Figure S3 Genome-wide association study (GWAS) for total β-xanthophylls content in maize grain. (A) Scatter plot of association results from a unified mixed model analysis of total β-xanthophylls and linkage disequilibrium (LD) estimates ($r^2$) across the zep1 chromosome region. Negative log₁₀-transformed $P$-values (left y-axis) from a GWAS for total β-xanthophylls and $r^2$ values (right y-axis) are plotted against physical position (B73 RefGen_v2) for a 1.2 Mb region on chromosome 2 that encompasses zep1. The blue vertical lines are –log₁₀ $P$-values for SNPs that are statistically significant for total β-xanthophylls at 5% false discovery rate (FDR), while the gray vertical lines are –log₁₀ $P$-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 44,448,432 bp. The black horizontal dashed line indicates the –log₁₀ $P$-value of the least statistically significant SNP at 5% FDR. The black vertical dashed lines indicate the start and stop positions of zep1 (GRMZM2G127139). (B) Scatter plot of association results from a conditional unified mixed model analysis of total β-xanthophylls and LD estimates ($r^2$) across the zep1 chromosome region, as in (A). The peak SNP from the unconditional GWAS (S2_44448432; 44,448,432 bp) was included as a covariate in the unified mixed model to control for the zep1 effect.