Figure S8  Genome-wide association study (GWAS) for lutein content in maize grain. Scatter plot of association results from a unified mixed model analysis of lutein and linkage disequilibrium (LD) estimates ($r^2$) across the lcyE chromosome region. Negative log$_{10}$-transformed $P$-values (left y-axis) from a GWAS for lutein and $r^2$ values (right y-axis) are plotted against physical position (B73 RefGen_v2) for a 12 Mb region on chromosome 8 that encompasses lcyE. The blue vertical lines are $-\log_{10}$P-values for SNPs that are statistically significant for lutein at 5% false discovery rate (FDR), while the gray vertical lines are $-\log_{10}$P-values for SNPs that are non-significant at 5% FDR. Triangles are the $r^2$ values of each SNP relative to the peak SNP (indicated in red) at 138,883,206 bp. The black horizontal dashed line indicates the $-\log_{10}$P-value of the least statistically significant SNP at 5% FDR. The black vertical dashed lines indicate the start and stop positions of lcyE (GRMZM2G12966). (B) Scatter plot of association results from a conditional unified mixed model analysis of lutein and LD estimates ($r^2$) across the lcyE chromosome region, as in (A). The two SNPs (lcyE SNP216 and S8_138882897) from the optimal multi-locus mixed model (MLMM) model were included as covariates in the unified mixed model to control for the lcyE effect.