Figure 3: GWAS Cohort Simulation
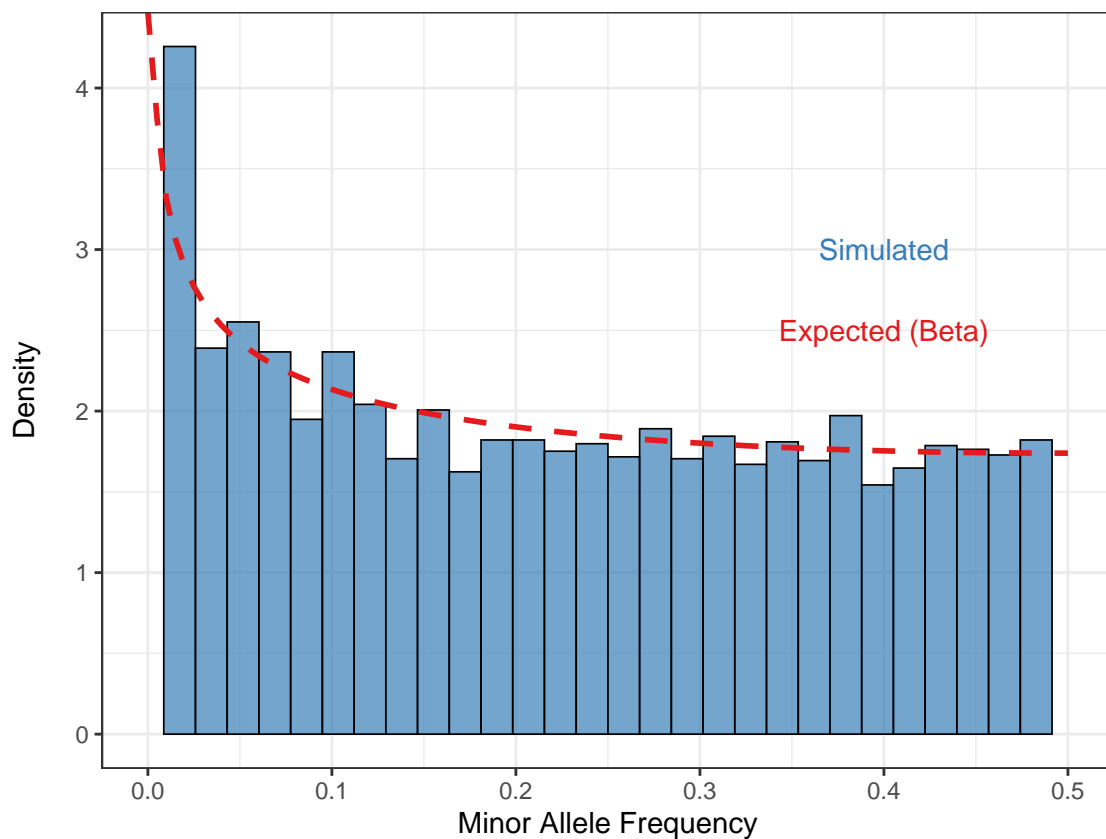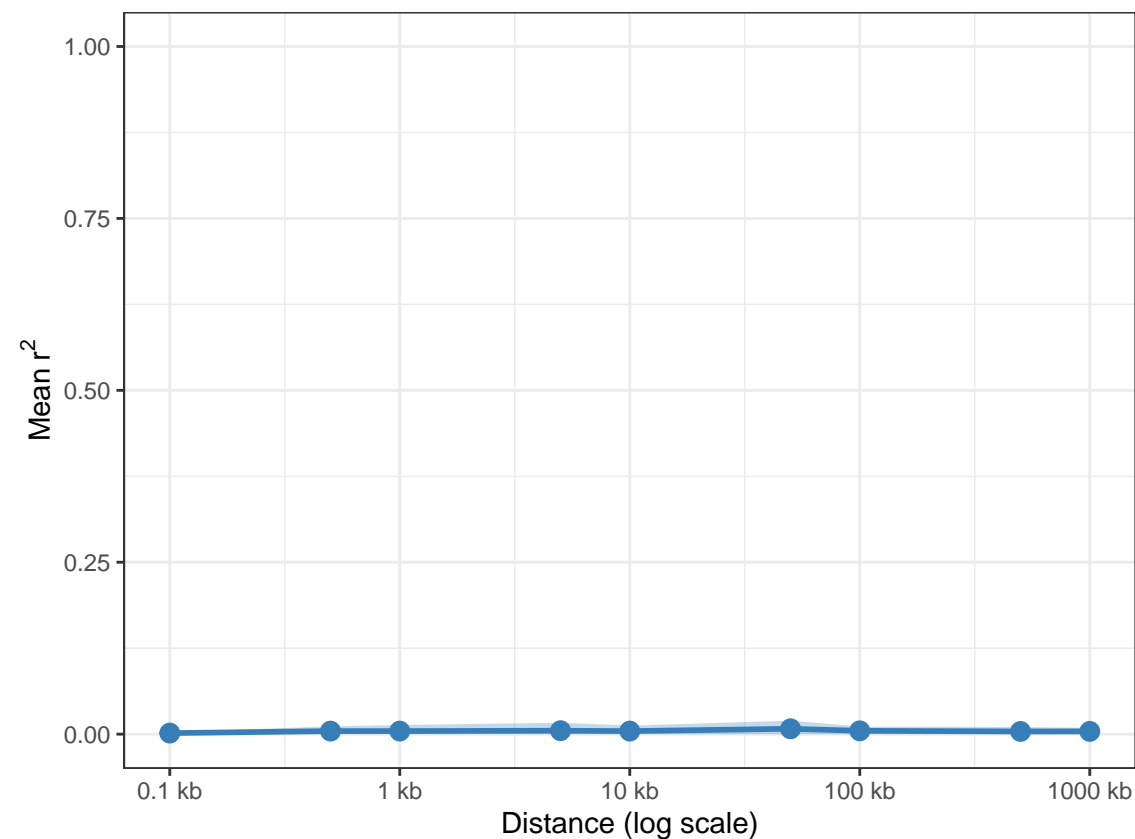
300 samples, 5000 variants, 3 populations (Fst=0.05), 50 causal variants
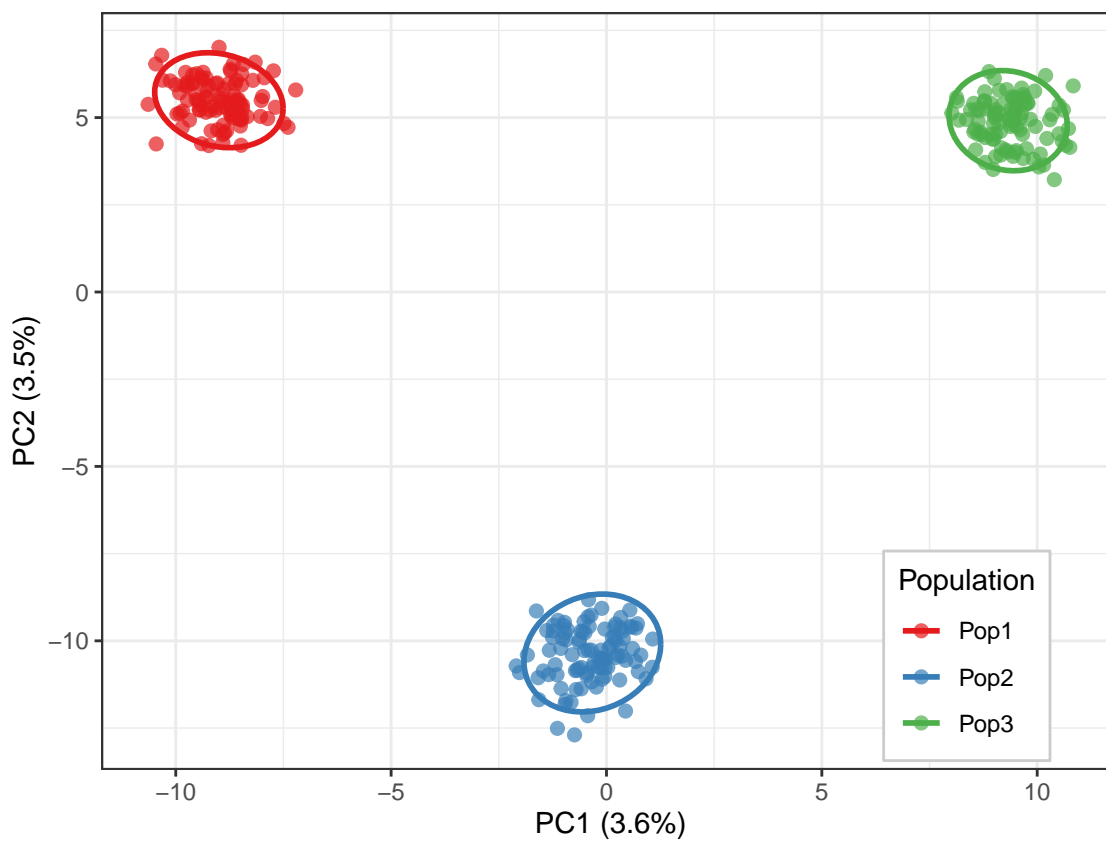
A. Minor Allele Frequency Spectrum

Simulated

Expected (Beta)

B. Linkage Disequilibrium Decay

C. Population Structure (PCA)

Population
- Pop1
- Pop2
- Pop3

D. Genotype–Phenotype Association

Non-causal

Causal

Bonferroni