Figure S10. Manhattan plot of results from a conditional genome-wide association study (GWAS) of five elemental grain phenotypes in the Ames panel. For each phenotype, the SNPs selected by the optimal multi-locus mixed model were included as covariates in the mixed linear model to control for large-effect loci. Each point represents a SNP with its -$\log_{10}$ P-value (y-axis) from a mixed linear model analysis plotted as a function of physical position (B73 RefGen_v4) across the 10 chromosomes of maize (x-axis). None of the tested SNPs in the conditional GWAS were significant at a genome-wide false-discovery rate of 5%.