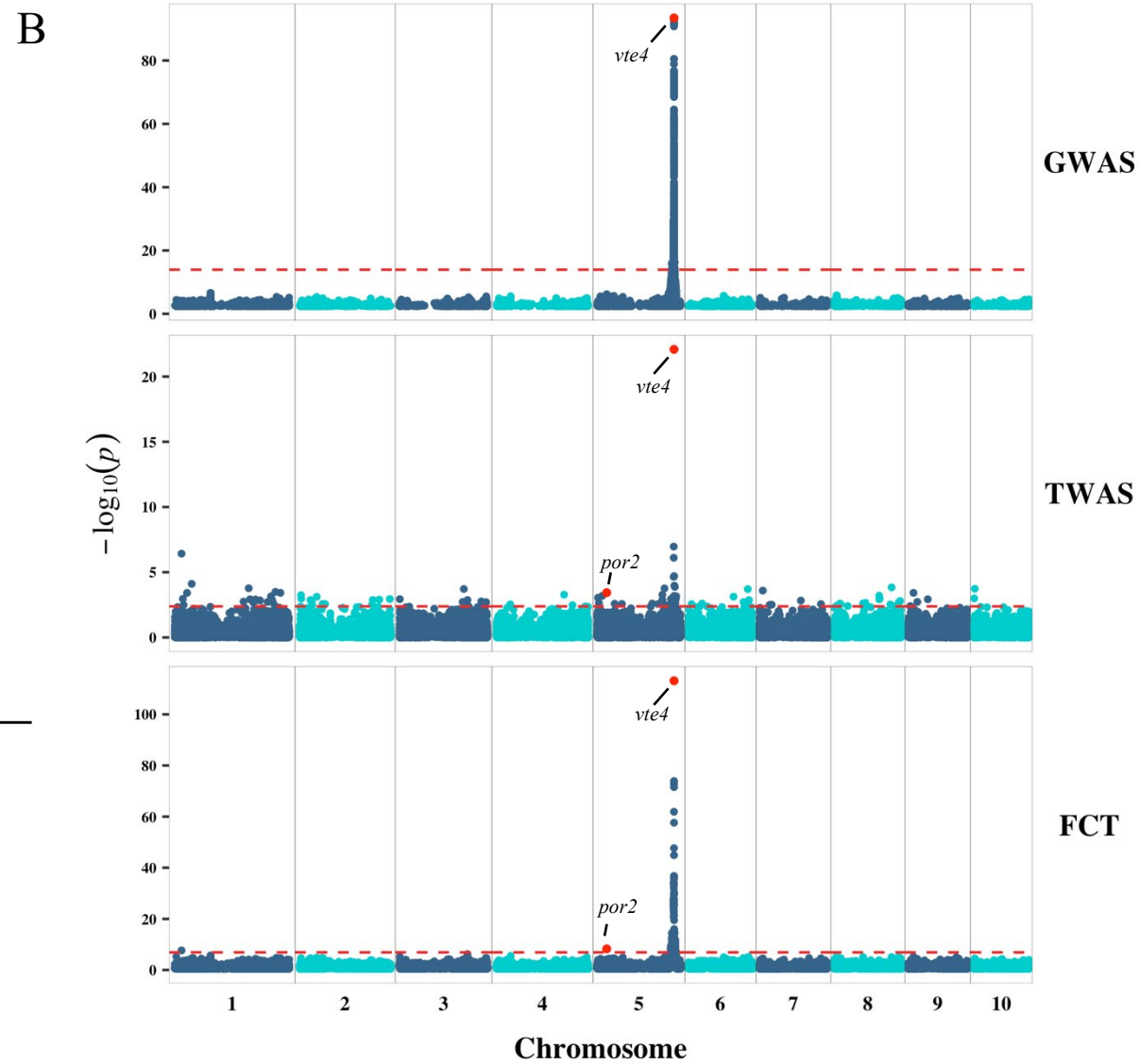
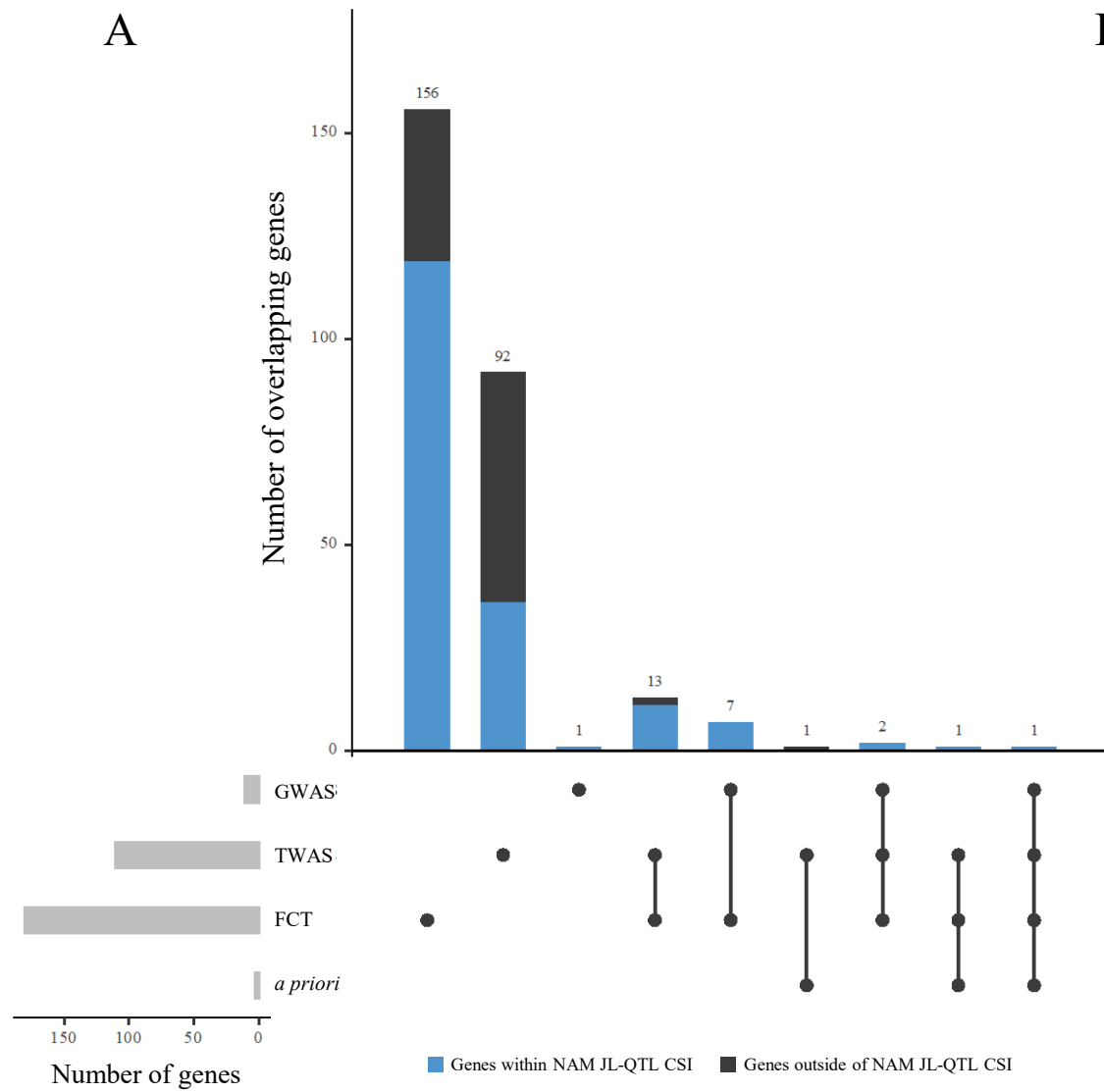
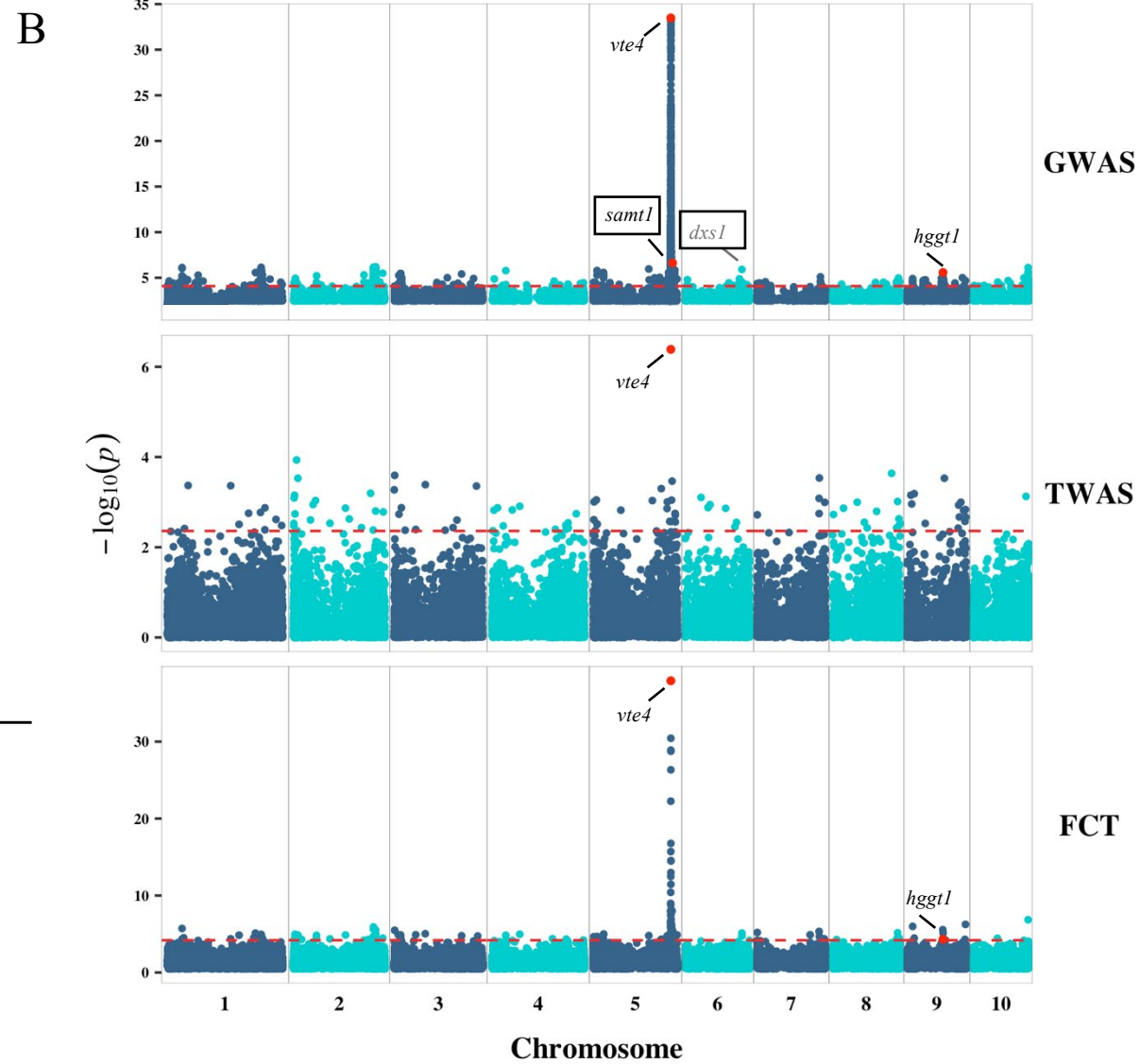
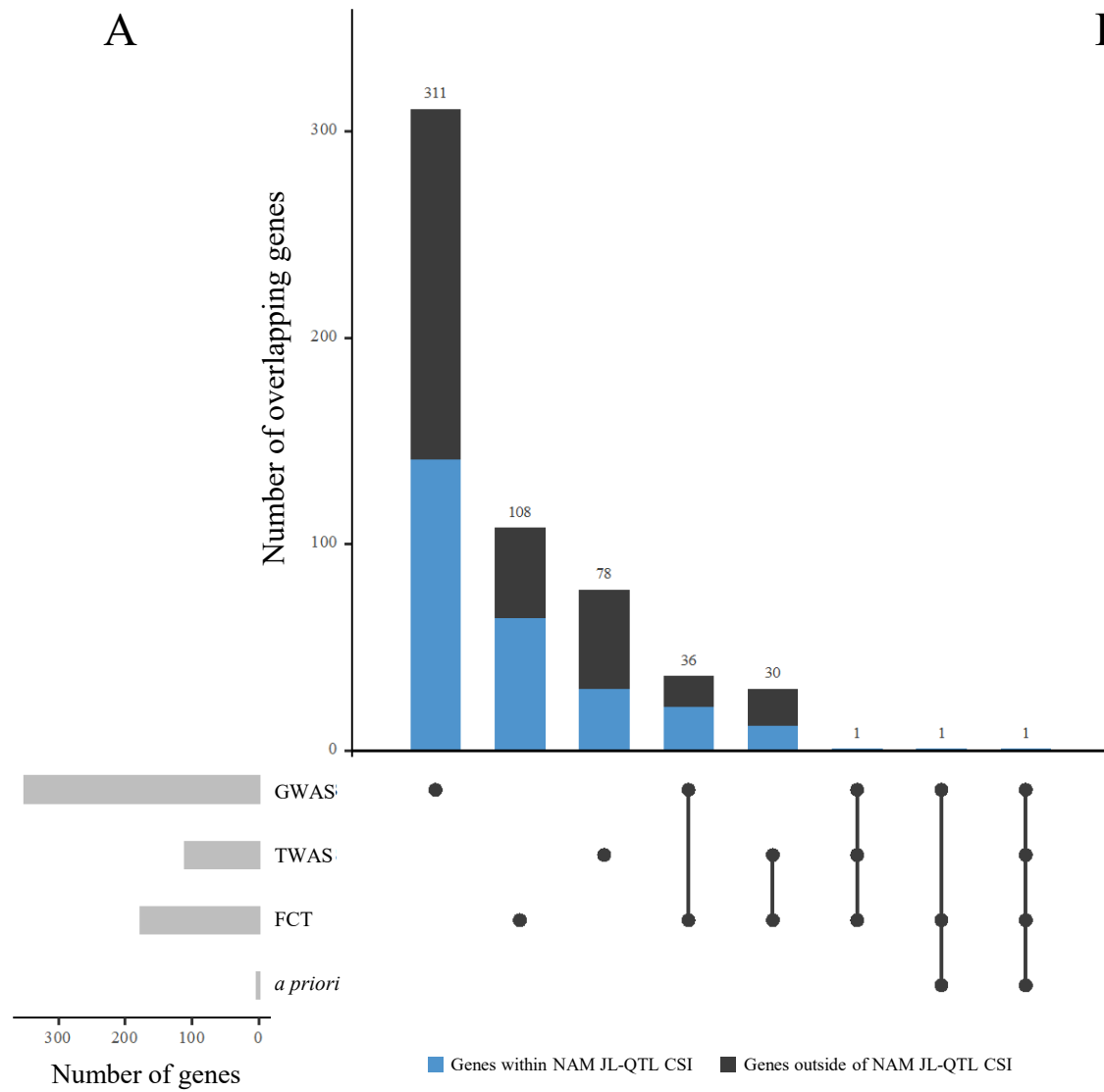
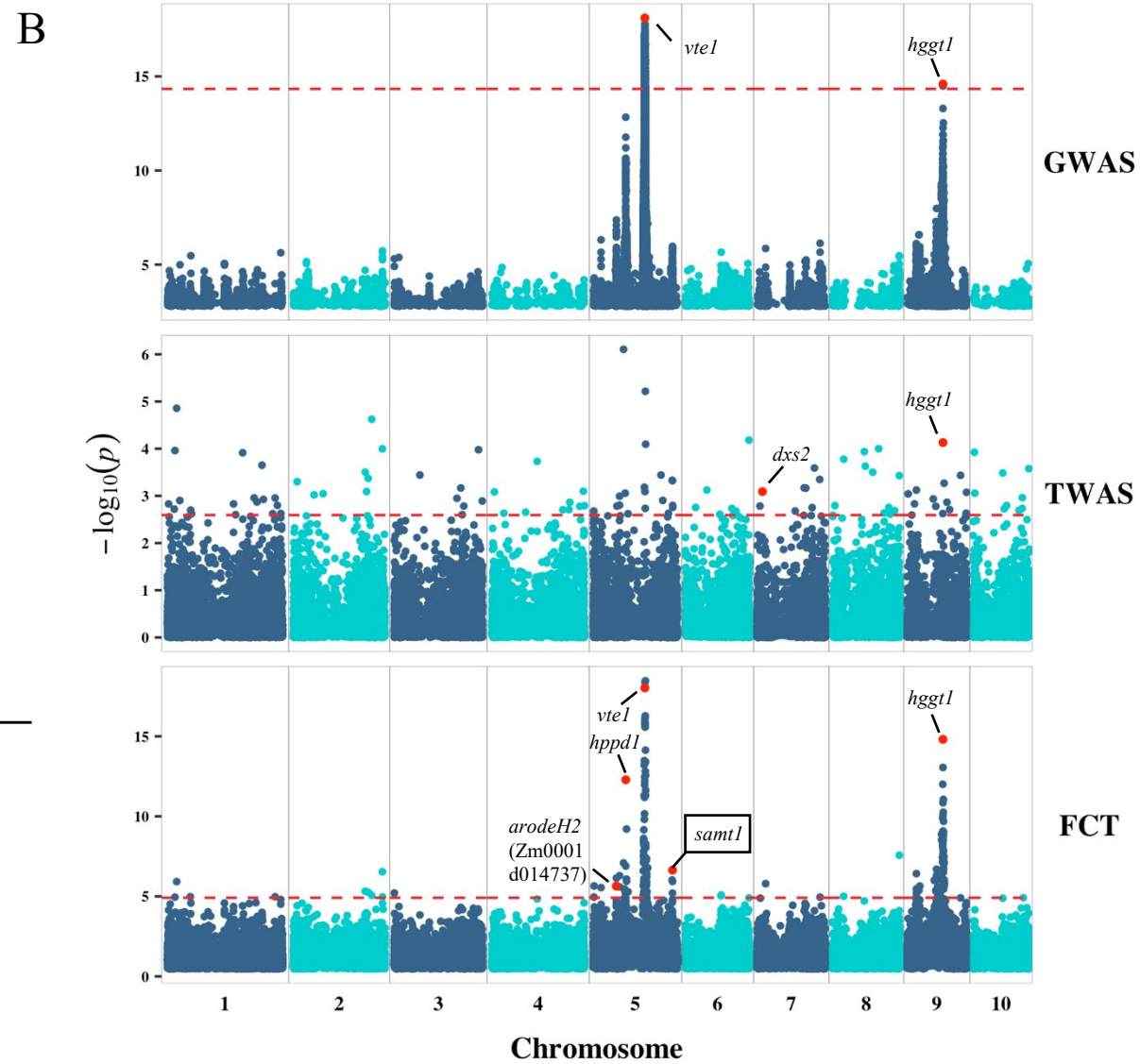
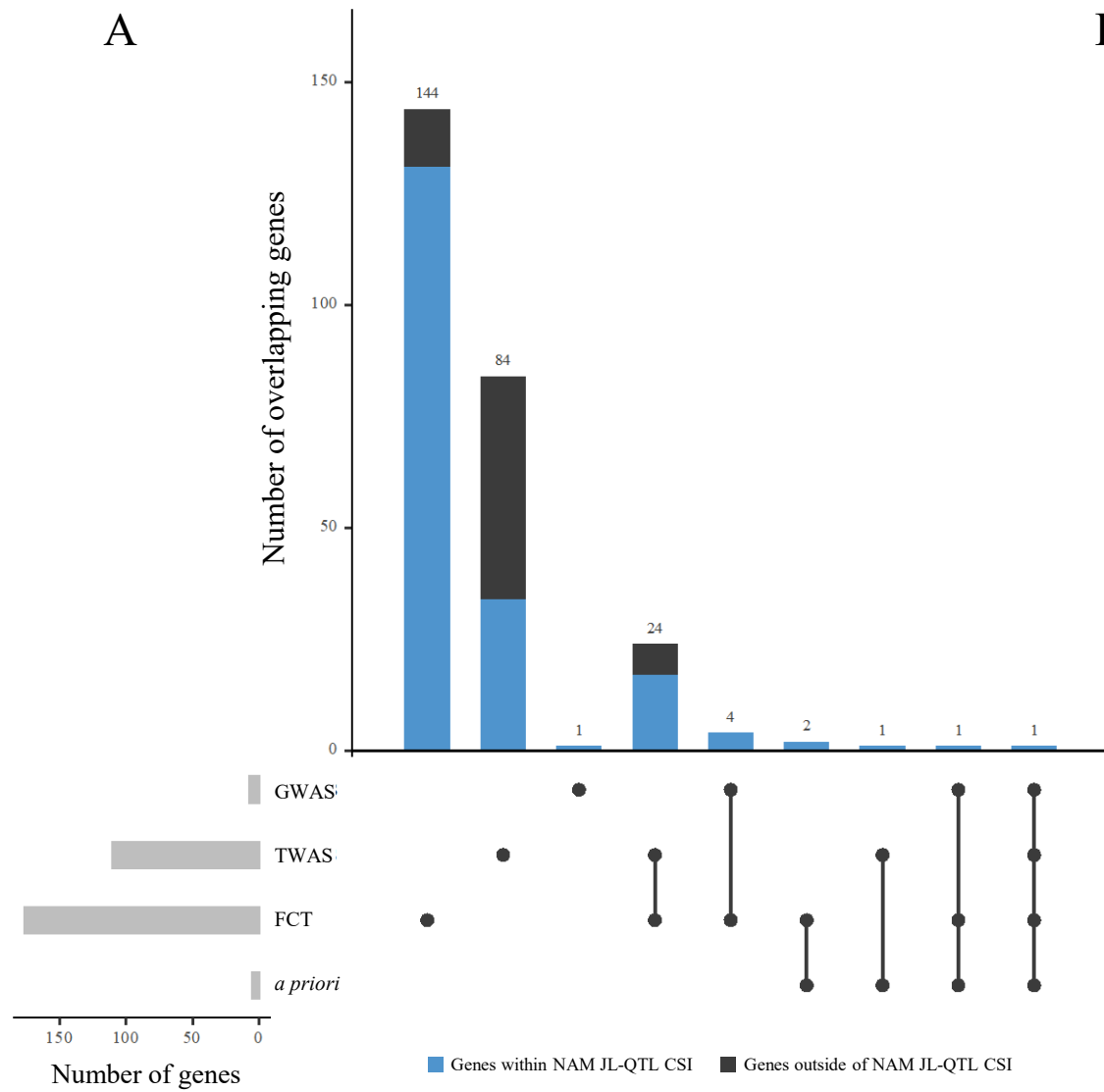
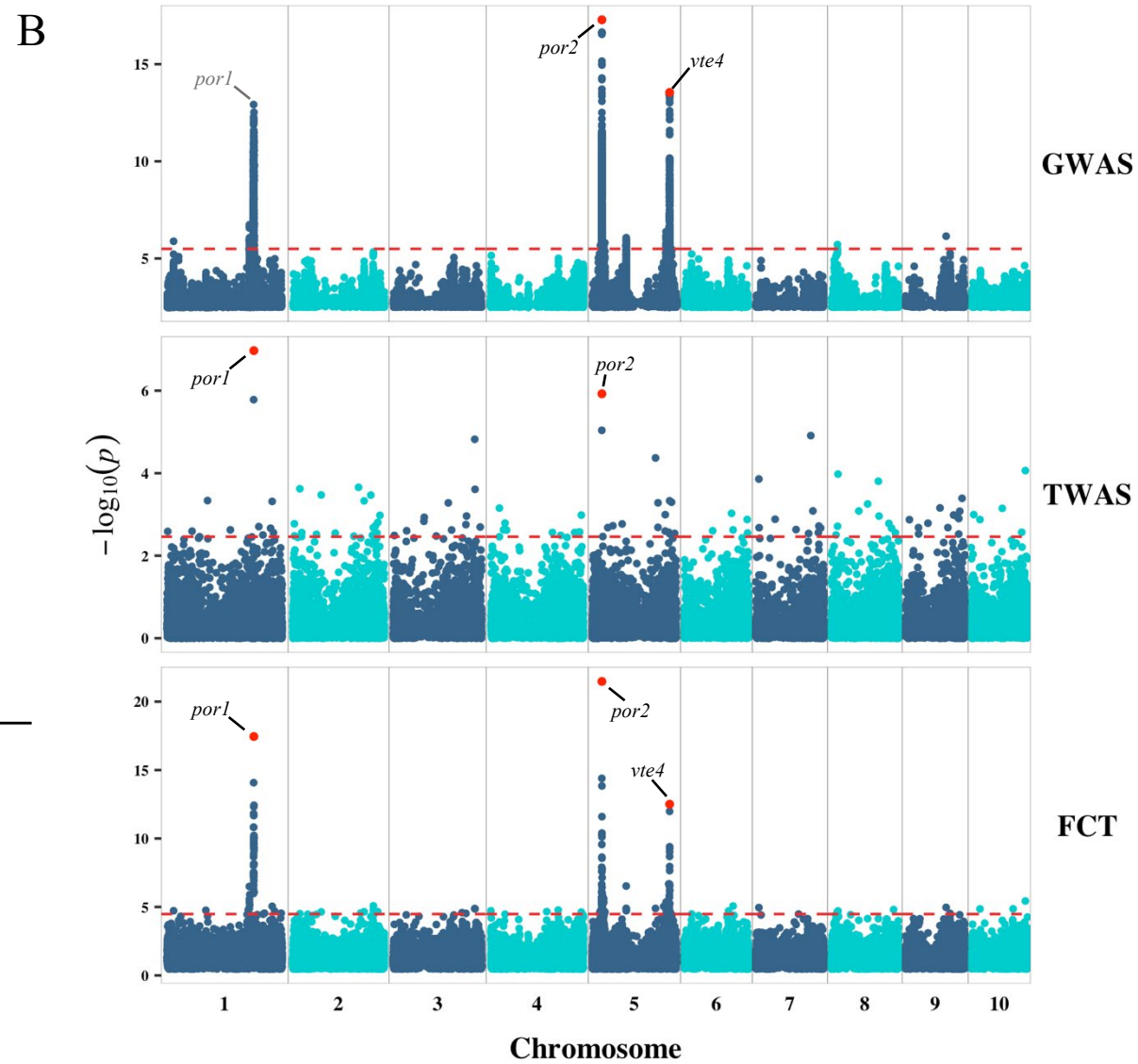
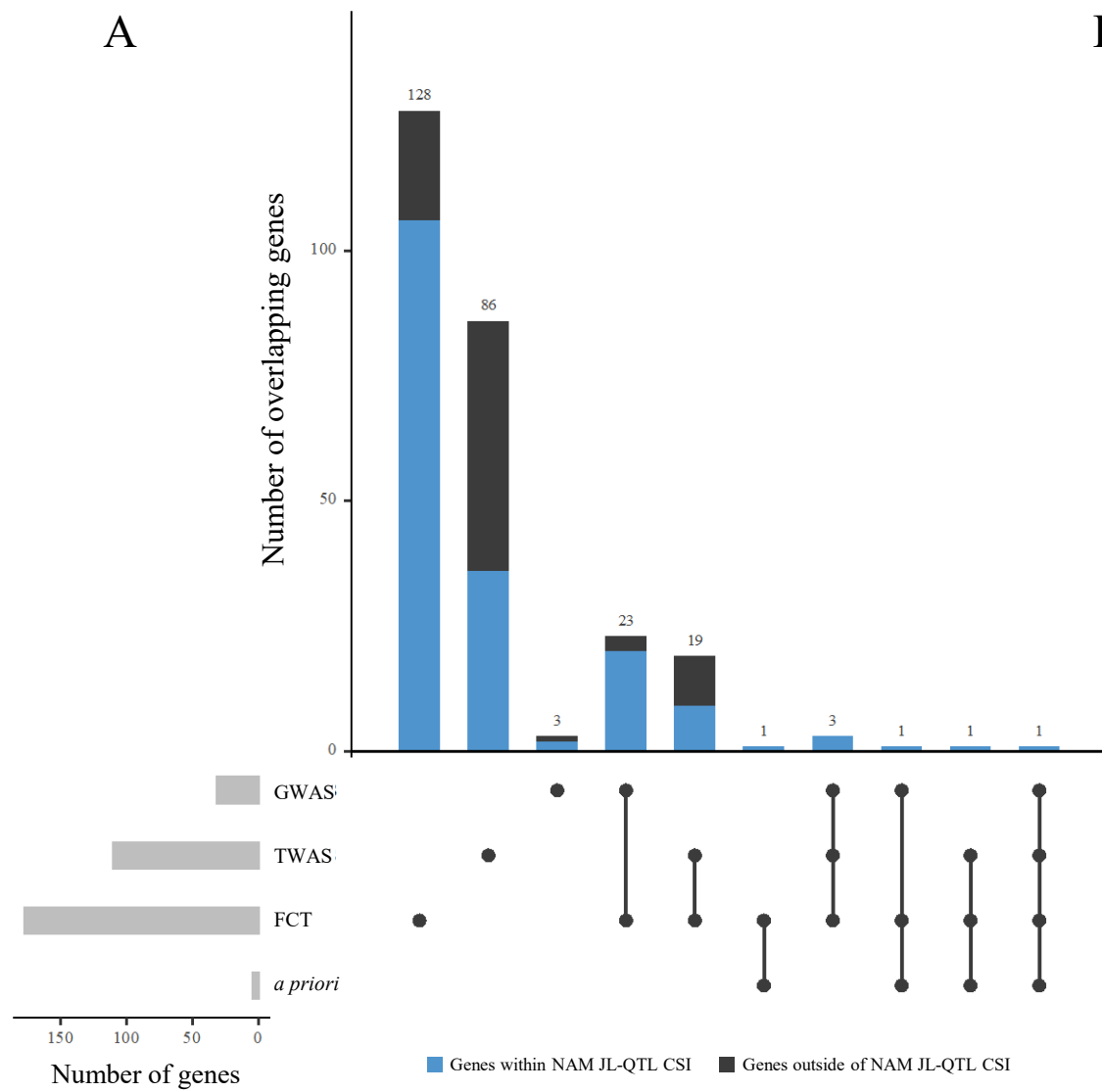


**Supplementary Figure S3.** Genome-wide association study (GWAS), transcriptome-wide association study (TWAS), and Fisher's combined test (FCT) results for eight tocochromanol grain phenotypes. A: Upset plot showing the number of overlapping genes between GWAS, TWAS, FCT, and *a priori* pathway genes involved in the biosynthesis of chlorophylls and tocochromanols (Supplementary Table S5). The number of genes located within the U.S. nested association mapping (NAM) joint linkage-quantitative trait loci (JL-QTL) common support interval (CSI) for each phenotype is highlighted in blue in the bar plots. B: Manhattan plots of GWAS, TWAS, and FCT results. Each point represents a SNP or gene with its  $-\log_{10} P$ -value (y-axis) from GWAS, TWAS, and FCT plotted as a function of physical position (Mb, B73 RefGen\_v4) across the 10 chromosomes of maize (x-axis). Red horizontal dashed lines indicate the thresholds of top 0.02%, top 0.5% and top 0.5% for GWAS, TWAS, and FCT, respectively. Candidate causal genes (Table 2) that are within 100 kb of a top 0.02% GWAS peak SNP or ranked top 0.5% in TWAS or FCT are highlighted with red dots and labeled in black in the Manhattan plots. Candidate causal genes that are within 1 Mb of a top 0.02% GWAS peak SNP are labeled in gray. Novel associations are marked with a solid line, black rectangle.

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