

Figure S1. Sample QC procedure in UK Biobank for 3 asthma phenotypes.

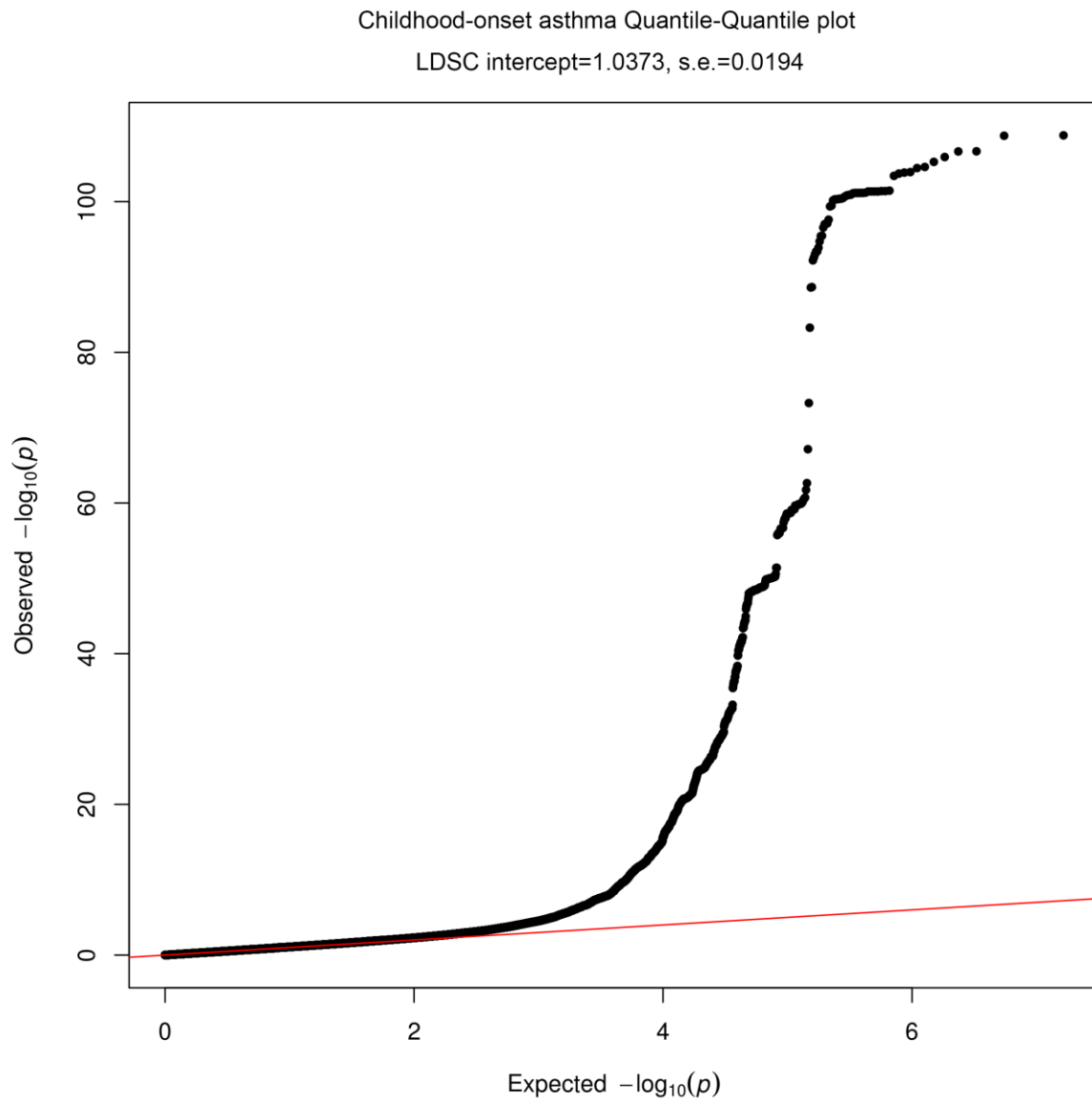


Figure S2. Quantile-quantile plot of childhood-onset asthma. LDSC intercept=1.04 showed no evidence of population stratification bias.

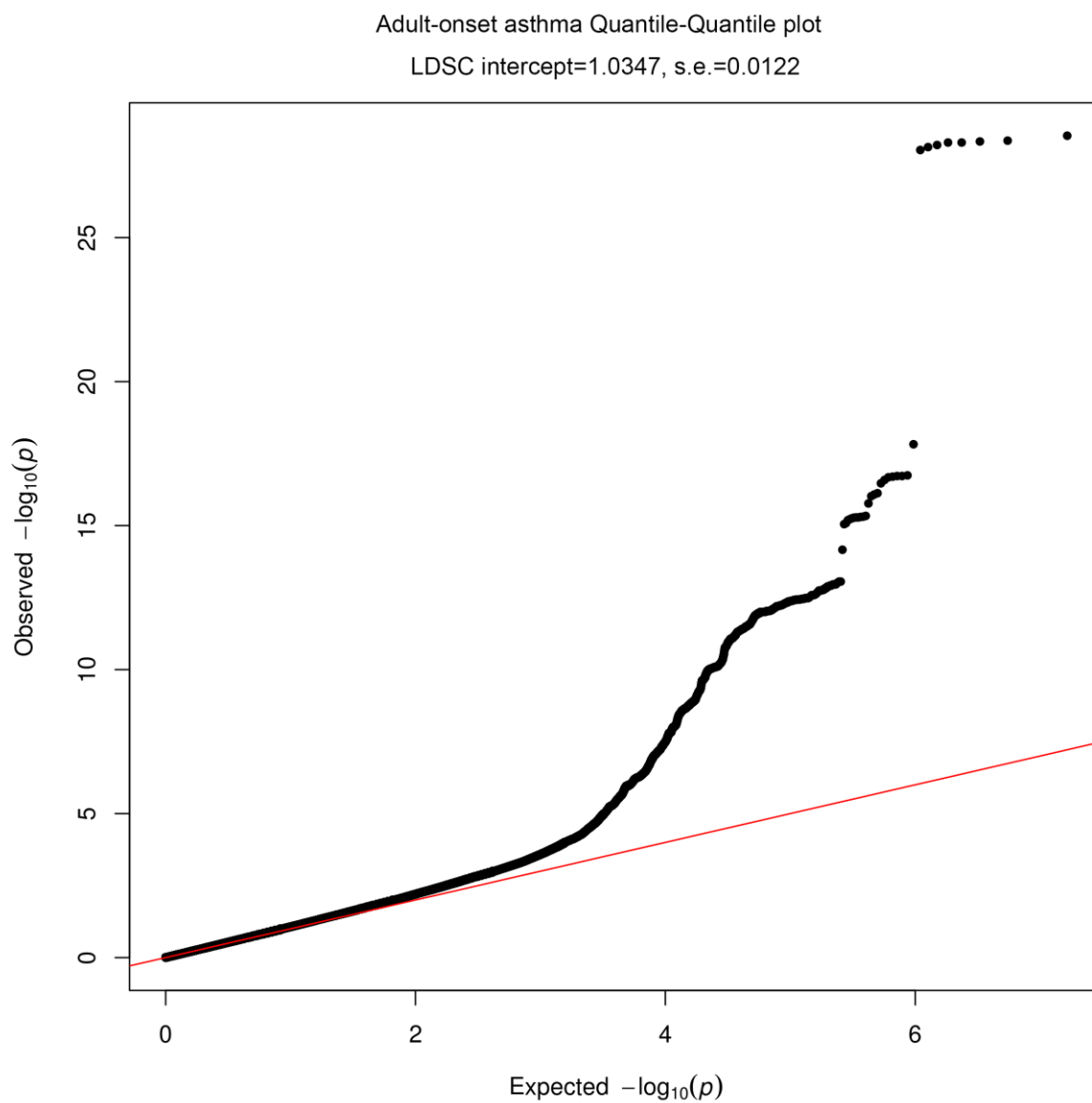


Figure S3. Quantile-quantile plot of adult-onset asthma. LDSC intercept=1.03 showed no evidence of population stratification bias.

Correlation of effect size of 10 novel loci between UK Biobank and TAGC multiancestry population

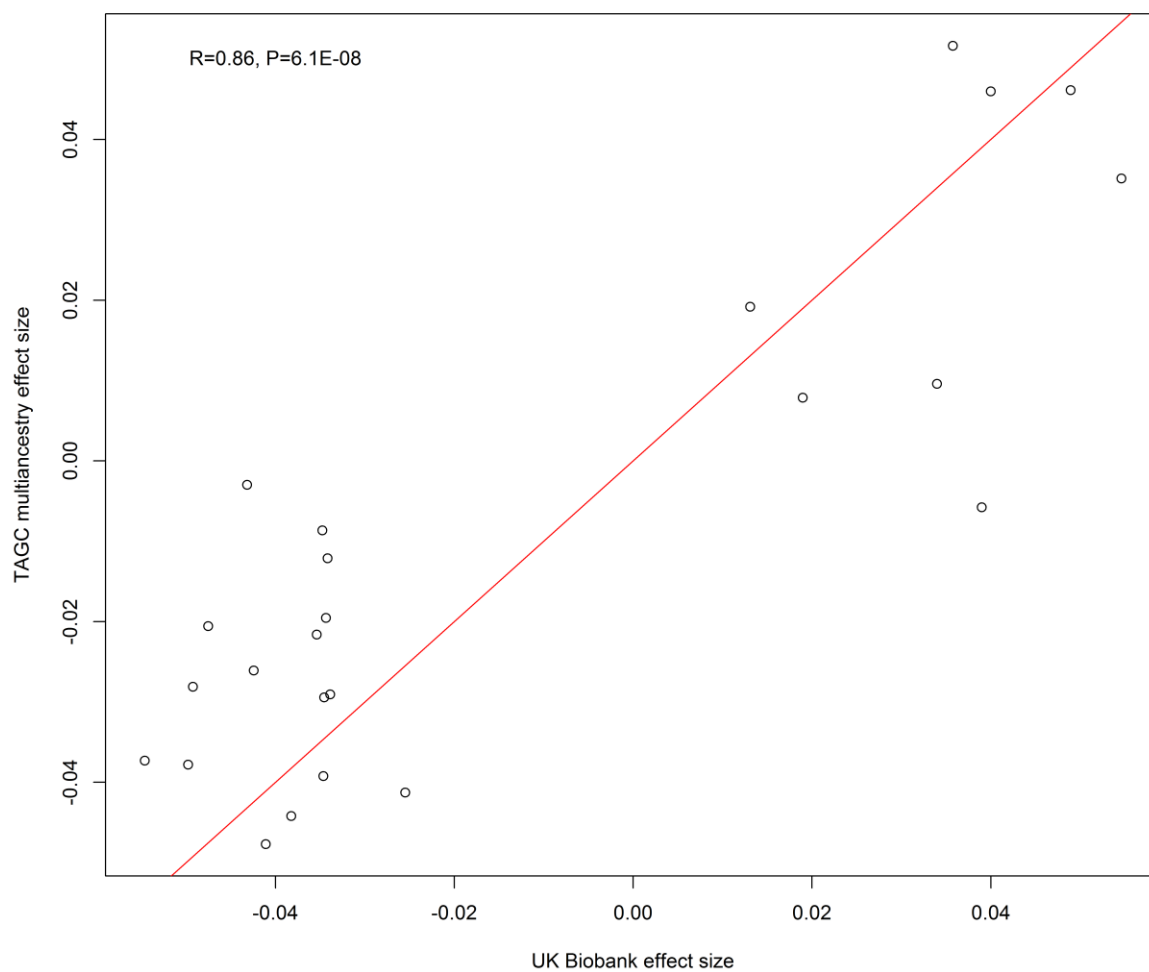


Figure S4. Correlation of effect size of 24 novel loci between UK Biobank and TAGC multiancestry population. R denotes Pearson correlation coefficient; P denotes P-value for Pearson correlation coefficient. Red line denotes diagonal line.

Correlation of effect size of 10 novel loci between UK Biobank and TAGC European population

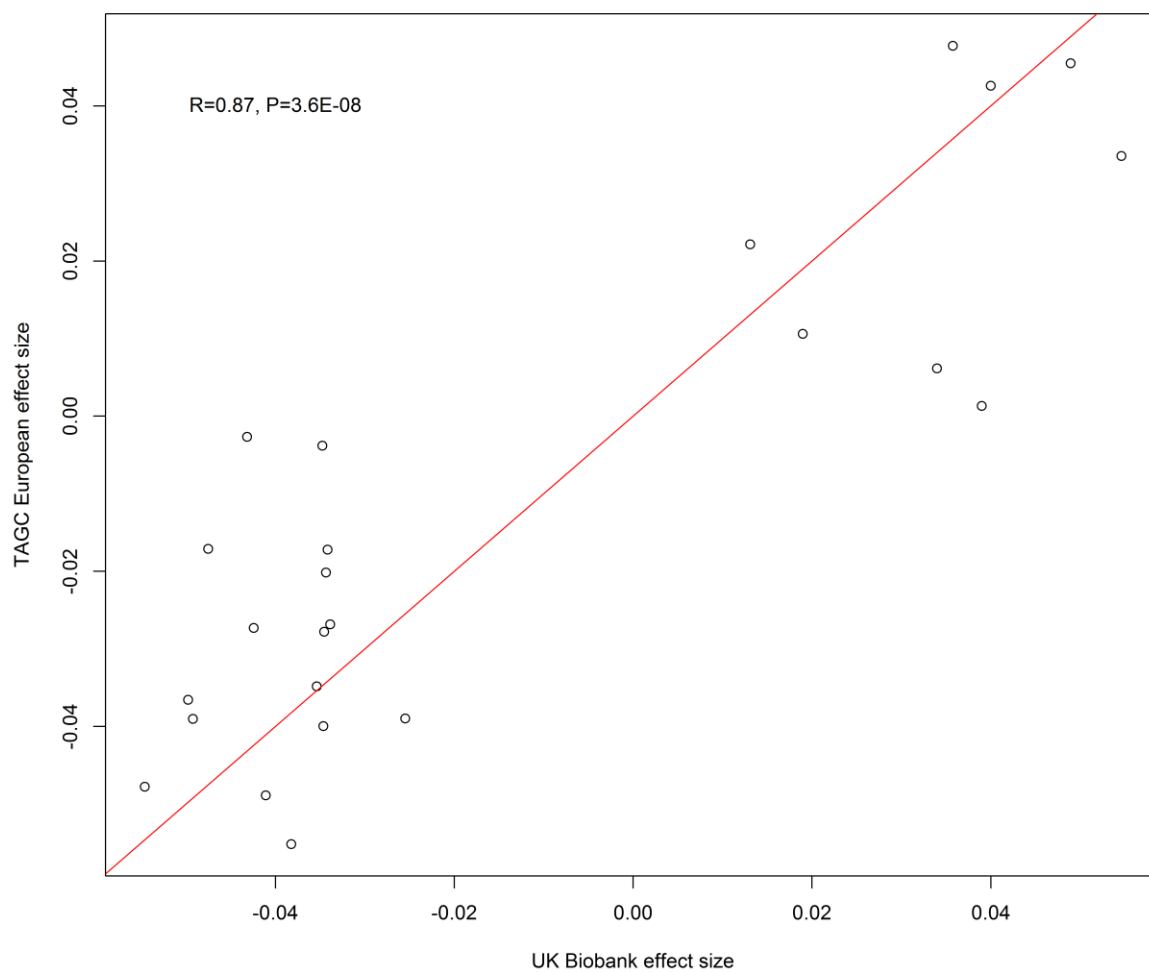


Figure S5. Correlation of effect size of 24 novel loci between UK Biobank and TAGC European population. R denotes Pearson correlation coefficient; P denotes P-value for Pearson correlation coefficient. Red line denotes diagonal line.

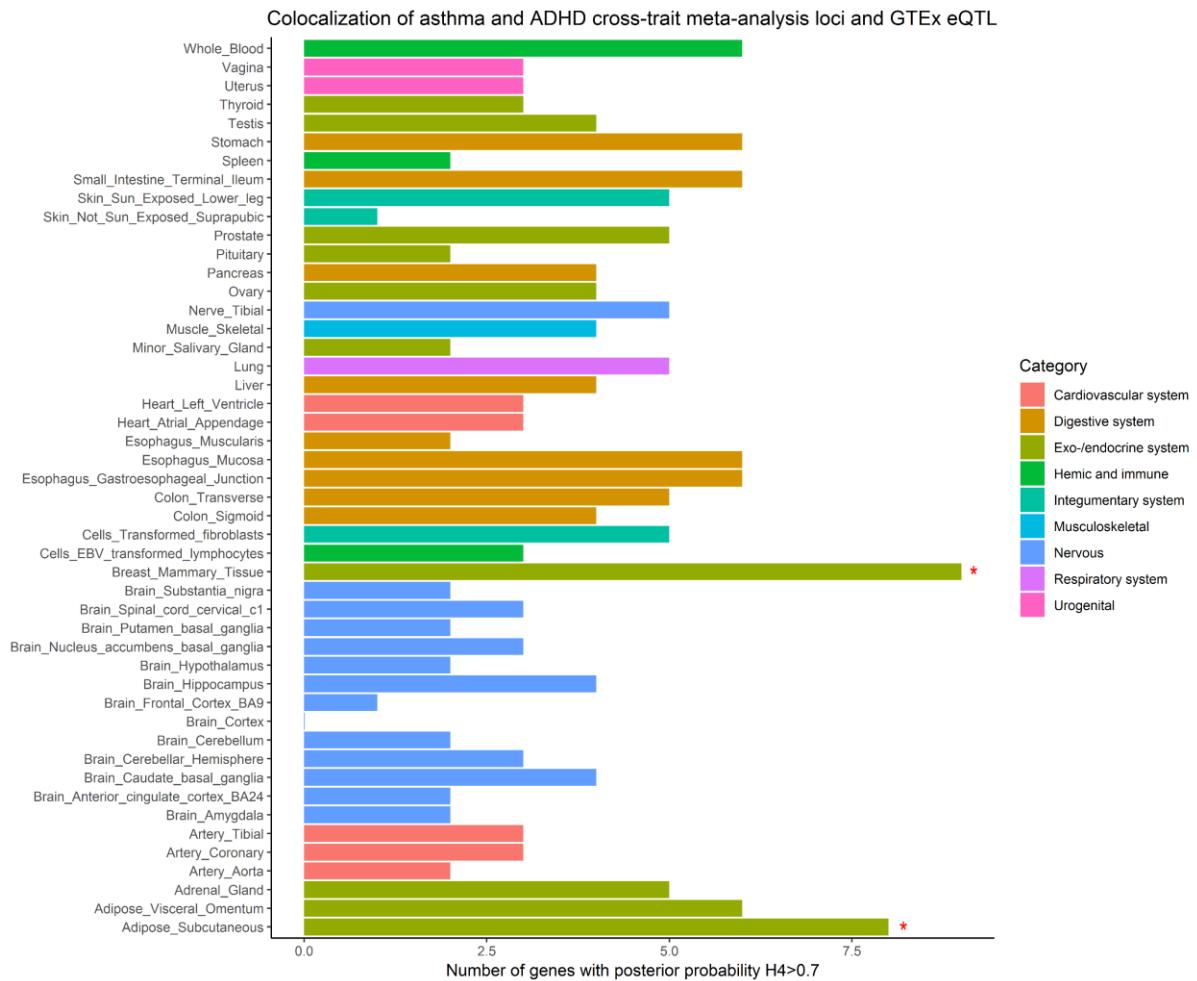


Figure S6. Colocalization of asthma and ADHD meta-analysis loci and GTEx eQTL. Tissues are categorized into organ/body system. X-axis denotes number of genes with posterior probability $H_4 > 0.7$ (GWAS cross-trait meta-analysis and GTEx eQTL were associated and shared one common causal variant). Enrichment test based on 1000 permutations was performed. We assigned the 1 red asterisk to the tissue if it's nominally significant enriched, 2 red asterisks if it's significantly enriched after multiple testing correction for 48 tissues.

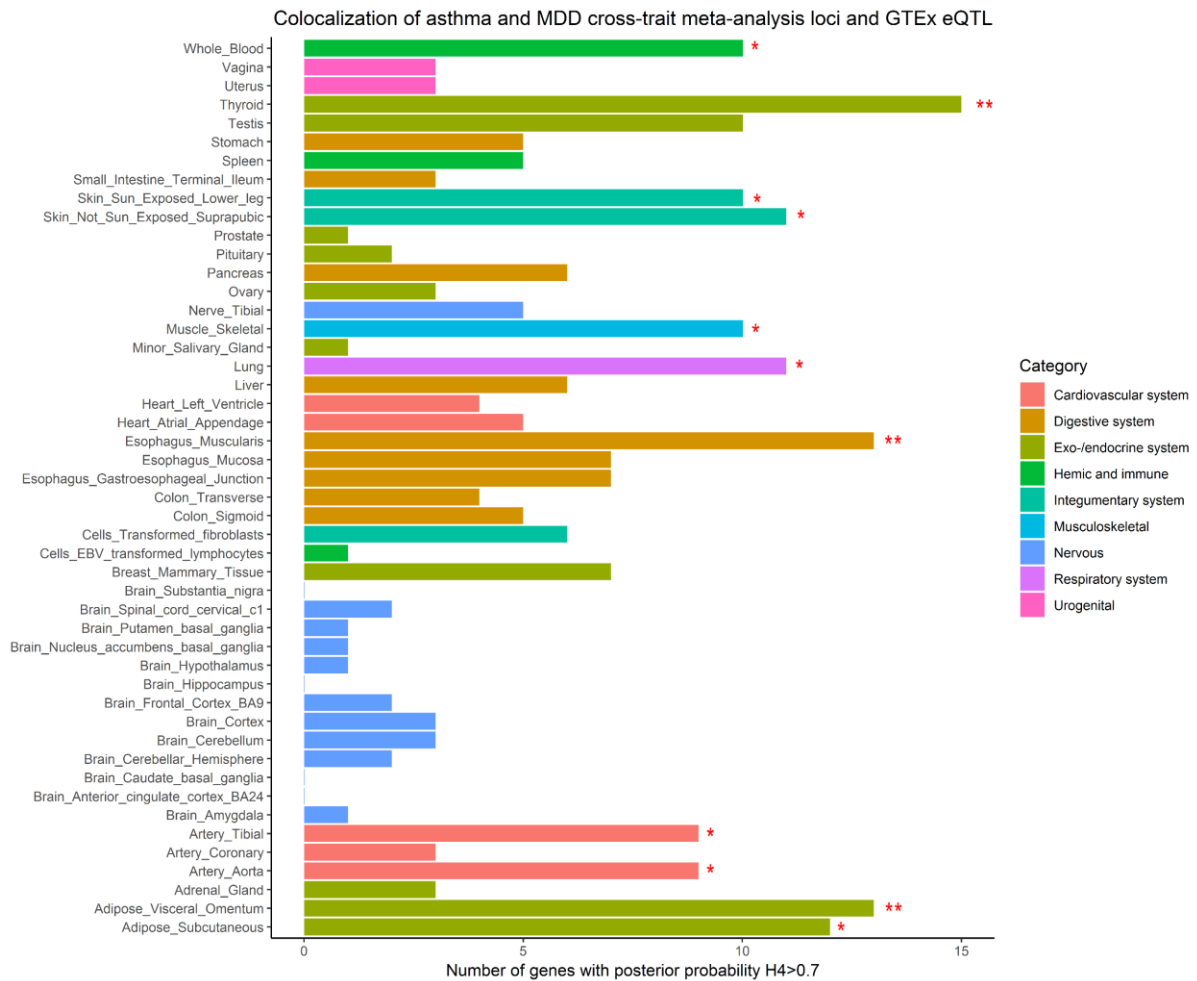


Figure S7. Colocalization of asthma and MDD meta-analysis loci and GTEx eQTL. Tissues are categorized into organ/body system. X-axis denotes number of genes with posterior probability $H4 > 0.7$ (GWAS cross-trait meta-analysis and GTEx eQTL were associated and shared one common causal variant). Enrichment test based on 1000 permutations was performed. We assigned the 1 red asterisk to the tissue if it's nominally significant enriched, 2 red asterisks if it's significantly enriched after multiple testing correction for 48 tissues.