

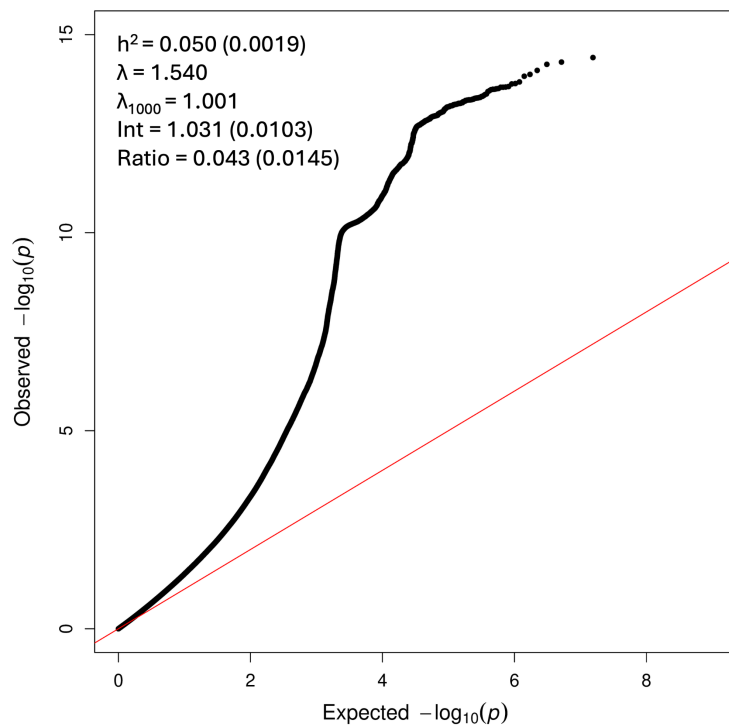
Genome-wide meta-analysis of quantitatively measured generalized anxiety symptoms in individuals of European ancestry

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Supplementary Information

QQ Plot of generalised anxiety symptom severity meta-GWAS.....	1
Supplementary Figure 1 Quantile-quantile plot of a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869).....	1
MAGMA tissue expression results from FUMA.....	2
Supplementary Figure 2 Gene-tissue results for a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869) using brain samples from BrainSpan taken at 29 different ages.....	2
Supplementary Figure 3 Gene-tissue results for a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869) using brain samples from BrainSpan taken at 11 general developmental stages.....	3
Supplementary Figure 4 Gene-tissue results for a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869) using 30 general tissue types from GTEx v8.....	4
Supplementary Figure 5 Gene-tissue results for a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869) using 54 tissue types from GTEx v8..	5

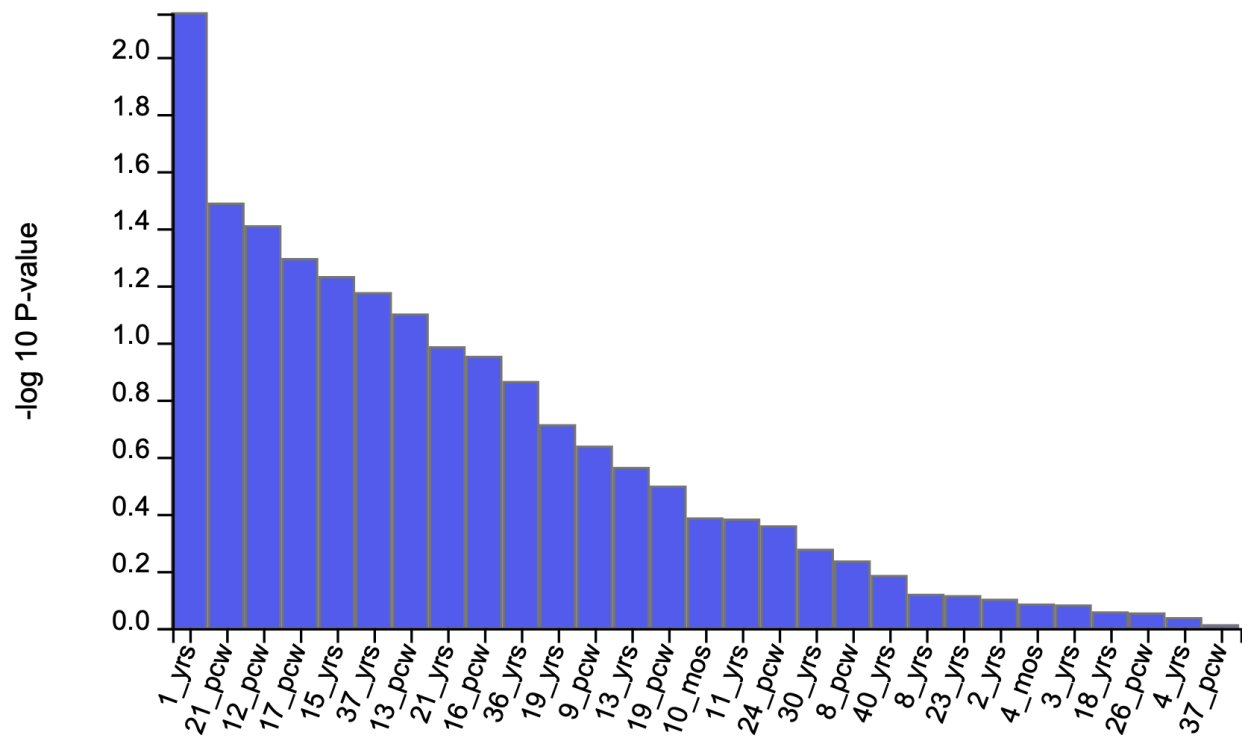
QQ Plot of generalised anxiety symptom severity meta-GWAS



Supplementary Figure 1 | Quantile-quantile plot of a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869).

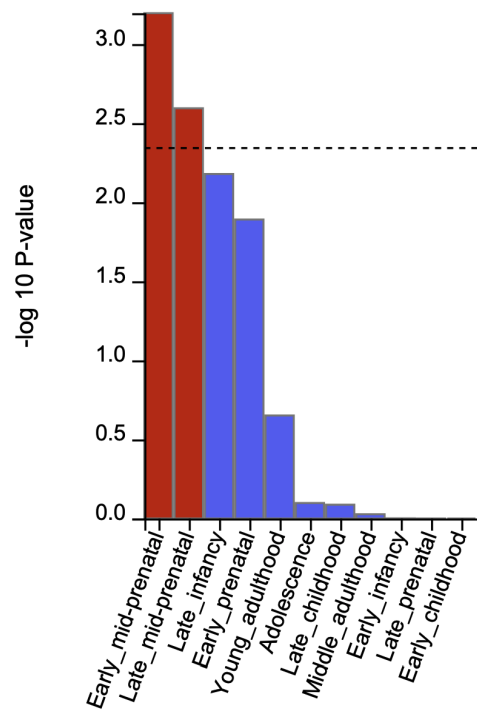
Note: The red line represents the expected $-\log_{10}(p)$ under the null and the black points represent the observed $-\log_{10}(p)$ values. Text is LDSC output, where h^2 = heritability, Int = intercept, values in brackets are standard errors of the estimates, λ = genomic inflation factor, λ_{1000} = genomic inflation factor for an equivalent study with a sample size of 1000.

MAGMA tissue expression results from FUMA



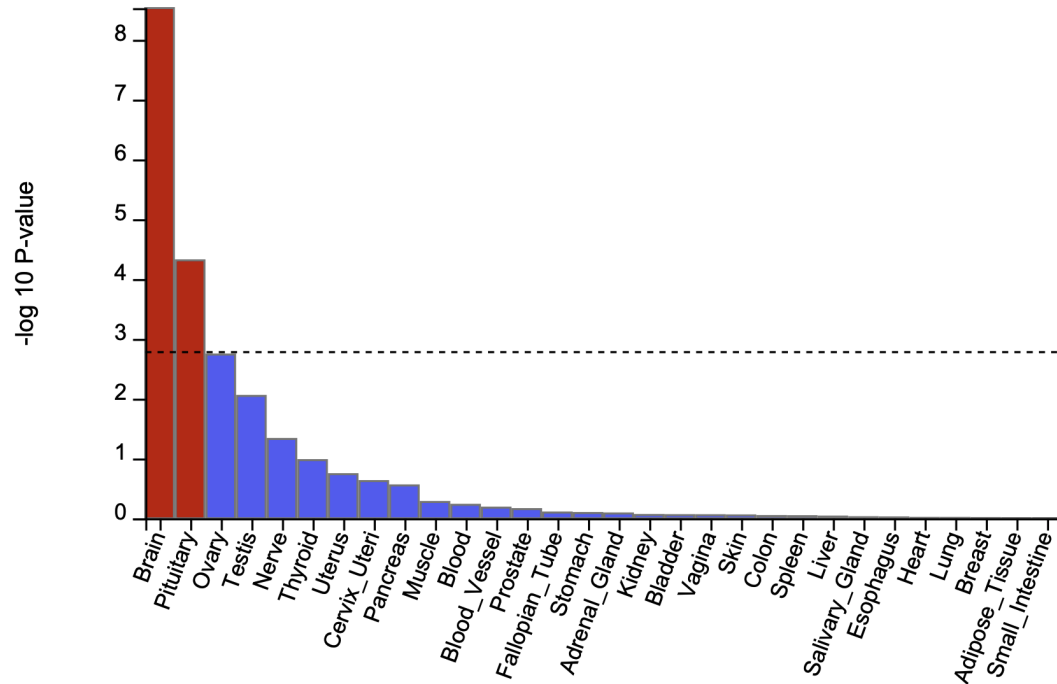
Supplementary Figure 2 | Gene-tissue results for a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869) using brain samples from BrainSpan taken at 29 different ages.

None passed a Bonferroni-corrected threshold for 29 tests ($p < 1.7 \times 10^{-3}$).

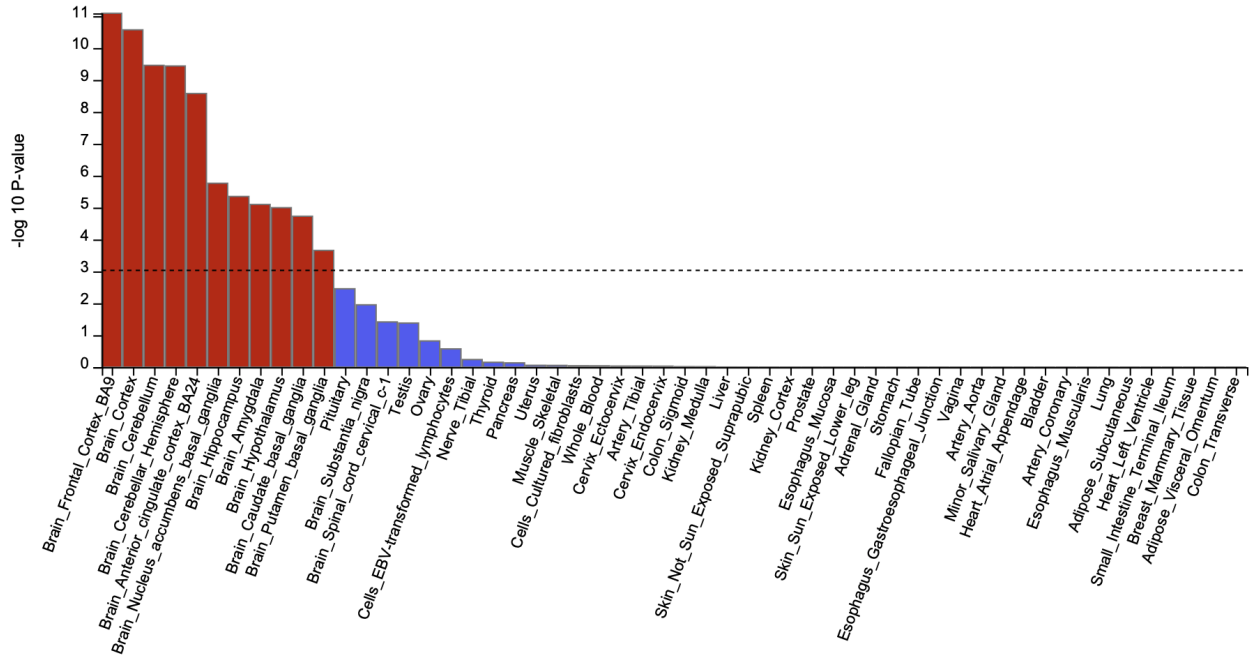


Supplementary Figure 3 | Gene-tissue results for a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869) using brain samples from BrainSpan taken at 11 general developmental stages.

The horizontal dotted line indicates a Bonferroni-corrected significance threshold for 11 tests ($p < 4.5 \times 10^{-3}$) and the red bars indicate tests that passed this threshold.



Supplementary Figure 4 | Gene-tissue results for a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869) using 30 general tissue types from GTEx v8. The horizontal dotted line indicates a Bonferroni-corrected significance threshold for 30 tests ($p < 1.7 \times 10^{-3}$) and the red bars indicate tests that passed this threshold.



Supplementary Figure 5 | Gene-tissue results for a genome-wide association meta-analysis of generalised anxiety symptom severity (N = 693,869) using 54 tissue types from GTEx v8. The horizontal dotted line indicates a Bonferroni-corrected significance threshold for 54 tests ($p < 9.26 \times 10^{-4}$) and the red bars indicate tests that passed this threshold. Full results are provided in Table S16.