



**Figure S5** Genome-wide association study (GWAS) for the ratio of zeinoxanthin to lutein content in maize grain. (A) Scatter plot of association results from a unified mixed model analysis of the ratio of zeinoxanthin to lutein and linkage disequilibrium (LD) estimates ( $r^2$ ) across the *lut1* chromosome region. Negative  $\log_{10}$ -transformed  $P$ -values (left y-axis) from a GWAS for the ratio of zeinoxanthin to lutein and  $r^2$  values (right y-axis) are plotted against physical position (B73 RefGen\_v2) for a 1 Mb region on chromosome 1 that encompasses *lut1*. The blue vertical lines are  $-\log_{10} P$ -values for SNPs that are statistically significant for the ratio of zeinoxanthin to 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 86,844,203 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 *lut1* (GRMZM2G14322.) (B) Scatter plot of association results from a conditional unified mixed model analysis of the ratio of zeinoxanthin to lutein and LD estimates ( $r^2$ ) across the *lut1* chromosome region, as in (A). The peak SNP from the unconditional GWAS (ss196425306; 86,844,203 bp) was included as a covariate in the unified mixed model to control for the *lut1* effect.