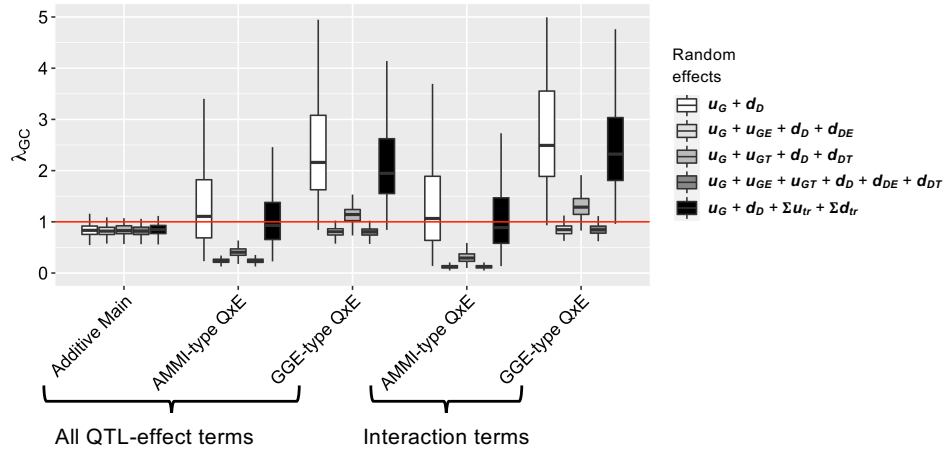


A



B

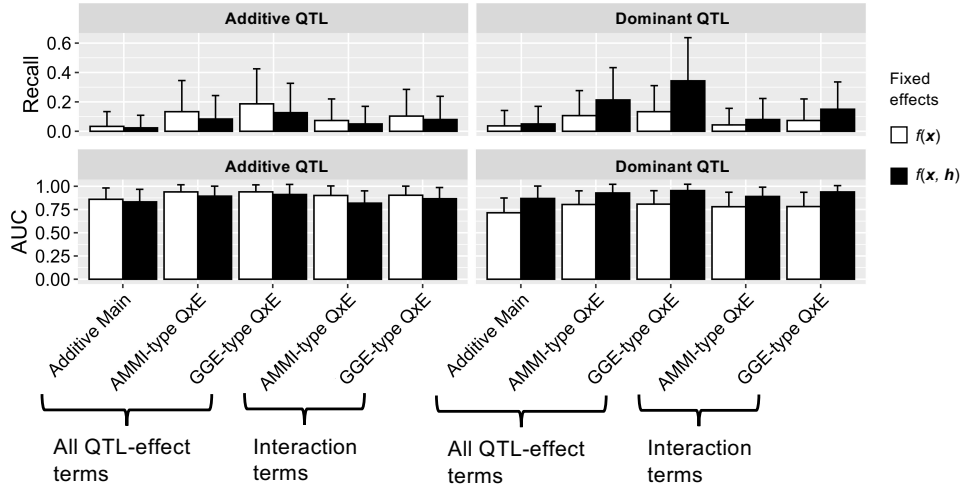


Figure S1. Evaluation of linear mixed models (LMMs) including dominant effect terms.

(A) Box and whisker plots of genomic inflation factors (λ_{GC}) for p values. Red horizontal line indicates the theoretically expected value (i.e., $\lambda_{GC} = 1$). (B) Bar plots of power to detect quantitative trait loci (QTLs) in simulated phenotypes, assuming multiple environments and multiple trials. Recall values were calculated using a false discovery rate of 0.05 as the genome-wide significance threshold. Values represent means of 100 simulations. The fixed and random effect terms used in this analysis was GGE-type $Q \times E$ and ' $u_G + u_{GE} + u_{GT} + d_D + d_{DE} + d_{DT}$,' respectively.