



Supplementary Figure S4. Manhattan plots of expression quantitative trait loci (eQTL) mapping results of 12 candidate causal genes. Each point represents a SNP with its $-\log_{10} P$ -value (y-axis) from a mixed linear model analysis plotted as a function of physical position (B73 RefGen_v4) across the 10 chromosomes of maize (x-axis). The red horizontal dashed line indicates the significant threshold after Bonferroni correction ($\alpha = 0.05$). The green vertical line indicates the genomic position of each candidate causal gene.