Table S4 GREML estimates of variance components and GBLUP accuracies with and without genomic relationships for phenotypes with additive and dominance effects of 1006 QTL (mean ± standard deviation, n=10 repeats)

h^2 and σ^2	Definition		$\hat{\sigma}^2_\alpha$	$\hat{h}^2_\alpha$	R_a	$\hat{R}_a$	$\hat{\sigma}^2_\delta$	$\hat{h}^2_\delta$	R_d	$\hat{R}_d$
h^2_α=0.05	None	Mean	1.68×10^{-4}	1.67×10^{-4}	0.46	0.50	2.47×10^{-4}	2.47×10^{-4}	0.29	0.36
		SD	4.12×10^{-5}	4.19×10^{-5}	0.04	0.04	1.38×10^{-4}	1.41×10^{-4}	0.10	0.03
h^2_δ=0.05	I	Mean	0.06	0.06	0.46	0.50	0.04	0.03	0.29	0.36
		SD	0.02	0.01	0.04	0.04	0.02	0.02	0.10	0.03
σ^2_α=0.06	II	Mean	0.06	0.06	0.46	0.50	0.04	0.03	0.29	0.36
		SD	0.02	0.01	0.04	0.04	0.02	0.02	0.10	0.03
σ^2_δ=0.06	III	Mean	0.06	0.06	0.46	0.50	0.04	0.03	0.29	0.36
		SD	0.01	0.01	0.04	0.04	0.02	0.02	0.11	0.03
h^2_α=0.15	None	Mean	6.53×10^{-4}	6.79×10^{-4}	0.66	0.68	1.51×10^{-3}	1.57×10^{-3}	0.60	0.58
		SD	1.01×10^{-4}	1.26×10^{-4}	0.02	0.02	2.82×10^{-4}	3.36×10^{-4}	0.04	0.02
h^2_δ=0.15	I	Mean	0.24	0.17	0.66	0.68	0.23	0.16	0.60	0.58
		SD	0.04	0.02	0.02	0.02	0.04	0.03	0.04	0.02
σ^2_α=0.21	II	Mean	0.24	0.17	0.66	0.68	0.22	0.16	0.60	0.58
		SD	0.04	0.02	0.02	0.02	0.04	0.03	0.04	0.02
σ^2_δ=0.21	III	Mean	0.24	0.17	0.66	0.68	0.22	0.16	0.60	0.58
		SD	0.04	0.02	0.03	0.02	0.04	0.03	0.04	0.02
h^2_α=0.30	None	Mean	1.90×10^{-3}	1.91×10^{-3}	0.78	0.80	5.02×10^{-3}	5.06×10^{-3}	0.76	0.76
		SD	1.53×10^{-4}	1.93×10^{-4}	0.01	0.01	5.04×10^{-4}	6.63×10^{-4}	0.02	0.01
h^2_δ=0.30	I	Mean	0.71	0.29	0.78	0.80	0.75	0.31	0.76	0.76
		SD	0.06	0.02	0.01	0.01	0.08	0.03	0.02	0.01
σ^2_α=0.75	II	Mean	0.69	0.29	0.78	0.80	0.74	0.31	0.76	0.76
		SD	0.06	0.02	0.01	0.01	0.07	0.03	0.02	0.01
σ^2_δ=0.75	III	Mean	0.69	0.29	0.78	0.80	0.74	0.31	0.77	0.75
		SD	0.06	0.02	0.01	0.01	0.07	0.03	0.02	0.01

h^2_α is true additive heritability, h^2_δ is true dominance heritability, σ^2_α is true additive variance, σ^2_δ is true dominance variance, R_a is predicted accuracy of GBLUP of breeding values, $\hat{R}_a$ is observed accuracy of GBLUP of breeding values, R_d is predicted accuracy of GBLUP of dominance deviations, $\hat{R}_d$ is observed accuracy of GBLUP of dominance deviations, R_g is predicted accuracy of GBLUP

of genotypic values, $\hat{R}_g$ is observed accuracy of GBLUP of genotypic values, 'None': using the original mixed model of Equation 3 without genomic relationships.