

Table S4 P-values by the Kolmogorov-Smirnov Test

	Permut	Bootstr	GeneDr	GRAIP
$\sigma = 0.7$	0.60200	0.32428	0.00000	0.00000
$\sigma = 1$	0.44558	0.44988	0.00000	0.00000
$\sigma = 1.5$	0.43282	0.10871	0.00000	0.00000

Based on 6000 simulations under the null hypothesis that when no QTL effects existed, the distribution estimated by a testing method when relatedness was ignored was identical to the distribution estimated by the same method when relatedness was taken into account. Data was generated by each of the testing methods: permuting genotypic data (Permut), bootstrapping phenotypic data (Bootstr), gene dropping (GeneDr) and GRAIP. The distribution of the residual was normal with a standard deviation 0.7, 1 or 1.5.