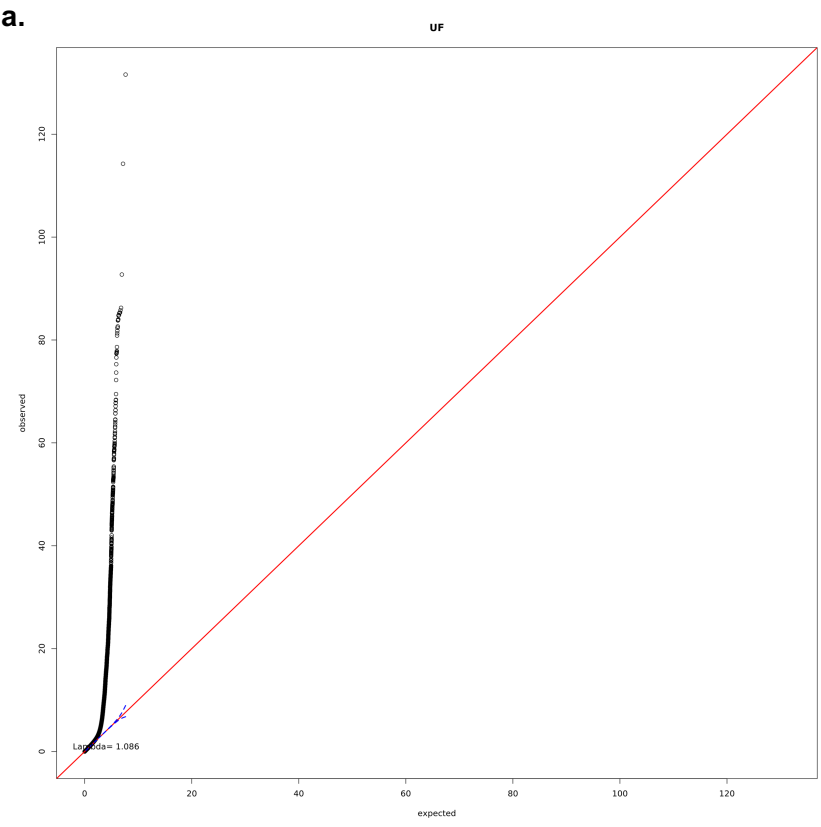
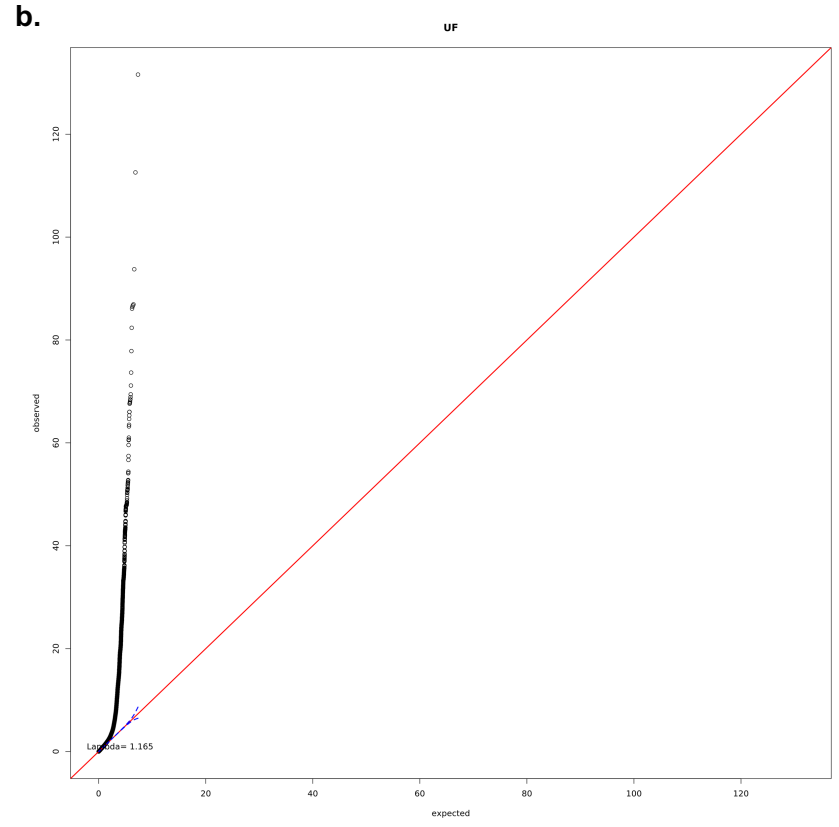


Genome-wide meta-analysis identifies novel risk loci for uterine fibroids within and across multiple ancestry groups

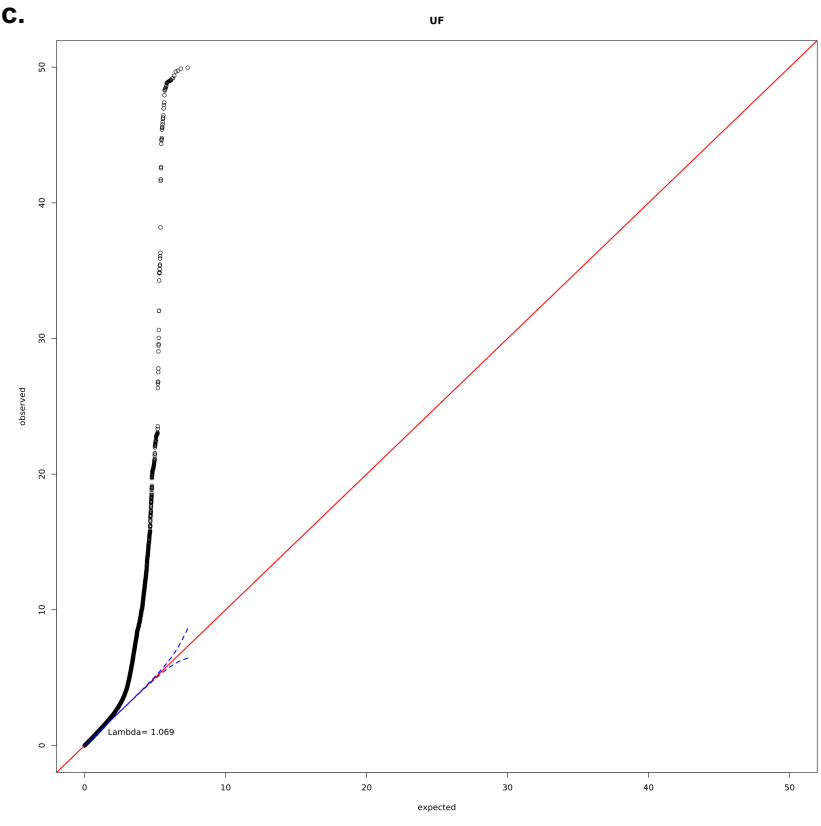
a.



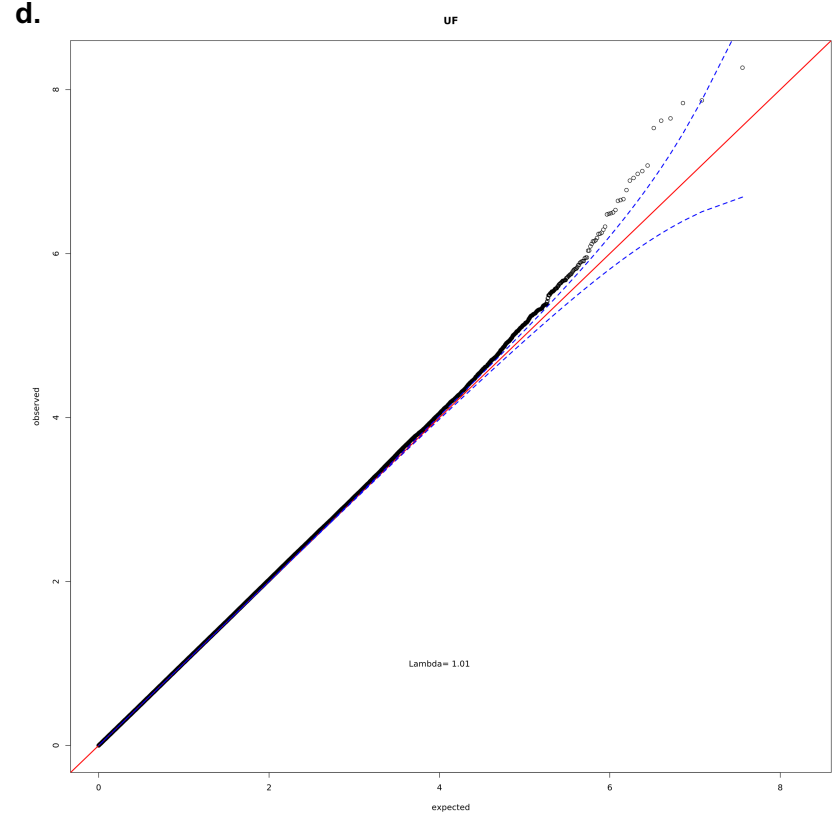
b.



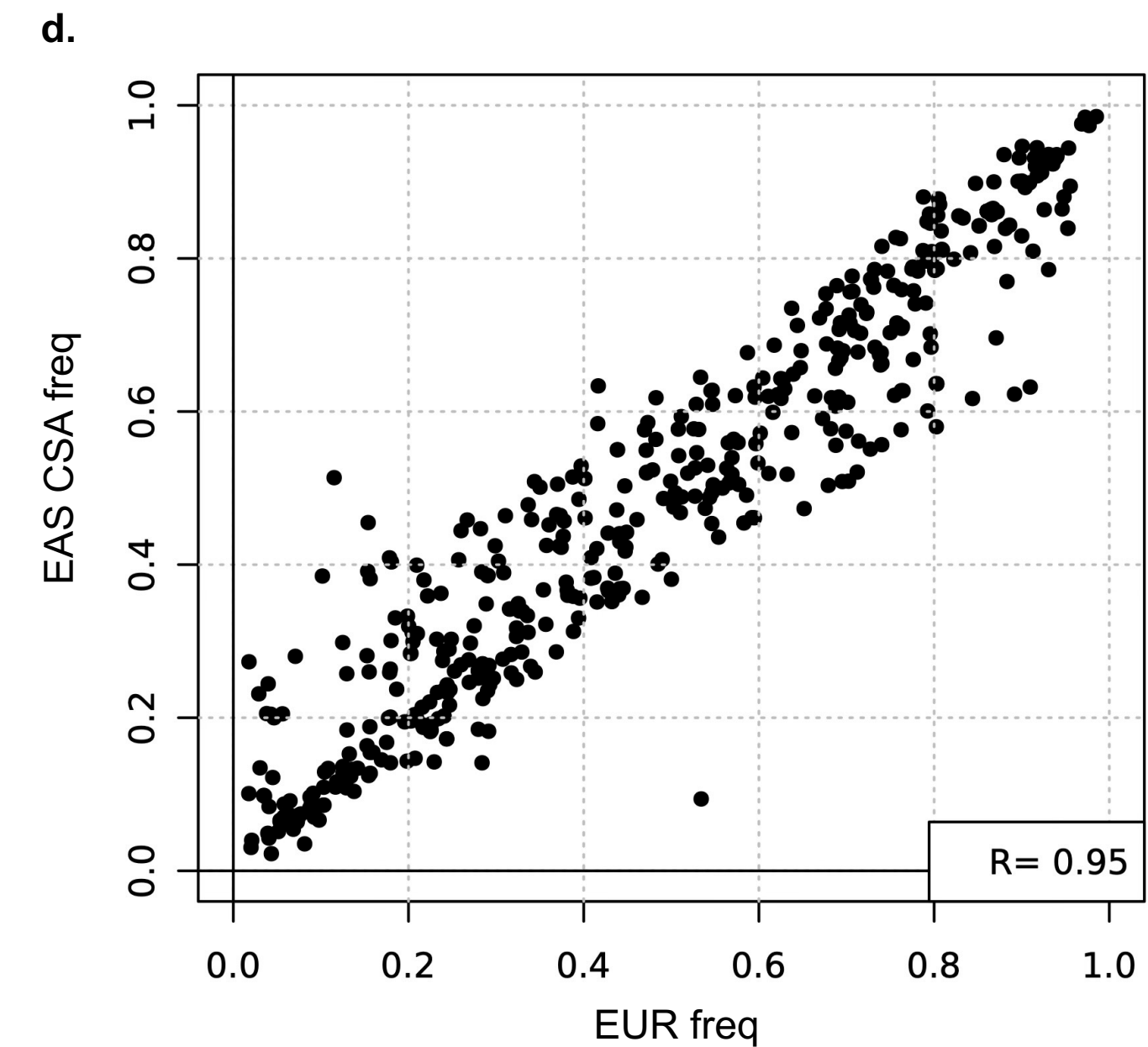
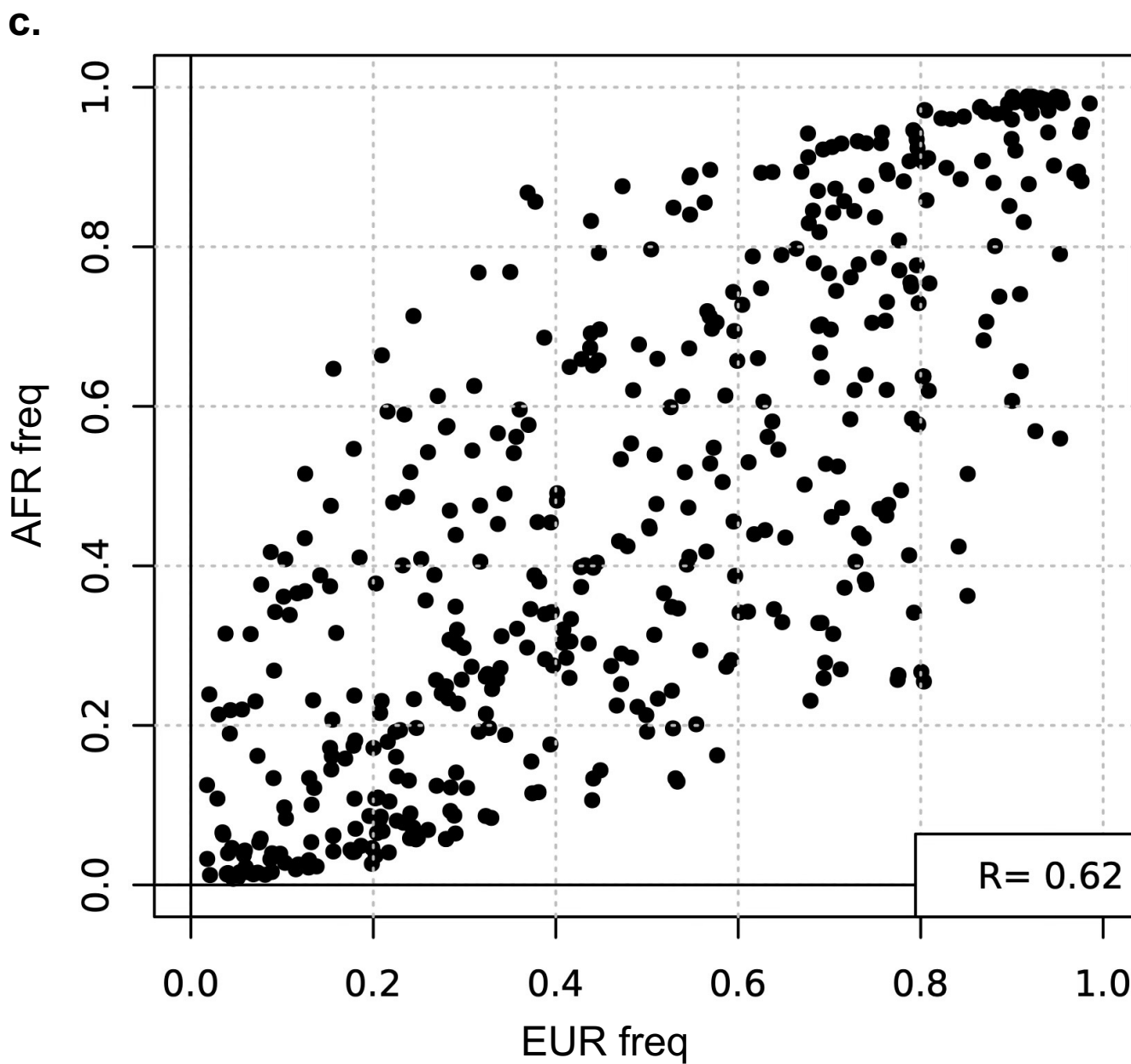
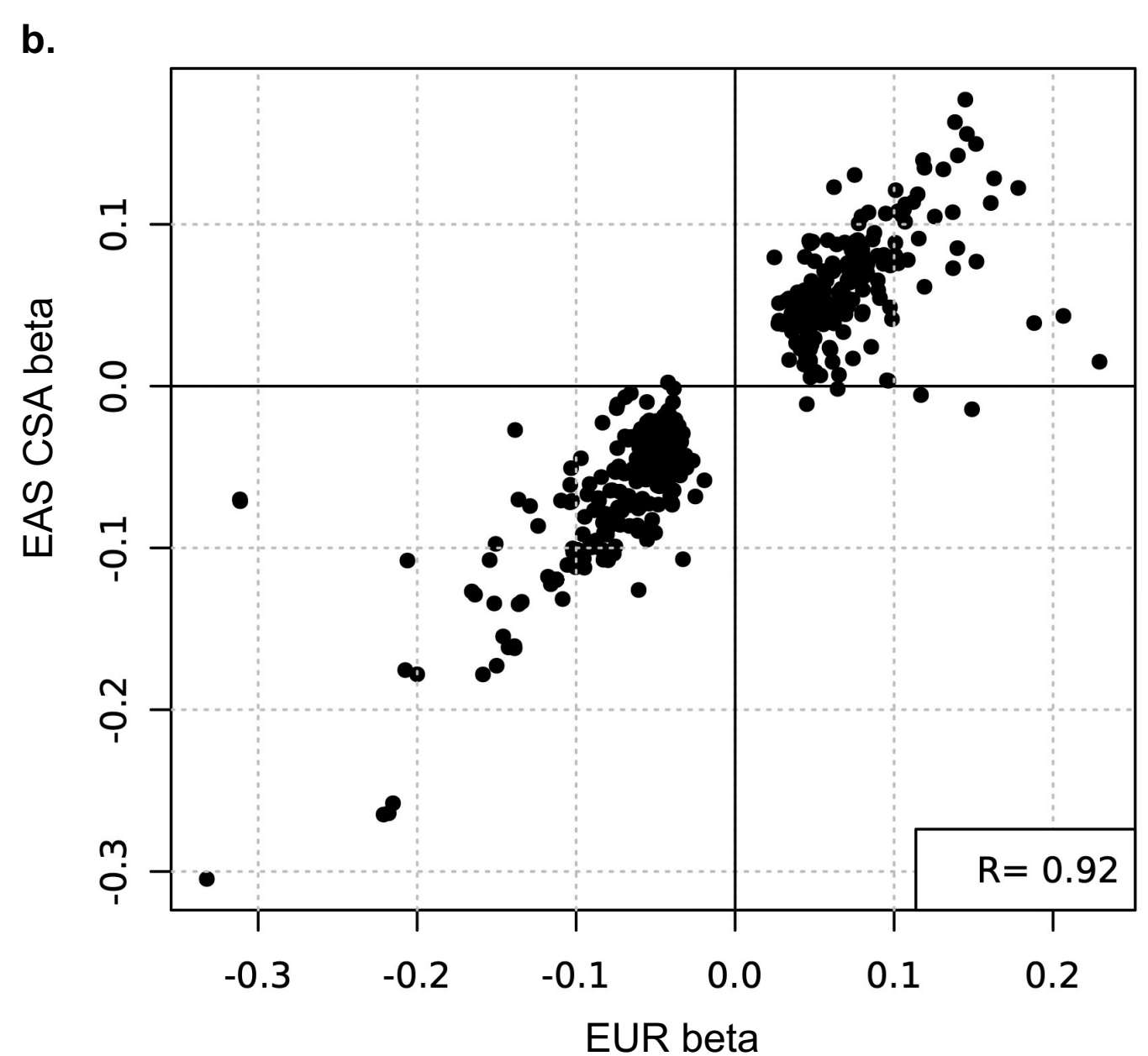
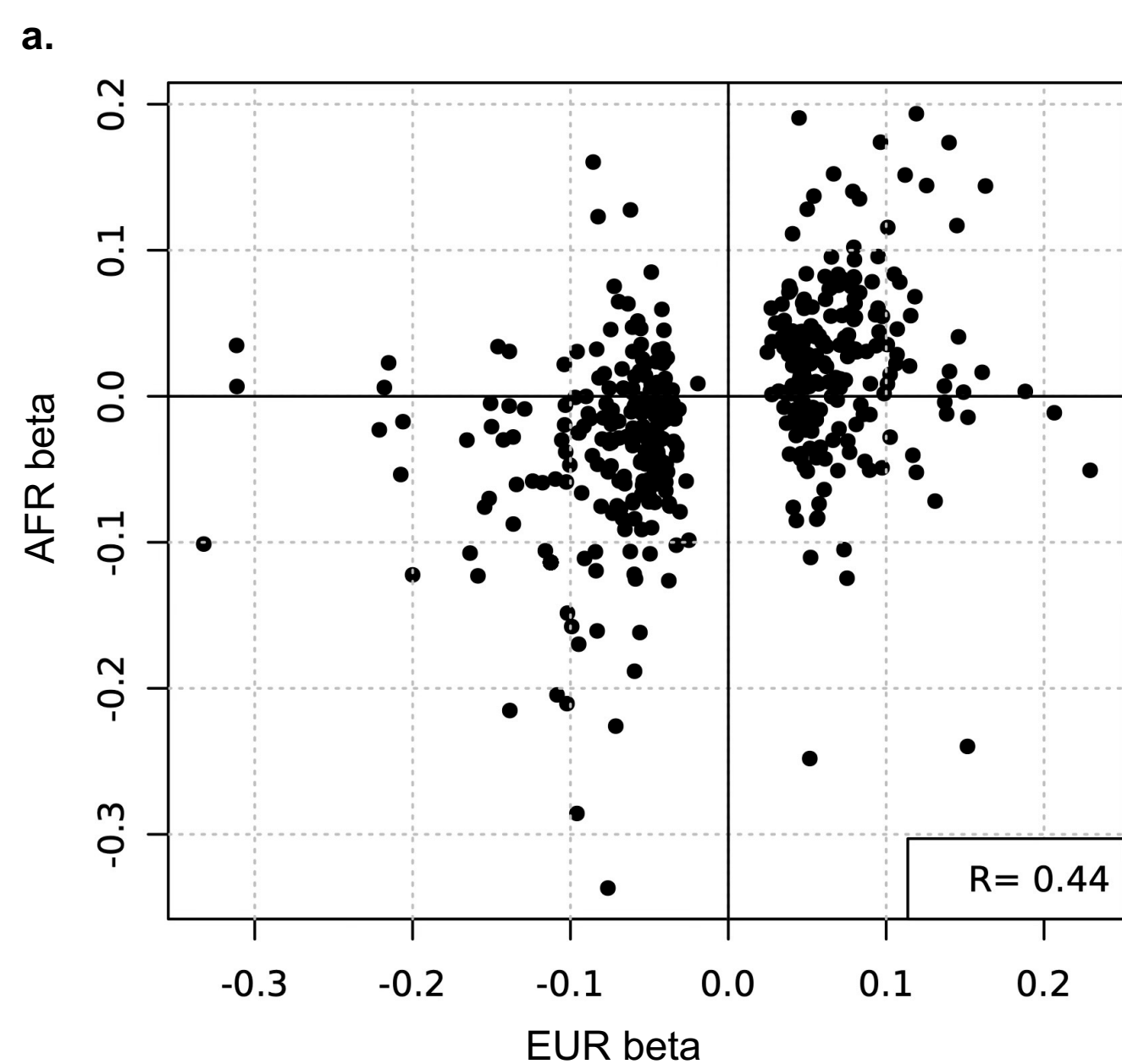
c.



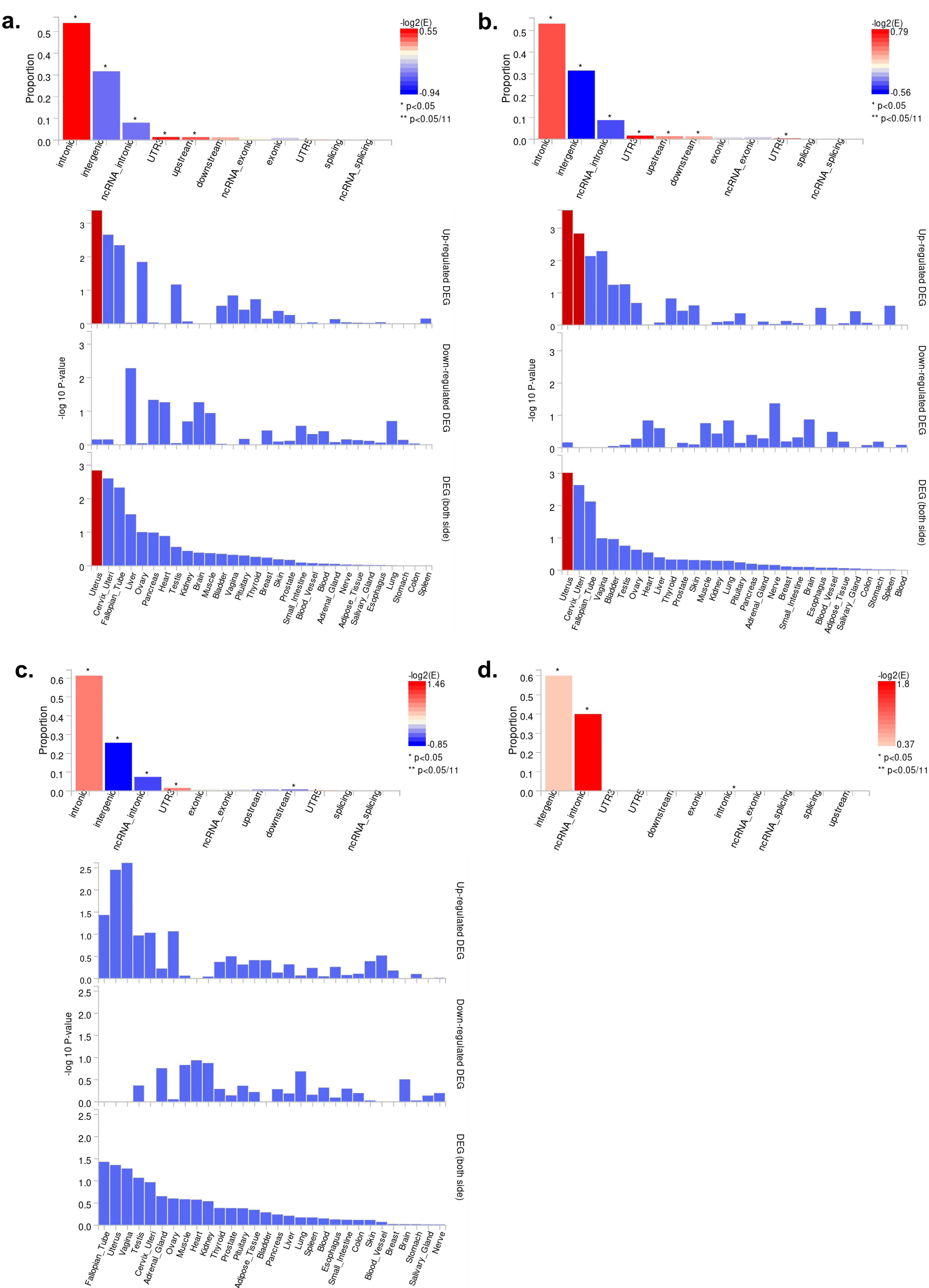
d.



Supplementary Figure 1. Quantile-quantile (QQ) plots of meta-analyses with lambda values. a = Multi-ancestry, b =European ancestry, c = East Asian/Central South Asian ancestry, d = African ancestry. Lambda value calculated from median chi-squared values.

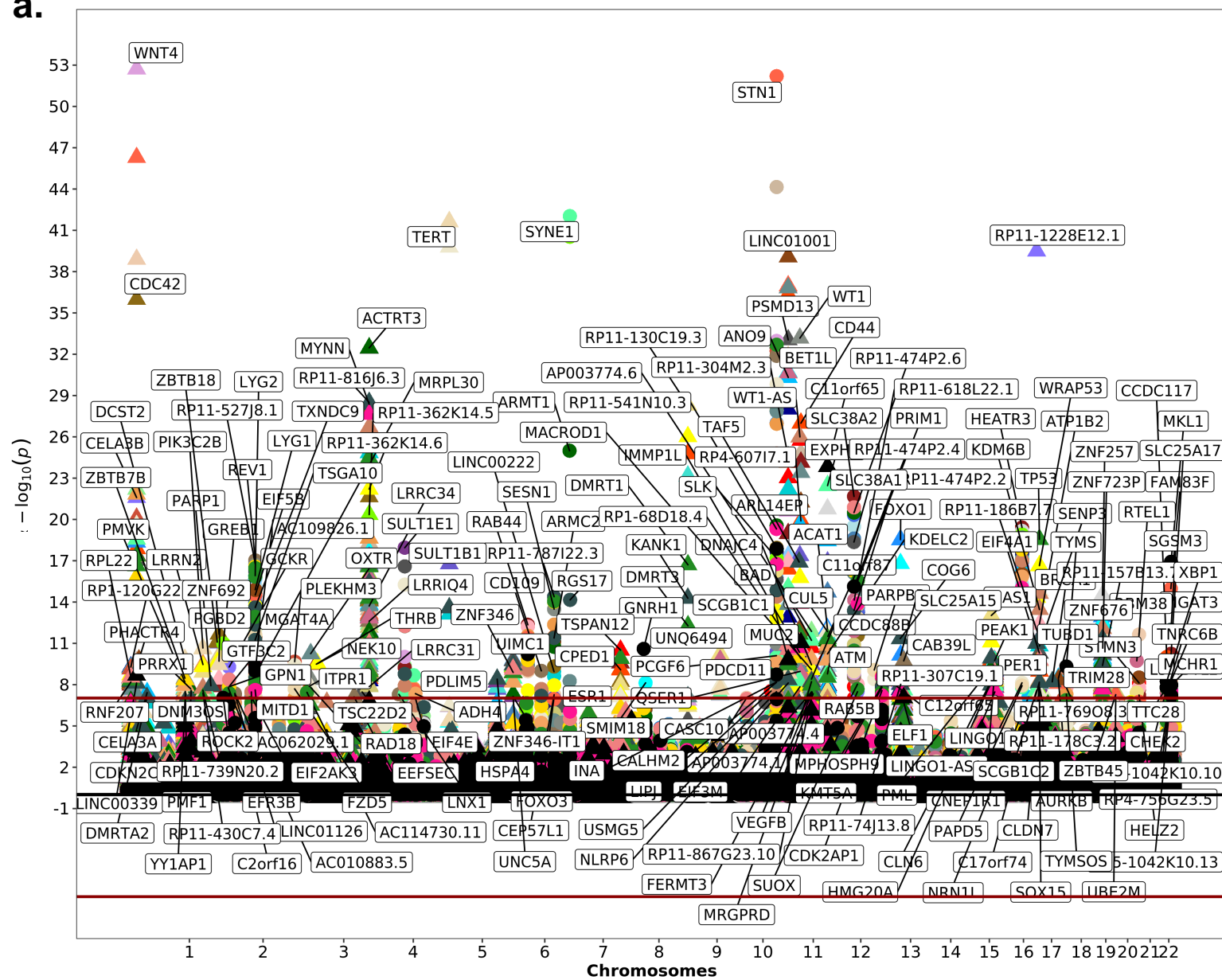


Supplementary Figure 2. Effect and frequency plots between ancestry groups for variants limited to those that were in the multi-ancestry summary statistics. a = effect size comparisons between African ancestry and European ancestry, b = effect size comparisons between East Asian/Central South Asian ancestry and European ancestry, c = effect allele frequency comparisons between African ancestry and European ancestry, d = effect allele frequency comparisons between East Asian/Central South Asian ancestry and European ancestry. Correlation statistical test with R function corr.

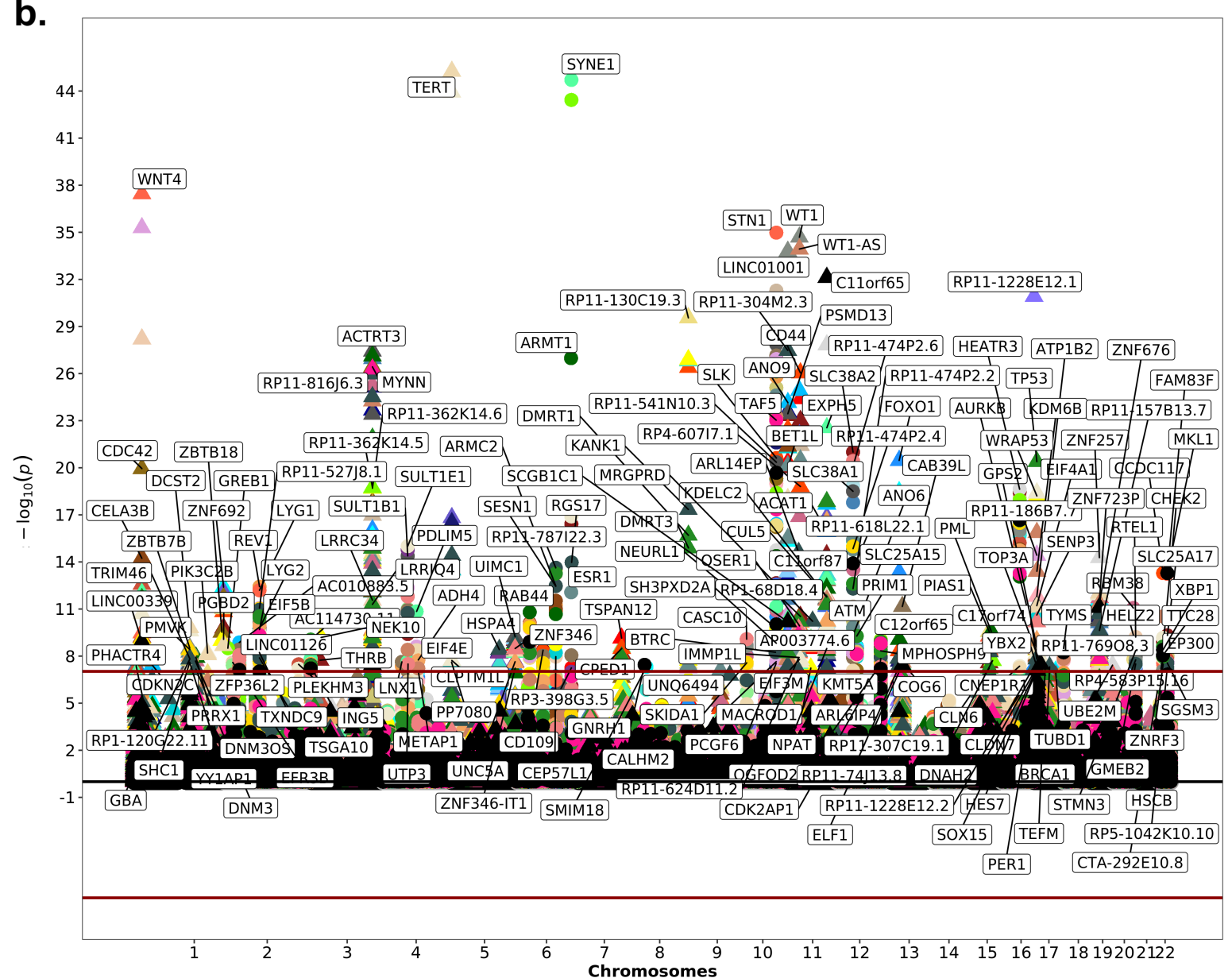


Supplementary Figure 3. Functional Mapping and Annotation (FUMA) results with annotated significant variants results of enrichment (upper panels) and differentially expressed gene enrichment (lower panels) tests. a = Multi-ancestry, b = European ancestry, c = East Asian/Central South Asian ancestry, d =African ancestry. Enrichment tests, empiric p-value threshold (0.05).

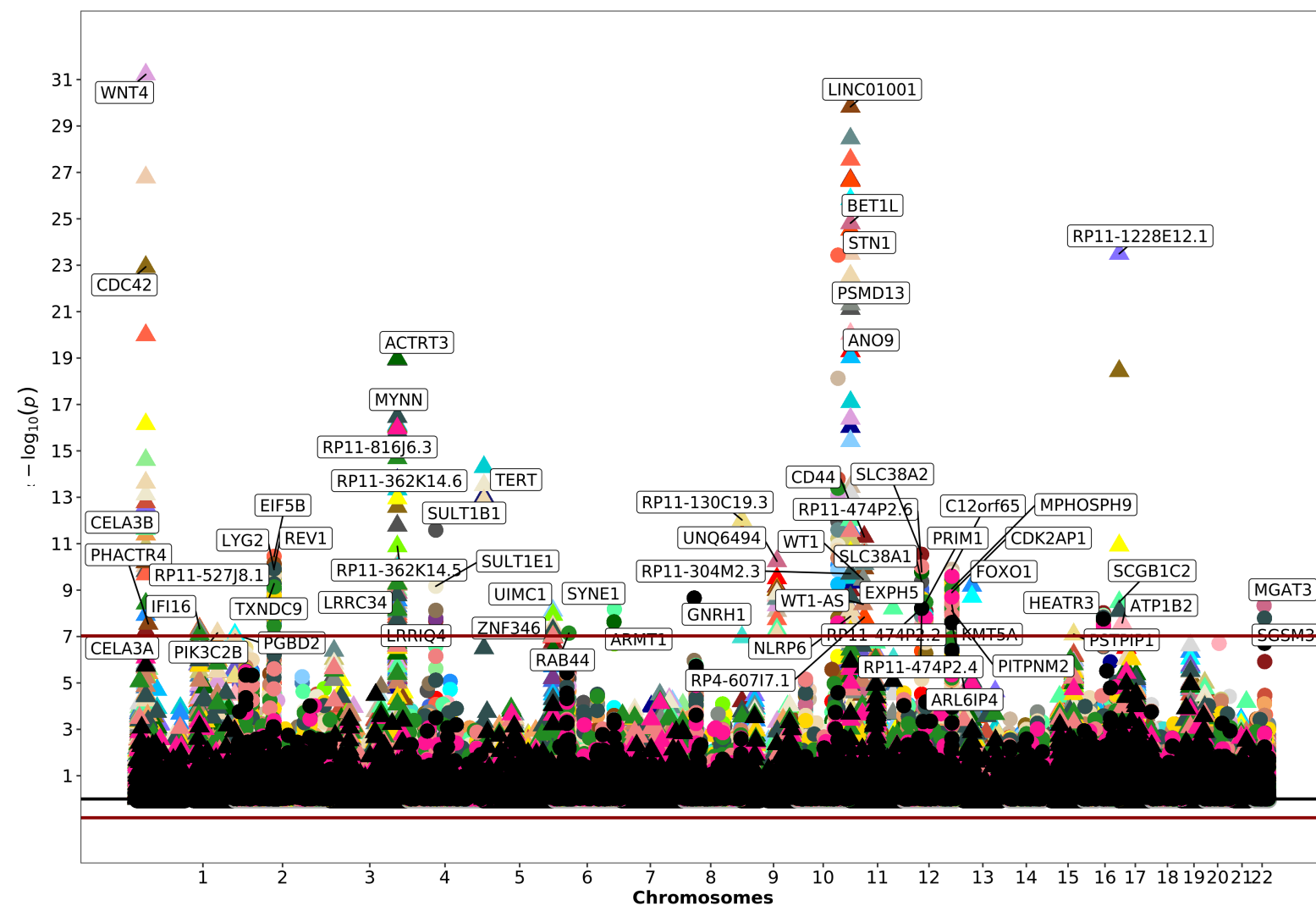
a.



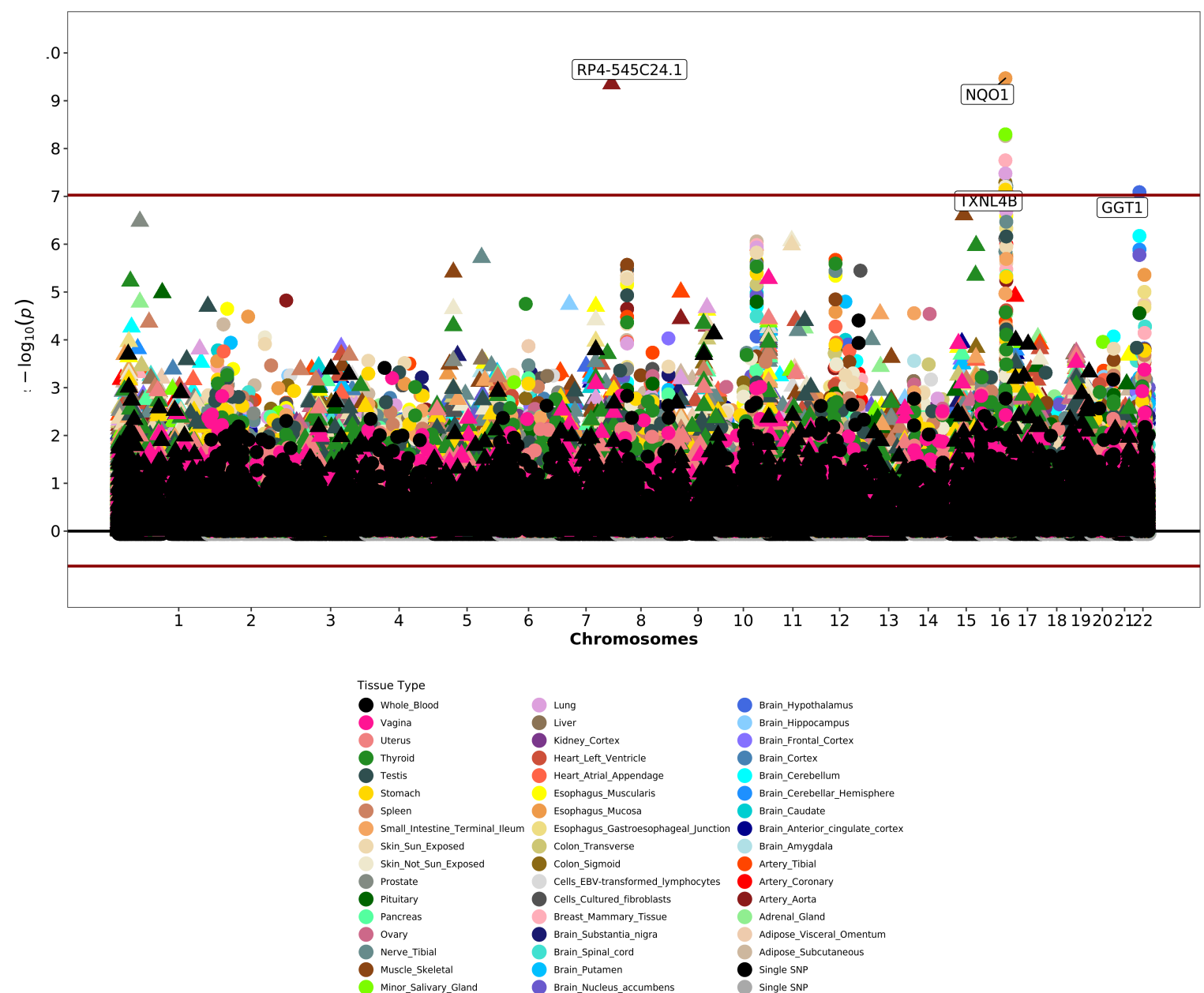
b.



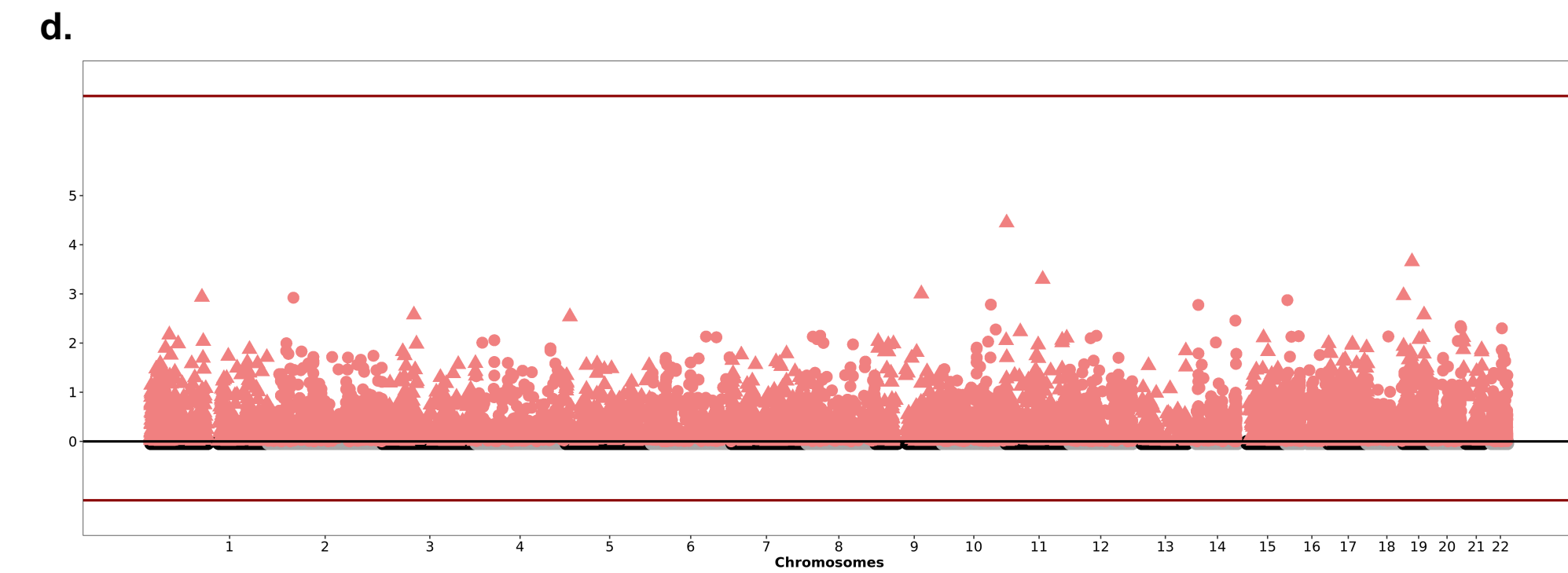
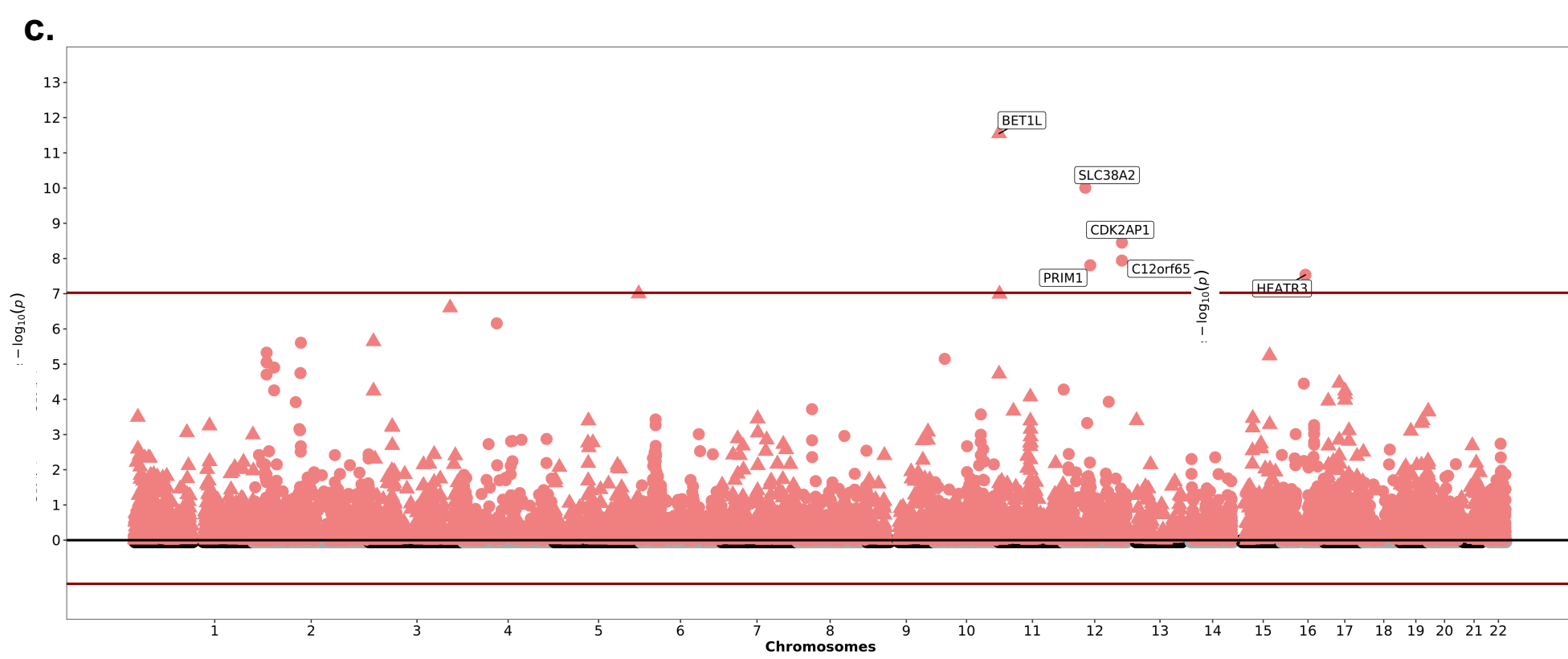
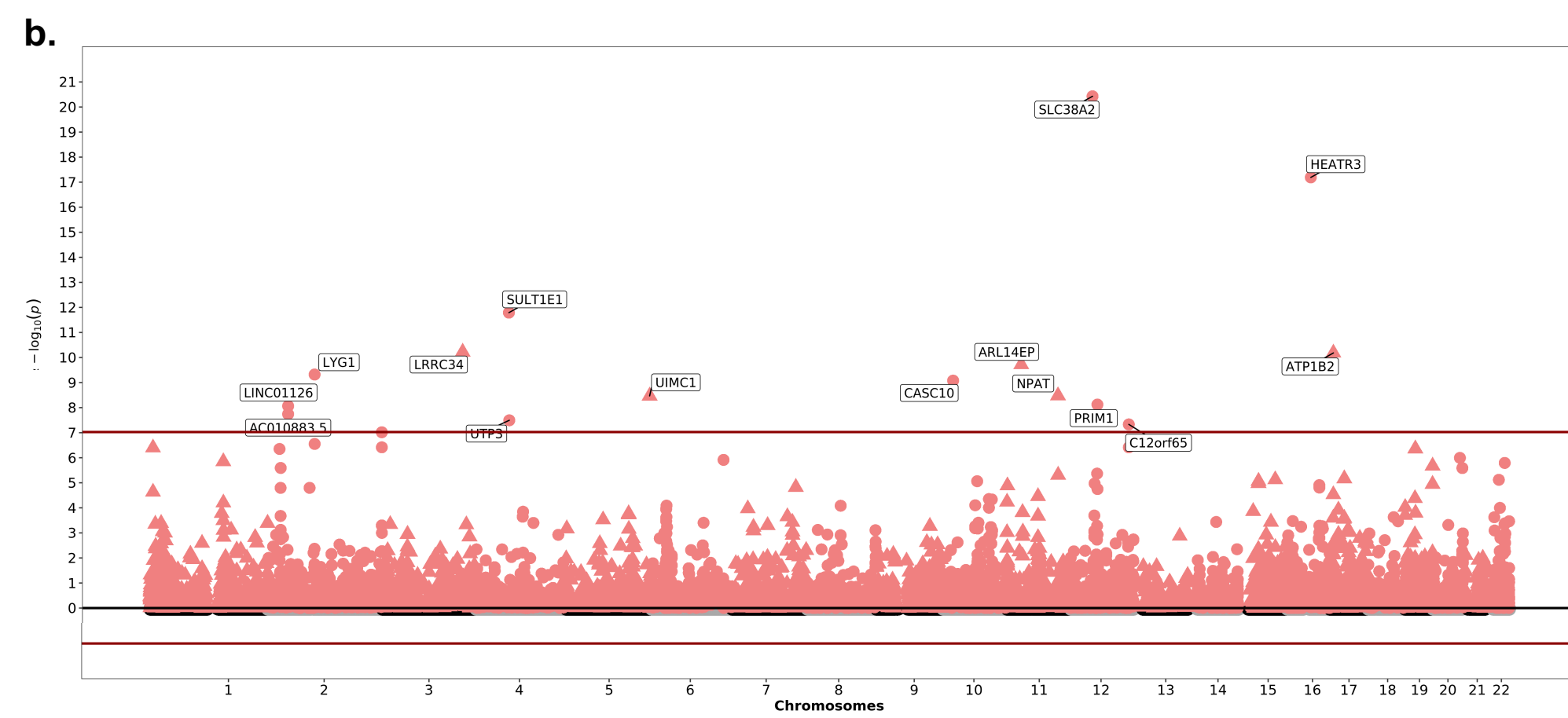
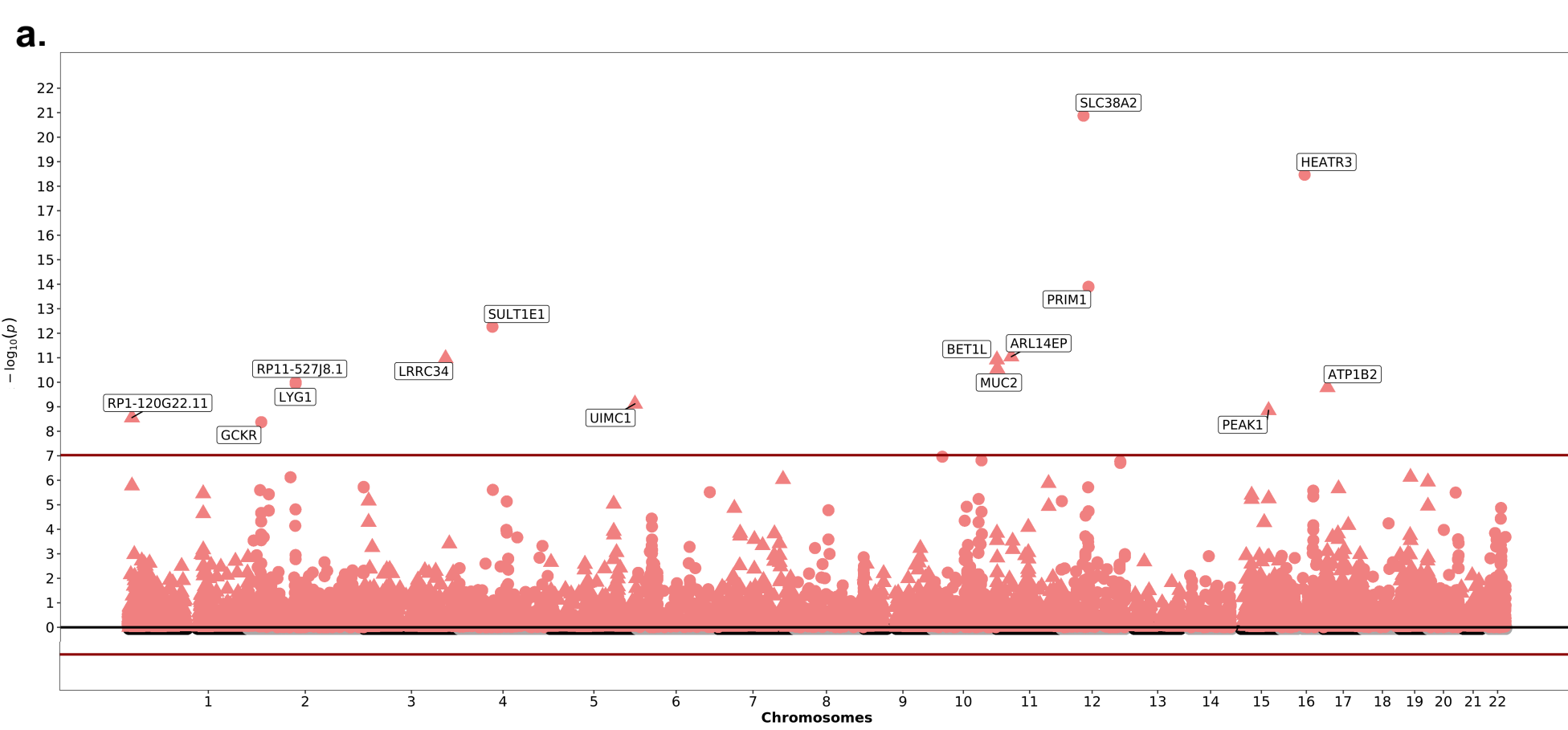
c.



d.



Supplementary Figure 4. S-PrediXcan results for 49 GTEx v8 tissues using JTI models. a = Multi-ancestry, b = European ancestry, c = East Asian/Central South Asian ancestry, d = African ancestry. Two-sided Wald test; multiple testing correction p-value threshold used (9.4×10^{-8}).



Supplementary Figure 5. S-PrediXcan results for the uterine tissue shown using JTI models. a = Multi-ancestry, b = European ancestry, c = East Asian/Central South Asian ancestry, d = African ancestry. Two-sided Wald test; multiple testing correction p-value threshold used (9.4×10^{-8}).

