Overlap of Hapmap 321 SNPs that meet filtering criteria across populations

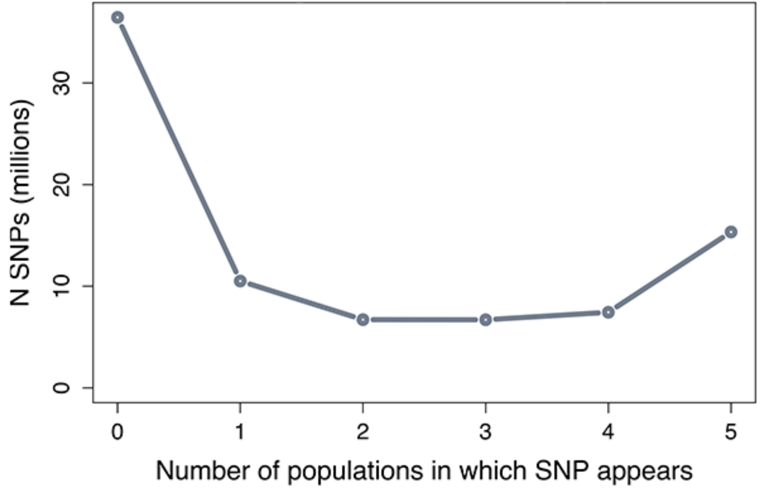

Figure S1. SNP overlap between populations in filtered projected Hapmap3.21 genotypes.

Difference in frequency of major allele in Hapmap 321 by population sharing

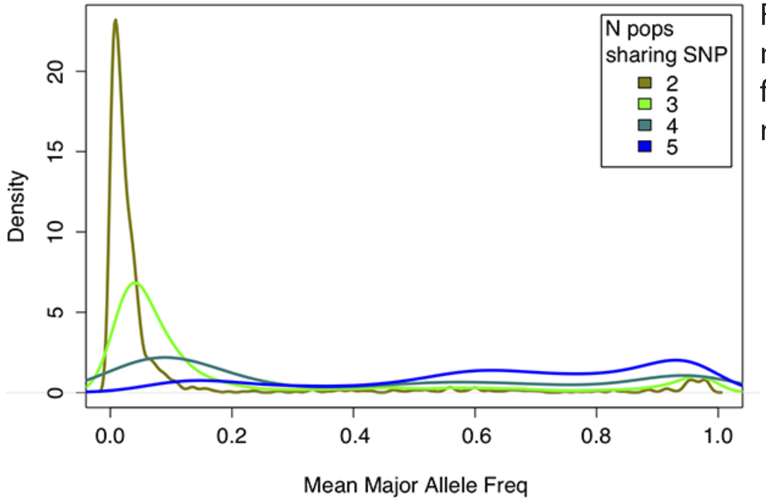

Figure S2. Density of the difference between the minimum and maximum Hapmap 3.21 major allele frequencies in shared filtered projected Hapmap3.21 genotypes.

Increase in predictive ability for DTA using genomic annotation subsets over all WGS SNPs

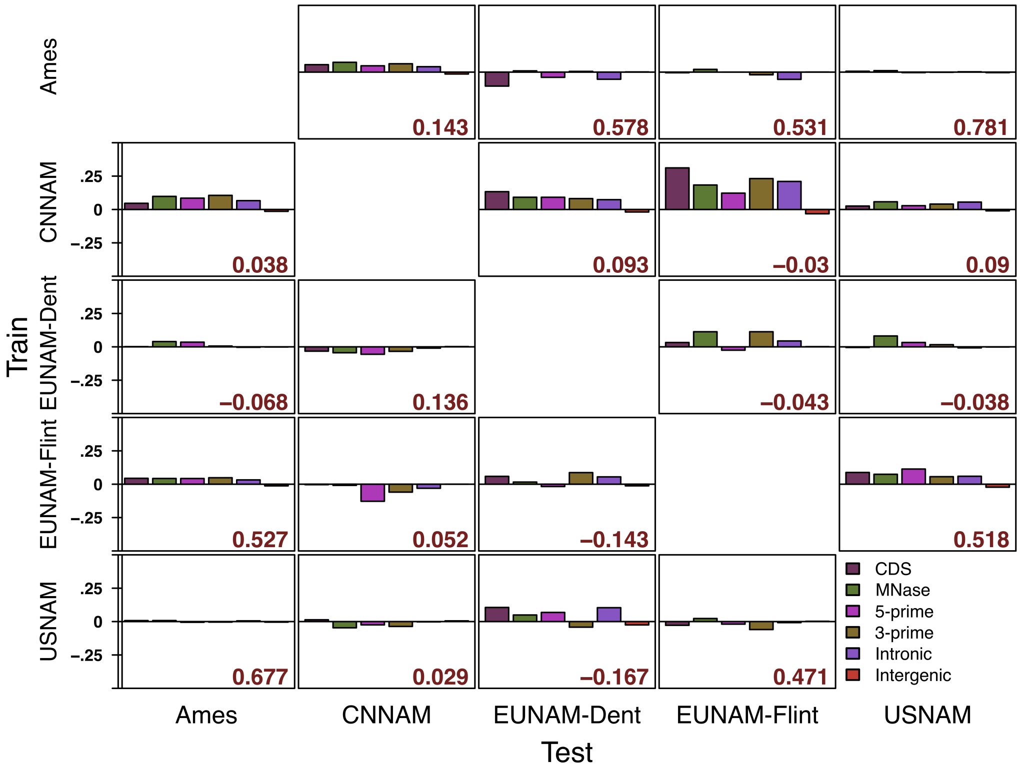

Figure S3. Increase in predictive ability for DTA using subsets of SNPs based on genomic annotations.

ROC curves for between population GWAS results with other populations as predictors

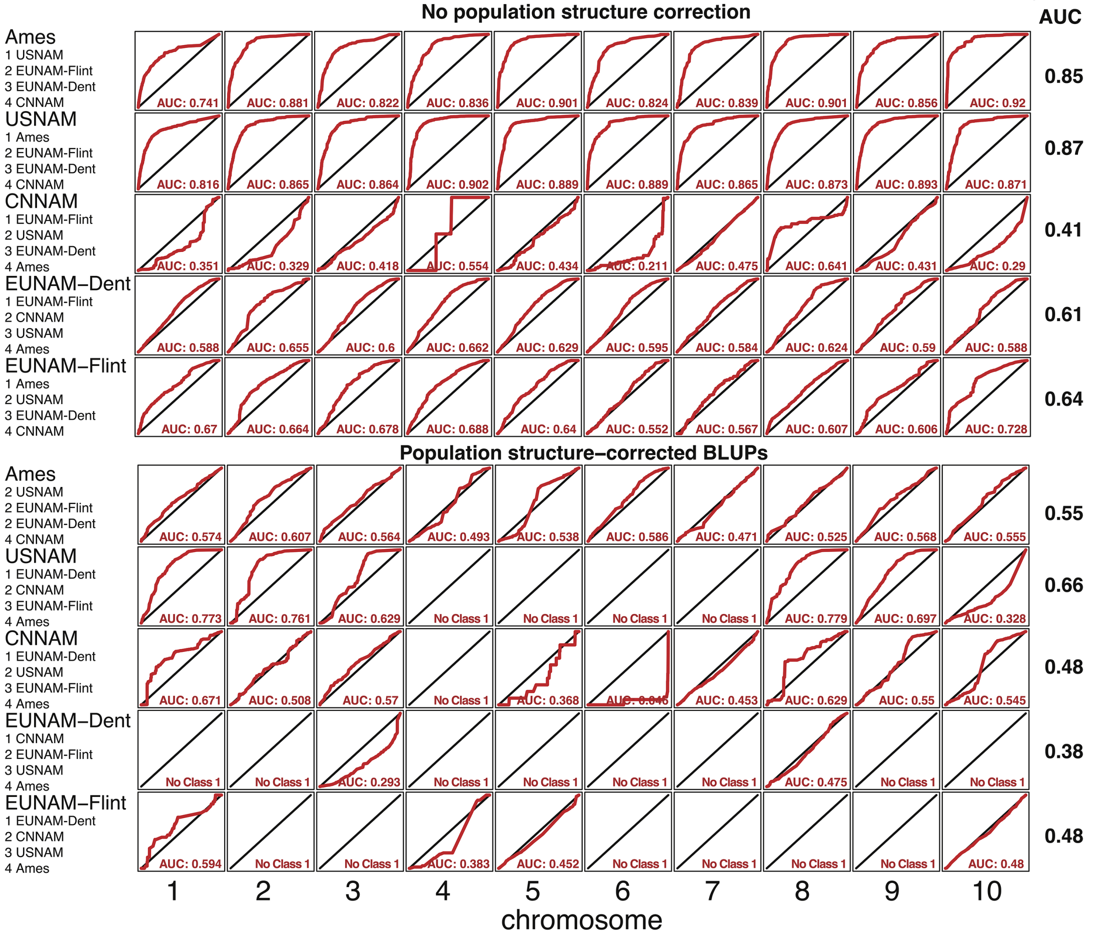

Figure S4. Random forest classifier for GWAS results between populations to evaluate overlap in GWAS results between populations. Predictors are equivalent GWAS (with or without population structure correction) for the other populations. Trained on nine chromosomes and tested on the 10th. Not all chromosomes for the population structure corrected results have top predictors, and are excluded from overall AUC calculations.

ROC curves for between population GWAS results with North American F_{ST}s as predictors

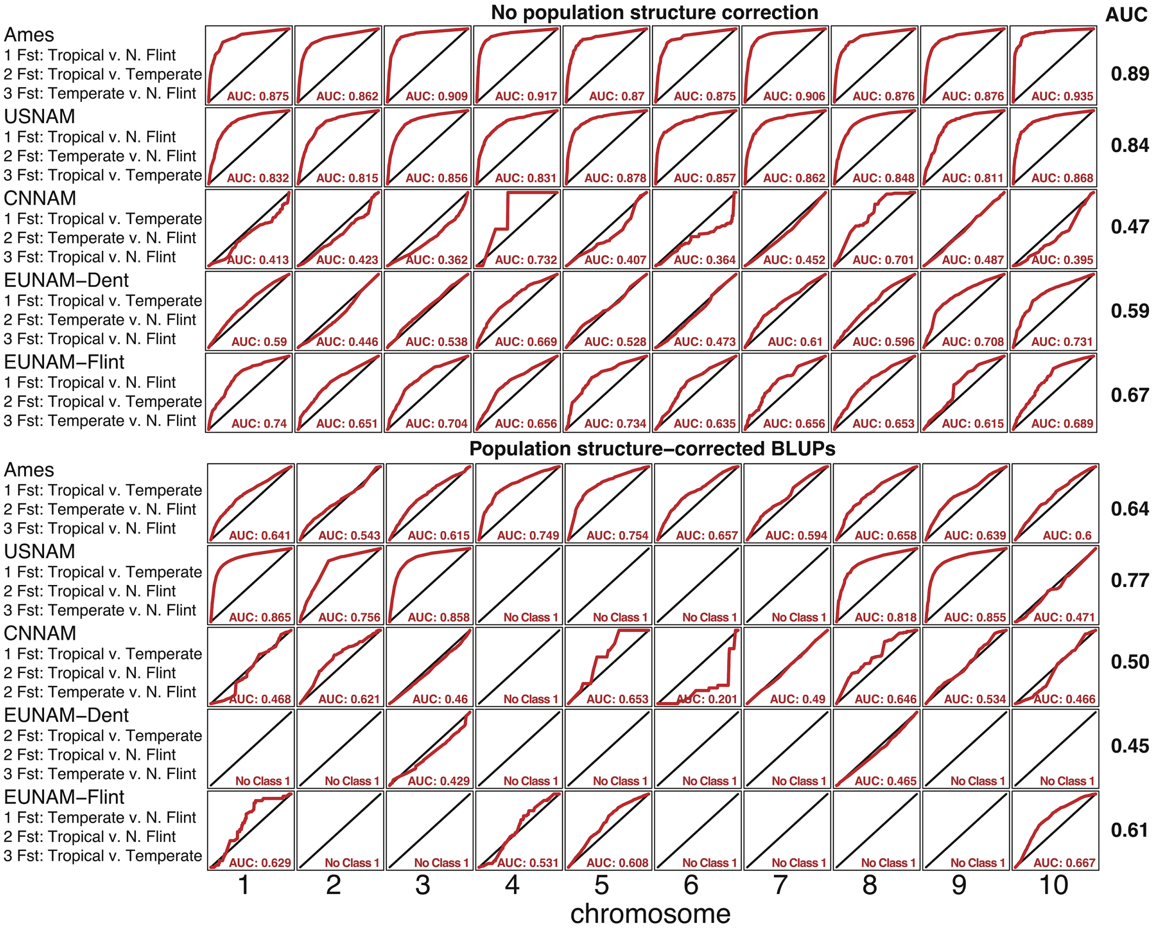

Figure S5. Random forest classifier with GWAS additive p-values as the response, and N. American FSTs as the predictors. Trained on nine chromosomes and tested on the 10th. Not all chromosomes for the population structure corrected results have top predictors, and are excluded from overall AUC calculations.