Supplementary Online Content

Montano C, Taub MA, Jaffe A, et al. Association of DNA methylation differences with schizophrenia in an epigenome-wide association study. *JAMA Psychiatry*. Published online April 13, 2016. doi:10.1001/jamapsychiatry.2016.0144.

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eMETHODS

Genome-wide measurement of DNA methylation

For the discovery set, whole blood samples from the multi-site consortia were processed at the Rutgers University Cell and DNA repository (RUCDR) for DNA isolation using Qiagen Autopure LS and the pellets were hydrated in TE buffer. The samples were shipped to JHU for analysis, and DNA integrity and concentration were confirmed by gel electrophoresis and NanoDrop. A total of 3168 samples, randomized for case-control status to minimize batch effects, were hybridized to the Infinium array for the discovery set (including technical replicates from 277 blood samples and liver and placenta samples across every plate for quality control, and blood samples from family members of probands for a separate study). For the replication set, DNA also was isolated at RUCDR. Of those, 516 samples were hybridized to the array (with 16 replicates from liver and placenta). For each sample, 1 µg of genomic DNA was bisulfite-converted using the EZ DNA Methylation™ Kit (Zymo Research, catalog No. D5001), according to the manufacturer's guidelines for the 450K array. DNAm for the discovery and the replication sets was measured using the Infinium HumanMethylation450 BeadChip assay (Illumina, San Diego, CA). We chose to use the same methylation platform for discovery and replication to accurately calculate and model cell proportion differences between cases and controls and maximize data harmonization (see Data processing and statistical modeling section).

Data processing and statistical modeling

Assessment of cell heterogeneity and potential confounders. Several efforts were made to quantify and correct for confounders known to affect DNAm in blood. First, self-reported race was confirmed via multidimensional scaling of beta scale methylation ratios from 65 SNPs selected to discriminate genetic background in the 450K array[1](**eFigure 1**). For a subset of samples, the 450K race prediction was confirmed with genotyping data (N=374, see genotyping section). Given the large proportion of African American participants, samples were separated in two categories: African American (AA) and non-African American (non-AA). Second, cell proportion estimates for six cell types (CD8+ and CD4+ T cells, B cells, monocytes, granulocytes, and natural killer cells) were calculated for each sample using software available in the *minfi* Bioconductor package, using an adaptation of a published algorithm[2,3]. Third, we compared gender estimates calculated using software available in *minfi* and from genotype data with self-reported gender. Fourth, self-reported current smoking status was ascertained for all individuals, and samples with missing smoking information were dropped. Moreover, to ensure that potential methylation differences revealed in the present study were not due to residual smoking confounding (even after explicitly modeling smoking in linear regression), we further removed 294 CpGs associated with smoking status in previous publications from our association results[4,5]. Fifth, we used ANOVA to test the effects of medication on predicted cell proportions, using the following antipsychotic medication categories: 0=No antipsychotics, 1=Typical antipsychotics, 2=Atypical antipsychotics, and 3=Typical and Atypical antipsychotics. Sixth, we applied the "Remove Unwanted Variation, 2-step" (RUV-2) method[6] to correct potential batch effects by unmeasured factors, using the first two principal components of the raw intensities in the green and red channels of the negative control probes of the 450K array.

Replication analysis. We fit a similar robust linear regression model to that of the discovery set, using the same covariates except for race (all of the samples were identified as non-AA). We considered only the statistically significant DMPs from the discovery results. We applied a threshold of nominal p-value <0.05 and same direction of association to declare replication. We also assessed quadrant correlations (akin to a Kappa statistic) between the discovery and replication regression estimates across these DMPs. Post-hoc analysis to assess the influence of antipsychotic treatment on DNA methylation levels was performed using the 679 cases with complete medication information, correcting for multiple testing using the Sidak test in the *mutoss* package[7].

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Gene ontology and pathway analyses. To investigate the potential biological meaning and functional significance of the SZ-DMPs identified, we undertook gene ontology and pathway analyses. We tested for enrichment of genes for SZ-associated DMPs based on Gene Ontology (Biology Processes database) using the *GOstats* bioconductor package[8]. Network analyses were generated through the use of QIAGEN's Ingenuity Pathway Analysis (IPA®, QIAGEN, Redwood City, www.qiagen.com/ingenuity) and GeneMania (http://www.genemania.org).

Illumina genome-wide genotyping and meQTL analysis. A subset of the case-control samples (N=380) were genotyped using the HumanOmni5Exome-4v1 chip. Genotyping was conducted at the Genetic Resources Core Facility, Johns Hopkins Institute of Genetic Medicine, Baltimore, MD. QC was performed following the CHARGE consortium best practices[9]. Samples included for analysis had >99% call rates (N=1 dropped) and consistent inferred and recorded gender (N=5 dropped). SNP filtering eliminated monomorphic SNPs, those with call rates <95%, and duplicated SNPs. This resulted in 3,796,870 autosomal SNPs on 374 samples (165 SZ cases and 209 controls). QC and quantification of population stratification were performed using the package PLINK (http://pngu.mgh.harvard.edu/purcell/plink/). To identify meQTL SNPs, 209 control individuals with both DNAm and SNP data were selected, and 456,513 autosomal methylation probes were tested for association with autosomal SNPs. Cis-meQTLs were selected for having a maximum distance of less than 50 Kb between the CpG and the SNP. Analysis was carried out using the package *MatrixEQTL* and a significance level of FDR <0.01[10]. The PGC2 SZ-associated SNP set was derived from the published Psychiatric Genomics Consortium latest mega-analysis[11]. Significance of overlap between SZ-DMPs and PGC2 regions was assessed using Fisher's exact test. To assess replication between these studies, we looked for overlap of significant meQTLs with statistically significant SZ-SNPs reported by the PGC.

Regression modeling formulas for identification of SZ-associated differentially methylated positions (DMSPs).

The formula for the primary regression analysis was:

$$DNAm \sim \beta_0+\beta_1(Diagnosis)+\beta_2(sex)+\beta_3(age)+\beta_4(current\ smoking)+\beta_5(race)+\beta_6(CD8T)+\beta_7(CD4T)+\beta_8(NK)+\beta_9(B\ cell)+\beta_{10}(monocytes)+\beta_{11}(granulocytes)+\beta_{12}(PC1_{\text{negative control probes}})+\beta_{13}(PC2_{\text{negative control probes}})$$

For the additional analyses stratified by race and gender, the formulae were:

$$DNAm_{[AA]} \sim \beta_0+\beta_1(Diagnosis+\beta_2(sex)+\beta_3(age)+\beta_4(current\ smoking)+\beta_5(CD8T)+\beta_6(CD4T)+\beta_7(NK)+\beta_8(B\ cell)+\beta_9(monocytes)+\beta_{10}(granulocytes)+\beta_{11}(PC1_{\text{negative control probes}})+\beta_{12}(PC2_{\text{negative control probes}})$$

$$DNAm_{[non\text{-}AA]} \sim \beta_0+\beta_1(Diagnosis+\beta_2(sex)+\beta_3(age)+\beta_4(current\ smoking)+\beta_5(CD8T)+\beta_6(CD4T)+\beta_7(NK)+\beta_8(B\ cell)+\beta_9(monocytes)+\beta_{10}(granulocytes)+\beta_{11}(PC1_{\text{negative control probes}})+\beta_{12}(PC2_{\text{negative control probes}})$$

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$$DNAm_{[males]} \sim \beta_0+\beta_1(Diagnosis+\beta_2(age)+\beta_3(current\ smoking)+\beta_4(race)+\beta_5(CD8T)+\beta_6(CD4T)+\beta_7(NK)+\beta_8(B\ cell)+\beta_9(monocytes)+\beta_{10}(granulocytes)+\beta_{11}(PC1_{negative\ control\ probes})+\beta_{12}(PC2_{negative\ control\ probes})$$

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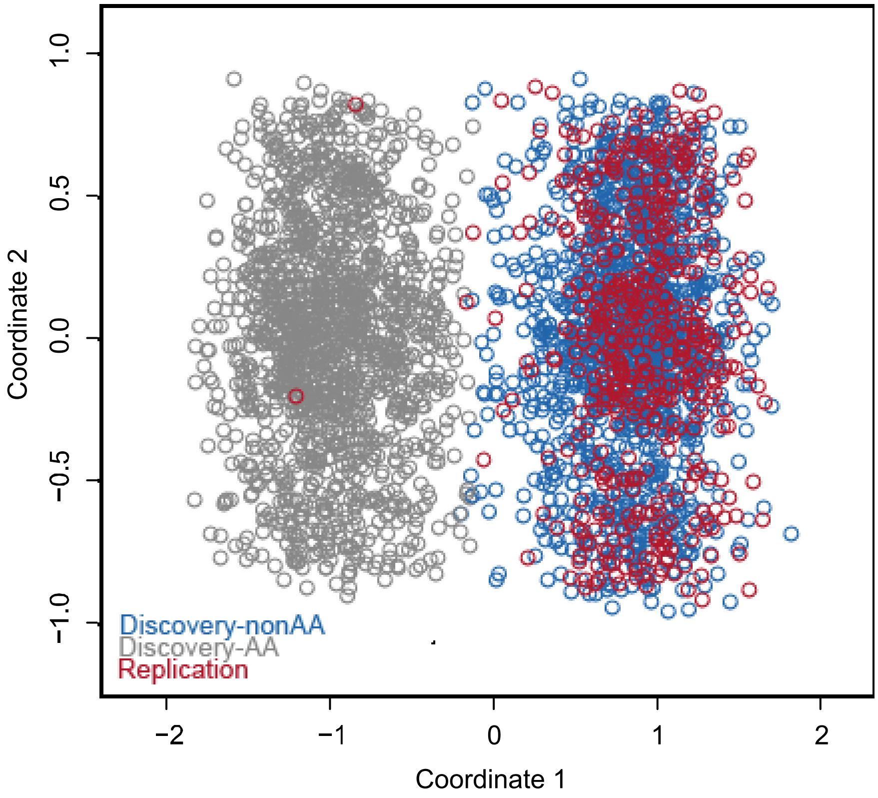
SUPPLEMENTARY FIGURES AND TABLES

eFigure 1



eFigure 1. Self-identified race check using 65 Infinium450K SNPs. MDS plot of beta scale methylation ratios from selected SNPs discriminates African American and non-African American samples. Discovery set African American samples in grey color, Discovery non-African American samples in blue, and replication samples in red. All but 2 replication samples clustered with the non-African American samples.

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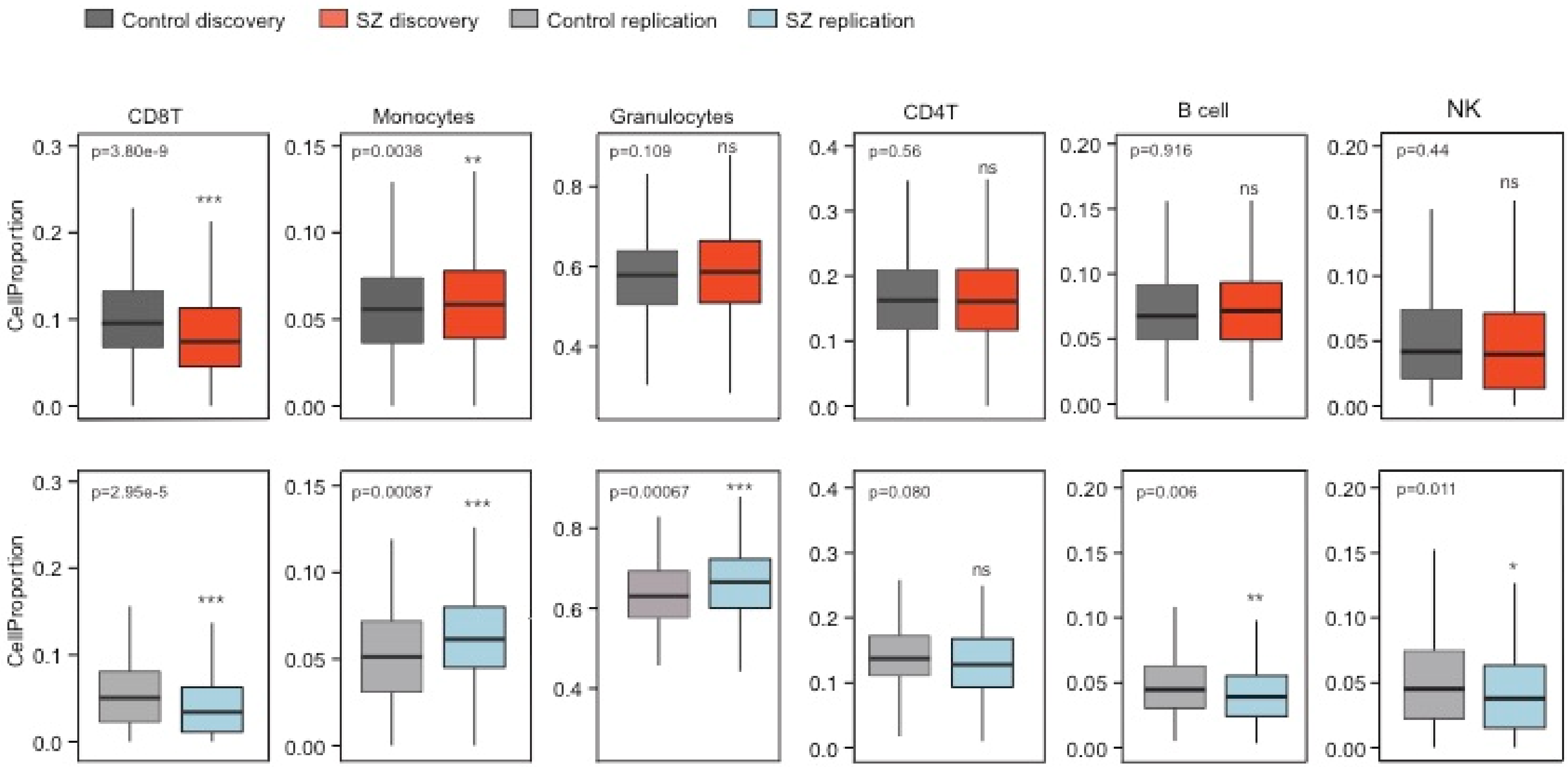
eFigure 2



eFigure 2. Estimated cell proportion differences in SZ cases vs. controls. Calculated cell proportions in the discovery set (top panel) and replication set (bottom panel) for six cell types (CD8+ and CD4+ T cells, monocytes, granulocytes, B cells, and natural killer (NK) cells).

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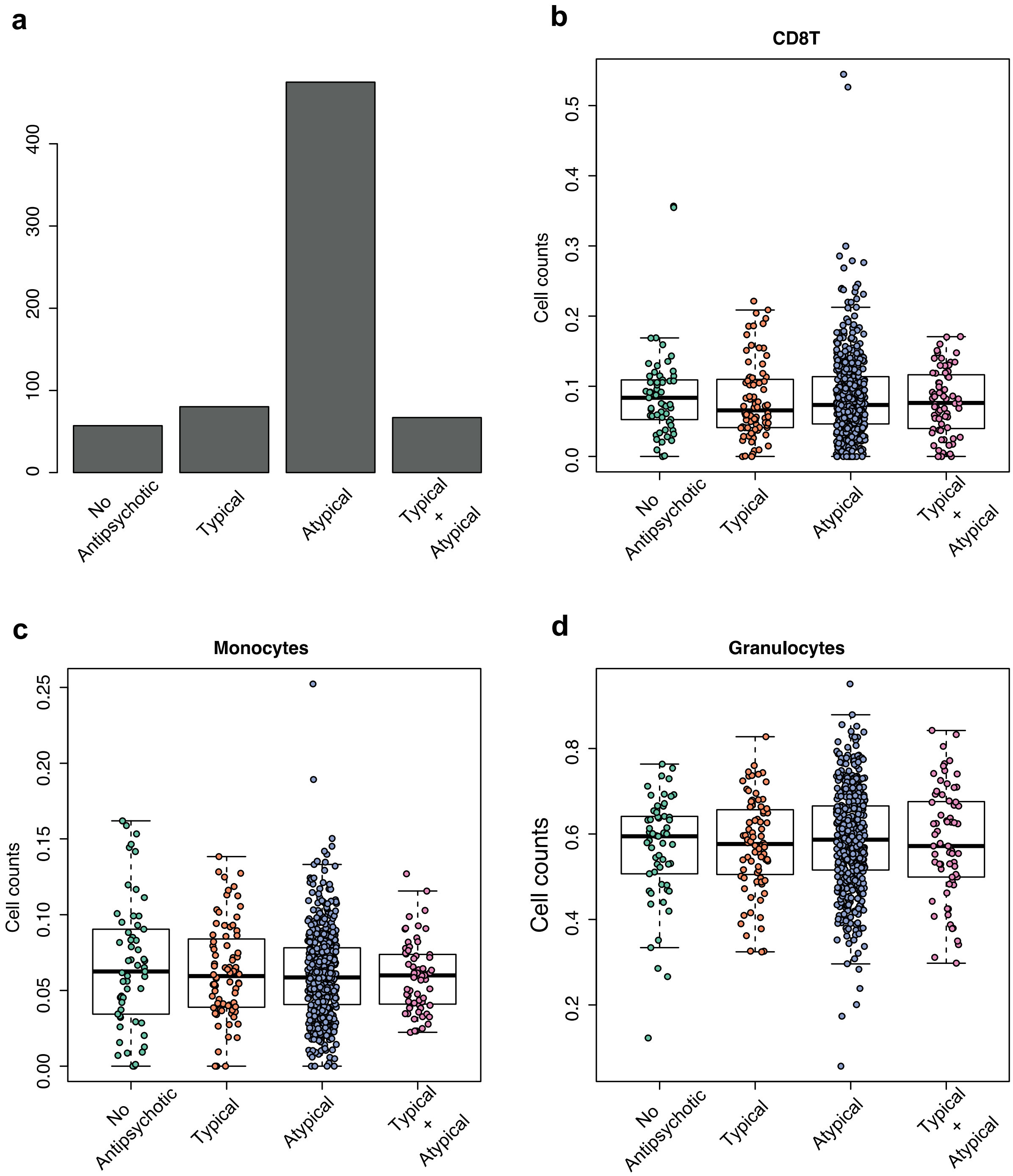
eFigure 3



eFigure 3. Association of estimated cell proportions and pharmacological treatment in SZ cases. (a) Distribution of SZ probands by treatment categories (No antipsychotic, typical antipsychotic, atypical antipsychotics, and combination of both typical and atypical). 70% of the probands were treated with atypical antipsychotics. Estimated **(b)** CD8+T counts (p-value = 0.623), (**c**) monocytes (p-value= 0.579), and **(d)** and granulocytes (p-value= 0.535) in each category.

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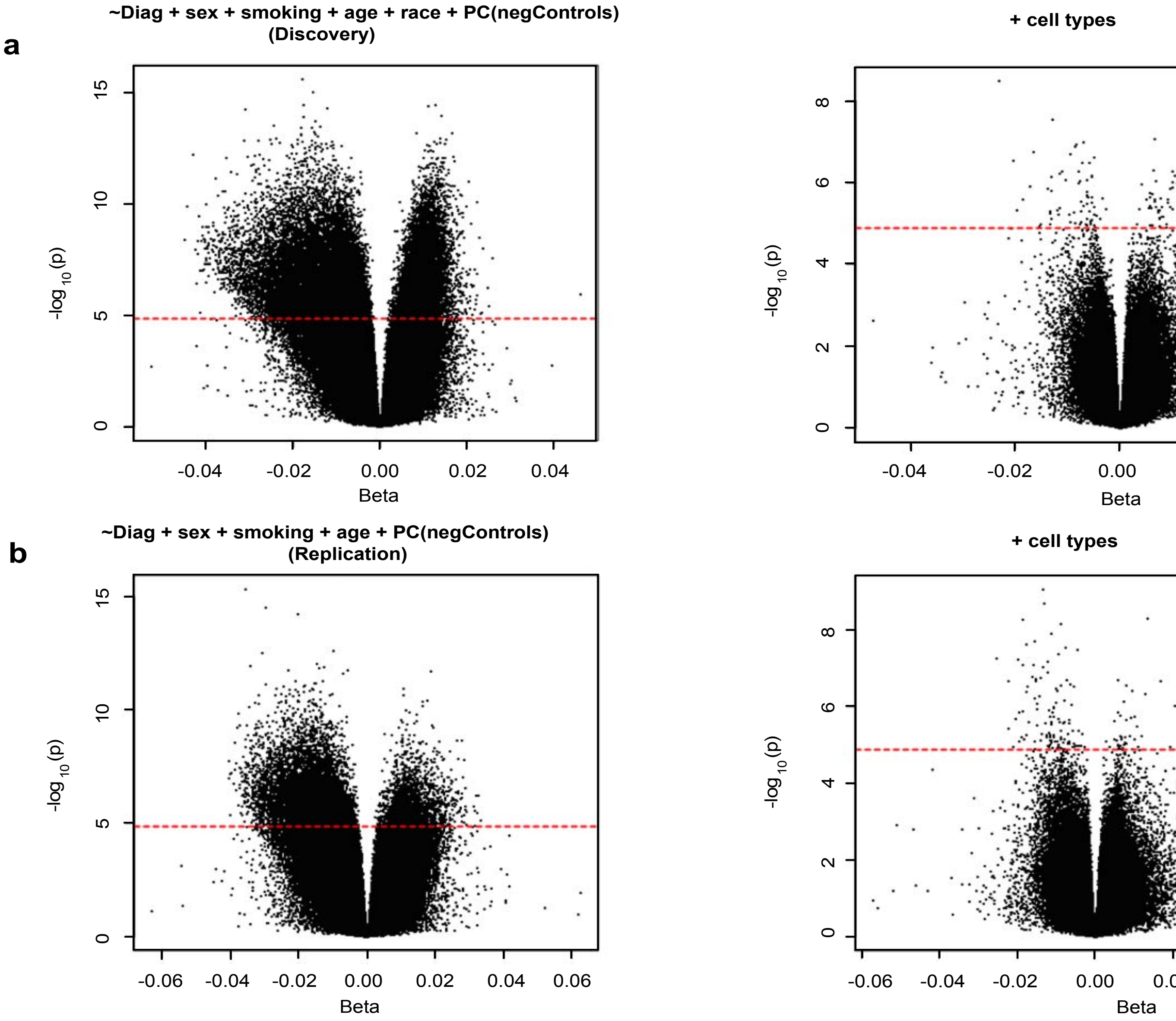
eFigure 4



eFigure 4. Volcano plots of DMPs with and without adjusting for cell type. (a) Plots of $-\log_{10}$ (p-value) against beta scale methylation ratios of the methylation difference between SZ cases and controls in the discovery set, without (left) or with (right) cell type adjustment. Both models adjust for sex, smoking, age, race, and batch. **(b)** Same analysis as in **(a)**, but in the replication set. The dashed line represents the approximate p-value for an FDR = 0.20, the cutoff used in this study.

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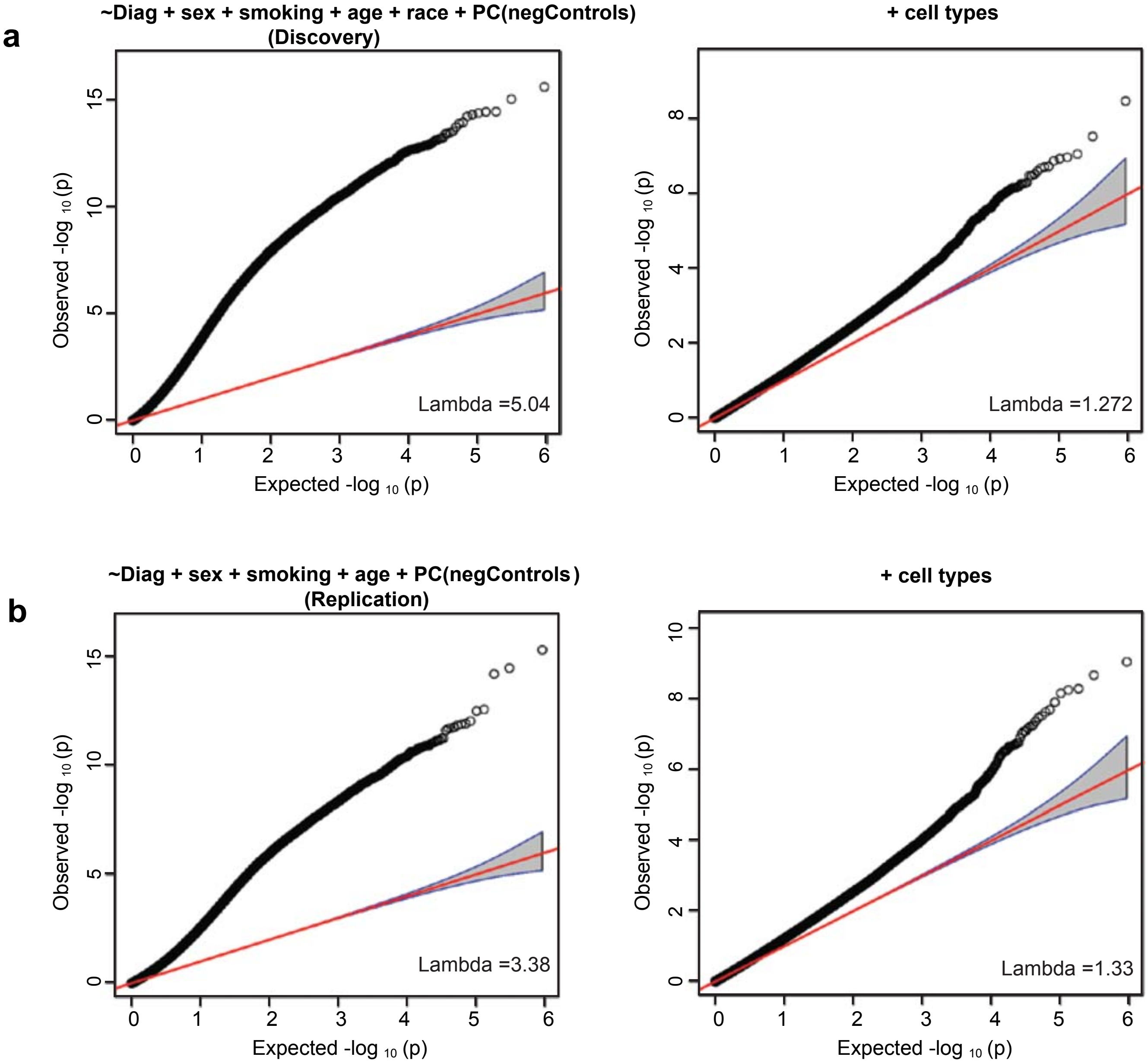
eFigure 5



eFigure 5. QQ plots of p-values with and without adjusting for cell type. Expected vs. observed P-value distributions from the case-control analysis, for the discovery **(a)** and replication **(b)** sets. Blue lines represent the 95% confidence intervals for the null distribution. Lambda represents the genomic inflation factor.

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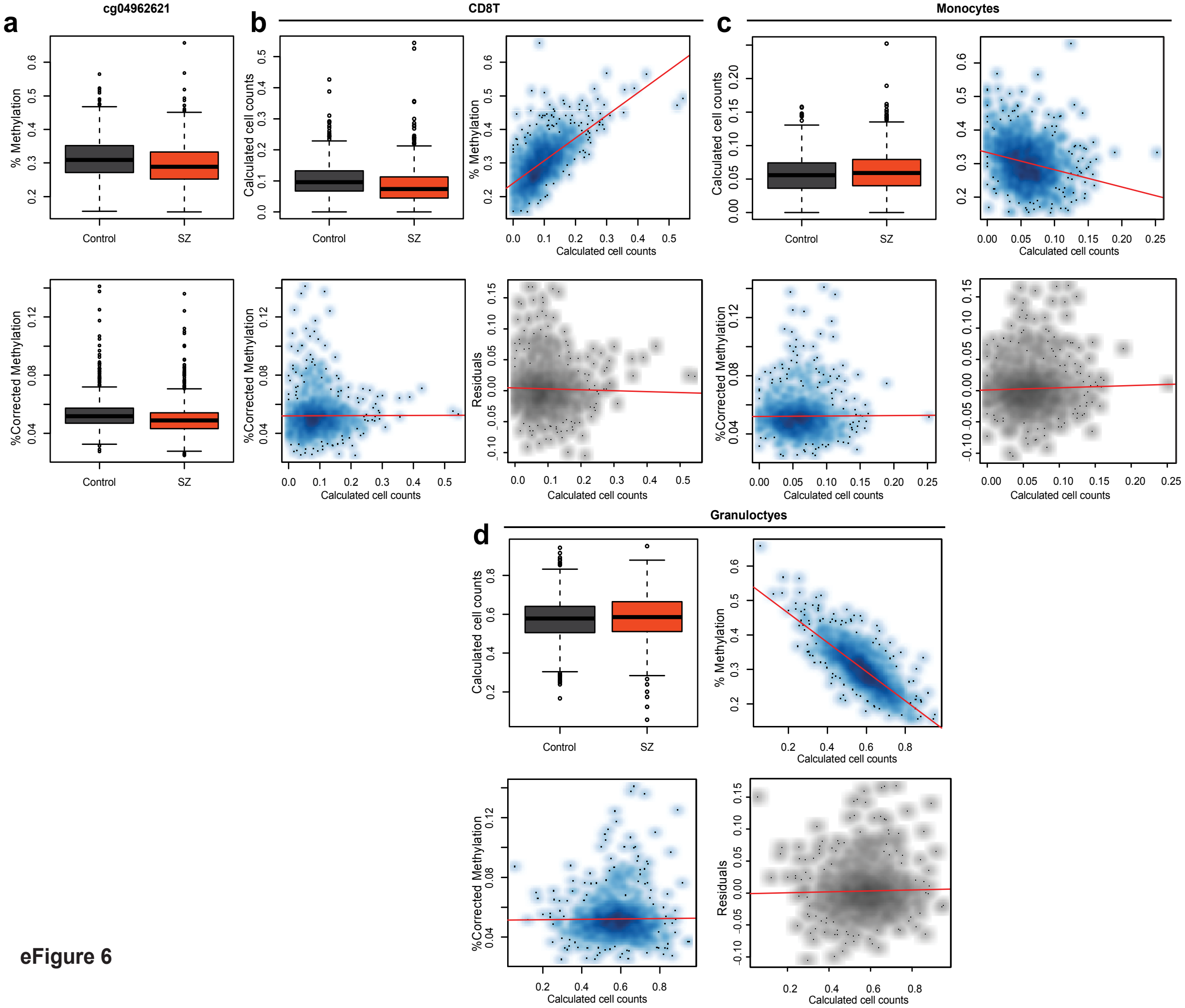

eFigure 6

eFigure 6. Testing for residual confounding after regression using loci where CD8+T cell counts and methylation change are positively correlated. (a) Top panel shows unadjusted methylation change for locus cg04962621, bottom panel shows methylation after adjusting for covariates. **(b)** Top left, calculated CD8+T cell counts by diagnosis; top right: correlation of calculated CD8+T cell counts and unadjusted methylation; bottom left: correlation of calculated CD8+T cell counts and adjusted methylation; bottom right: correlation of calculated CD8+T cell counts and residuals from linear regression. **(c)** and **(d)** show the same analysis for monocytes and granulocytes, respectively.

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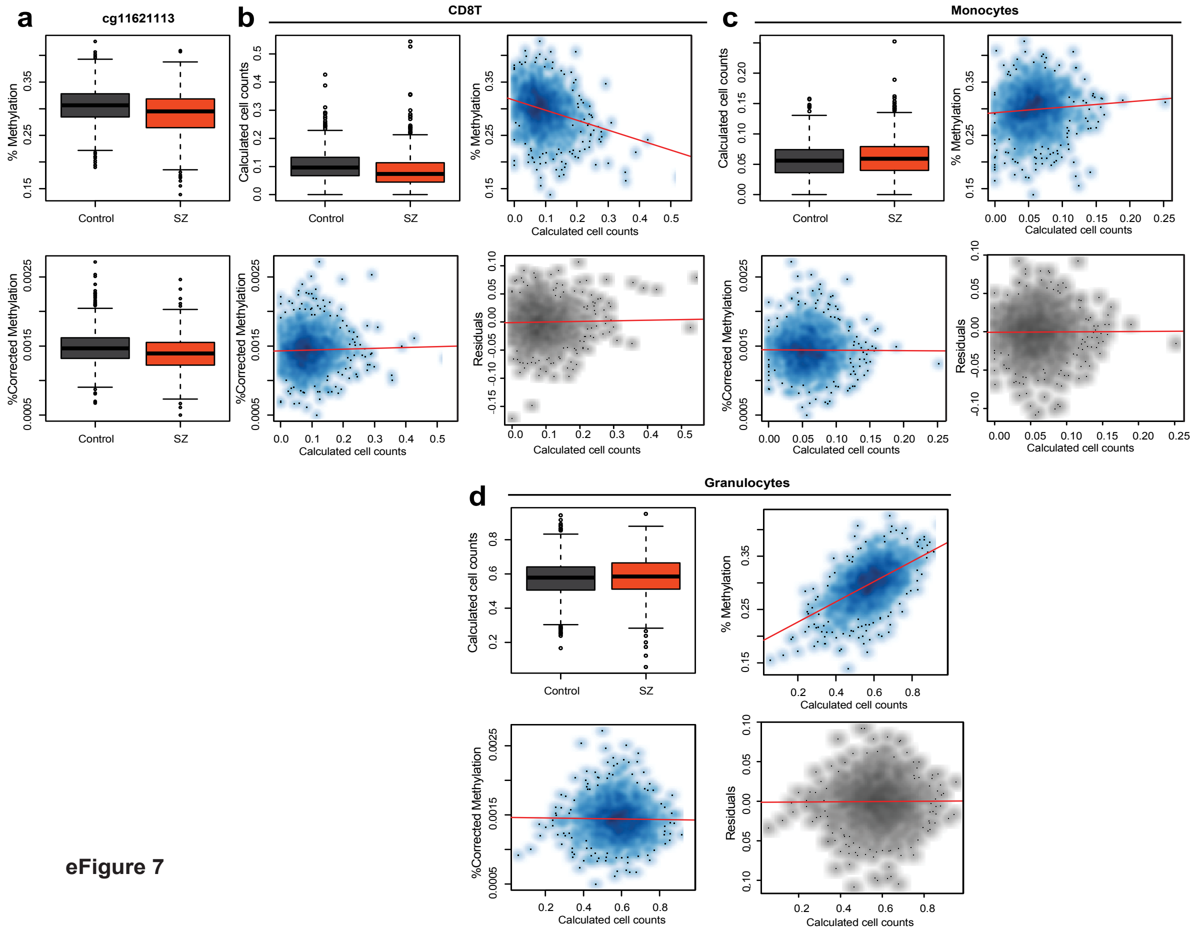

eFigure 7

eFigure 7. Testing for residual confounding after regression using loci where CD8T cell counts and methylation change are negatively correlated. (a) Top panel shows unadjusted methylation change for locus cg11621113, bottom panel shows methylation after adjusting for covariates. **(b)** Top left, calculated CD8+T cell counts by diagnosis; top right: correlation of calculated CD8+T cell counts and unadjusted methylation; bottom left: correlation of calculated CD8+T cell counts and adjusted methylation; bottom right: correlation of calculated CD8+T cell counts and residuals from linear regression. **(c)** and **(d)** show the same analysis for monocytes and granulocytes, as in eFigure 6.

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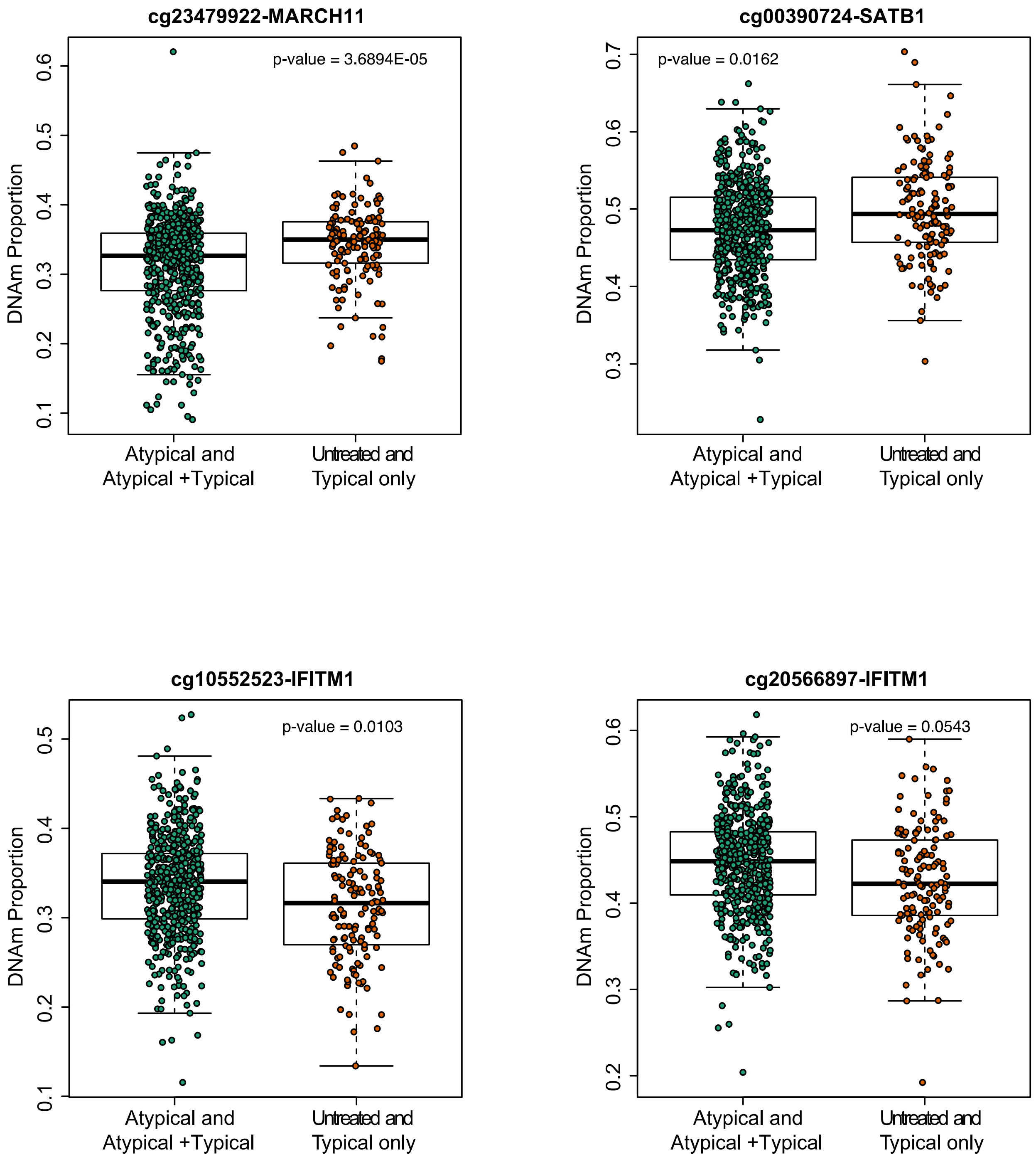
eFigure 8



eFigure 8. Post-hoc testing for the effect of atypical antipsychotic medication on methylation levels. The four methylated loci affected by atypical antipsychotic treatment (p-value ≤0.05). They correspond to three genes: *MARCH11*, *SATB2*, and *IFITM1*.

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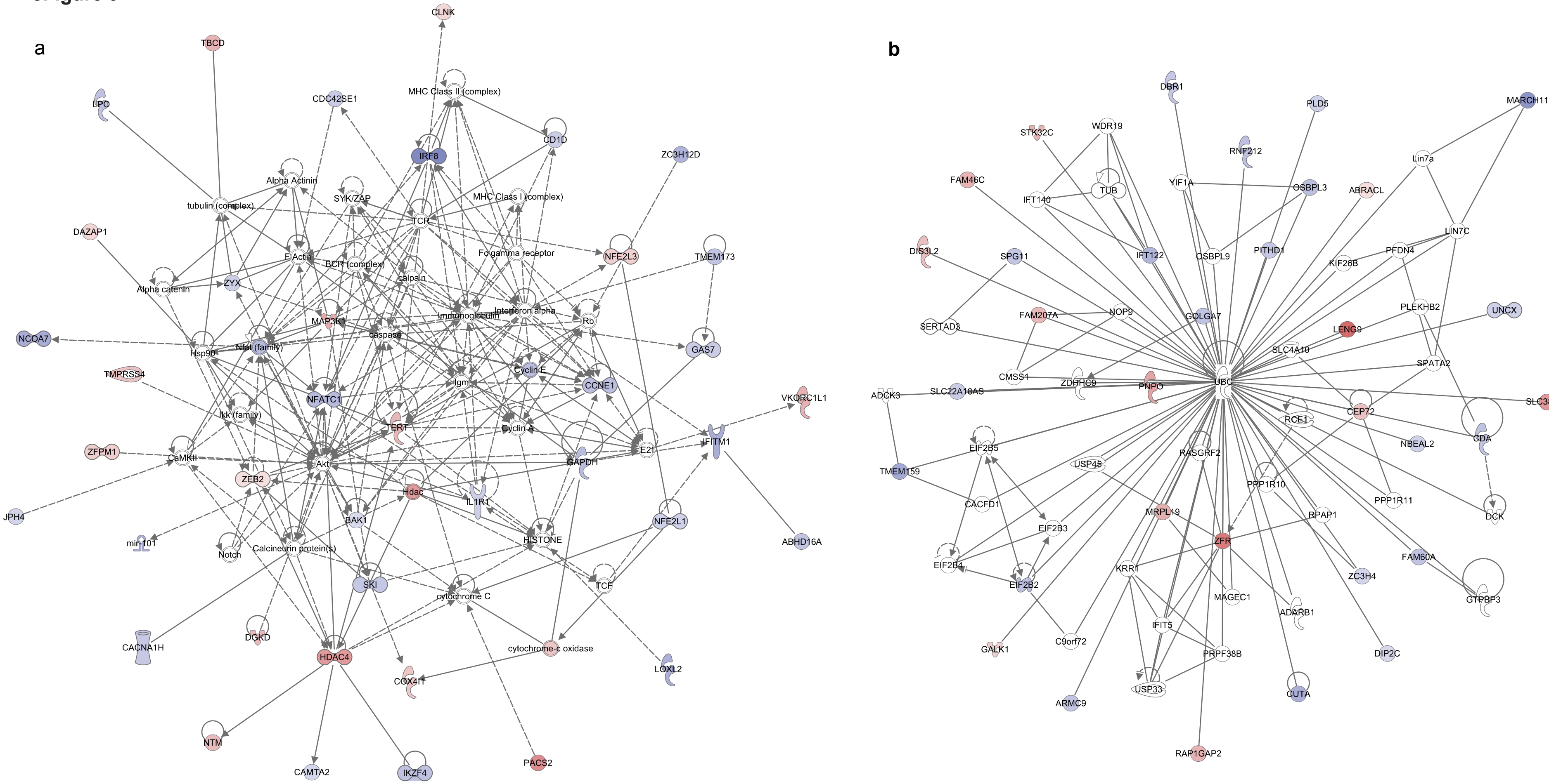
eFigure 9



eFigure 9. IPA Network analysis of genes identified in our genome-wide study. Top two regulatory networks included **(a)**Amino Acid Metabolism, Energy Production, Post-Translational Modification, and **(b)** Hereditary Disorder, Neurological Disease, Psychological Disorders.

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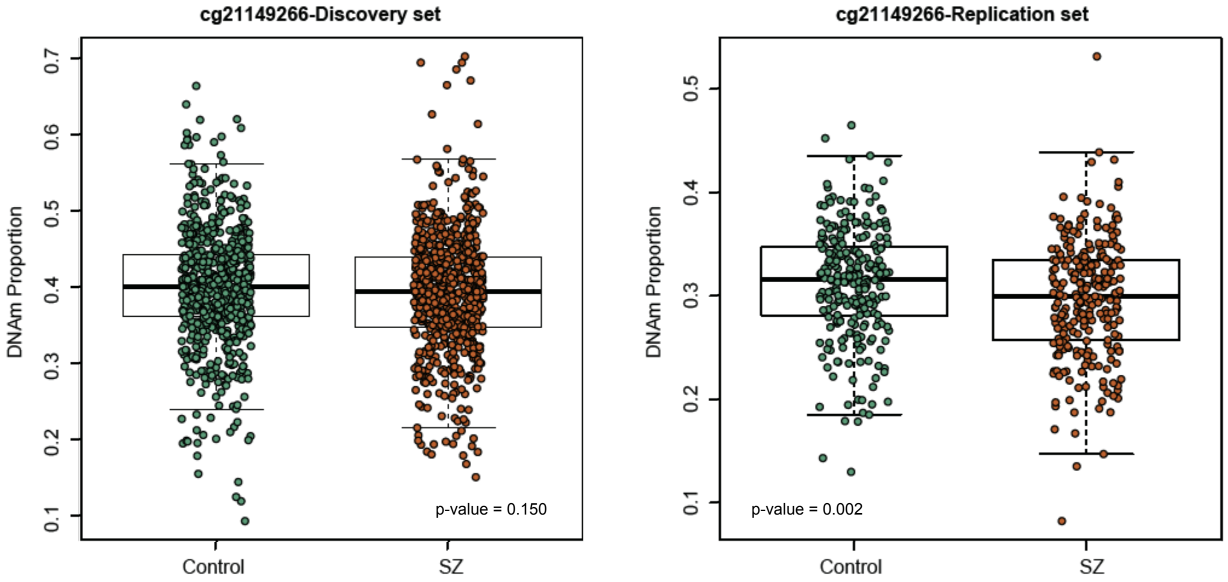
eFigure 10



eFigure 10. Methylation levels at closest locus to Aberg *et al*. MWAS top result *FAM63B*. Methylation levels in the discovery set for cg21149266 in position chr15: 59146882, 126 bp away from the closest validated position at chr15: 59146756. Left, values for discovery set. Right, values for replication set.

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eTable 1. Characteristics of the discovery and replication populations (blood tissue samples)

Variable	Controls	Cases	Total
Discovery			
No.Participants	645	689	1334
Sex, n (%)			
Male	273 (42.3%)	477(69.2%)	
Female	372 (57.7%)	212(30.8%)	
Race/Ethnicity, n (%)			
non-African American	419 (65%)	258 (37.4%)	
African American	226 (35%)	431 (62.6%)	
Study, n (%)			
Study-Cogs	412 (63.9%)	238 (34.5%)	
Study-MGI	84 (13%)	28 (4.1%)	
Study-Paartners	149 (23.1%)	423 (61.4%)	
Age	39.53	37.65	
Smoking			
Current Smoker	97(15%)	402(58.3%)	
Psychiatric treatment, n (%)			
No antipsychotic	633[a](100%)	57 (8.4%)	
Typical antipsychotic	0	80 (11.8%)	
Atypical antipsychotic	0	475 (70.0%)	
Both typical and atypical antipsychotic	0	67 (9.9%)	
Replication			
No.Participants	250	247	497
Sex, n (%)			
Male	190 (76%)	188 (76.1%)	
Female	60 (24%)	59 (23.9%)	
Race/Ethnicity, n (%)			
non-African American	250 (100%)	247 (100%)	
Age	35.1	34.96	
Smoker	125 (50%)	123 (49.8%)	

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eTable 2. Summary of discovery and replication results

Discovery Study			Replication Study								
FDR	All	Minus 294 Smoking CpGs	No. CpGs with Δ methylation in same direction				No. CpGs with Δ methylation in different direction				% Replication
			P<0.05	P 0.05-0.10	P>0.10	Total	P<0.05	P 0.05-0.10	P>0.10	Total	Quadrant Correspondence
0.05	120	113	36	8	46	90	1	1	21	23	79.65
0.1	248	234	68	17	94	179	3	3	49	55	76.50
0.15	547	527	125	29	223	377	9	5	136	150	71.54
0.2	945	923	172	48	405	625	16	17	265	298	67.71

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eTable 3. SZ-associated DMPs (all samples)								
Probe	**Illumina annotation (nearest gene)**	**chr**	**position**	**Discovery set (N=1334)**			**Replication set (N=497)**	
				Δ Beta	**P Value**	**FDR**	**Δ Beta**	**P Value**
cg04792777	KIAA0125	chr14	106322429	-0.007	1.06E-07	0.010	-0.008	2.13E-04
cg13092108	RPS6KA1	chr1	26857284	-0.008	1.16E-07	0.010	-0.009	4.38E-05
cg04962621	MGRN1	chr16	4714733	-0.009	1.32E-07	0.010	-0.007	6.95E-05
cg13997435	S100A2	chr1	153538406	-0.007	3.26E-07	0.011	-0.005	2.77E-02
cg26385126	NCOR2	chr12	124912021	0.006	4.99E-07	0.014	0.010	3.91E-07
cg07458272	KIAA0355	chr19	34744396	0.010	5.39E-07	0.014	0.007	2.10E-02
cg13549638	RPTOR	chr17	78860076	0.013	6.70E-07	0.014	0.008	3.72E-02
cg10975863	RAD51B	chr14	68830704	0.011	6.90E-07	0.014	0.010	1.62E-02
cg22891595	RP11-699L21.1	chr3	193570256	0.011	6.94E-07	0.014	0.006	4.98E-02
cg06996599	C6orf136	chr6	30619232	0.007	9.39E-07	0.015	0.006	3.28E-03
cg23387863	PEAK1	chr15	77472416	0.010	1.02E-06	0.015	0.011	6.62E-04
cg25323444	MAD1L1	chr7	2111060	0.011	1.07E-06	0.016	0.011	2.32E-04
cg11621113	MAN2B1	chr19	12776725	-0.008	1.09E-06	0.016	-0.013	8.72E-10
cg23009327	TCF3	chr19	1630248	0.010	1.32E-06	0.017	0.007	7.92E-03
cg12939085	PPP1CA	chr11	67166104	0.008	2.45E-06	0.023	0.006	4.65E-03
cg06721411	AUP1	chr2	74753759	0.009	2.67E-06	0.023	0.006	3.72E-02
cg12619262	CHST12	chr7	2480493	0.016	2.85E-06	0.024	0.012	7.44E-03
cg03038262	IFITM1	chr11	315262	-0.007	3.02E-06	0.024	-0.006	2.27E-02
cg19769147	PACS2	chr14	105860954	0.009	3.08E-06	0.024	0.007	2.27E-02
cg16038738	FAM102B	chr1	109103731	-0.006	3.27E-06	0.025	-0.005	1.23E-03
cg14827056	AGO2	chr8	141550539	0.006	3.78E-06	0.028	0.004	4.65E-02
cg25792439	CARD14	chr17	78163268	0.007	4.89E-06	0.029	0.006	2.28E-02
cg11186858	SEC14L1	chr17	75096382	0.011	4.93E-06	0.029	0.014	1.38E-04
cg13390284	MIR101-1	chr1	65531864	-0.007	5.11E-06	0.029	-0.004	2.76E-02
cg00417304	PRDM11	chr11	45124456	-0.009	5.39E-06	0.030	-0.013	2.95E-05
cg04535902	GFI1	chr1	92947332	-0.013	5.73E-06	0.031	-0.011	1.90E-02
cg27457201	RPTOR	chr17	78854232	0.008	7.92E-06	0.038	0.009	8.35E-03
cg04232128	TMEM173	chr5	138861241	-0.005	8.39E-06	0.040	-0.003	2.49E-02
cg20359445	IKZF4	chr12	56415591	-0.006	9.06E-06	0.042	-0.004	1.69E-03
cg24489015	LPO	chr17	56316162	-0.006	9.34E-06	0.043	-0.006	1.04E-04
cg11977605	RNF212	chr4	1076247	-0.006	1.04E-05	0.045	-0.005	7.14E-04
cg00994936	DAZAP1	chr19	1423902	0.003	1.08E-05	0.045	0.004	2.61E-02
cg14114377	MARK4	chr19	45756845	-0.008	1.07E-05	0.045	-0.008	1.31E-03
cg13451416	AGAP1	chr2	236671149	-0.005	1.15E-05	0.046	-0.005	7.72E-03
cg03497652	ANKS3	chr16	4751569	0.009	1.26E-05	0.049	0.012	7.00E-05
cg24517501	GFI1	chr1	92952702	-0.008	1.30E-05	0.050	-0.008	4.99E-04
cg07333545	MCM3	chr6	52170606	-0.011	1.44E-05	0.052	-0.009	1.12E-02
cg11597902	SEC14L1	chr17	75096239	0.010	1.49E-05	0.054	0.011	4.65E-04
cg27093918	MIR1538	chr16	69564625	-0.012	1.71E-05	0.059	-0.015	7.17E-05

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cg23542902	HES1	chr3	193807749	-0.005	1.73E-05	0.059	-0.004	1.47E-02
cg08940169	ZFPM1	chr16	88540241	0.004	1.89E-05	0.063	0.006	2.87E-05
cg26581729	NPDC1	chr9	139939792	-0.010	1.95E-05	0.063	-0.016	1.72E-07
cg08869118	MLXIP	chr12	122617908	0.004	1.99E-05	0.064	0.003	2.36E-02
cg09308580	ZFP36L2	chr2	43405947	-0.006	2.31E-05	0.066	-0.004	8.91E-03
cg27431877	NCOR2	chr12	124911924	0.005	2.29E-05	0.066	0.008	1.64E-04
cg10397932	SKI	chr1	2166155	-0.005	2.33E-05	0.066	-0.003	2.37E-02
cg21581415	SCAP	chr3	47460784	0.006	2.38E-05	0.067	0.005	1.94E-02
cg22887491	NTM	chr11	131618277	0.005	2.43E-05	0.067	0.002	3.22E-02
cg05036937	ITGA2	chr5	52283760	-0.006	2.50E-05	0.068	-0.005	6.13E-03
cg03078690	VPS52	chr6	33235504	0.006	2.97E-05	0.074	0.006	5.65E-03
cg17901584	DHCR24	chr1	55353706	-0.010	3.14E-05	0.076	-0.011	6.95E-03
cg01115923	KIFC3	chr16	57793728	-0.005	3.16E-05	0.076	-0.003	4.81E-02
cg01765406	HS6ST1	chr2	129231478	-0.007	3.35E-05	0.077	-0.006	1.46E-02
cg16111190	DDR1	chr6	30860887	0.011	3.78E-05	0.084	0.009	1.27E-02
cg01676795	POR	chr7	75586348	0.011	4.03E-05	0.086	0.010	2.46E-02
cg26253134	TGFA	chr2	70751721	-0.006	4.15E-05	0.088	-0.005	9.43E-04
cg04359840	XYLT1	chr16	17563300	-0.011	4.14E-05	0.088	-0.017	2.28E-05
cg00066663	CHD3	chr17	7792674	-0.004	4.38E-05	0.091	-0.003	5.23E-03
cg20384132	RANBP3L	chr5	36302349	0.009	4.39E-05	0.091	0.007	2.03E-02
cg06315217	GMDS	chr6	1629850	0.006	4.51E-05	0.093	0.006	4.58E-03
cg03762242	GAS7	chr17	9940004	-0.005	4.76E-05	0.096	-0.003	2.69E-02
cg27115863	CARD10	chr22	37921640	-0.010	4.77E-05	0.096	-0.011	1.30E-03
cg02117086	B3GNT7	chr2	232265670	0.010	4.90E-05	0.097	0.006	4.79E-02
cg19148201	DDR1	chr6	30860237	0.011	5.09E-05	0.098	0.009	4.53E-02
cg04462774	AQP6	chr12	50368110	0.005	5.22E-05	0.098	0.005	3.32E-02
cg00812833	PLD5	chr1	242687412	-0.004	5.20E-05	0.098	-0.003	3.34E-02
cg25722983	STK40	chr1	36840028	-0.007	5.27E-05	0.098	-0.012	4.95E-06
cg14741228	FAM60A	chr12	31476479	-0.005	5.36E-05	0.099	-0.005	1.33E-03
cg10236687	EMP2	chr16	10626884	-0.011	5.65E-05	0.102	-0.009	1.94E-02
cg10839385	VSIG8	chr1	159825049	0.006	5.68E-05	0.102	0.004	8.76E-03
cg23479922	MARCH11	chr5	16179633	-0.010	5.85E-05	0.103	-0.009	1.43E-02
cg11356547	ZFR	chr5	32355062	0.010	5.96E-05	0.103	0.007	2.89E-02
cg04189320	KLF13	chr15	31691214	-0.005	5.98E-05	0.103	-0.005	1.72E-02
cg20143111	CLNK	chr4	10673188	0.003	5.98E-05	0.103	0.002	4.81E-02
cg16660971	RPTOR	chr17	78860029	0.011	5.97E-05	0.103	0.017	1.03E-04
cg19235307	IFT122	chr3	129160154	-0.007	6.25E-05	0.104	-0.006	4.67E-03
cg15246238	FSCN1	chr7	5635134	-0.010	6.41E-05	0.105	-0.019	1.32E-06
cg07791897	MAP3K1	chr5	55897584	0.007	6.39E-05	0.105	0.006	1.03E-02
cg13442969	DYRK2	chr12	68044208	-0.007	6.52E-05	0.105	-0.006	1.18E-02
cg09277709	FBXO46	chr19	46224285	0.007	6.52E-05	0.105	0.009	1.87E-03
cg07552087	MLST8	chr16	2258457	0.005	6.62E-05	0.105	0.005	9.28E-03
cg11311053	NCOR2	chr12	124912049	0.006	6.70E-05	0.105	0.013	5.07E-09
cg10626063	SPRED3	chr19	38881032	0.011	6.87E-05	0.106	0.023	1.86E-06

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cg20930290	RPS6KA4	chr11	64138764	0.007	7.30E-05	0.108	0.004	3.42E-02
cg20610950	SEC14L1	chr17	75096202	0.012	7.93E-05	0.112	0.021	9.21E-05
cg05919456	PXDC1	chr6	3722818	-0.009	8.02E-05	0.113	-0.008	2.65E-02
cg10836392	SULT4A1	chr22	44258132	-0.008	8.86E-05	0.118	-0.007	2.85E-02
cg16815625	TRAPPC9	chr8	141229477	0.011	9.19E-05	0.119	0.009	3.89E-02
cg13871900	SLC38A10	chr17	79235968	0.008	9.14E-05	0.119	0.008	1.03E-02
cg23565821	CUTA	chr6	33385056	-0.007	9.36E-05	0.119	-0.016	8.09E-08
cg07781445	RAP1GAP2	chr17	2886250	0.006	9.35E-05	0.119	0.007	6.06E-03
cg04172533	NOD2	chr16	50743027	-0.005	9.43E-05	0.119	-0.004	3.26E-02
cg00159243	SELPLG	chr12	109023799	-0.007	9.61E-05	0.119	-0.011	1.10E-06
cg04777348	GFI1	chr1	92952897	-0.007	9.77E-05	0.120	-0.012	3.10E-05
cg02027561	NCOA7	chr6	126110790	-0.008	1.01E-04	0.121	-0.006	4.69E-02
cg17879299	DDR1	chr6	30860300	0.015	9.97E-05	0.120	0.019	1.91E-03
cg06636316	CCNE1	chr19	30303495	-0.006	1.07E-04	0.123	-0.006	9.50E-04
cg05006142	RP5-1086L22.1	chr6	170536124	0.011	1.08E-04	0.124	0.015	1.69E-04
cg00695799	ZC3H12D	chr6	149803087	-0.007	1.09E-04	0.125	-0.007	4.55E-05
cg03897436	UNKL	chr16	1425469	0.004	1.20E-04	0.131	0.004	2.59E-02
cg00390724	SATB1	chr3	18484742	-0.013	1.22E-04	0.132	-0.010	4.03E-02
cg10552523	IFITM1	chr11	313478	-0.010	1.24E-04	0.132	-0.009	1.43E-02
cg06902929	PPT2	chr6	32123258	-0.004	1.27E-04	0.134	-0.005	9.64E-03
cg07558761	SLC7A5	chr16	87866696	0.007	1.32E-04	0.135	0.008	1.48E-02
cg26687842	FOXO1	chr13	41055491	0.007	1.36E-04	0.136	0.011	7.66E-05
cg18431951	PUF60	chr8	144906507	0.008	1.39E-04	0.136	0.007	3.72E-02
cg10134910	RNF212	chr4	1076041	-0.006	1.42E-04	0.139	-0.009	1.63E-03
cg00834988	AUTS2	chr7	70060153	0.008	1.42E-04	0.139	0.006	2.22E-02
cg07021906	SLC7A5	chr16	87866833	0.008	1.43E-04	0.139	0.014	1.76E-04
cg25338134	GXYLT2	chr3	72940510	-0.006	1.45E-04	0.139	-0.006	3.99E-03
cg09778958	LRFN3	chr19	36427721	-0.006	1.46E-04	0.139	-0.006	7.65E-03
cg02203067	SLC7A5	chr16	87866800	0.006	1.47E-04	0.139	0.006	1.49E-02
cg22091236	RPTOR	chr17	78853966	0.007	1.52E-04	0.141	0.005	3.48E-02
cg03620886	FDX1L	chr19	10420353	-0.003	1.52E-04	0.141	-0.003	3.93E-02
cg10987503	GET4	chr7	922825	0.006	1.52E-04	0.141	0.009	2.34E-03
cg15742245	CD177	chr19	43857717	0.011	1.55E-04	0.142	0.014	7.99E-03
cg21302812	CDC37	chr19	10506915	0.004	1.59E-04	0.142	0.005	1.16E-02
cg06647844	MRPL19	chr2	75888565	0.006	1.59E-04	0.142	0.007	3.19E-02
cg07328664	DIS3L2	chr2	233125062	0.005	1.62E-04	0.143	0.004	3.79E-02
cg00933443	DBR1	chr3	137892432	-0.005	1.62E-04	0.143	-0.004	4.99E-02
cg19190163	PSMB8	chr6	32810785	-0.007	1.63E-04	0.143	-0.007	7.63E-03
cg02731632	UNCX	chr7	1328627	-0.004	1.64E-04	0.143	-0.004	8.03E-03
cg25290355	LENG9	chr19	54975087	0.012	1.71E-04	0.147	0.007	1.43E-02
cg23606421	ENTPD8	chr9	140330621	-0.005	1.73E-04	0.148	-0.007	6.13E-03
cg21220247	KIAA0125	chr14	106321936	-0.008	1.77E-04	0.149	-0.010	1.86E-03
cg00916854	VPS37B	chr12	123350361	0.005	1.85E-04	0.152	0.005	1.82E-02
cg12754982	IGF2R	chr6	160409942	0.008	1.86E-04	0.152	0.008	2.42E-02

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cg07336872	ULBP3	chr6	150393535	-0.008	1.88E-04	0.152	-0.007	2.63E-02
cg21746997	BMPR1B	chr4	95679381	-0.007	1.96E-04	0.155	-0.005	4.27E-02
cg13171679	GOLGA7	chr8	41258634	-0.005	1.98E-04	0.155	-0.004	1.93E-02
cg17636309	EEF1D	chr8	144672242	0.007	2.06E-04	0.158	0.007	2.96E-02
cg03370704	MIR143HG	chr5	148785408	-0.015	2.11E-04	0.159	-0.013	4.08E-02
cg14078053	IRS1	chr2	227661656	0.006	2.15E-04	0.160	0.011	1.20E-04
cg05028773	LOC284454	chr19	13947162	-0.004	2.15E-04	0.160	-0.004	9.82E-03
cg20566897	IFITM1	chr11	313527	-0.010	2.18E-04	0.160	-0.008	1.48E-02
cg21019522	SLC22A18AS	chr11	2920789	-0.005	2.27E-04	0.164	-0.005	1.22E-03
cg24502330	CDA	chr1	20914028	-0.006	2.32E-04	0.164	-0.005	1.56E-02
cg16931076	WNT5B	chr12	1702001	-0.007	2.31E-04	0.164	-0.012	1.23E-06
cg07979747	DDR1	chr6	30860136	0.007	2.31E-04	0.164	0.007	4.54E-02
cg25647583	FES	chr15	91427184	-0.005	2.33E-04	0.164	-0.003	1.26E-02
cg03940776	SYNJ2	chr6	158490013	-0.005	2.40E-04	0.167	-0.004	3.11E-02
cg22964469	SORL1	chr11	121337508	-0.005	2.49E-04	0.170	-0.006	6.97E-04
cg09665571	TBCD	chr17	80861008	0.006	2.48E-04	0.170	0.007	3.89E-03
cg07722722	C1orf228	chr1	45187551	0.009	2.55E-04	0.171	0.004	4.90E-02
cg20562447	CPT1A	chr11	68611596	0.004	2.53E-04	0.171	0.003	2.43E-02
cg14986464	ABHD16A	chr6	31669902	-0.005	2.60E-04	0.172	-0.009	3.85E-05
cg00294109	CRBN	chr3	3219781	-0.004	2.60E-04	0.172	-0.003	3.12E-02
cg27241044	BASP1P1	chr13	23499838	-0.007	2.64E-04	0.172	-0.009	9.35E-03
cg17368760	THBD	chr20	23029287	-0.007	2.68E-04	0.173	-0.006	7.17E-03
cg18532239	CEP72	chr5	619883	0.005	2.64E-04	0.172	0.004	2.20E-02
cg25767870	FAM46C	chr1	118188756	0.006	2.69E-04	0.173	0.006	1.56E-02
cg05541096	TTLL11	chr9	124854664	-0.005	2.86E-04	0.177	-0.010	3.76E-07
cg16568360	TAOK2	chr16	29987261	-0.005	2.86E-04	0.177	-0.006	1.02E-03
cg20054248	IKZF4	chr12	56414508	-0.004	2.89E-04	0.177	-0.003	1.60E-02
cg22675767	ACAP3	chr1	1234367	0.005	2.97E-04	0.179	0.004	3.88E-02
cg12002745	FAM83A	chr8	124179875	-0.004	3.10E-04	0.182	-0.004	7.12E-03
cg17126555	ICAM3	chr19	10445516	0.006	3.17E-04	0.183	0.006	2.21E-02
cg17343451	AP2M1	chr3	183899704	0.006	3.20E-04	0.184	0.007	7.39E-03
cg20817228	LINC00623	chr1	149614778	0.007	3.33E-04	0.186	0.008	1.86E-02
cg26076905	PIK3R1	chr5	67522298	0.006	3.44E-04	0.191	0.005	1.38E-02
cg09801824	DNAJB12	chr10	74076930	-0.005	3.54E-04	0.193	-0.004	2.07E-03
cg03459202	DIP2C	chr10	676740	-0.003	3.57E-04	0.193	-0.004	1.10E-02
cg23344523	IGF2R	chr6	160380572	0.006	3.60E-04	0.193	0.007	4.45E-03
cg22996004	PNPO	chr17	46018654	0.007	3.63E-04	0.193	0.006	6.19E-03
cg15943584	EIF2B2	chr14	75472643	-0.006	3.63E-04	0.193	-0.006	8.71E-03
cg06784563	NFATC1	chr18	77284509	-0.006	3.67E-04	0.193	-0.007	1.29E-03
cg23622878	PWWP2B	chr10	134225120	0.006	3.70E-04	0.193	0.005	3.33E-02
cg08933467	FCRL1	chr1	157776690	-0.004	3.69E-04	0.193	-0.005	2.31E-03
cg27225680	GALK1	chr17	73760817	0.004	3.92E-04	0.197	0.003	8.12E-04
cg27300045	ZC3H4	chr19	47610813	-0.004	3.93E-04	0.197	-0.004	1.58E-03
cg09868768	ASPRV1	chr2	70188605	0.007	3.98E-04	0.198	0.006	2.97E-02

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cg20914572	PRRT1	chr6	32119874	-0.006	4.04E-04	0.198	-0.005	4.71E-03

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eTable 4. SZ-associated DMPs (stratified analysis, males only)

Probe	Illumina annotation (nearest gene)	chr	position	Discovery set (N=750)			Replication set (N=497)	
				Δ Beta	P Value	FDR	Δ Beta	P Value
cg13092108	RPS6KA1	chr1	26857284	-0.011	5.64E-08	0.009	-0.008	9.80E-04
cg04792777	KIAA0125	chr14	106322429	-0.008	5.52E-06	0.094	-0.007	5.45E-03
cg23565821	CUTA	chr6	33385056	-0.011	6.71E-06	0.096	-0.013	1.88E-04
cg14986464	ABHD16A	chr6	31669902	-0.008	6.84E-06	0.096	-0.008	2.32E-03
cg14326196	KIF12	chr9	116860650	-0.023	8.44E-06	0.096	-0.013	3.48E-02
cg10626063	SPRED3	chr19	38881032	0.016	9.87E-06	0.104	0.027	4.23E-07
cg04962621	MGRN1	chr16	4714733	-0.009	1.27E-05	0.109	-0.007	3.02E-04
cg08933467	FCRL1	chr1	157776690	-0.006	1.65E-05	0.126	-0.005	4.32E-03
cg10785394	FAM20B	chr1	178993006	-0.009	1.83E-05	0.127	-0.007	8.24E-03
cg05541096	TTLL11	chr9	124854664	-0.008	1.85E-05	0.127	-0.011	7.00E-07
cg16660971	RPTOR	chr17	78860029	0.015	1.92E-05	0.129	0.016	1.95E-03
cg11621113	MAN2B1	chr19	12776725	-0.009	1.94E-05	0.129	-0.012	1.83E-06
cg10615591	RTEL1	chr20	62318433	-0.008	2.51E-05	0.133	-0.007	1.50E-02
cg09778958	LRFN3	chr19	36427721	-0.009	2.64E-05	0.133	-0.006	1.60E-02
cg11597902	SEC14L1	chr17	75096239	0.012	2.97E-05	0.137	0.010	3.41E-03
cg06096184	LRIG1	chr3	66549732	-0.009	4.24E-05	0.155	-0.005	2.75E-02
cg06682039	RP5-1086L22.1	chr6	170536047	0.014	4.45E-05	0.156	0.008	2.58E-02
cg25647583	FES	chr15	91427184	-0.007	4.96E-05	0.159	-0.004	8.06E-03
cg16568360	TAOK2	chr16	29987261	-0.007	5.66E-05	0.166	-0.007	1.47E-03
cg10836392	SULT4A1	chr22	44258132	-0.010	5.74E-05	0.166	-0.010	1.31E-02
cg14239983	SORL1	chr11	121337384	-0.008	8.16E-05	0.186	-0.008	2.73E-03
cg23968113	SNTG2	chr2	1234756	-0.004	8.99E-05	0.190	-0.003	4.39E-02
cg05006142	RP5-1086L22.1	chr6	170536124	0.014	9.94E-05	0.194	0.018	1.64E-04

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eTable 5. SZ-associated DMPs (stratified analysis, only non-African Americans)

Probe	Illumina annotation (nearest gene)	chr	position	Discovery set (N=677)			Replication set (N=497)	
				Δ Beta	P Value	FDR	Δ Beta	P Value
cg15132169	ZC3H12D	chr6	149805995	-0.017	4.92081E-07	0.028	-0.008	1.93E-02
cg22891595	RP11-699L21.1	chr3	193570256	0.013	7.33932E-06	0.073	0.006	4.98E-02
cg09502149	SLC2A1	chr1	43406792	0.011	1.08666E-05	0.087	0.006	2.23E-02
cg11699125	ACOT7	chr1	6341327	0.006	0.000011777	0.090	0.004	6.32E-03
cg13549638	RPTOR	chr17	78860076	0.014	1.26229E-05	0.090	0.008	3.72E-02
cg09249800	ACOT7	chr1	6341287	0.005	1.38433E-05	0.090	0.003	9.78E-03
cg13136655	ZC3H12D	chr6	149806131	-0.012	0.000014062	0.090	-0.005	2.12E-02
cg04983687	ZFPM1	chr16	88558223	0.007	1.81063E-05	0.098	0.006	4.61E-04
cg09802688	TRAF3IP3	chr1	209942066	-0.011	1.95438E-05	0.099	-0.007	1.55E-03
cg22344793	TRIM29	chr11	120039642	-0.008	2.23543E-05	0.104	-0.003	3.92E-02
cg00390724	SATB1	chr3	18484742	-0.021	2.22985E-05	0.104	-0.010	4.03E-02
cg16660971	RPTOR	chr17	78860029	0.016	2.32846E-05	0.104	0.017	1.03E-04
cg18082788	ZC3H12D	chr6	149806339	-0.017	2.56209E-05	0.105	-0.008	3.61E-02
cg23479922	MARCH11	chr5	16179633	-0.017	3.17613E-05	0.116	-0.009	1.43E-02
cg09391371	PDCD1	chr2	242790370	-0.005	3.36901E-05	0.120	-0.004	1.35E-03
cg13997435	S100A2	chr1	153538406	-0.008	3.90229E-05	0.130	-0.005	2.77E-02
cg14389122	EDC3	chr15	74945851	-0.009	4.38037E-05	0.136	-0.007	3.89E-03
cg10836392	SULT4A1	chr22	44258132	-0.012	4.44516E-05	0.136	-0.007	2.85E-02
cg00812833	PLD5	chr1	242687412	-0.006	6.16995E-05	0.152	-0.003	3.34E-02
cg21019522	SLC22A18AS	chr11	2920789	-0.007	7.18738E-05	0.161	-0.005	1.22E-03
cg19003304	TOX	chr8	60029914	0.006	7.35323E-05	0.161	0.003	2.22E-02
cg12946371	NDUFC2-KCTD14	chr11	77757383	0.004	0.000090358	0.168	0.002	2.95E-02
cg00682367	RP11-290F20.1	chr20	48963280	-0.007	9.40389E-05	0.168	-0.004	2.00E-03
cg13046440	UBE3A	chr15	25684837	0.008	9.44532E-05	0.168	0.004	7.85E-03
cg08940169	ZFPM1	chr16	88540241	0.005	9.75324E-05	0.169	0.006	2.87E-05
cg09308580	ZFP36L2	chr2	43405947	-0.007	0.000110849	0.172	-0.004	8.91E-03
cg07458272	KIAA0355	chr19	34744396	0.011	0.000130475	0.184	0.007	2.10E-02
cg04276536	CCDC102A	chr16	57567813	-0.006	0.000134158	0.186	-0.005	9.43E-04
cg22887491	NTM	chr11	131618277	0.006	0.000150868	0.193	0.002	3.22E-02

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eTable 6. SZ-associated DMPs (stratified analysis, only African Americans, first 100 DMPs)

Probe	Illumina annotation (nearest gene)	chr	position	Discovery study (N=657)			Replication study (N=497)	
				Δ Beta	P Value	FDR	Δ Beta	P Value
cg23565821	CUTA	chr6	33385056	-0.014	5.30E-08	0.004	-0.016	8.09E-08
cg14114377	MARK4	chr19	45756845	-0.013	1.55E-07	0.006	-0.008	1.31E-03
cg12939085	PPP1CA	chr11	67166104	0.012	2.87E-07	0.008	0.006	4.65E-03
cg07722722	C1orf228	chr1	45187551	0.018	2.96E-07	0.008	0.004	4.90E-02
cg05419096	LINC00443	chr13	107467865	-0.010	4.17E-07	0.009	-0.005	1.73E-02
cg19190163	PSMB8	chr6	32810785	-0.014	4.87E-07	0.010	-0.007	7.63E-03
cg12582905	IFITM2	chr11	310771	-0.006	7.88E-07	0.012	-0.002	2.00E-02
cg20170777	COX10-AS1	chr17	13972099	-0.015	8.89E-07	0.014	-0.009	1.47E-02
cg07622001	AC008697.1	chr5	158758903	-0.009	1.11E-06	0.014	-0.005	5.56E-04
cg19465320	STAT5B	chr17	40426890	-0.012	1.29E-06	0.015	-0.010	1.29E-04
cg11977605	RNF212	chr4	1076247	-0.010	1.86E-06	0.017	-0.005	7.14E-04
cg03762242	GAS7	chr17	9940004	-0.008	3.99E-06	0.025	-0.003	2.69E-02
cg01435039	PTCHD3P1	chr10	29700804	-0.008	4.68E-06	0.026	-0.006	7.95E-04
cg19939130	IFI16	chr1	158978468	-0.012	5.30E-06	0.028	-0.006	3.23E-02
cg23429047	HS6ST1	chr2	129028542	0.009	5.63E-06	0.028	0.004	1.48E-02
cg00417304	PRDM11	chr11	45124456	-0.014	5.58E-06	0.028	-0.013	2.95E-05
cg18906043	GRAP	chr17	18967111	-0.007	5.96E-06	0.028	-0.003	5.15E-03
cg07678266	GLT1D1	chr12	129444630	0.021	8.37E-06	0.034	0.011	4.42E-02
cg03147185	NCAPH	chr2	97008030	-0.009	8.82E-06	0.035	-0.007	8.75E-04
cg25247520	PVT1	chr8	128808017	-0.011	9.87E-06	0.037	-0.010	3.04E-04
cg03438552	TAP2	chr6	32805548	-0.013	1.01E-05	0.037	-0.006	4.11E-02
cg00094412	GABBR1	chr6	29592854	-0.013	1.04E-05	0.037	-0.007	2.34E-02
cg13092108	RPS6KA1	chr1	26857284	-0.011	1.09E-05	0.037	-0.009	4.38E-05
cg09605818	TRPV1	chr17	3489147	0.006	1.10E-05	0.037	0.004	8.14E-03
cg19235307	IFT122	chr3	129160154	-0.013	1.15E-05	0.037	-0.006	4.67E-03
cg16472834	AC098823.3	chr2	231533021	-0.014	1.18E-05	0.037	-0.005	3.96E-02
cg26581729	NPDC1	chr9	139939792	-0.014	1.22E-05	0.037	-0.016	1.72E-07
cg11356290	ZCWPW2	chr3	28390998	-0.002	1.25E-05	0.037	-0.001	4.13E-02
cg20930290	RPS6KA4	chr11	64138764	0.010	1.39E-05	0.039	0.004	3.42E-02
cg01062024	IMPDH2	chr3	49065979	-0.013	1.48E-05	0.039	-0.008	7.77E-03
cg02220008	PHACTR1	chr6	13192742	-0.011	1.51E-05	0.039	-0.007	2.21E-02
cg24351076	ITPRIPL1	chr2	96992044	-0.010	1.55E-05	0.039	-0.005	2.11E-02
cg20842997	UGDH-AS1	chr4	39529386	-0.008	1.58E-05	0.039	-0.003	3.28E-02
cg16778018	MGRN1	chr16	4736225	0.011	1.70E-05	0.041	0.006	4.31E-02
cg23965590	CBL	chr11	119133451	-0.010	1.78E-05	0.042	-0.008	6.70E-04
cg14827056	AGO2	chr8	141550539	0.008	1.81E-05	0.042	0.004	4.65E-02
cg20384132	RANBP3L	chr5	36302349	0.016	1.81E-05	0.042	0.007	2.03E-02
cg11186858	SEC14L1	chr17	75096382	0.014	2.03E-05	0.045	0.014	1.38E-04
cg19845878	TACC3	chr4	1742857	0.009	2.19E-05	0.046	0.008	1.74E-03

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cg04172533	NOD2	chr16	50743027	-0.008	2.36E-05	0.048	-0.004	3.26E-02
cg08880817	TXNDC5	chr6	7909642	-0.009	2.50E-05	0.049	-0.003	4.46E-02
cg11356547	ZFR	chr5	32355062	0.016	2.50E-05	0.049	0.007	2.89E-02
cg02505676	ACSF3	chr16	89220516	0.005	2.55E-05	0.049	0.003	3.80E-03
cg25628989	SSRP1	chr11	57093345	-0.017	2.64E-05	0.049	-0.010	3.73E-02
cg19769147	PACS2	chr14	105860954	0.013	2.90E-05	0.051	0.007	2.27E-02
cg05438719	CMIP	chr16	81476518	-0.008	2.96E-05	0.051	-0.004	4.56E-02
cg18529294	CENPO	chr2	25016799	-0.004	3.09E-05	0.052	-0.002	3.52E-02
cg23962746	MIR205HG	chr1	209105888	-0.010	3.17E-05	0.053	-0.005	4.53E-02
ch.3.638689R	GADL1	chr3	31240746	-0.003	3.25E-05	0.054	-0.001	4.28E-02
cg15922057	KSR1	chr17	25784714	-0.010	3.36E-05	0.055	-0.004	1.31E-02
cg14741228	FAM60A	chr12	31476479	-0.008	3.41E-05	0.055	-0.005	1.33E-03
cg24143729	RASA3	chr13	114820861	0.007	3.47E-05	0.055	0.007	1.61E-03
cg26812615	MAP1LC3B2	chr12	116996773	-0.008	3.67E-05	0.056	-0.007	5.41E-03
cg08932533	CD47	chr3	107812758	0.008	3.68E-05	0.056	0.004	3.30E-02
cg11003133	AIM2	chr1	159046391	-0.013	3.75E-05	0.056	-0.008	1.33E-02
cg21742048	NEURL1B	chr5	172099681	-0.010	3.79E-05	0.056	-0.005	4.42E-02
cg23222278	LINC00312	chr3	8623867	-0.007	3.83E-05	0.056	-0.004	1.40E-02
cg19668951	SLC39A13	chr11	47430812	-0.009	3.94E-05	0.057	-0.010	7.69E-07
cg09132240	NCOR2	chr12	124922727	0.008	4.58E-05	0.061	0.006	2.97E-03
cg12619262	CHST12	chr7	2480493	0.021	4.69E-05	0.061	0.012	7.44E-03
ch.2.113772948R	PAX8	chr2	114056478	-0.005	4.88E-05	0.062	-0.001	3.27E-02
cg16111190	DDR1	chr6	30860887	0.016	5.40E-05	0.065	0.009	1.27E-02
cg05146536	FAM47E	chr4	77140678	-0.007	5.46E-05	0.065	-0.003	2.91E-02
cg04962621	MGRN1	chr16	4714733	-0.011	5.93E-05	0.066	-0.007	6.95E-05
cg01408817	FXYD3	chr19	35606534	-0.008	5.88E-05	0.066	-0.005	1.48E-02
cg15072976	GAL3ST2	chr2	242715549	0.011	6.12E-05	0.067	0.006	2.10E-02
cg08112313	XRCC1	chr19	44079105	-0.008	6.67E-05	0.070	-0.005	2.54E-02
cg16568360	TAOK2	chr16	29987261	-0.008	6.66E-05	0.070	-0.006	1.02E-03
cg02772266	PARP11	chr12	4060781	0.008	6.91E-05	0.070	0.005	1.13E-02
cg04239024	CENPE	chr4	104119155	-0.005	6.98E-05	0.070	-0.002	2.18E-02
cg14986464	ABHD16A	chr6	31669902	-0.009	6.97E-05	0.070	-0.009	3.85E-05
cg15921436	ARL17A	chr17	44337874	-0.008	7.01E-05	0.070	-0.006	4.76E-02
cg23542902	HES1	chr3	193807749	-0.008	7.20E-05	0.070	-0.004	1.47E-02
cg19835796	ZNF608	chr5	123637793	-0.006	7.17E-05	0.070	-0.004	4.51E-02
cg02100497	DAPK1	chr9	90273707	-0.007	7.39E-05	0.070	-0.004	3.47E-02
cg10921517	MOB2	chr11	1520881	0.006	7.43E-05	0.070	0.003	4.92E-02
cg27115863	CARD10	chr22	37921640	-0.016	7.48E-05	0.070	-0.011	1.30E-03
cg05809481	ISG20L2	chr1	156696467	-0.012	7.53E-05	0.071	-0.006	2.68E-02
cg02023550	GPC1	chr2	241294007	-0.007	7.73E-05	0.071	-0.005	3.70E-03
cg22515589	BAHCC1	chr17	79426432	0.011	7.85E-05	0.071	0.007	2.73E-02
cg09247619	PTPRC	chr1	198648849	-0.009	7.95E-05	0.071	-0.006	6.09E-03
cg22422264	USP8	chr15	50792856	0.014	7.98E-05	0.071	0.012	1.64E-03

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cg23009327	TCF3	chr19	1630248	0.012	8.12E-05	0.071	0.007	7.92E-03
cg03897436	UNKL	chr16	1425469	0.007	8.49E-05	0.073	0.004	2.59E-02
cg01511901	HMGB1	chr13	31004719	-0.011	8.83E-05	0.073	-0.006	1.76E-02
cg16759443	ACSF3	chr16	89200506	0.005	8.90E-05	0.073	0.003	4.57E-02
cg13442969	DYRK2	chr12	68044208	-0.011	8.92E-05	0.073	-0.006	1.18E-02
cg22052056	DNMT3B	chr20	31351813	-0.010	9.10E-05	0.073	-0.006	4.55E-02
cg06696905	PDE12	chr3	57539284	-0.007	9.48E-05	0.075	-0.004	3.08E-02
cg26385126	NCOR2	chr12	124912021	0.007	9.96E-05	0.077	0.010	3.91E-07
cg14819242	GRAMD3	chr5	125782749	-0.008	1.02E-04	0.077	-0.005	1.05E-02
cg22129111	ALOXE3	chr17	8009699	-0.008	1.02E-04	0.077	-0.005	1.89E-02
cg01765406	HS6ST1	chr2	129231478	-0.009	1.04E-04	0.077	-0.006	1.46E-02
cg22940798	TAP2	chr6	32805554	-0.011	1.07E-04	0.078	-0.006	3.53E-02
cg10919344	OR5A1	chr11	59210634	-0.010	1.12E-04	0.079	-0.006	2.74E-02
cg09186031	METTL9	chr16	21677966	-0.010	1.12E-04	0.079	-0.008	5.02E-05
cg12378753	ABLIM1	chr10	116527201	-0.011	1.14E-04	0.079	-0.011	3.99E-04
cg11344352	ERCC1	chr19	45927696	-0.013	1.15E-04	0.080	-0.008	6.94E-07
cg13463033	SEC16A	chr9	139360276	0.007	1.16E-04	0.080	0.005	5.66E-03
cg08348165	OR2A12	chr7	143791397	0.010	1.19E-04	0.081	0.008	1.60E-02

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eTable 7. Gene Ontology characterization of SZ-associated DMPs in blood

	GO.ID	Term	Annotated	Significant	Expected	Odds Ratio	p-value (FDR)
1	GO:0051056	regulation of small GTPase mediated signal transduction	546	15	4.69	3.56	0.114
2	GO:0031929	TOR signaling	60	5	0.51	10.88	0.114
3	GO:0009966	regulation of signal transduction	2487	38	21.34	2.12	0.114
4	GO:0023051	regulation of signaling	2773	41	23.80	2.07	0.114
5	GO:0010646	regulation of cell communication	2786	41	23.91	2.06	0.114
6	GO:0061462	protein localization to lysosome	16	3	0.14	27.26	0.148
7	GO:0051058	negative regulation of small GTPase mediated signal transduction	41	4	0.35	12.85	0.163
8	GO:0046578	regulation of Ras protein signal transduction	520	13	4.46	3.18	0.185
9	GO:0097264	self proteolysis	5	2	0.04	78.20	0.191
10	GO:0035556	intracellular signal transduction	2194	33	18.83	2.02	0.191
11	GO:0032006	regulation of TOR signaling	48	4	0.41	10.80	0.191
12	GO:0032007	negative regulation of TOR signaling	22	3	0.19	18.65	0.196
13	GO:0035023	regulation of Rho protein signal transduction	486	12	4.17	3.12	0.199
14	GO:0007264	small GTPase mediated signal transduction	488	12	4.19	3.11	0.199
15	GO:0008216	spermidine metabolic process	6	2	0.05	58.64	0.199

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eTable 8. meQTLs that overlap with SZ-SNPs from PGC

Probe	P Value	FDR	chr	position	SNPs	PGC Ranks
cg25647583	2.29E-07	2.55E-05	15	91428636	rs7177338	11
cg25647583	7.89E-06	0.000621	15	91428197	rs2071382	11

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