Figure S6. Genome-wide association study (GWAS) for zeinoxanthin content in maize grain. (A) Scatter plot of association results from a unified mixed model analysis of zeinoxanthin 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 zeinoxanthin 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 zeinoxanthin 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 $lut1$ (GRMZM2G143223). (B) Scatter plot of association results from a conditional unified mixed model analysis of zeinoxanthin and LD estimates ($r^2$) across the $lut1$ chromosome region, as in (A). The peak SNP from the unconditional GWAS (ss19642359; 86,844,203 bp) was included as a covariate in the unified mixed model to control for the $lut1$ effect.