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Supplemental information

Genetic interactions drive heterogeneity

in causal variant effect sizes

for gene expression and complex traits

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Supplementary Figures

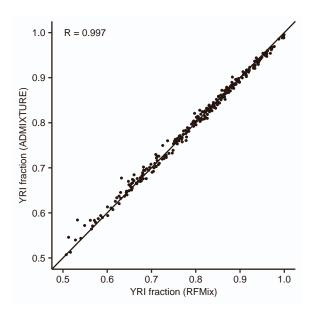


Figure S1: Comparison of ancestry inference methods. We observe a strong correlation between RFMix and ADMIXTURE estimates of global African ancestry fraction for African American individuals in MESA.

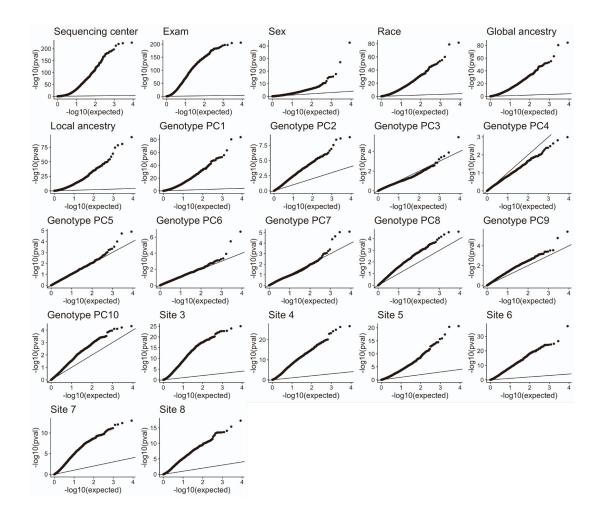


Figure S2: Association between gene expression phenotypes and covariates. We tested for statistical association between phenotypes of all 4,236 significant genes and 22 covariates, including 2 batch covariates (sequencing center and time of exam), sex, race, global and local ancestry, 10 genotype principal components (PCs), and 6 covariates corresponding to a one-hot encoding of recruitment site. We show the resulting QQ plots of association p-values, demonstrating that expression phenotypes are significantly associated with sequencing center, time of exam, sex, race, global and local ancestry, recruitment site, and the first two genotype PCs.

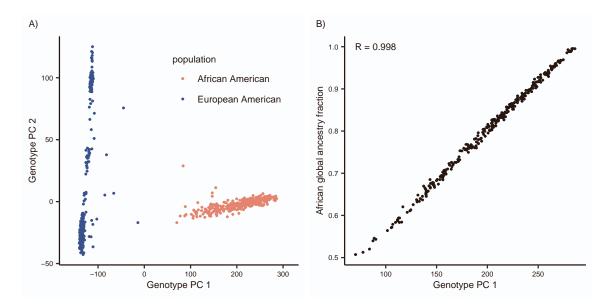


Figure S3: Principal components analysis of MESA genotypes. A) We computed principal components from the genotypes of 296 African Americans and 482 European Americans in MESA. The first genotype PC stratifies the African Americans and the second genotype PC stratifies the European Americans. B) Within African Americans, the first genotype PC is highly correlated with African global ancestry fraction.

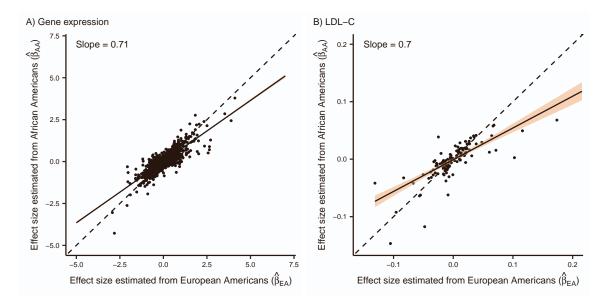


Figure S4: Ordinary least squares regression of β_{AA} on β_{EA} for **A**) gene expression and **B**) LDL-C. We represent the 95% CI with the shaded region.

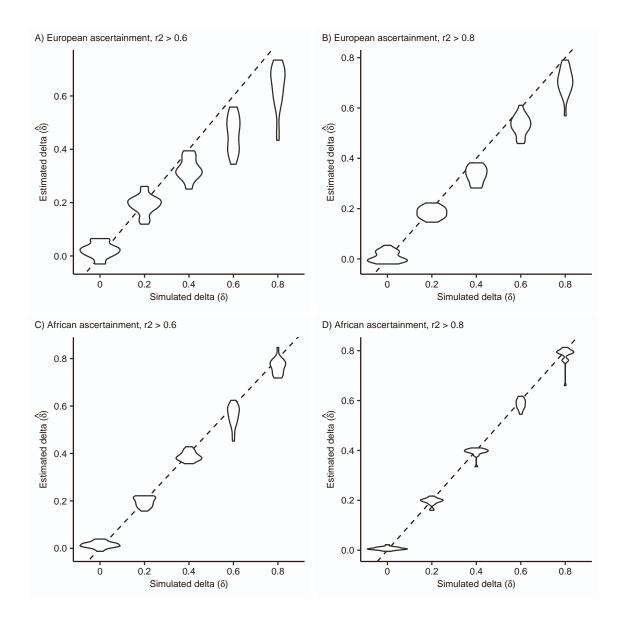


Figure S5: Estimates of δ from simulations where causal variant effect sizes are allowed to differ between populations. We simulated ascertainment in both European and African ancestries and required that the squared correlation between the causal SNP and the tag SNP was either greater than 0.6 or 0.8.

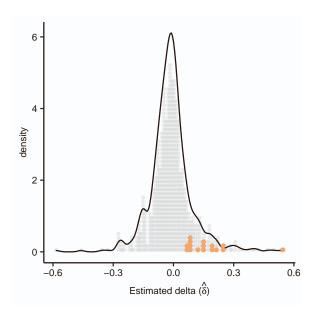


Figure S6: Estimates of δ from 700 simulations where causal variant effect sizes are identical between populations. Orange points represent simulations where the null hypothesis was rejected in favor of the alternative hypothesis (i.e. type I error).

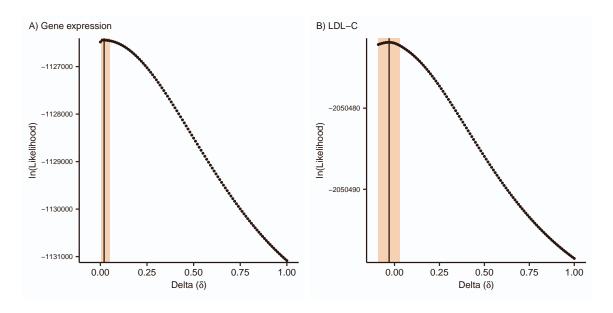


Figure S7: Likelihood surface for δ when comparing causal variant effect sizes between two subsets of European Americans. Maximum likelihood estimates and 95% bootstrap CI are **A)** 0.008 (0.003, 0.05) for gene expression and **B)** -0.03 (-0.09, 0.03) for LDL-C. We denote the MLE and 95% bootstrap CI with the vertical line and shaded region, respectively.

Supplementary Acknowledgments

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