.04	0.15	0.16	-0.01
cg07815131	chr6:99289733			0.39	0.44	-0.06	0.44	0.44	0.00
cg05583087	chr3:12894947			0.46	0.51	-0.06	0.47	0.49	-0.02
cg03724006	chr11:62790783			0.48	0.54	-0.06	0.50	0.52	-0.03
cg10535500	chr6:33398610	SYNGAP1	Body	0.43	0.47	-0.04	0.38	0.41	-0.02
cg09235936	chr2:242170211	HDLBP	Body	0.68	0.74	-0.06	0.77	0.80	-0.03
cg12473775	chr11:66824650	RHOD	Body	0.72	0.68	0.04	0.66	0.66	-0.01
cg27252696	chr6:100912940	SIM1	TSS1500	0.07	0.09	-0.01	0.05	0.05	0.00
cg00172872	chr12:89461426			0.77	0.82	-0.04	0.77	0.78	-0.02
cg07780199	chr19:18830892	CRTC1	Body	0.73	0.77	-0.05	0.70	0.71	0.00
cg19671331	chr8:143509438			0.72	0.80	-0.08	0.82	0.81	0.00
cg26925590	chr16:139752	C16orf35	Body	0.85	0.90	-0.05	0.91	0.91	0.00
cg02064366	chr17:79045526	BAIAP2	Body	0.62	0.67	-0.05	0.71	0.75	-0.04
cg17244485	chr2:103443515			0.38	0.32	0.05	0.27	0.26	0.01
cg23236908	chr14:55819305	FBXO34	3'UTR	0.77	0.81	-0.04	0.77	0.78	-0.01
cg03962217	chr7:154796431	LOC202781	Body	0.65	0.69	-0.05	0.60	0.62	-0.02
cg17356733	chr21:34774627	IFNGR2	TSS1500	0.64	0.70	-0.06	0.70	0.70	0.00
cg16040341	chr15:83544284	HOMER2	Body	0.69	0.75	-0.05	0.72	0.73	-0.01

cg24038762	chr1:87817476			0.73	0.77	-0.04	0.72	0.73	-0.01
cg05529091	chr12:111475875	CUX2	Body	0.65	0.70	-0.05	0.64	0.68	-0.04
cg05374733	chr12:42853791	PRICKLE1	Body	0.80	0.83	-0.03	0.83	0.83	0.00
cg06746318	chr7:101755186	CUX1	Body	0.70	0.76	-0.06	0.78	0.79	-0.01
cg08404546	chr22:37910993	CARD10	Body	0.76	0.82	-0.05	0.78	0.80	-0.02
cg14905600	chr10:134226361	PWWP2B	3'UTR	0.75	0.81	-0.06	0.84	0.84	-0.01
cg10976478	chr2:241263838			0.84	0.80	0.04	0.79	0.79	0.00
cg21399807	chr2:54955581	EML6	Body	0.74	0.78	-0.04	0.69	0.70	-0.01
cg21776682	chr8:1387801			0.68	0.73	-0.05	0.68	0.69	-0.02
cg26593722	chr16:87376314	FBXO31	Body	0.80	0.85	-0.05	0.90	0.91	-0.01
cg04543233	chr20:21689105	PAX1	Body	0.16	0.19	-0.04	0.14	0.15	-0.01
cg06614697	chr1:3696285			0.62	0.67	-0.05	0.64	0.66	-0.02

SUPPLEMENTARY TABLE 12 - Top 20 enriched GO terms for genes in the WGCNA modules most highly associated with schizophrenia ('black' and 'pink'). GO enrichment for biological processes was performed using EASE (DAVID). Table shows GO term, number of genes (count), and p-values for EASE score and Benjamini-Hochberg adjustment.

Gene Ontology Term	GO:ID	Count	p-value	FDR Value
Black module				
neuron projection	GO:0043005	224	2.09E-14	1.32E-10
neuron part	GO:0097458	247	1.24E-11	3.92E-08
dendrite	GO:0030425	124	1.97E-11	4.02E-08
synapse	GO:0045202	170	2.99E-11	4.02E-08
nervous system development	GO:0007399	453	3.19E-11	4.02E-08
cytoskeletal protein binding	GO:0008092	207	2.89E-10	3.03E-07
cell projection	GO:0042995	344	7.85E-10	7.06E-07
synapse part	GO:0044456	126	5.42E-09	4.27E-06
generation of neurons	GO:0048699	303	6.26E-09	4.39E-06
transmission of nerve impulse	GO:0019226	184	8.17E-09	5.15E-06
multicellular organismal signaling	GO:0035637	188	1.37E-08	7.87E-06
neuron projection morphogenesis	GO:0048812	153	1.50E-08	7.89E-06
neuron projection development	GO:0031175	175	1.93E-08	9.37E-06
neurogenesis	GO:0022008	313	3.07E-08	1.38E-05
synaptic transmission	GO:0007268	176	3.50E-08	1.47E-05
neuron development	GO:0048666	200	5.10E-08	2.01E-05
cell junction	GO:0030054	213	6.27E-08	2.32E-05
cell morphogenesis involved in neuron differentiation	GO:0048667	145	1.51E-07	5.28E-05
synaptic membrane	GO:0097060	81	2.60E-07	8.63E-05
axon development	GO:0061564	139	4.88E-07	1.54E-04
Pink module				
cell junction	GO:0030054	161	2.58E-10	1.54E-06
nervous system development	GO:0007399	302	4.11E-09	1.23E-05
homophilic cell adhesion	GO:0007156	47	7.42E-09	1.48E-05
synapse	GO:0045202	110	5.87E-08	8.56E-05
neuron projection development	GO:0031175	122	7.18E-08	8.56E-05
neurogenesis	GO:0022008	213	1.95E-07	1.83E-04
calcium ion binding	GO:0005509	129	2.14E-07	1.83E-04
generation of neurons	GO:0048699	202	3.04E-07	1.95E-04
neuron projection morphogenesis	GO:0048812	104	3.19E-07	1.95E-04

neuron projection	GO:0043005	132	3.26E-07	1.95E-04
neuron development	GO:0048666	137	3.72E-07	2.01E-04
neuron differentiation	GO:0030182	160	5.70E-07	2.83E-04
cell development	GO:0048468	220	8.21E-07	3.77E-04
dendrite	GO:0030425	75	1.07E-06	4.55E-04
system development	GO:0048731	488	1.89E-06	7.50E-04
synaptic membrane	GO:0097060	56	2.58E-06	8.62E-04
cell morphogenesis involved in neuron differentiation	GO:0048667	98	2.60E-06	8.62E-04
synapse part	GO:0044456	81	2.60E-06	8.62E-04
transmission of nerve impulse	GO:0019226	119	2.86E-06	8.97E-04

SUPPLEMENTARY TABLE 13 - Correlation between DNA methylation and brain development (days post conception) in a cohort of 179 human fetal brain samples, for the top 100 ranked DMPs between SZ and controls in prefrontal cortex. DMP=differentially methylated probe.

SZ DMP rank	Probe ID	Gene name	Pearson's R	p-value	FDR
74	cg03724006		-0.62	1.31E-20	1.28E-18
62	cg07665929	STK10	-0.58	2.44E-17	1.20E-15
6	cg00236305	MYT1L	-0.54	4.24E-15	1.39E-13
59	cg25790133	FAM193A	-0.53	1.40E-14	3.43E-13
69	cg27097992		0.53	2.49E-14	4.88E-13
86	cg03962217	LOC202781	-0.51	3.39E-13	5.54E-12
41	cg07114544	NTN1	0.45	2.18E-10	3.05E-09
87	cg17356733	IFNGR2	-0.44	9.63E-10	1.18E-08
53	cg07289133	FAM92B	0.43	2.33E-09	2.51E-08
77	cg12473775	RHOD	0.43	2.56E-09	2.51E-08
89	cg24038762		0.41	1.70E-08	1.36E-07
93	cg08404546	CARD10	-0.41	1.80E-08	1.36E-07
100	cg06614697		-0.41	1.67E-08	1.36E-07
4	cg08171022	PPFIA1	-0.4	2.33E-08	1.63E-07
92	cg06746318	CUX1	0.4	2.68E-08	1.75E-07
8	cg13079528	SDK1	0.36	6.13E-07	3.75E-06
95	cg10976478		0.36	6.70E-07	3.86E-06
31	cg05860371		-0.35	1.40E-06	7.53E-06
75	cg10535500	SYNGAP1	-0.35	1.46E-06	7.53E-06
21	cg04922803	GLT8D2	-0.35	1.71E-06	8.38E-06
67	cg24079702	FHL2	0.34	3.93E-06	1.83E-05
83	cg02064366	BAIAP2	-0.32	9.07E-06	4.04E-05
12	cg09507608		-0.3	4.49E-05	1.91E-04
90	cg05529091	CUX2	-0.29	7.18E-05	2.93E-04
22	cg18857062	CRIP3	-0.28	1.65E-04	6.47E-04
49	cg03991188	MYH16	-0.27	2.39E-04	9.01E-04
97	cg21776682		0.26	3.40E-04	1.23E-03
35	cg21390682	MCF2L	0.25	6.90E-04	2.42E-03
47	cg04691233	JAM3	0.24	1.08E-03	3.65E-03
48	cg07500432	PARD6G	0.24	1.15E-03	3.76E-03
9	cg14429765	MCPH1	0.23	1.90E-03	6.01E-03
57	cg07421682	PCSK6	0.22	3.27E-03	1.00E-02
85	cg23236908	FBXO34	0.22	3.65E-03	1.08E-02
81	cg19671331		-0.2	6.06E-03	1.75E-02
26	cg26182253		-0.2	6.45E-03	1.81E-02
63	cg21375204	CLIP2	0.2	8.15E-03	2.22E-02
66	cg06168875	NANOS3	0.19	1.10E-02	2.91E-02
61	cg01936649		0.19	1.15E-02	2.97E-02

15	cg21847368	MCF2L	0.18	1.47E-02	3.69E-02
51	cg12198176	RTDR1	0.18	1.63E-02	3.99E-02
29	cg16393877		0.17	2.01E-02	4.76E-02
72	cg07815131		-0.17	2.07E-02	4.76E-02
79	cg00172872		-0.17	2.09E-02	4.76E-02
24	cg27363226	KHSRP	-0.17	2.24E-02	4.99E-02
7	cg14966346	KLC1	0.17	2.61E-02	5.44E-02
46	cg09942424	MGAT5B	0.17	2.56E-02	5.44E-02
88	cg16040341	HOMER2	0.17	2.58E-02	5.44E-02
76	cg09235936	HDLBP	0.16	2.88E-02	5.88E-02
28	cg14527262	LOC100130872-SPON2	0.16	3.26E-02	6.52E-02
20	cg21341878	ZFYVE28	0.15	4.02E-02	7.88E-02
13	cg23844013	C8A	0.15	4.22E-02	8.11E-02
37	cg20930320	SORT1	-0.15	4.53E-02	8.54E-02
18	cg03445663	HDLBP	0.14	5.52E-02	1.02E-01
55	cg20011075		0.14	6.32E-02	1.15E-01
64	cg23203234		0.13	8.72E-02	1.55E-01
96	cg21399807	EML6	0.13	9.39E-02	1.64E-01
71	cg23996071	HOOK1	-0.12	1.04E-01	1.79E-01
34	cg27608031	ADAMTS18	-0.12	1.15E-01	1.94E-01
2	cg24803255	RASA3	-0.11	1.26E-01	2.09E-01
54	cg11945824	PRRT1	-0.11	1.51E-01	2.47E-01
70	cg22060153	SNORD89	0.11	1.59E-01	2.55E-01
98	cg26593722	FBXO31	-0.1	1.63E-01	2.58E-01
33	cg21609813	LGI3	-0.1	1.72E-01	2.68E-01
91	cg05374733	PRICKLE1	0.1	1.82E-01	2.79E-01
19	cg15079231	VIPR1	0.09	2.08E-01	3.09E-01
44	cg13280041	NHSL1	-0.09	2.08E-01	3.09E-01
94	cg14905600	PWWP2B	0.09	2.11E-01	3.09E-01
14	cg26578910	PRKD2	-0.09	2.25E-01	3.24E-01
17	cg10248981	LHPP	0.09	2.31E-01	3.28E-01
99	cg04543233	PAX1	0.09	2.55E-01	3.57E-01
80	cg07780199	CRTC1	-0.08	2.60E-01	3.59E-01
27	cg14370653		0.08	2.78E-01	3.78E-01
25	cg02187259	FAM49A	0.08	3.02E-01	4.03E-01
43	cg25778661		-0.08	3.04E-01	4.03E-01
30	cg26130533	LOC100130872-SPON2	-0.07	3.41E-01	4.46E-01
73	cg05583087		0.07	3.57E-01	4.60E-01
16	cg03607729	LCMT1	-0.07	3.81E-01	4.85E-01
78	cg27252696	SIM1	0.06	3.90E-01	4.90E-01
52	cg19643441	SF4	-0.06	4.04E-01	5.01E-01
5	cg02857643	CACNA1G	0.06	4.21E-01	5.16E-01

56	cg14752965		0.05	4.74E-01	5.73E-01
39	cg13119928	KRT79	-0.05	5.01E-01	5.99E-01
10	cg08602214	RHOBTB2	-0.05	5.21E-01	6.14E-01
58	cg22697364		0.05	5.26E-01	6.14E-01
42	cg09419102		-0.04	5.69E-01	6.56E-01
3	cg00903099	HTR5A	-0.04	5.86E-01	6.62E-01
82	cg26925590	C16orf35	0.04	5.88E-01	6.62E-01
11	cg19735533		0.04	6.27E-01	6.98E-01
32	cg03363012	C20orf54	-0.03	6.70E-01	7.30E-01
36	cg27654476		0.03	6.79E-01	7.30E-01
38	cg12864185		-0.03	6.85E-01	7.30E-01
65	cg04215055	MGAT5B	-0.03	6.64E-01	7.30E-01
68	cg25900150	ZC3H3	0.03	6.97E-01	7.34E-01
23	cg27138871		0.02	8.29E-01	8.64E-01
1	cg26173173	GSDMD	0.01	8.55E-01	8.73E-01
60	cg10622536	C1orf113	0.01	8.48E-01	8.73E-01
45	cg14772639	SAP130	-0.01	8.72E-01	8.81E-01
50	cg21843517	SNRNP35	0.01	8.92E-01	8.92E-01
40	cg20681783		NA	NA	NA
84	cg17244485		NA	NA	NA