Figure S3  Genome-wide association study (GWAS) for the ratio of γ- to (γ- + α-tocopherols) [γT/(γT+αT)] in maize grain. (A) Scatter plot of association results from a unified mixed model analysis of γT/(γT+αT) and linkage disequilibrium (LD) estimates ($r^2$) across the ZmVTE4 chromosome region. Negative $\log_{10}$-transformed $P$-values (left $y$-axis) from a GWAS for γT/(γT+αT) and $r^2$ values (right $y$-axis) are plotted against physical position (B73 RefGen_v2) for a 7 Mb region on chromosome 5 that encompasses ZmVTE4. The blue vertical lines are −$\log_{10}$ $P$-values for SNPs that are statistically significant for γT/(γT+αT) 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 200,367,532 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 positions of four genes (from left to right): a WYRKY transcription factor (GRMZM5G823157), ZmVTE4 (GRMZM2G035213), a pentatricopeptide repeat-containing protein (GRMZM2G325019), and an amino acid permease (GRMZM2G161641). (B) Scatter plot of association results from a conditional unified mixed model analysis of γT/(γT+αT) and LD estimates ($r^2$) across the ZmVTE4 chromosome region, as in (A). The three SNPs (ss196416269, S5_200369534, and S5_200369481) from the optimal multi-locus mixed model (MLMM) model were included as covariates in the unified mixed model to control for the ZmVTE4 effect. (C) Gene model diagram for ZmVTE4 with γT/(γT+αT) associated SNPs. Blue vertical lines indicate the physical position (RefGen_v2) of SNPs within +/- 3 kb of the open reading frame start or stop position for ZmVTE4 that are significantly associated with γT/(γT+αT) at 5% FDR. Significant SNPs at 10% FDR are shown as gray vertical lines. The peak SNP is indicated by a red triangle, while the three SNPs included in the optimal MLMM model are indicated by inverted red triangles.