

Supplementary files

Supplementary Table 1. Pathway analysis of the top five results from MAGENTA.

Database	Gene set	ORIG _GS_ SIZE	EFF_ GS_ SIZE	MED_ GENE_ _SIZE_ _KB	MEAN_ GENE_ SIZE_KB	NOMINAL_ GSEA_PVAL_ 75PERC_ CUTOFF	FDR_75 PERC_ CUTOFF	OBS_GENES_ ABOVE_75 PERC_ CUTOFF
Panther	Panther	36	34	76	160	1.30×10^{-3}	8.66×10^{-2}	17
GOTERM	GOTERM	91	85	51	134	1.26×10^{-4}	2.74×10^{-1}	37
GOTERM	GOTERM	41	40	42	75	2.00×10^{-4}	3.09×10^{-1}	20
KEGG	KEGG	22	20	44	87	3.60×10^{-3}	3.43×10^{-1}	11
BIOCARTA	BIOCARTA	31	28	75	92	1.12×10^{-2}	4.15×10^{-1}	13

ORIG_GS_SIZE: original number of genes per gene set; EFF_GS_SIZE: effective number of genes per gene set analysed, after removing genes that were not assigned a gene score; MED_GENE_SIZE_KB: median gene size of all genes in gene set in kilobase units; MEAN_GENE_SIZE_KB: mean gene size of all genes in gene set in kilobase units; NOMINAL_GSEA_PVAL_75PERC_CUTOFF: GSEA *P*-value using 75 percentile of all gene scores for the enrichment cutoff; FDR_75PERC_CUTOFF: estimated false discovery rate (q-value)

using 75 percentile cutoff; OBS_GENES_ABOVE_75PERC_CUTOFF: observed number of genes with a corrected gene *P*-value above the 75 percentile enrichment cutoff.

Supplementary Table 2. eQTL analysis to evaluate the correlation between rs1346665 and nearby gene expression levels.

Chr	SNP	BP	GWAS <i>P</i> -value	Gene	eQTL <i>P</i> -value	Effect size	Tissue
7	rs10252923	90905041	2.01×10 ⁻⁶	<i>CDK14</i>	0.05	-0.16	Brain - Nucleus accumbens (basal ganglia)
				<i>FZD1</i>	0.01	-0.02	Esophagus - Gastroesophageal Junction

eQTL: expression quantitative trait locus; Chr: chromosome; SNP: single nucleotide polymorphism; BP: base pair; GWAS: genome-wide association study; *CDK14*: Cyclin Dependent Kinase 14; *FZD1*: Frizzled Class Receptor 1.

Supplementary Figure 1A. Principal component analysis plot of GWAS (genome-wide association study) of schizophrenia. All cases and controls together with the five super-population from the 1000 Genomes Project Phase III integrated release version 5 database (European: EUR; American: AMR; East Asian: EAS; South Asian: SAS and African: AFR) were plotted based on the first two eigenvectors.

([insert Supplementary Figure 1A])

Supplementary Figure 1B. Principal component analysis plot of GWAS (genome-wide association study) of schizophrenia. All retained cases and controls were plotted based on the first two eigenvectors.

([insert Supplementary Figure 1B])

Supplementary Figure 2. Quantile-quantile plot and λ_{GC} value for the association analysis result. Under the null hypothesis of no association at any locus, the points would be expected to follow the purple line ($y=x$). The genomic inflation factor (λ_{GC}) for the analysis is shown on the graph.

([insert Supplementary Figure 2])

Supplementary Figure 3. eQTL (expression quantitative trait locus) analysis of rs10252923 with *FZD1* (Frizzled Class Receptor 1) or *CDK14* (Cyclin Dependent Kinase 14) in different tissues. Homo ref stands for homozygotes for the reference allele, het stands for heterozygotes, and homo alt stands for homozygotes for the alternative allele.

([insert Supplementary Figure 3])

Supplementary Figure 4. GARFIELD functional enrichment analysis. Wheel plot displaying functional enrichment of associations with schizophrenia within DNase I hypersensitive site (DHS) peaks in ENCODE (Encyclopedia of DNA Elements) and Roadmap studies. Radial lines show the fold enrichment (FE) values calculated at seven different GWAS (genome-wide association study) P -value thresholds (10^{-1} to 10^{-7}) for each of 424 cell types. Cell types are sorted by tissue on the outer circle with font size proportional to the number of cell types from that tissue. Boxes and circles next to the tissue labels are coloured with respect to tissue (right legend). FE values at different thresholds are plotted with different colours on the inner side of the circle (e.g. $P < 10^{-4}$ in black, bottom legend). Dots in the outer ring of the circle denote significant enrichment (if present) at $P < 10^{-4}$ for a given cell type. Results show the largest FE values obtained in fetal brain tissues.

([insert Supplementary Figure 4])