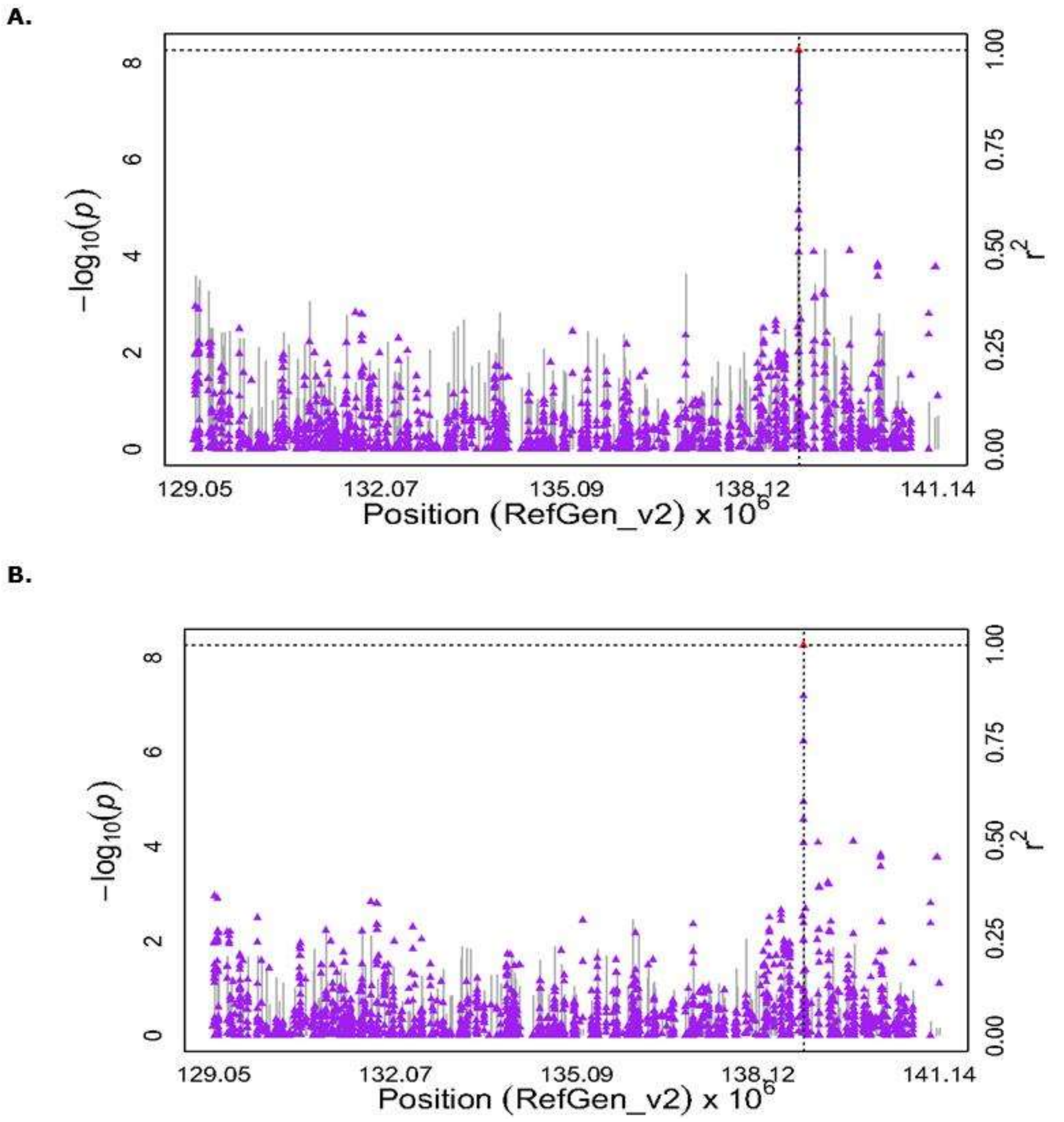

Figure S7 Genome-wide association study (GWAS) for zeaxanthin content in maize grain. Scatter plot of association results from a unified mixed model analysis of zeaxanthin and linkage disequilibrium (LD) estimates (r^2) across the *lcyE* chromosome region. Negative $\log_{10}$-transformed *P*-values (left y-axis) from a GWAS for zeaxanthin 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 zeaxanthin 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 zeaxanthin 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.