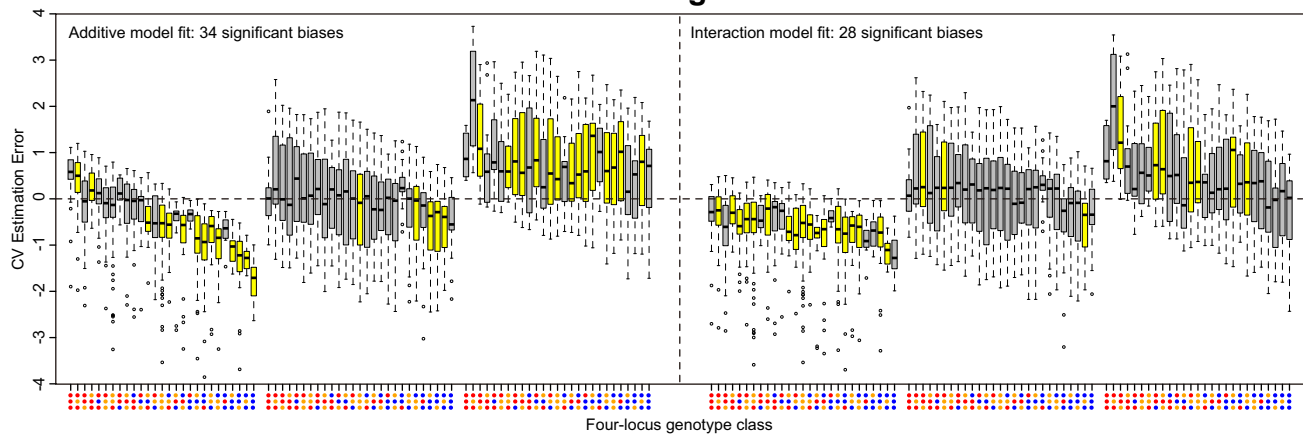
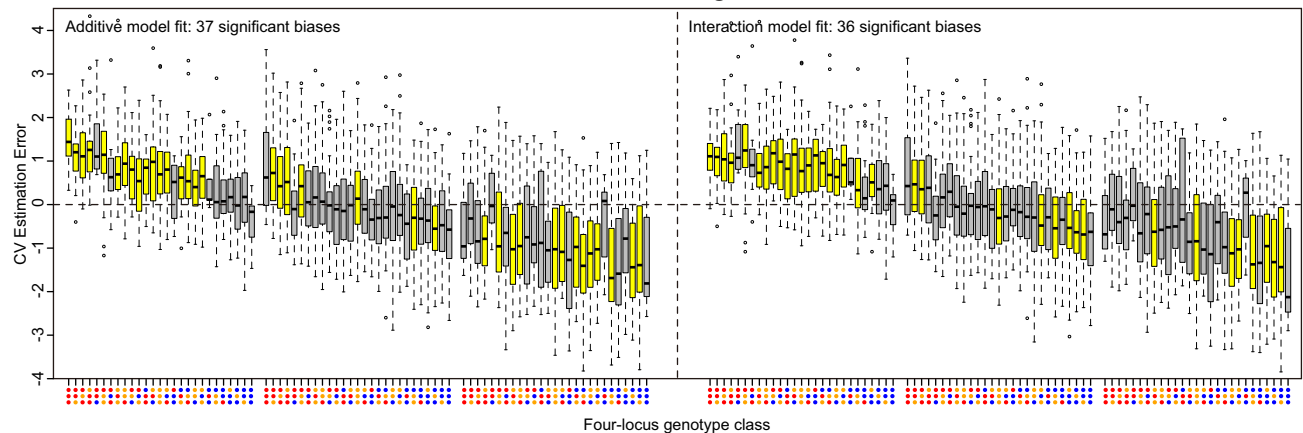


## Heading date



## Plant height



**Figure S14 Phenotype estimation bias for each of the 81 subpopulation with additive and interactive model in heading date and plant height, respectively.** Each  $y$  axis gives the cross-validated estimation error (bias) for the four-locus additive and interactive model, which represents the difference between predictive phenotype and actual phenotype ( $y - \hat{y}$ ). Each box plot shows the distribution of prediction errors for each of the 81 genotype classes. The 27 leftmost/middle/rightmost box plots represent the genotype classes with the MH63/heterozygous/ZS97 hub QTL allele. Significant biases, i.e., where the estimation errors deviate significantly from zero, are colored in yellow.