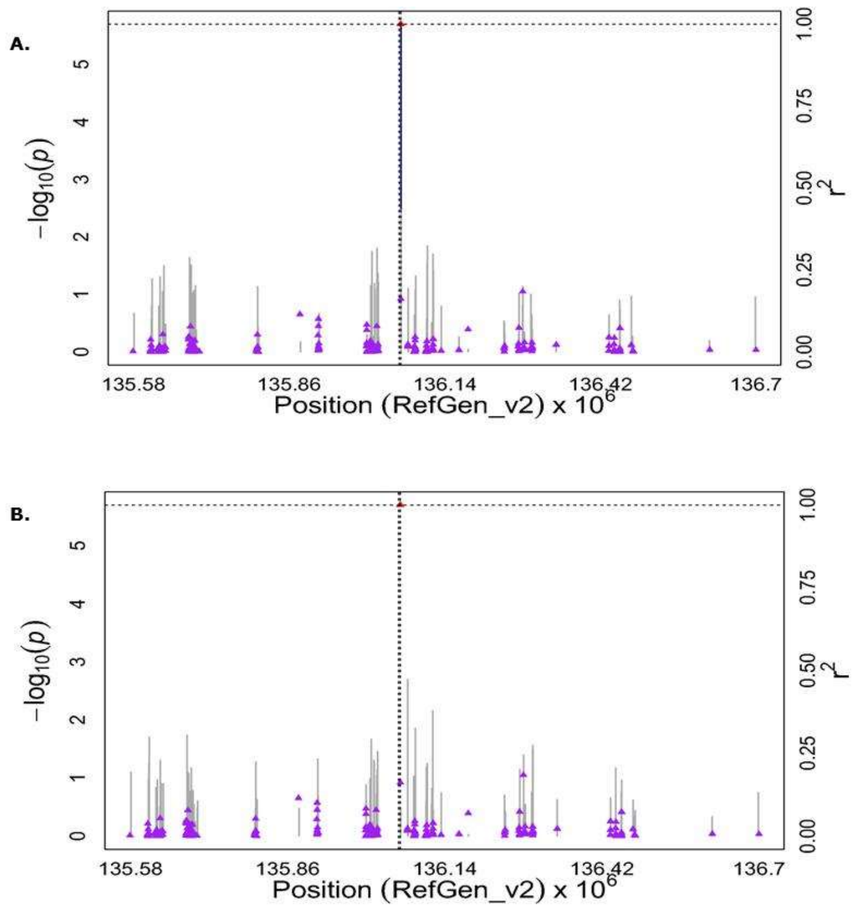

Figure S14 Genome-wide association study (GWAS) for total β-xanthophyll content in maize grain. (A) Scatter plot of association results from a unified mixed model analysis of total β-xanthophyll content and linkage disequilibrium (LD) estimates (r^2) across the *crtRB1* chromosome region. Negative $\log_{10}$-transformed *P*-values (left y-axis) from a GWAS of total β-xanthophyll content and r^2 values (right y-axis) are plotted against physical position (B73 RefGen_v2) for a 1.2 Mb region on chromosome 10 that encompasses *crtRB1*. The blue vertical lines are $-\log_{10}$ *P*-values for SNPs that are statistically significant for total β-xanthophyll content 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 polymorphism (indicated in red) at 136,059,748 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 *crtRB1* (GRMZM2G152135). (B) Scatter plot of association results from a conditional unified mixed model analysis of total β-xanthophyll and LD estimates (r^2) across the *crtRB1* chromosome region, as in (A). The peak polymorphism from the unconditional GWAS (*crtRB1* InDel4; 136,059,748 bp) was included as a covariate in the unified mixed model to control for the *crtRB1* effect.