

Figure S1. GWAS Manhattan plot of EHR defined CBP in European Ancestry (EUR) Participants

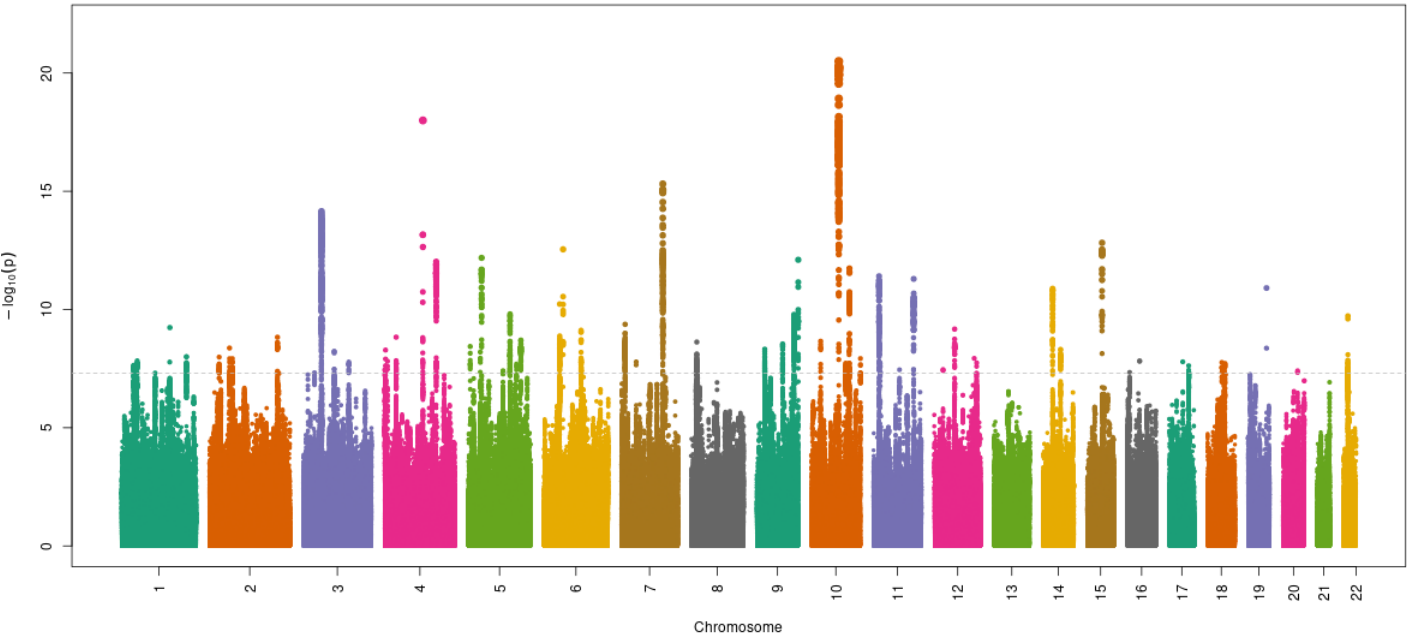


Figure S2. GWAS Manhattan plot of EHR defined CBP in African Ancestry (AFR) Participants

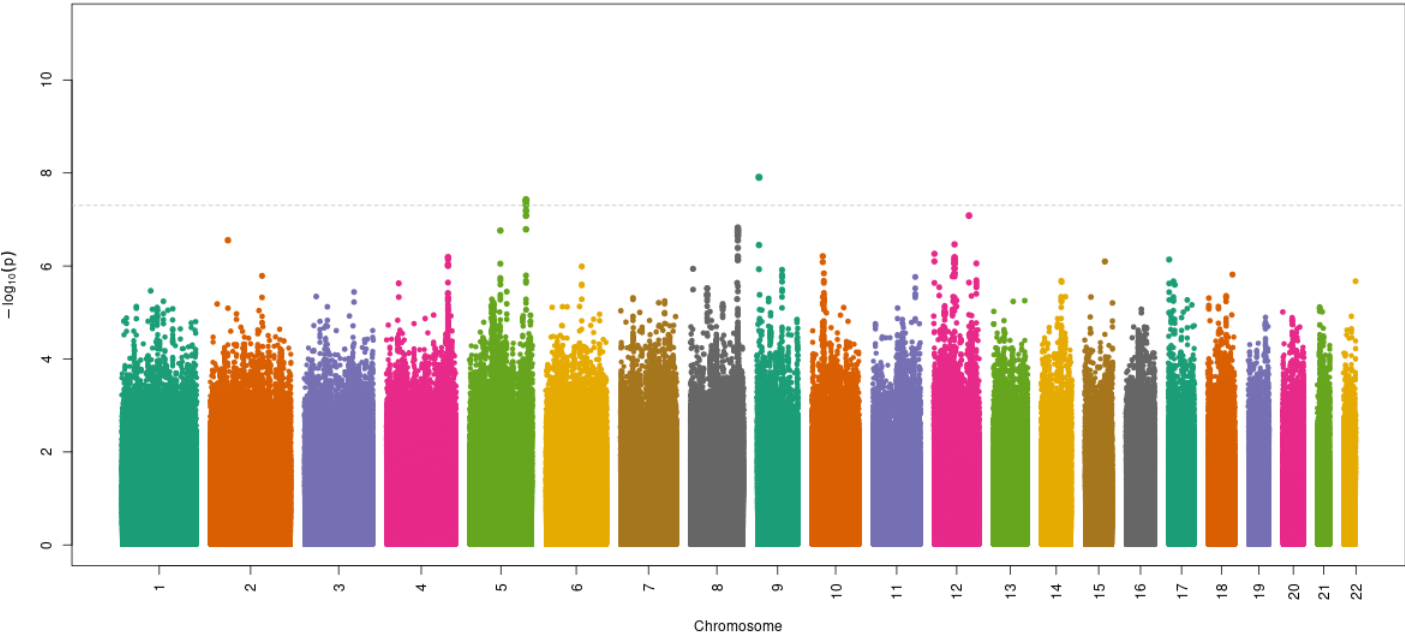


Figure S3. GWAS Manhattan plot of EHR defined CBP in Hispanic Ethnicity (HIS) Participants

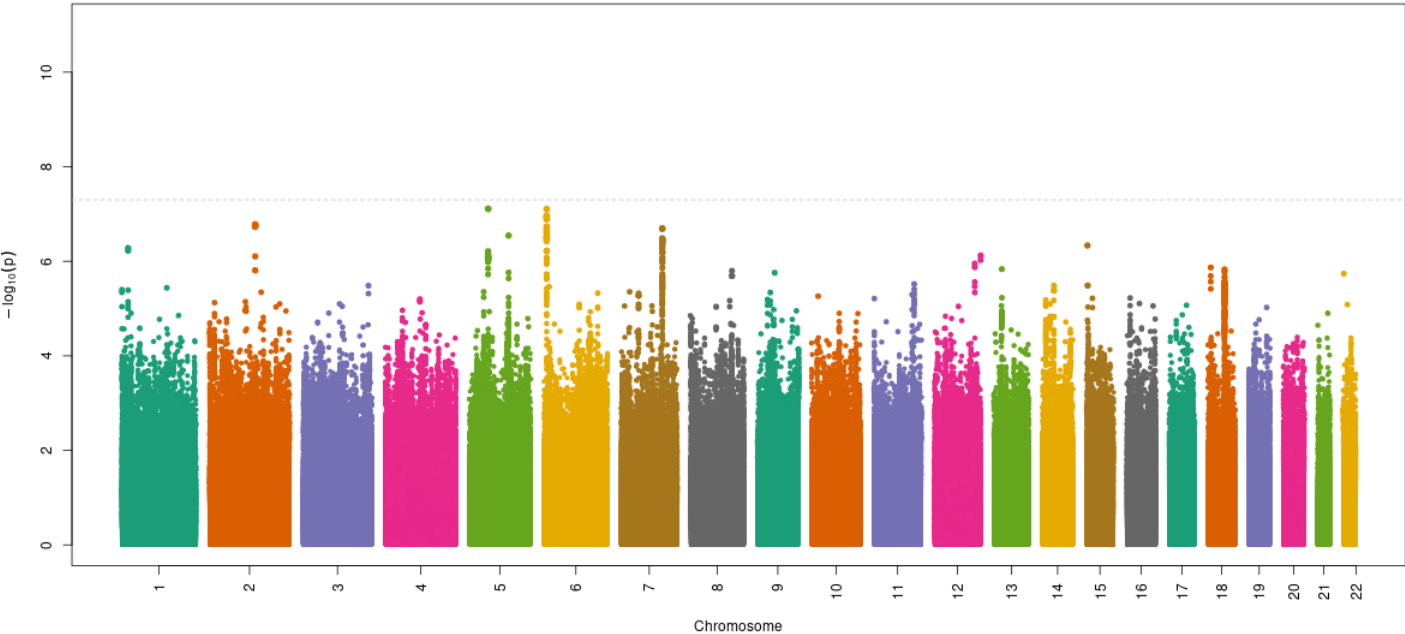


Figure S4. Multi-Ancestry Meta-Analysis GWAS QQ plot of EHR defined CBP

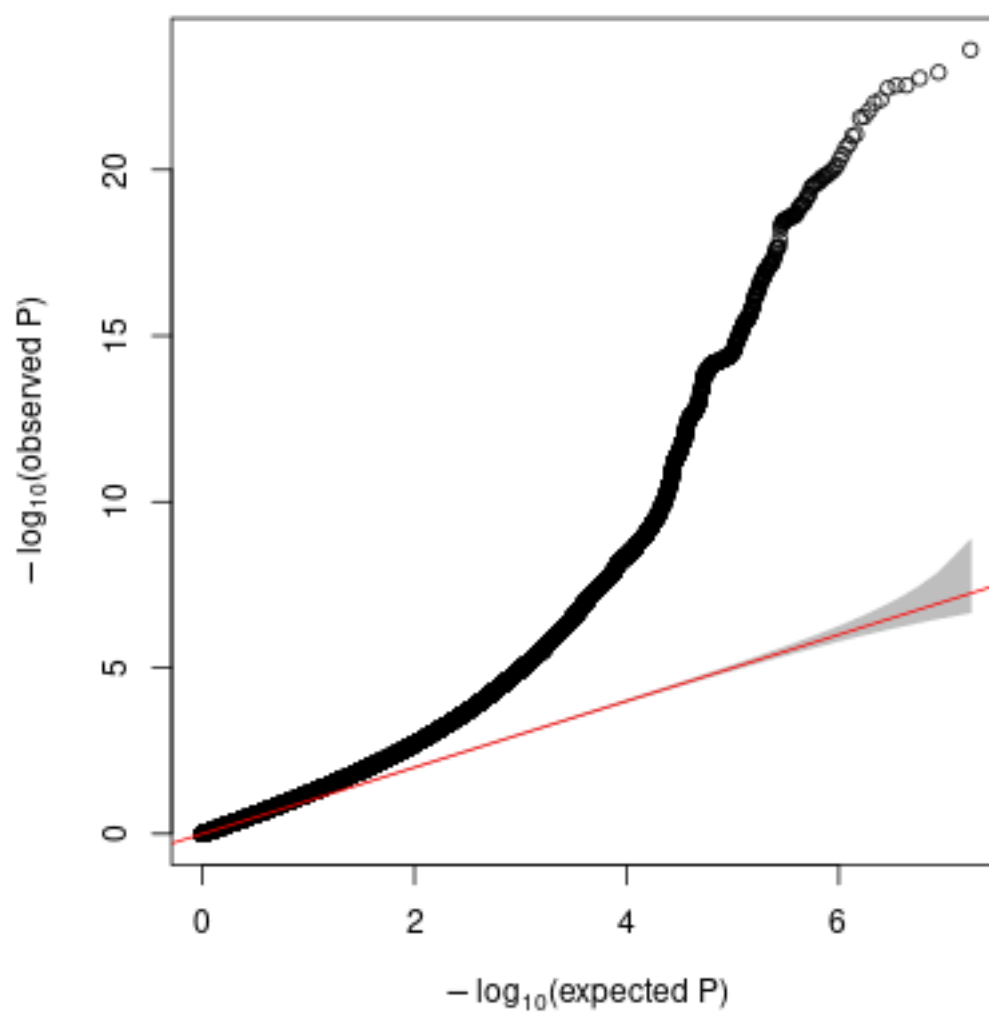


Figure S5. GWAS QQ plot of EHR defined CBP in European Ancestry (EUR) Participants

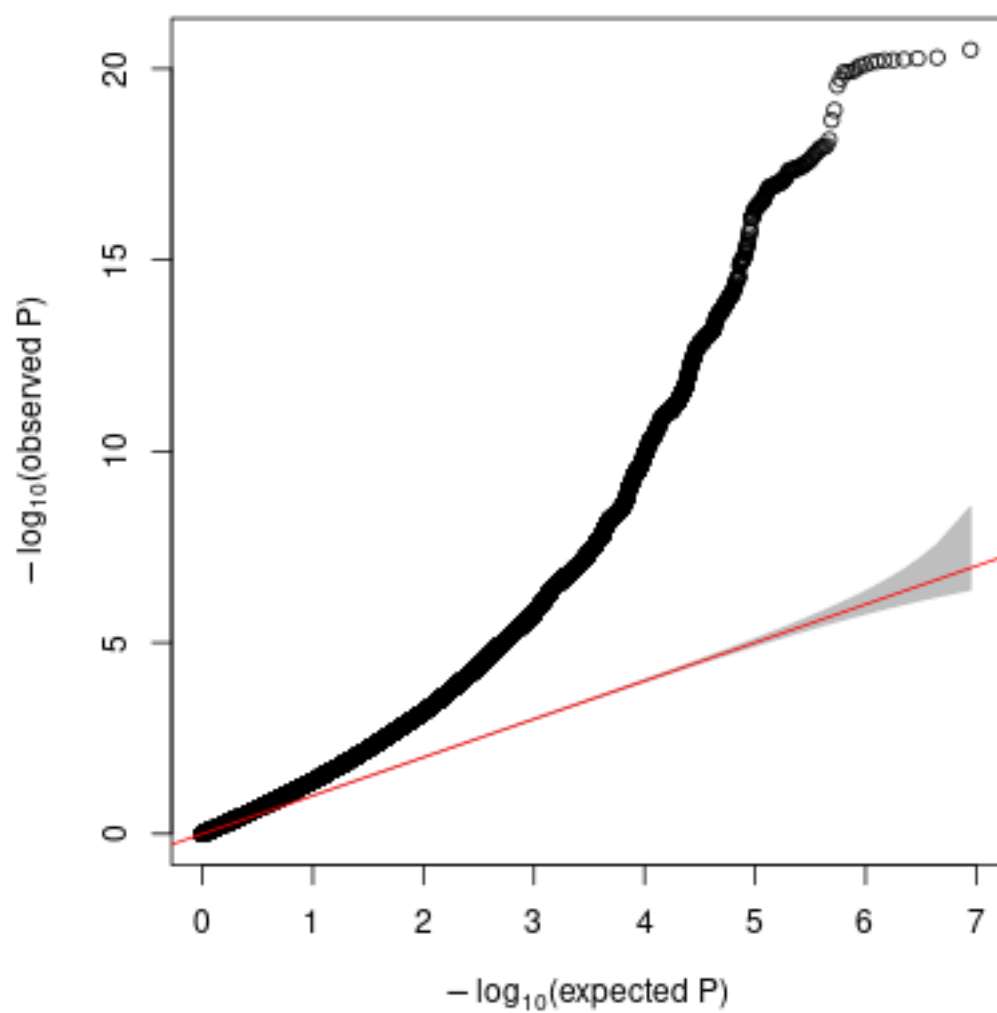


Figure S6. GWAS QQ plot of EHR defined CBP in African Ancestry (AFR) Participants

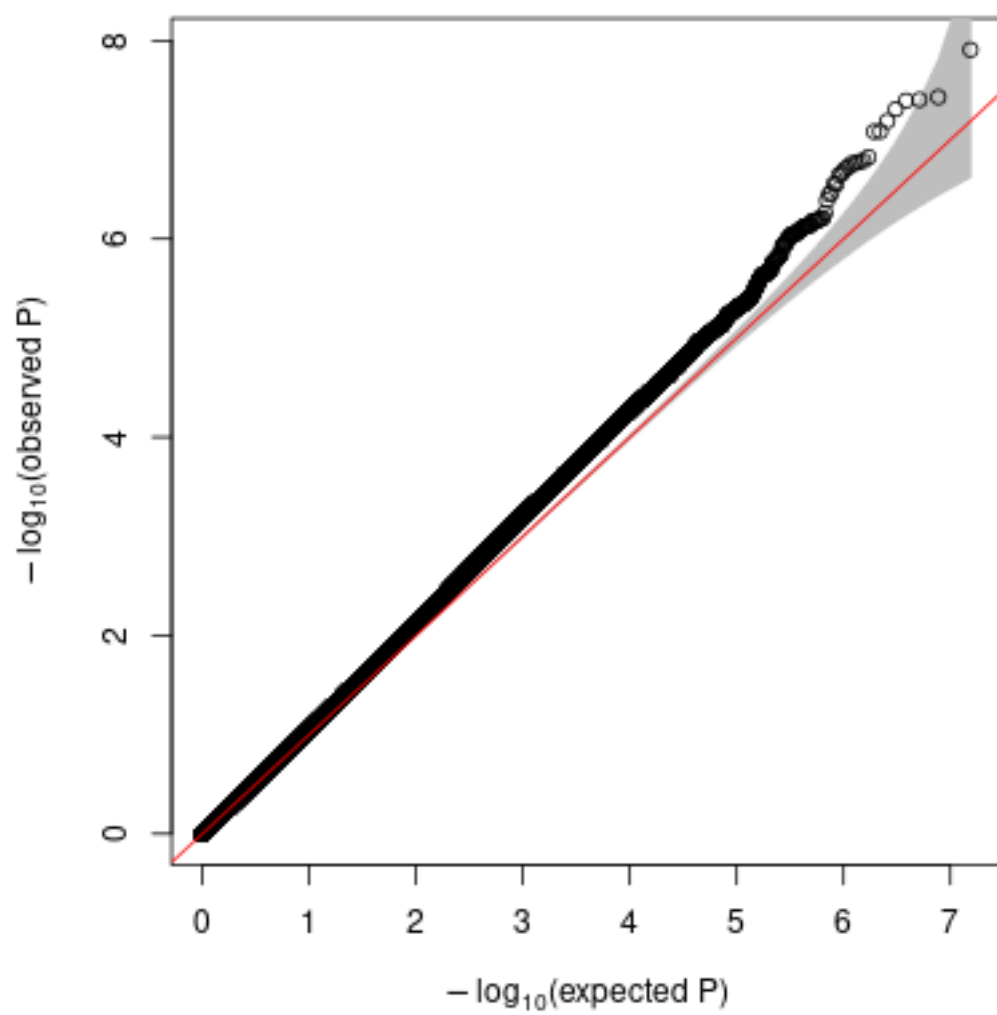


Figure S7. GWAS QQ plot of EHR defined CBP in Hispanic Ethnicity (HIS) Participants

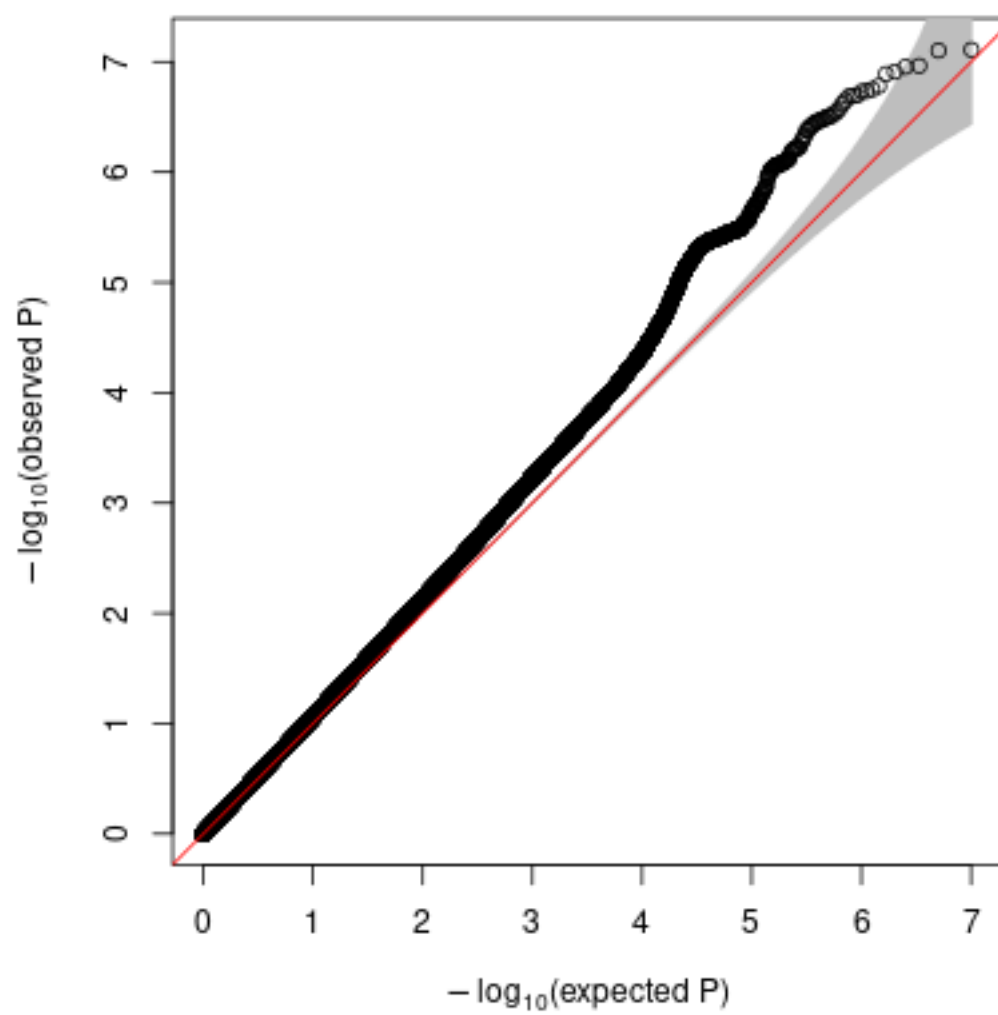
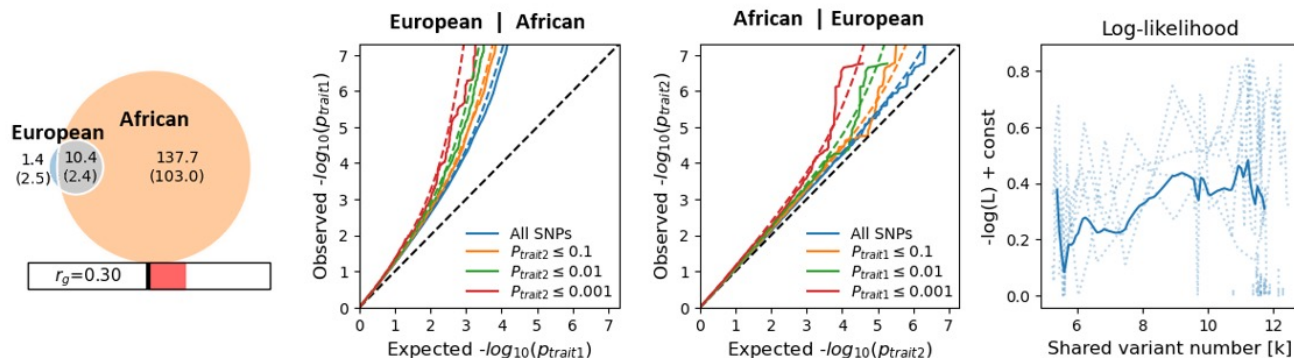
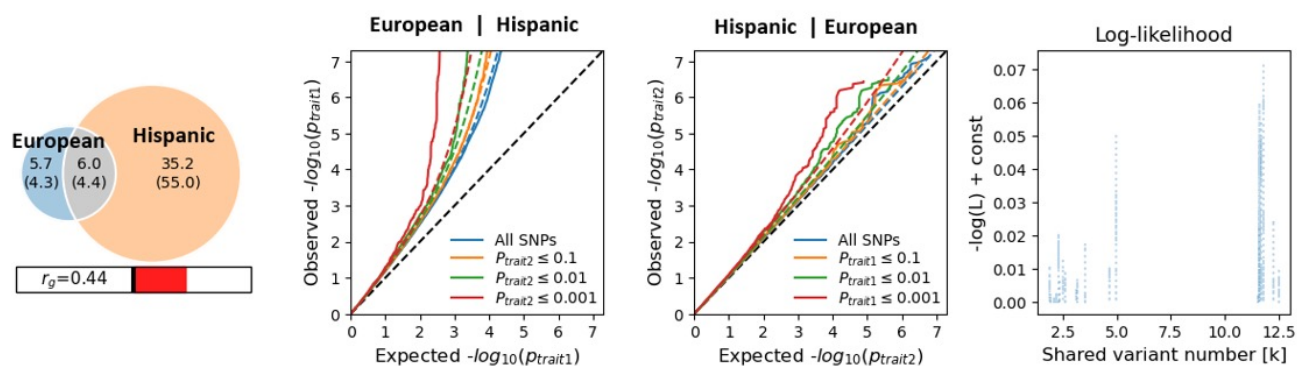


Figure S8. MiXeR genetic overlap between MVP (A) EUR and AFR HARE-defined ancestry cohorts (B) EUR and HIS HARE-defined ancestry cohorts, and (C) HIS and AFR HARE-defined ancestry cohorts. Venn diagrams report numbers in thousands of variant risk loci (standard error) related to the first trait (blue circle), second trait (orange circle), and the mutually shared variants (grey overlap). Genetic correlation is depicted as a number and red progress bar. Conditional QQ plot of trait 1 on subset 2 and trait 2 on subset 1 in the two center plots of each sub-figure. The model log likelihoods based on the number of causal variants are shown in the rightmost plots. The solid blue line reflects the average likelihood across the 20 MiXeR runs. Dotted blue lines reflect likelihoods of individual runs.

(A)



(B)



(C)

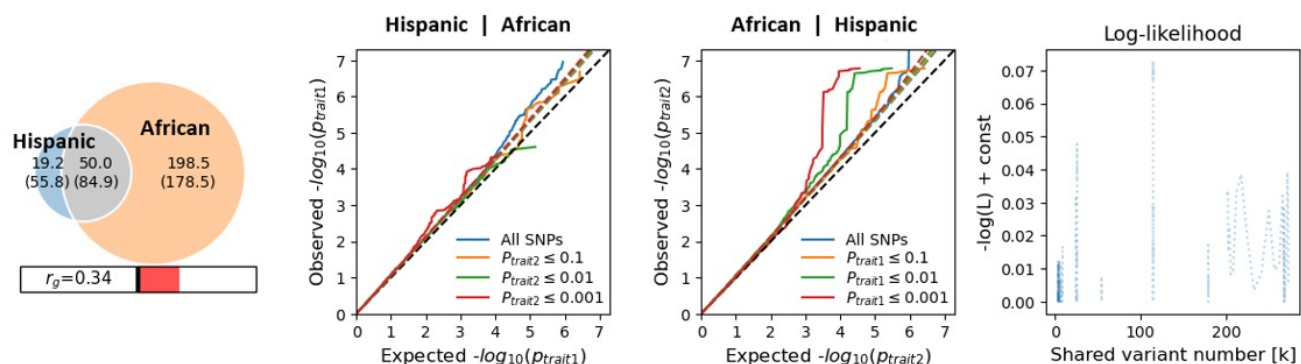


Figure S9. (A) FUMA multi-ancestry analysis MAGMA GTEx functional tissue enrichment histograms of tissue-specific localization of QTLs

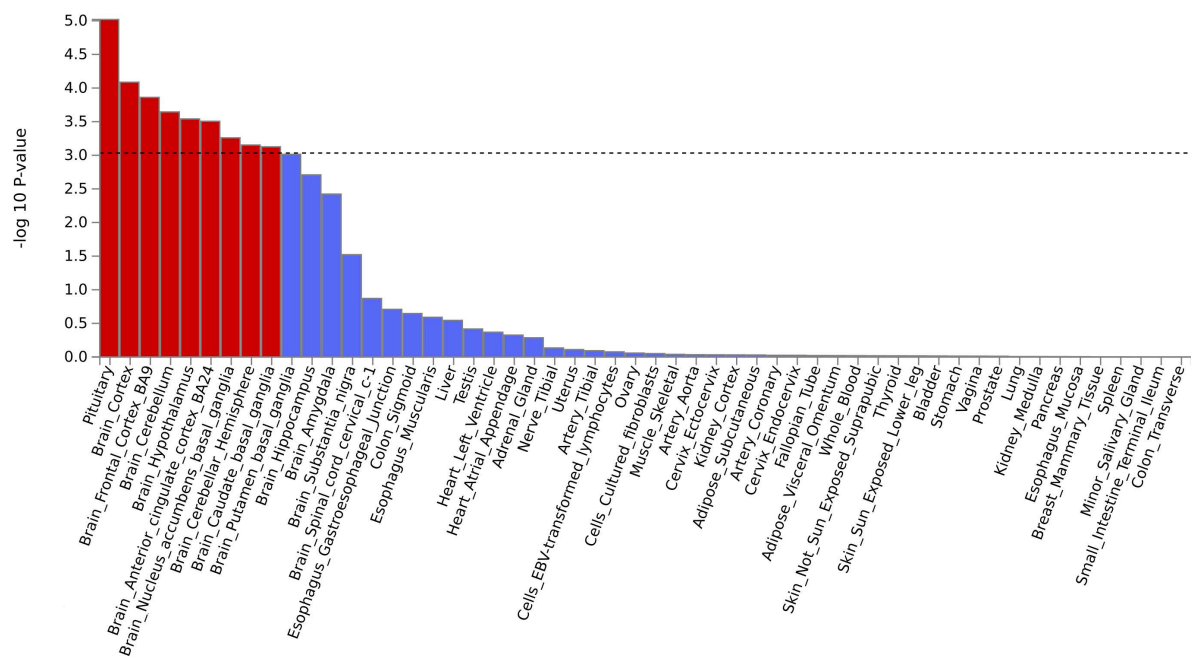
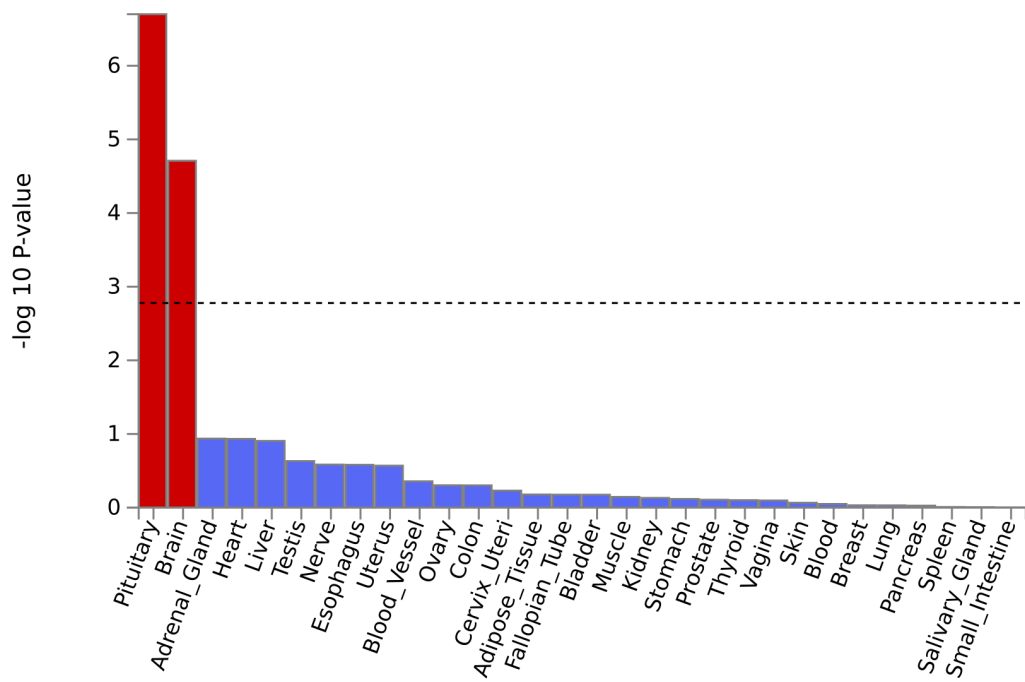


Figure S9 (B) FUMA multi-ancestry analysis MAGMA GTEx functional tissue enrichment histograms grouped by tissue context



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