The American Journal of Human Genetics, Volume *101*

Supplemental Data

Leveraging Multi-ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations

Marc A. Coram, Huaying Fang, Sophie I. Candille, Themistocles L. Assimes, and Hua Tang

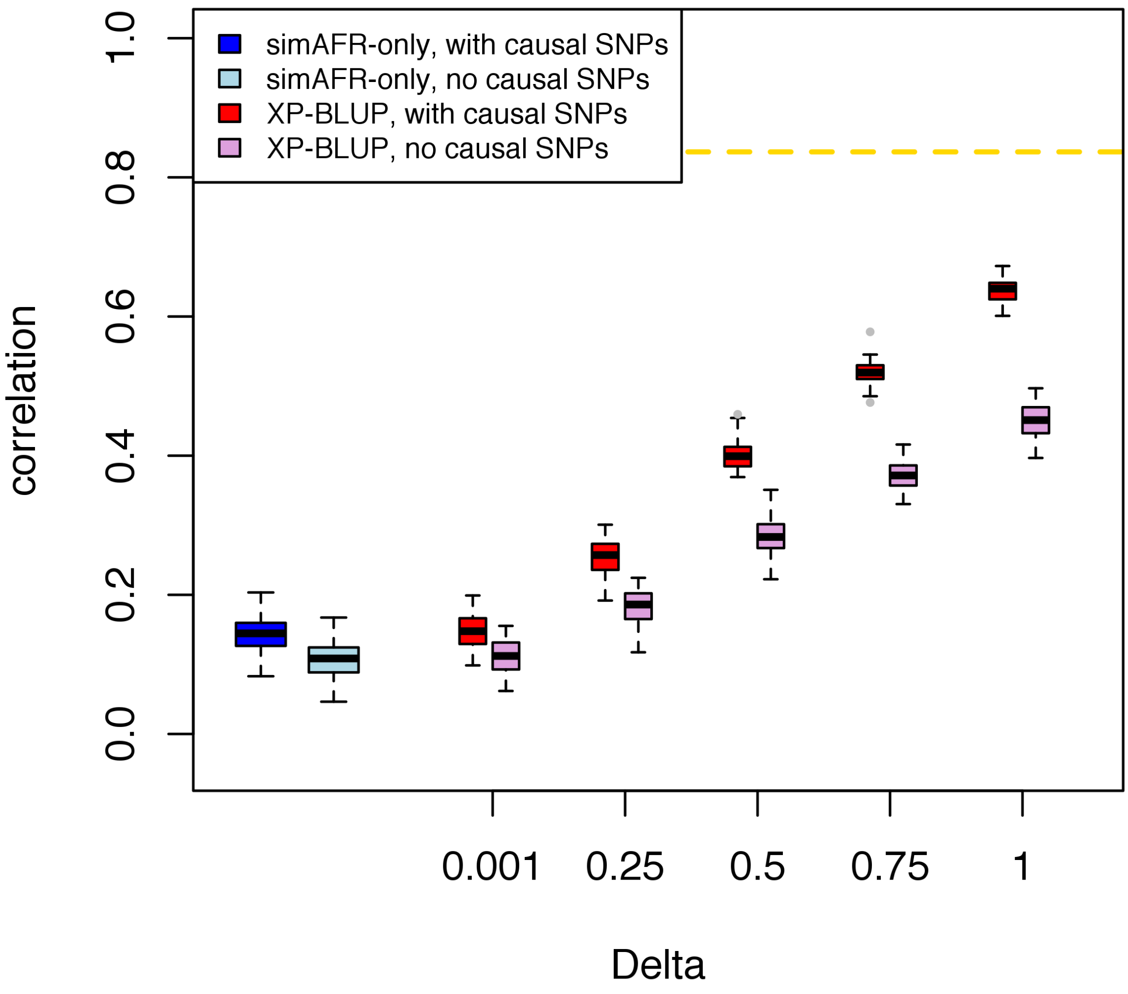

Figure S1. Comparison of predictive correlation, with or without the causal variants, by XP-BLUP to a single-component linear mixed-effects model (LMM) using the simAFR training data only. Delta specifies the proportion of overlapping loci between ethnicities. Dashed line is the theoretical maximum.

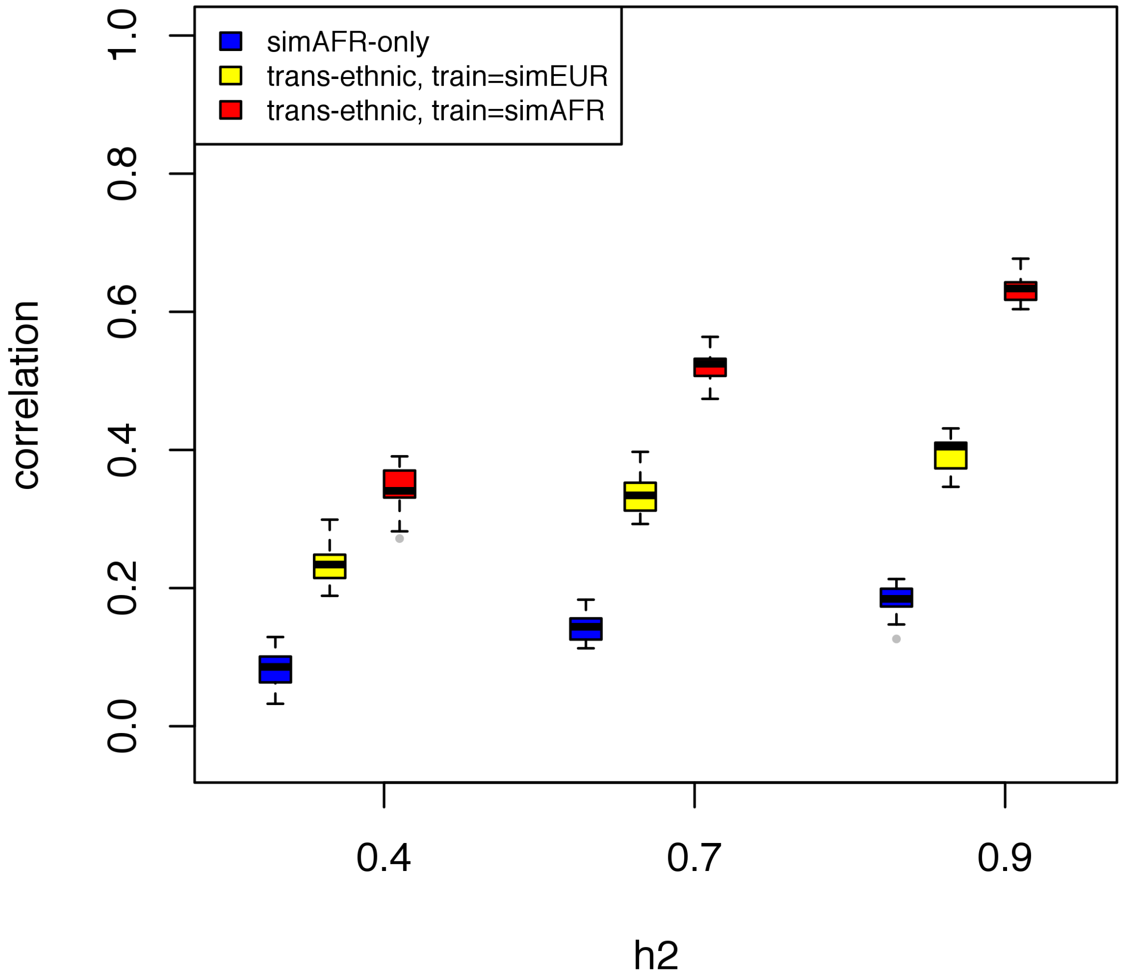

Figure S2. Predictive correlation of XP-BLUP and a single-component linear mixed-effects model (LMM) using the simAFR training data only, as a function of the underlying heritability (h2).

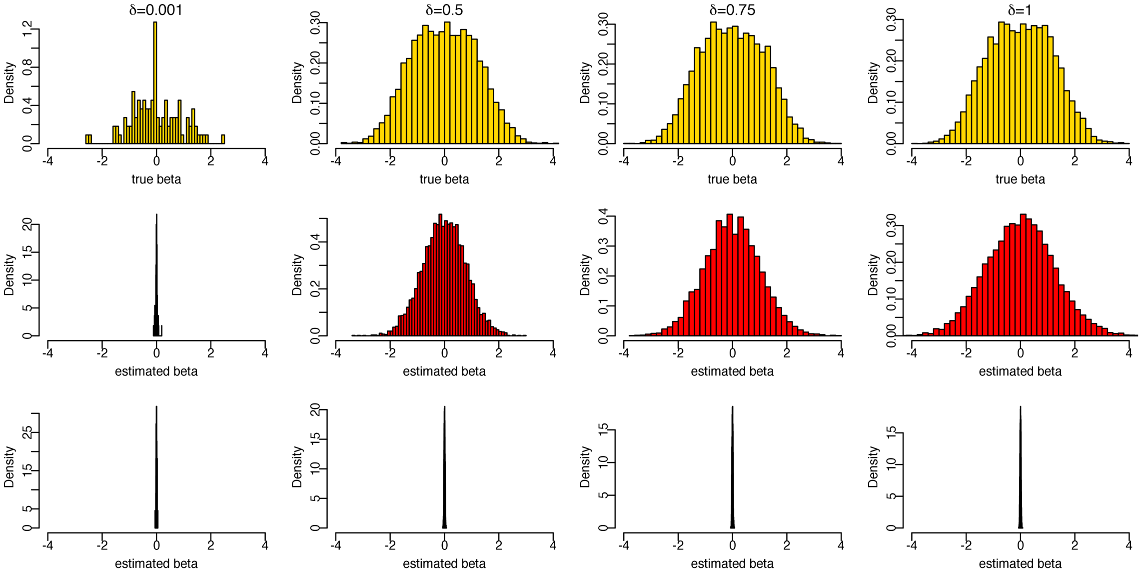

Figure S3. True and BLUP of trait-relevant SNP effects in simulations with varying degree of overlap between ethnicities. **Top row**: True effects of SNPs in C_1. **Middle row**: BLUP for SNPs in C_1; **bottom row**: BLUP for SNPs not C_1. Column heading δ indicates the degree of loci overlap between ethnicities: $\delta = 0.001$ represents independent genetic architecture, while $\delta = 1$ indicates all trait loci are shared.

p-threshold	$\|C_1\|$	VG_1 (SE)	Prediction r
5×10^{-8}	413	479.61 (113.09)	0.18
5×10^{-7}	518	471.74 (113.08)	0.19
5×10^{-6}	698	451.84 (112.87)	0.19
5×10^{-5}	1068	477.98 (113.89)	0.19
5×10^{-4}	1932	430.99 (112.72)	0.18
5×10^{-3}	6371	422.29 (117.29)	0.15
1	864472	609.335 (119.01)	0.095

Table S1: Predictive correlation coefficient for Low-density lipoprotein (LDL) level in WHI-SHARe at varying threshold (VG_1: variance explained by SNPs in C_1; Prediction r is evaluated on testing set).

p-threshold	$\|C_1\|$	VG_1 (SE)	Prediction r
5×10^{-8}	569	1.18×10^{-2} (3.58×10^{-3})	0.22
5×10^{-7}	706	1.14×10^{-2} (3.56×10^{-3})	0.23
5×10^{-6}	910	1.15×10^{-2} (3.57×10^{-3})	0.22
5×10^{-5}	1257	1.11×10^{-2} (3.59×10^{-3})	0.21
5×10^{-4}	2174	1.07×10^{-2} (3.63×10^{-3})	0.19
5×10^{-3}	6351	8.64×10^{-3} (3.72×10^{-3})	0.16
1	864472	1.69×10^{-2} (3.81×10^{-3})	0.086

Table S2: Predictive correlation coefficient for log high-density lipoprotein (HDL) in WHI-SHARe at varying threshold (VG_1: random effects variance explained by SNPs in C_1; Prediction r is evaluated on testing set).

p-threshold	**$\| C_1\|$**	**VG_1**	**Prediction r**
5×10^{-8}	413	4.32×10^{-2} (1.28×10^{-2})	0.17
5×10^{-7}	531	4.37×10^{-2} (1.29×10^{-2})	0.17
5×10^{-6}	726	4.03×10^{-2} (1.28×10^{-2})	0.17
5×10^{-5}	1065	3.81×10^{-2} (1.27×10^{-2})	0.17
5×10^{-4}	1996	3.77×10^{-2} (1.28×10^{-2})	0.16
5×10^{-3}	6508	2.90×10^{-2} (1.30×10^{-2})	0.15
1	864472	5.34×10^{-2} (1.33×10^{-2})	0.078

Table S3: Predictive correlation coefficient for log triglyceride (TG) level in WHI-SHARe at varying threshold (VG_1: variance explained by SNPs in C_1; Prediction r is evaluated on testing set).