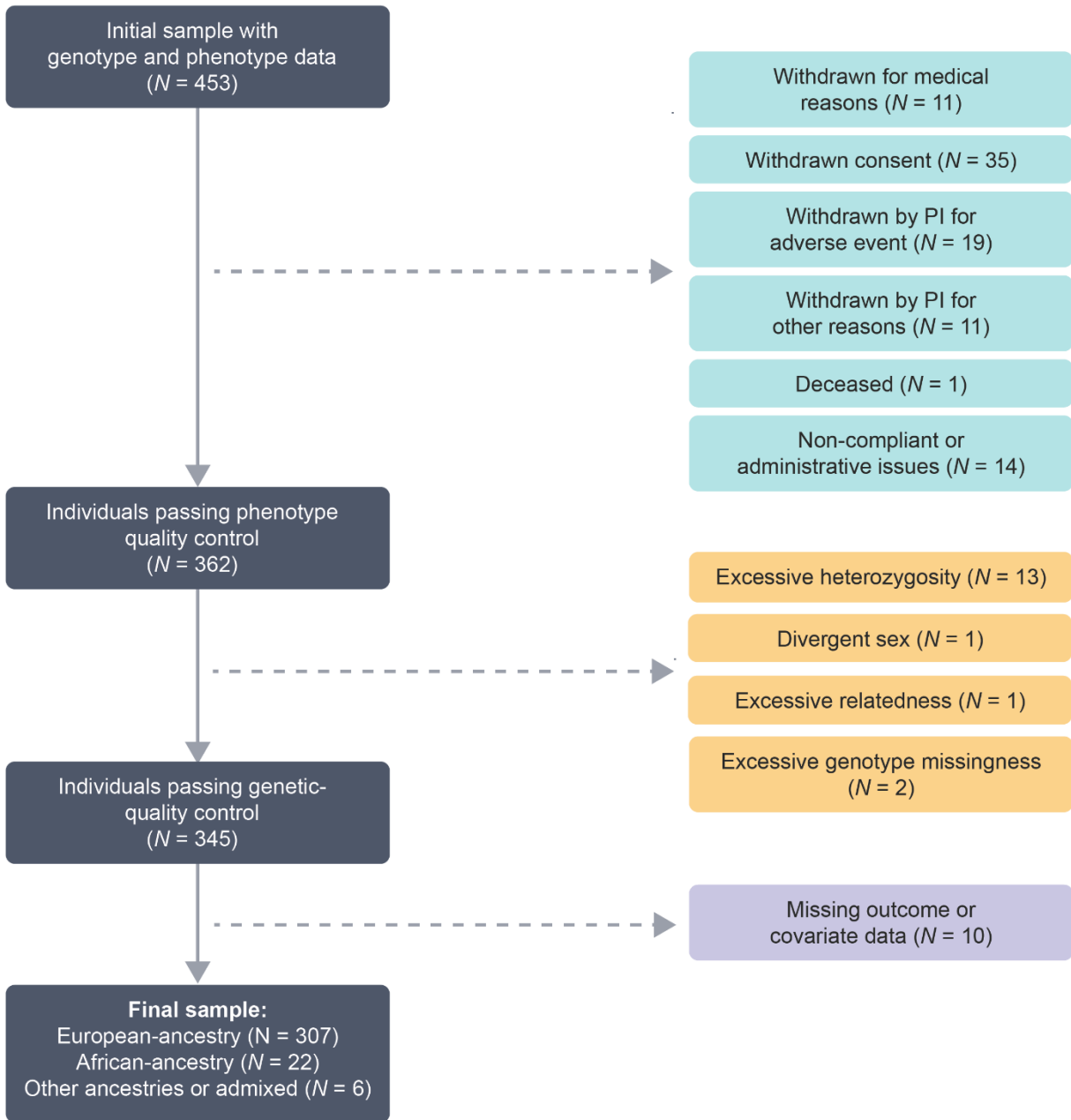
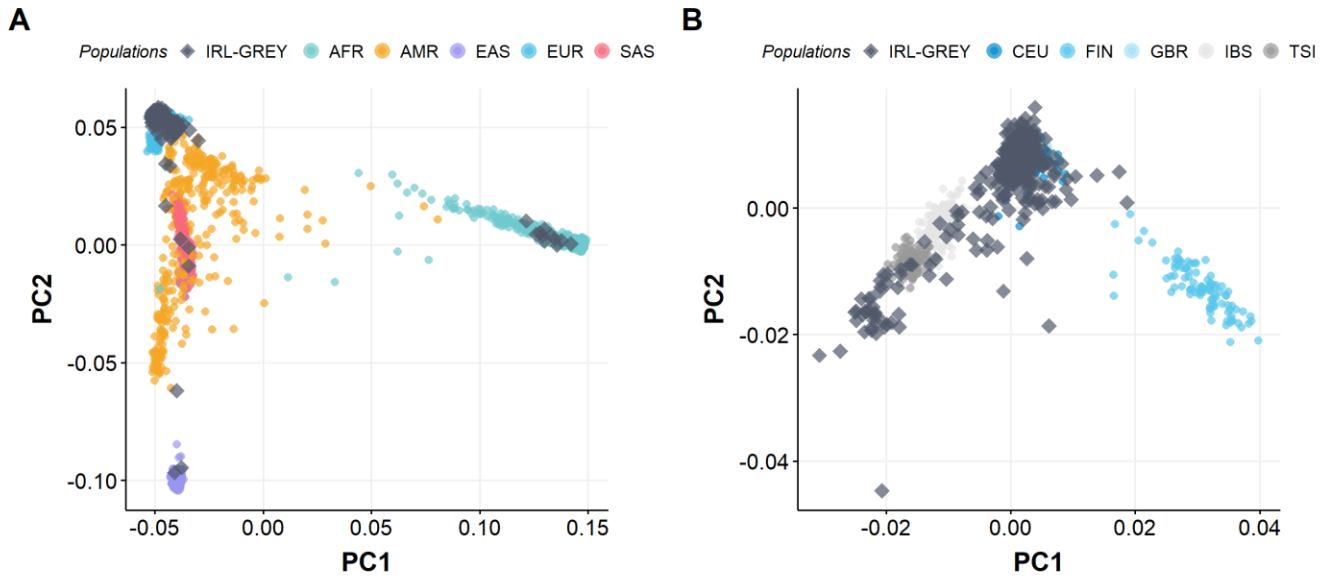


### Supplementary Figures

Genome-wide analysis suggests the importance of vascular processes and neuroinflammation in late-life antidepressant response

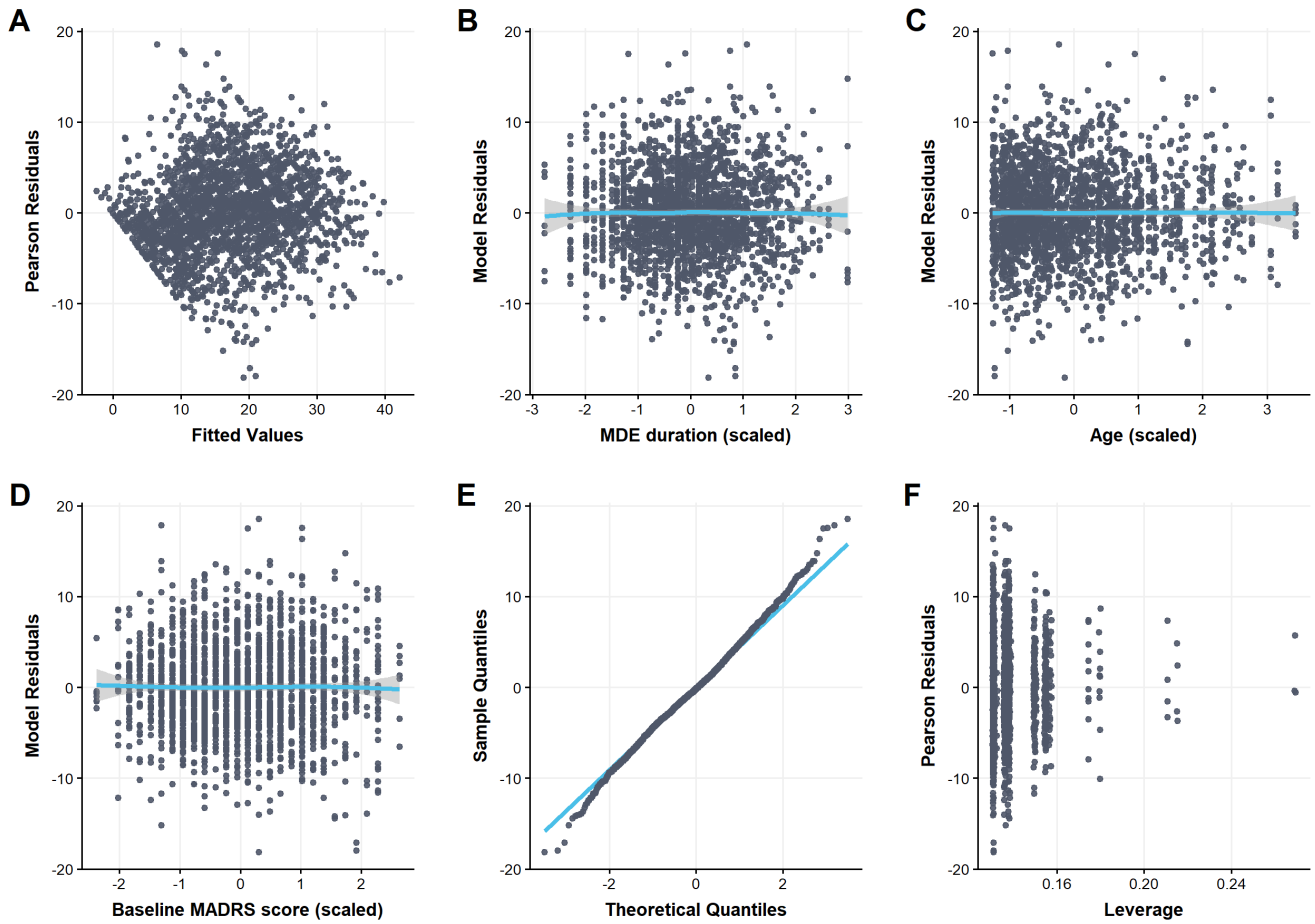


**Supplementary Figure 1.** Sample selection flow diagram.



**Supplementary Figure 2.** Ancestry analysis.

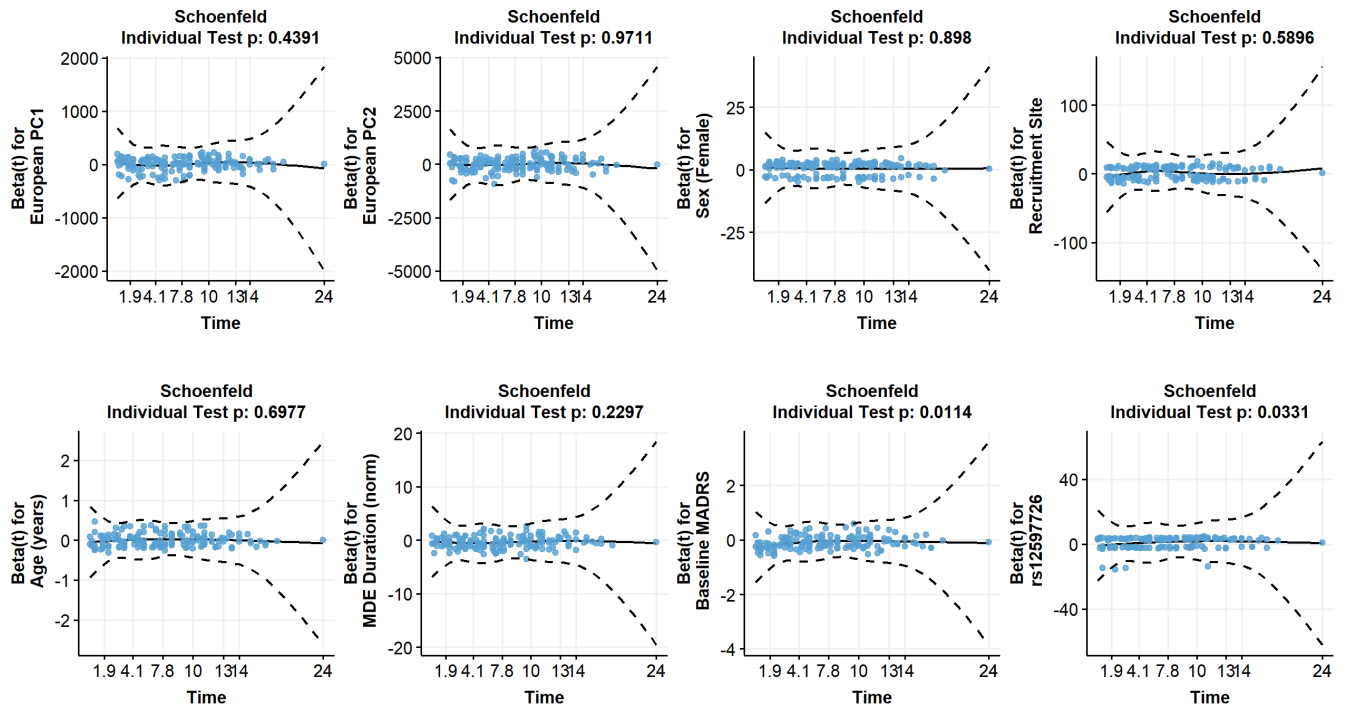
Principal component analysis in the total, mixed-ancestry sample ( $N=345$ ) and European sub-sample ( $N=307$ ) across four extracted principal components.



**Supplementary Figure 3.** Diagnostics of linear mixed-effects models.

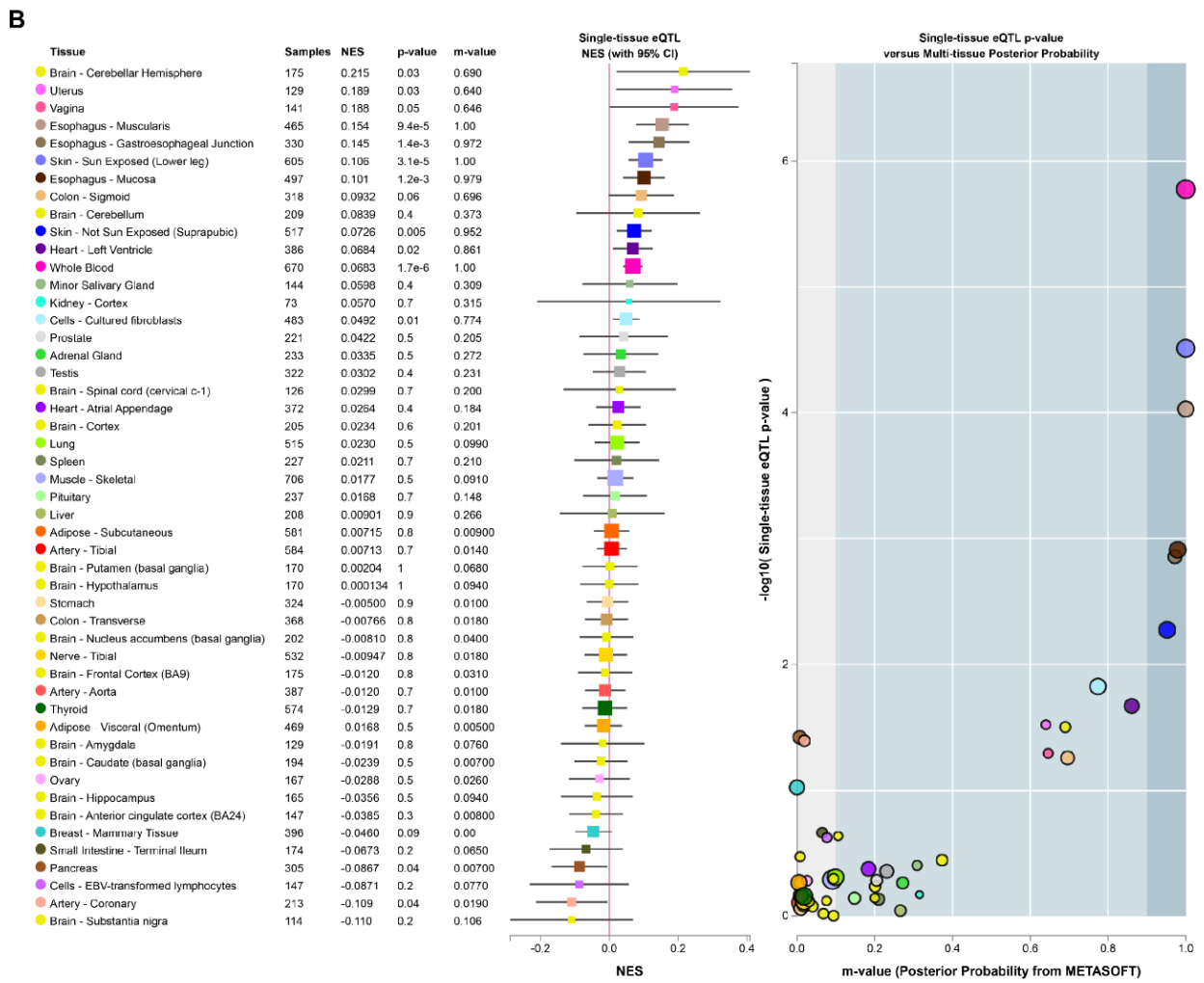
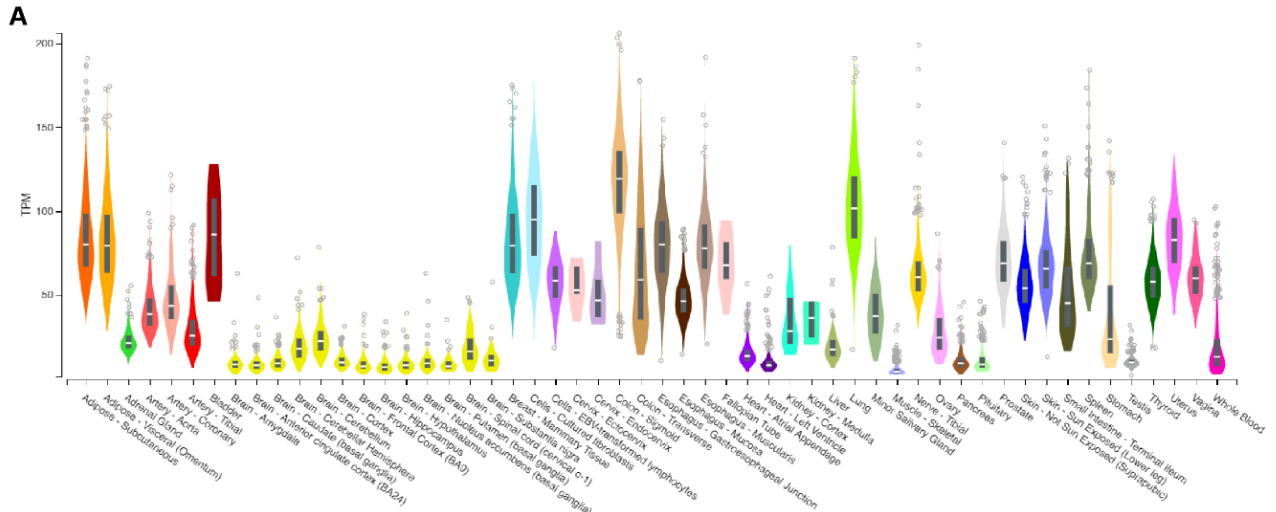
Diagnostic plots are shown for rs6916777, including checks for linearity, homoscedasticity, and normality. Similar results were observed for rs12597726.

Global Schoenfeld Test,  $p = 0.043$



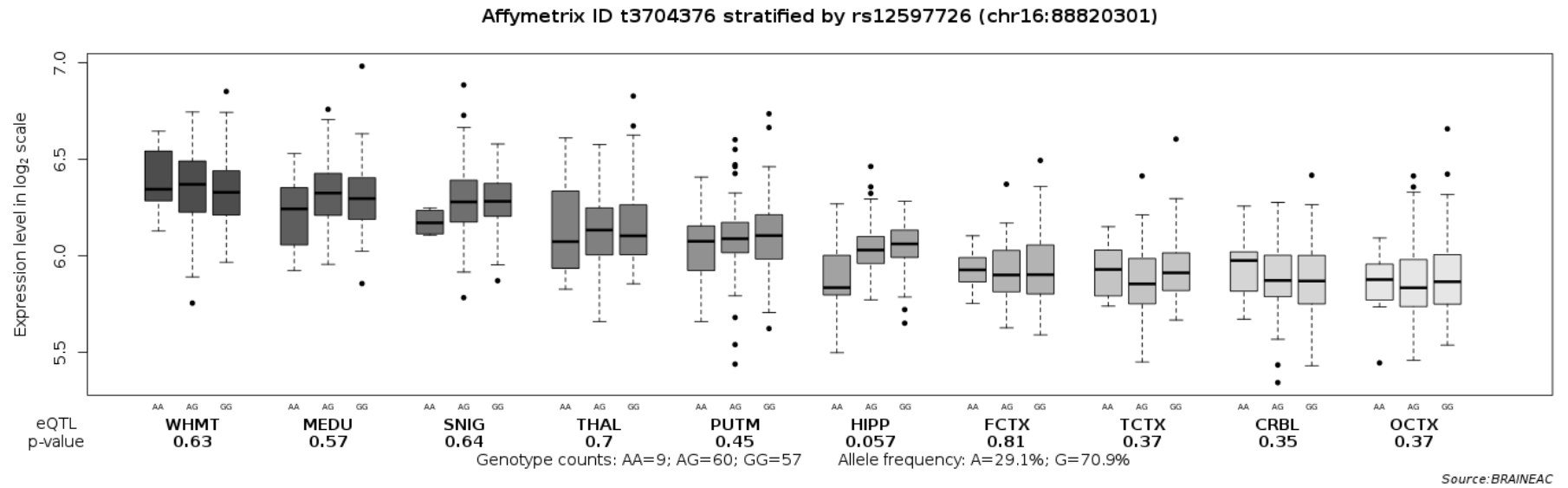
**Supplementary Figure 4.** Testing for proportional hazards.

Plots show scaled Schoenfeld residuals for all covariates included within the Cox proportional hazards model for rs12597726.



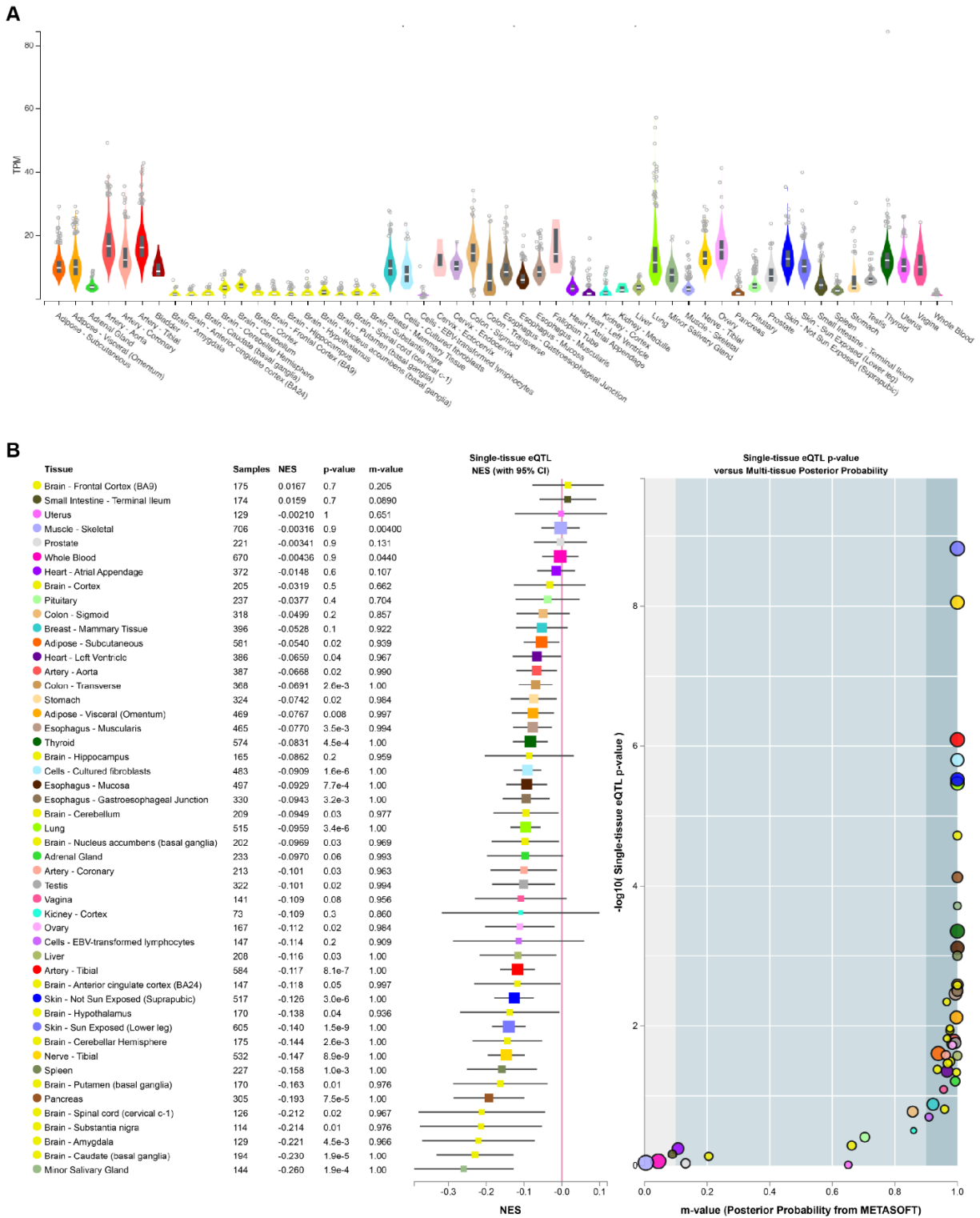
**Supplementary Figure 5.** GTEx expression information for *PIEZO1*.

(A) Expression *PIEZO1* across 54 GTEx tissues in transcripts per million (TPM; see <https://www.gtexportal.org/home/gene/PIEZO1>). (B) Effects of rs1259726 on the expression of *PIEZO1* across tissues where NES is the normalized effect size, with positive being an association of the minor allele with higher gene expression versus a negative value which would be decreased expression (see <https://www.gtexportal.org/home/snp/rs1259726>).



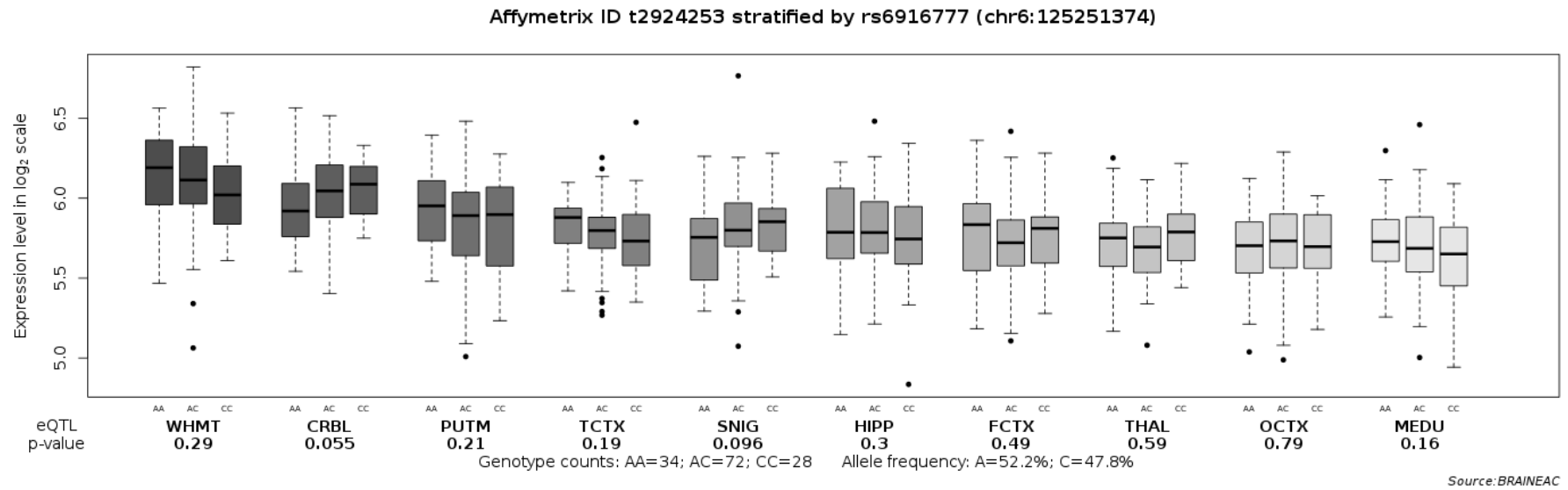
**Supplementary Figure 6.** Brain tissue expression of *PEIZO1*.

Expression levels are for the total transcripts across brain regions, stratified by rs12597726 genotypes, from *BRAINEAC*. *P*-values for eQTL below the names of brain regions compare levels of expression across genotypes.



Supplementary Figure 7. GTEx expression information for *RNF217*.

(A) Expression *RNF217* across 54 GTEx tissues in transcripts per million (TPM; see <https://www.gtexportal.org/home/gene/RNF217>). (B) Effects of rs6916777 on the expression of *RNF217* across tissues where *NES* is the normalized effect size, with positive being an association of the minor allele with higher gene expression versus a negative value which would be decreased expression (see <https://www.gtexportal.org/home/snp/rs6916777>).



**Supplementary Figure 8.** Brain tissue expression of *RNF217*.

Expression levels are for the total transcripts across brain regions, stratified by rs12597726 genotypes, from *BRAINEAC*. *P*-values for eQTL below the names of brain regions compare levels of expression across genotype.