Description of Additional Supplementary Files

Title: Supplementary Data 1:
Description: Number of individuals in each cohort. Columns include Cohort, cohort name; N, sample size; m, number of variants; Genotyping, genotyping method; and URL, source-data link. WGS: whole-genome sequencing.

Title: Supplementary Data 2:
Description: Significant ieQTLs identified across four brain cell types. Columns include CellType, brain cell type; phenotype_id, gene; variant_id, ieQTL; start_distance and end_distance, distances between the ieQTL and the gene; af, allele frequency; ma_samples and ma_count, minor-allele sample and count information; pval_g, b_g and b_g_se, P value, effect estimate and standard error for the genotype term; pval_i, b_i and b_i_se, P value, effect estimate and standard error for the cell-type-proportion term; pval_gi, b_gi and b_gi_se, P value, effect estimate and standard error for the genotype-by-cell-type-proportion interaction term; tests_emt, number of tests included in the empirical interaction test; pval_emt, P value from the empirical interaction test; pval_adj_bh, Benjamini–Hochberg-adjusted P value; eGeneType, gene category; SourceGene, source gene; and Direction, direction of the ieQTL effect. Regression tests were two-sided, and multiple testing was controlled using the Benjamini–Hochberg procedure. Significant ieQTLs were defined at FDR < 0.05.

Title: Supplementary Data 3:
Description: GWAS summary statistics. Columns include Trait, phenotype or trait name; Number of Cases and Number of Controls, numbers of cases and controls for binary traits; Sample Size, total GWAS sample size; Number of SNPs, number of SNPs analysed; Category, trait category; Population, study population; and Pubmed ID, PubMed identifier of the corresponding GWAS.

Title: Supplementary Data 4:
Description: Colocalization results from COLOC analyses. Columns include Cell, brain cell type; Trait, phenotype or trait; eGene, eGene identifier; eGene_chr and eGene_pos, eGene chromosome and genomic position; eGene_topSNP and eGene_topSNP_p, the top eQTL SNP and its P value; GWAS_topSNP and GWAS_topSNP_p, the top GWAS SNP and its P value; nsnp, number of SNPs included in the colocalization analysis; PP.H0–PP.H4, posterior probabilities for the five COLOC hypotheses; eGeneType, gene category; ieQTL_FDR, false-discovery rate; and ieQTLDirection, ieQTL direction.

Title: Supplementary Data 5:
Description: Summary-based Mendelian randomization (SMR) results. Columns include Cell, brain cell type; Trait, trait; probeID, Ensembl ID; ProbeChr and Probe_bp, probe chromosome and genomic position; Gene, gene symbol; topSNP, top SNP; topSNP_chr and topSNP_bp, top SNP chromosome and genomic position; A1 and A2, effect and alternative alleles; Freq, allele frequency; b_GWAS, se_GWAS and p_GWAS, GWAS effect estimate, standard error and P

value; b_eQTL, se_eQTL and p_eQTL, eQTL effect estimate, standard error and P value; b_SMR, se_SMR and p_SMR, SMR effect estimate, standard error and P value; p_HEIDI, HEIDI-test P value; nsnp_HEIDI, number of SNPs included in the HEIDI test; eGeneType, gene category; ieQTL_FDR, false-discovery rate; and ieQTLDirection, ieQTL direction.