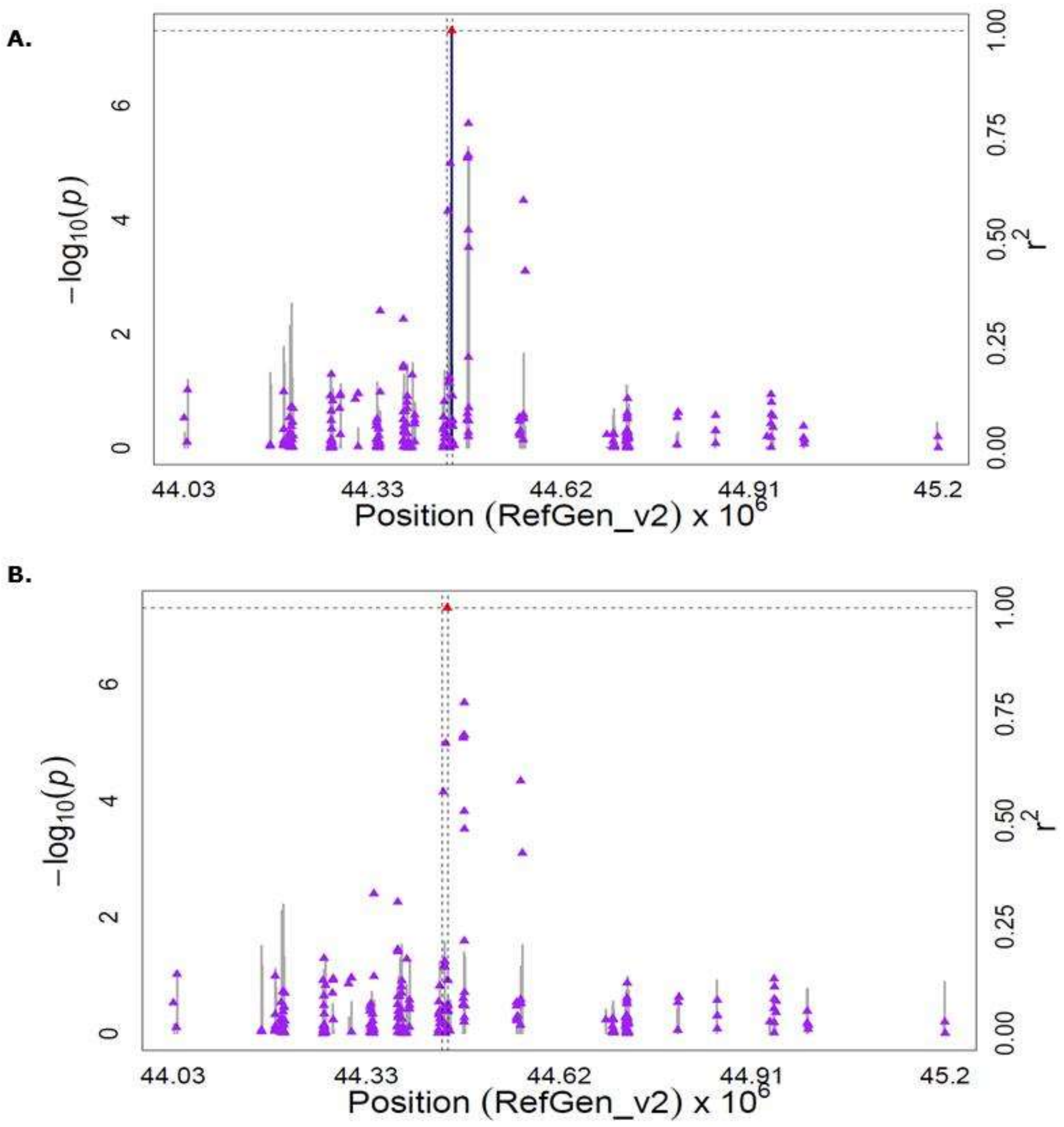

Figure S4 Genome-wide association study (GWAS) for the ratio of total β-xanthophylls to total α-xanthophylls content in maize grain. (A) Scatter plot of association results from a unified mixed model analysis of the ratio of total β-xanthophylls to total α-xanthophylls and linkage disequilibrium (LD) estimates (r^2) across the *zep1* chromosome region. Negative $\log_{10}$-transformed *P*-values (left y-axis) from a GWAS for the ratio of total β-xanthophylls to total α-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 $-\log_{10}$ P-values for SNPs that are statistically significant for the ratio of total β-xanthophylls to total α-xanthophylls 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 44,448,432 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 *zep1* (GRMZM2G127139). (B) Scatter plot of association results from a conditional unified mixed model analysis of the ratio of total β-xanthophylls to total α-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.