



Figure S12 Genome-wide association study (GWAS) for zeaxanthin content in maize grain. (A) Scatter plot of association results from a unified mixed model analysis of zeaxanthin and linkage disequilibrium (LD) estimates (r^2) across the surrounding 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 1.2 Mb region on chromosome 8. 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 171,705,574 bp. The black horizontal dashed line indicates the $-\log_{10} P$ -value of the least statistically significant SNP at 5% FDR. (B) Scatter plot of association results from a conditional unified mixed model analysis of zeaxanthin and LD estimates (r^2) across the 1.2 Mb chromosome region, as in (A). The peak SNP from the unconditional GWAS (S8_171705574; 171,705,574 bp) was included as a covariate in the unified mixed model to control for the novel effect detected on chromosome 8.