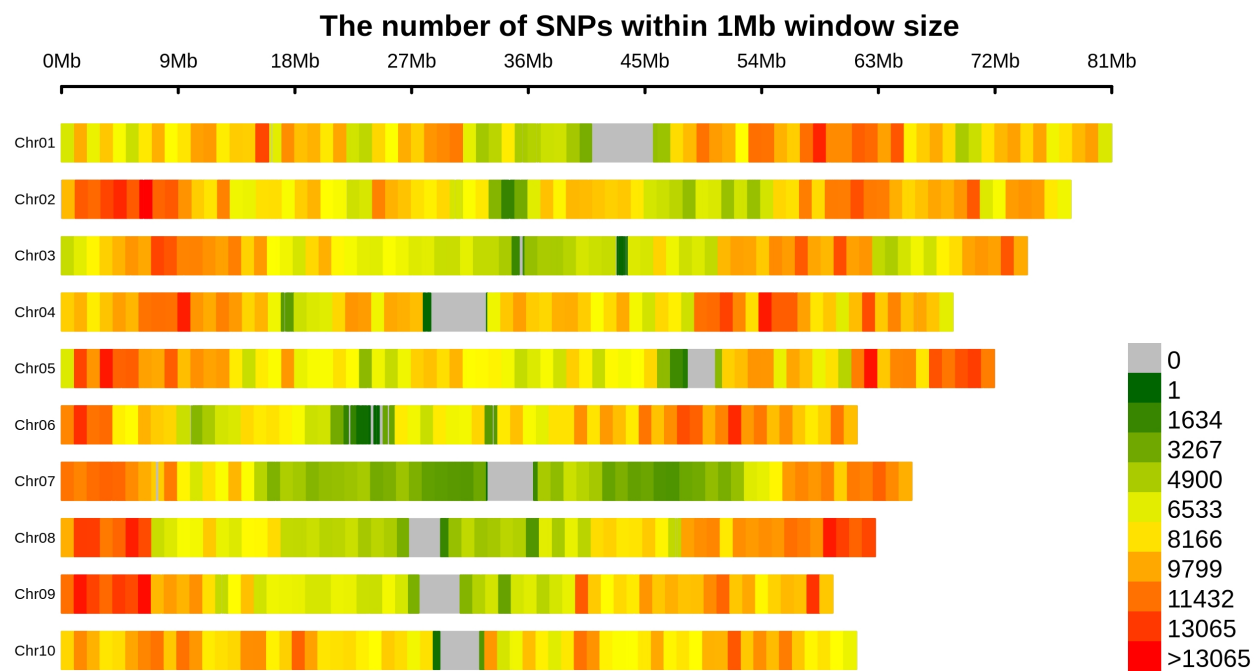


Supplemental Figures:

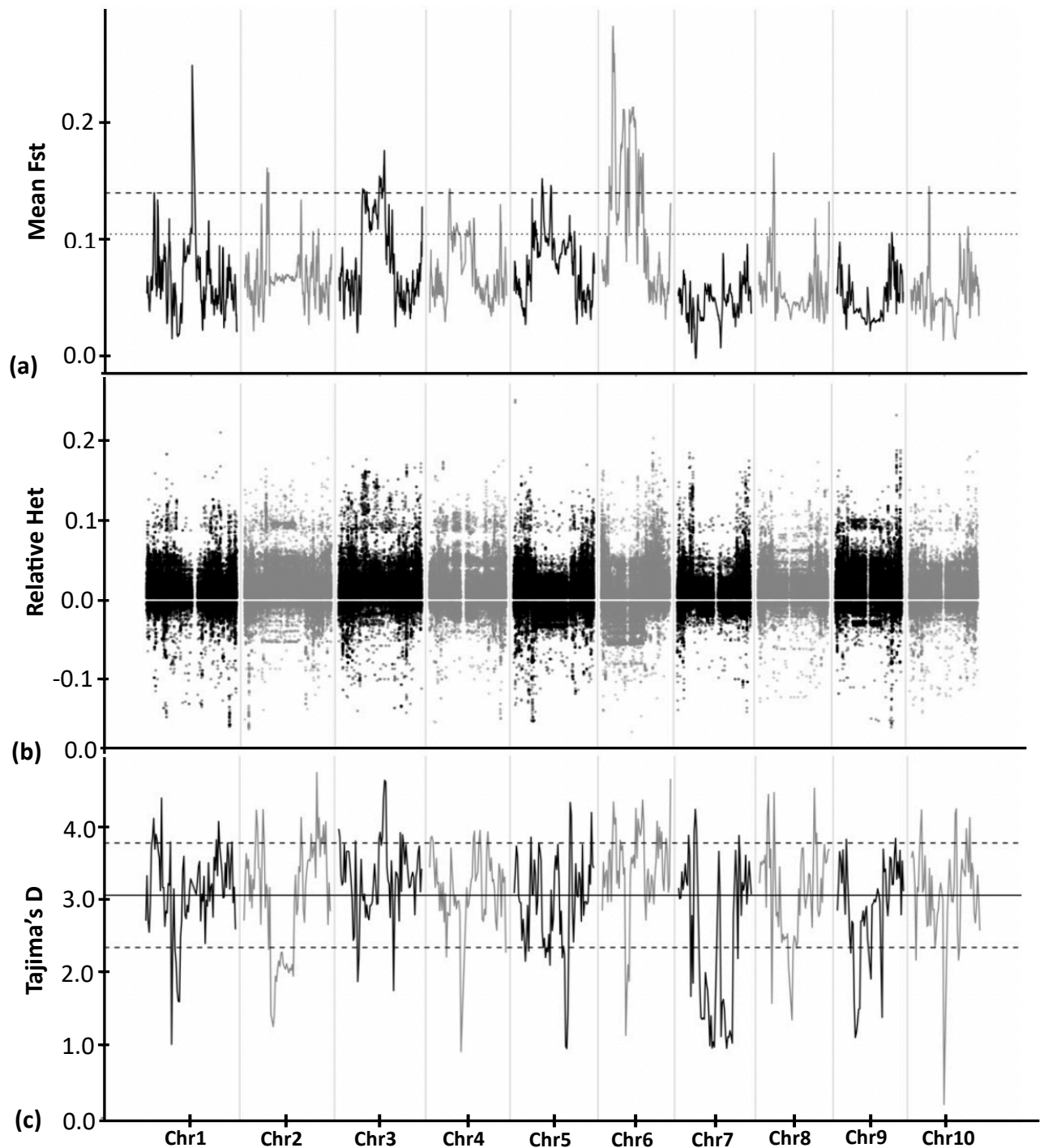
Identification of pleiotropic loci mediating structural and non-structural carbohydrate accumulation within the sorghum bioenergy association panel using high-throughput markers

Neeraj Kumar^{1,2,†,*}, J. Lucas Boatwright^{1,2,†,*}, Richard E. Boyles^{2,3}, Zachary W. Brenton^{1,4}, Stephen Kresovich^{1,2,5}

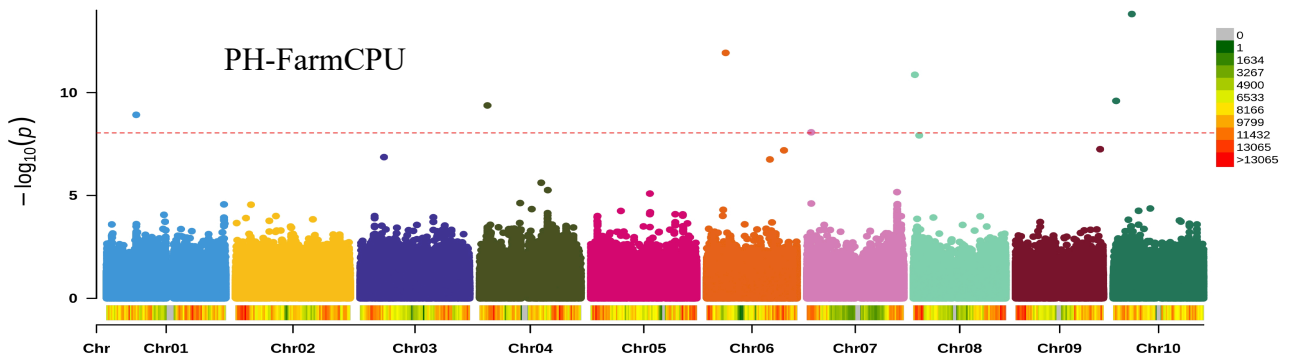
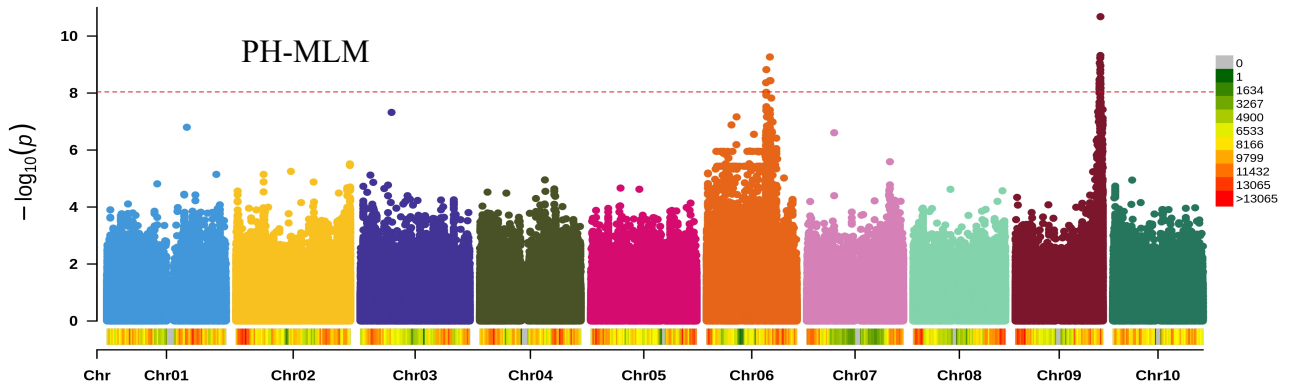
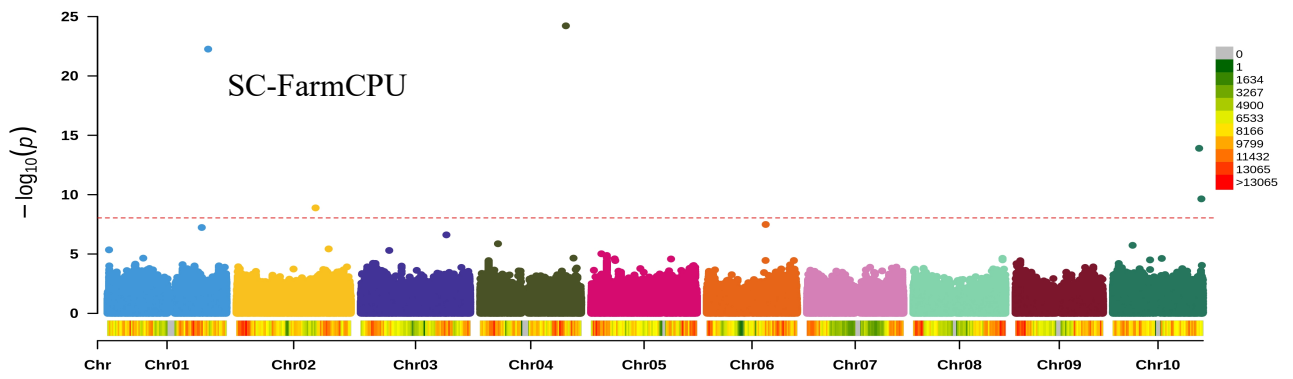
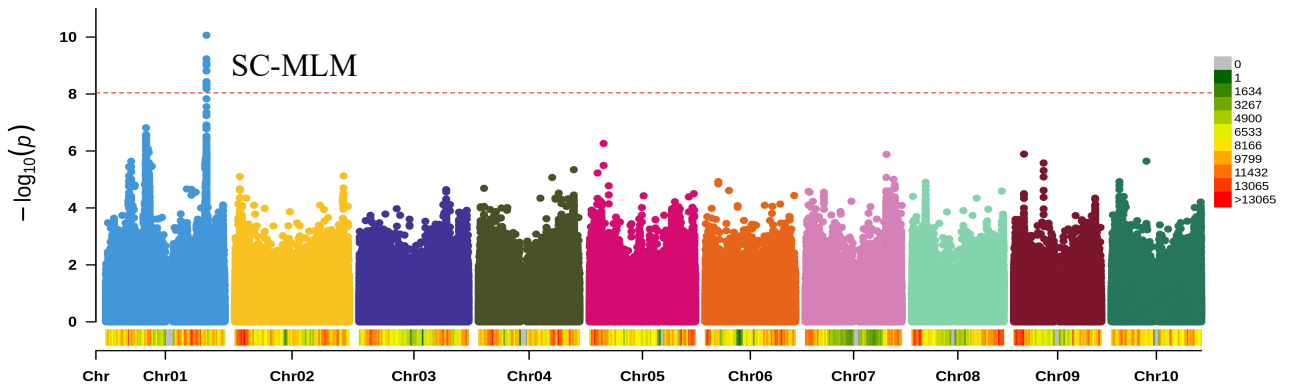
¹Advanced Plant Technology, Clemson University, Clemson, SC 29634, ²Department of Plant and Environmental Sciences, Clemson University, Clemson, SC 29634, ^{2,3}Pee Dee Research and Education Center, Clemson University, Florence, SC 29506, ⁴Carolina Seed Systems, Darlington, SC 29532, ⁵Feed the Future Innovation Lab for Crop Improvement, Cornell University, Ithaca, NY, USA, [†]These authors contributed equally to this work, ^{*}Corresponding authors.

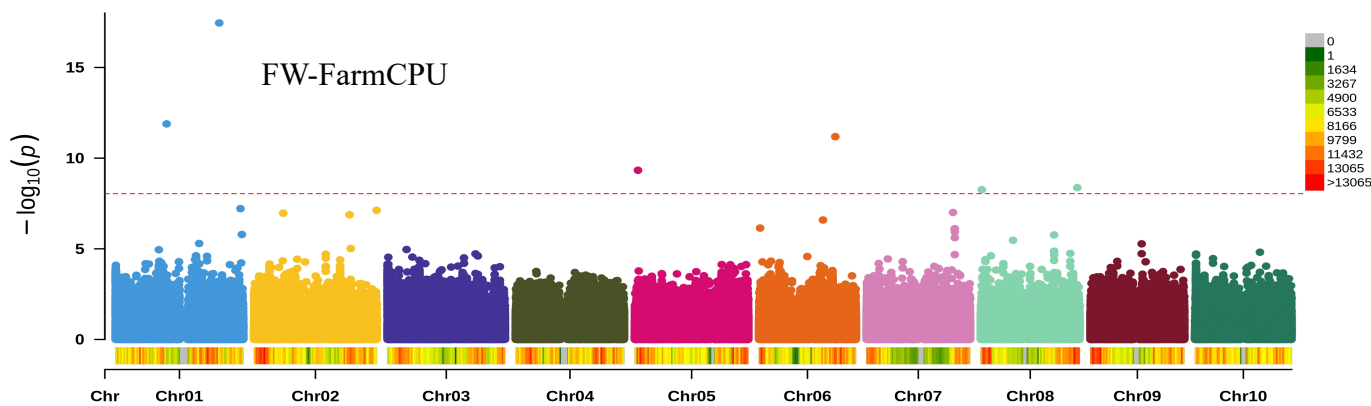
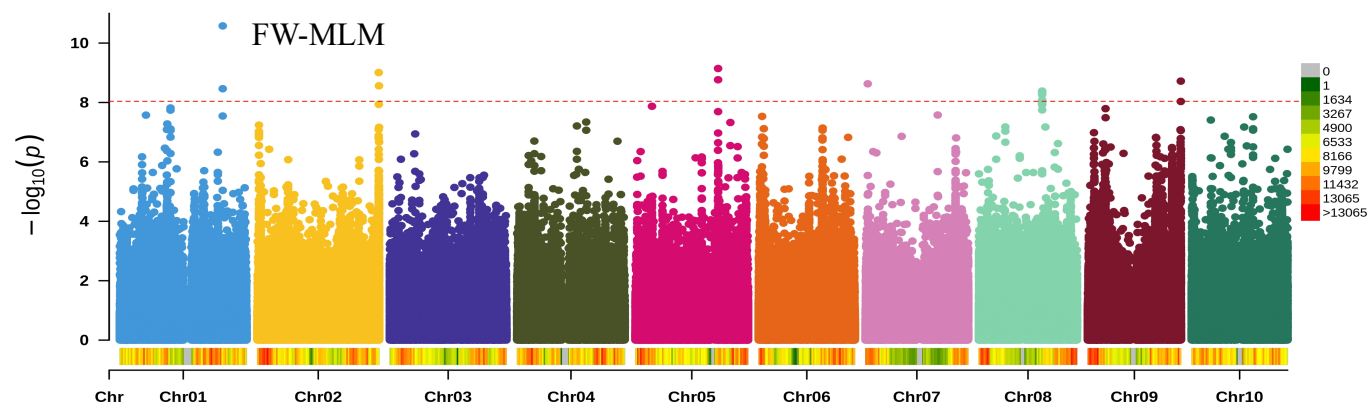
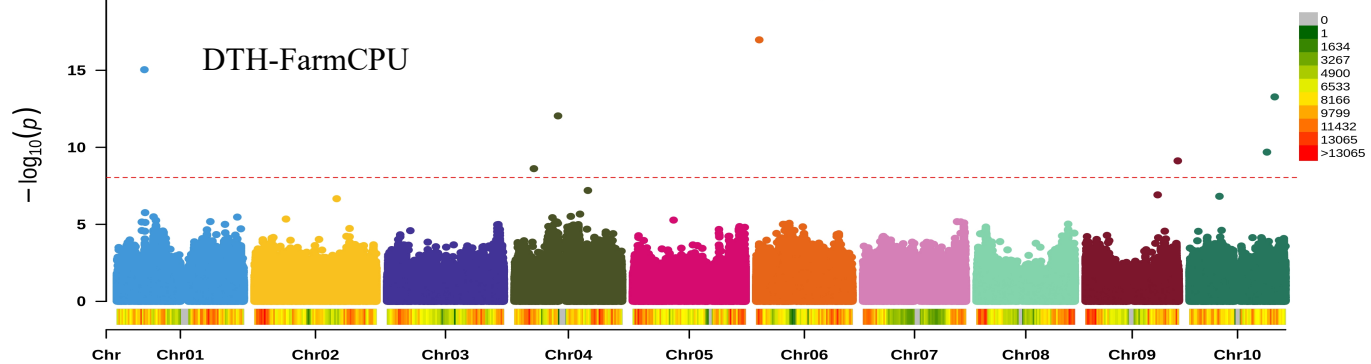
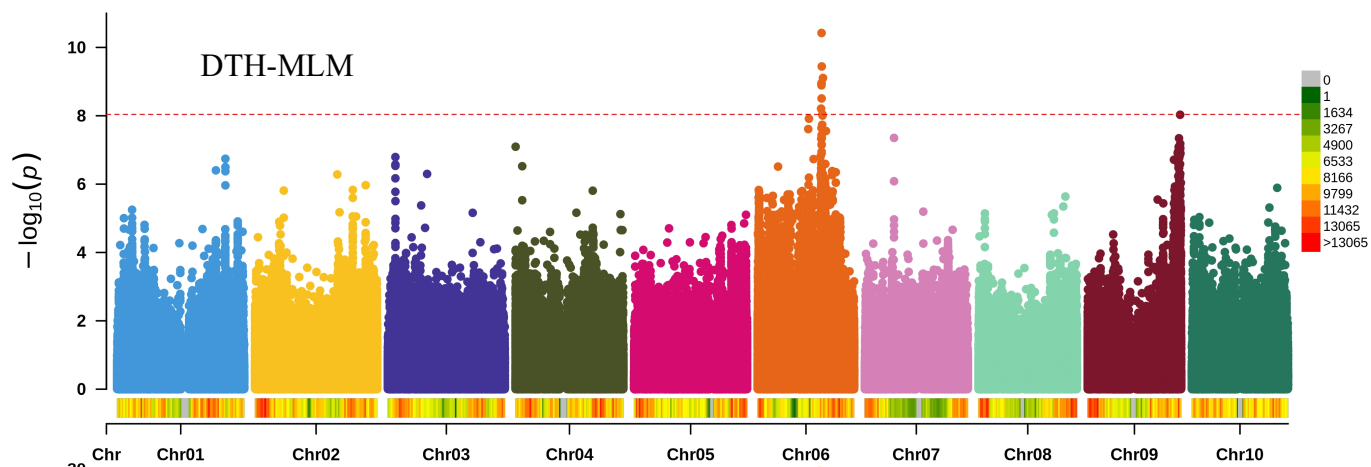


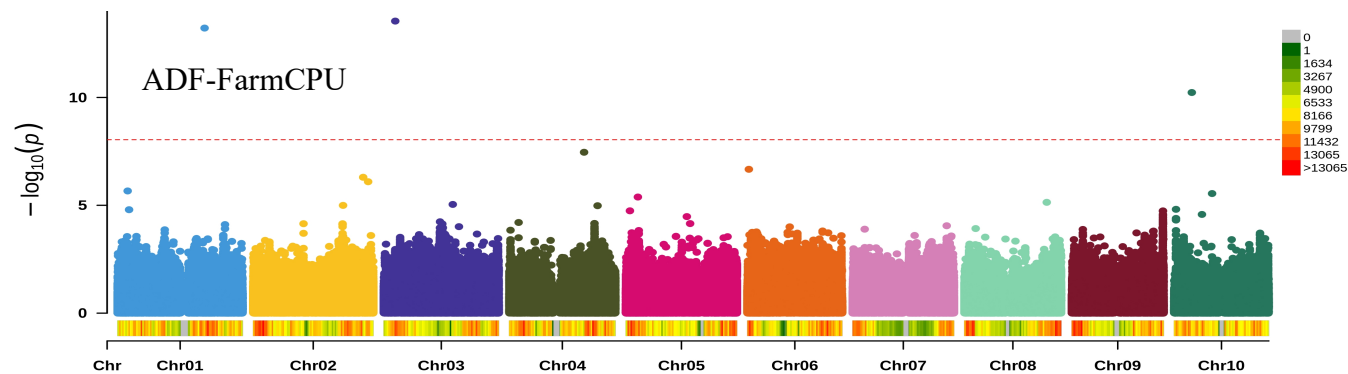
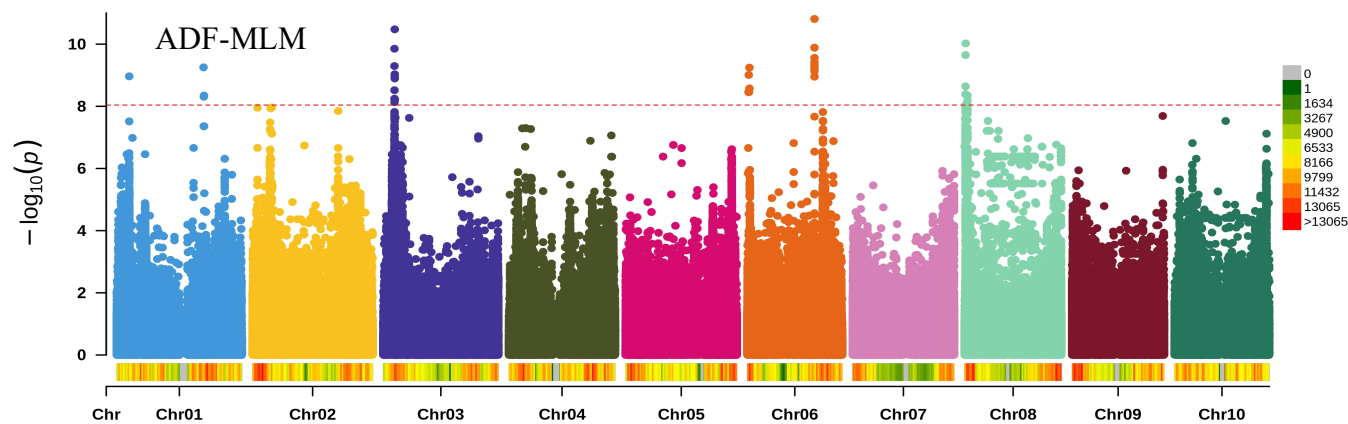
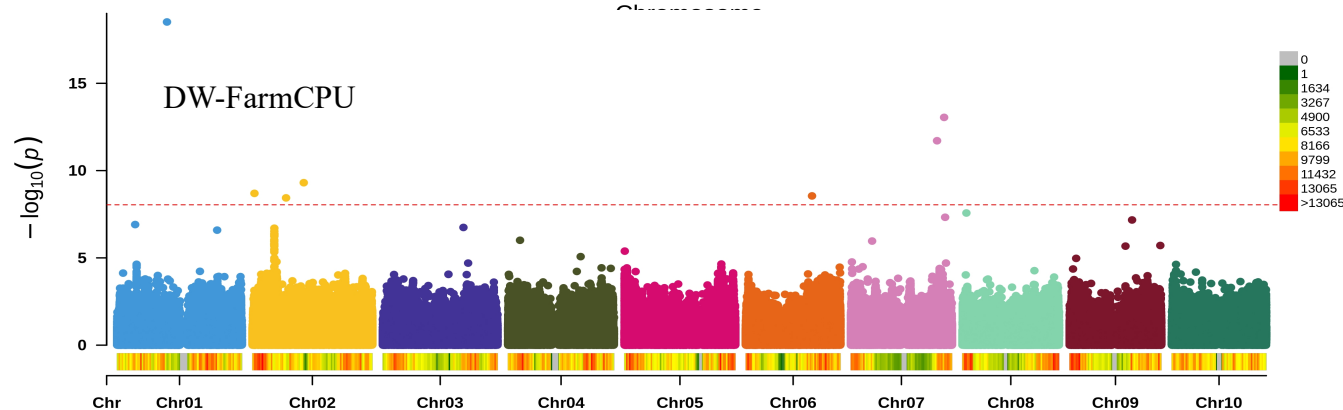
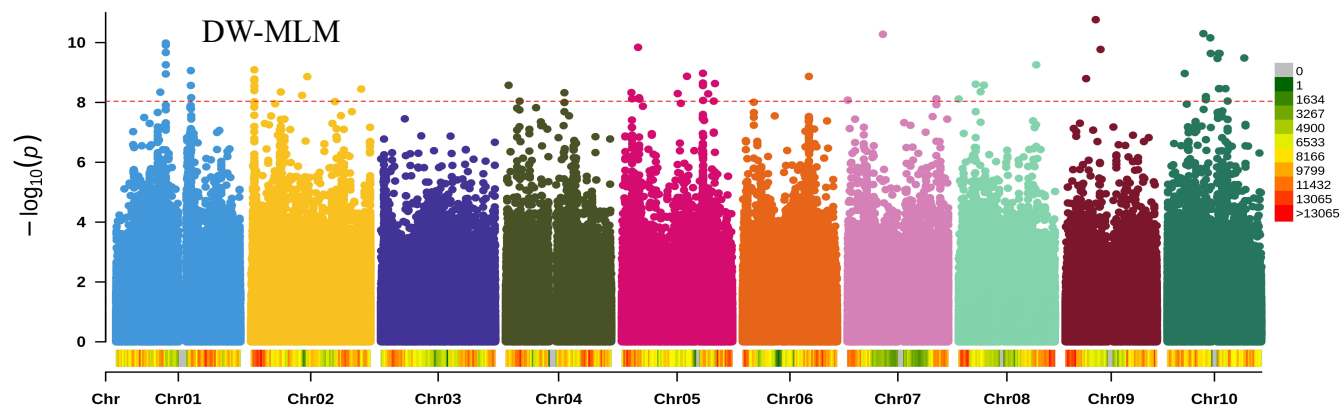
Supplementary Figure S1: Single nucleotide polymorphism (SNP) density on each chromosome of the bioenergy association panel (BAP).

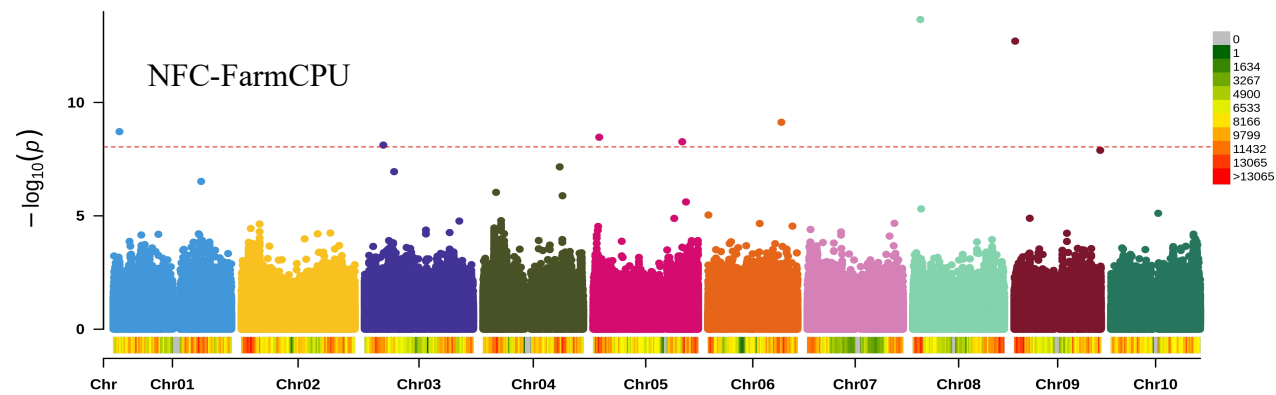
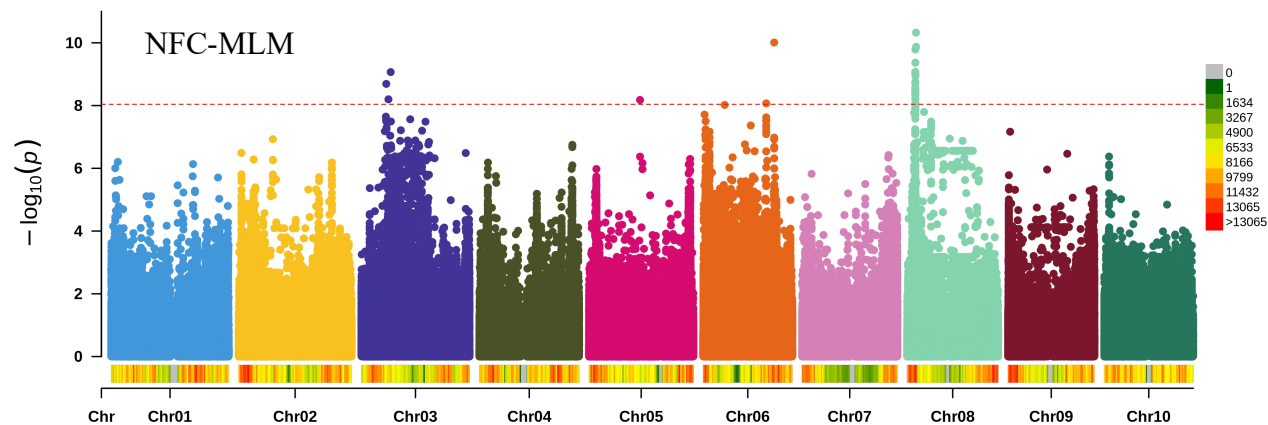
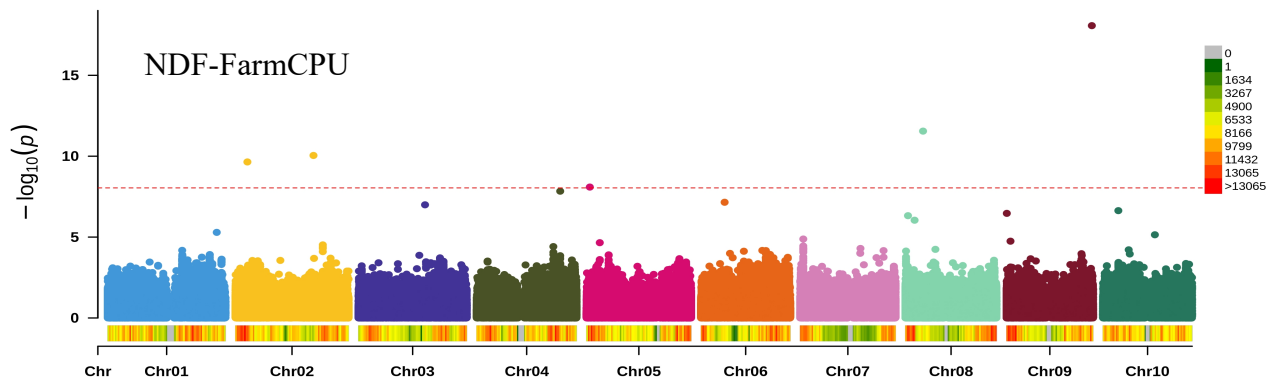
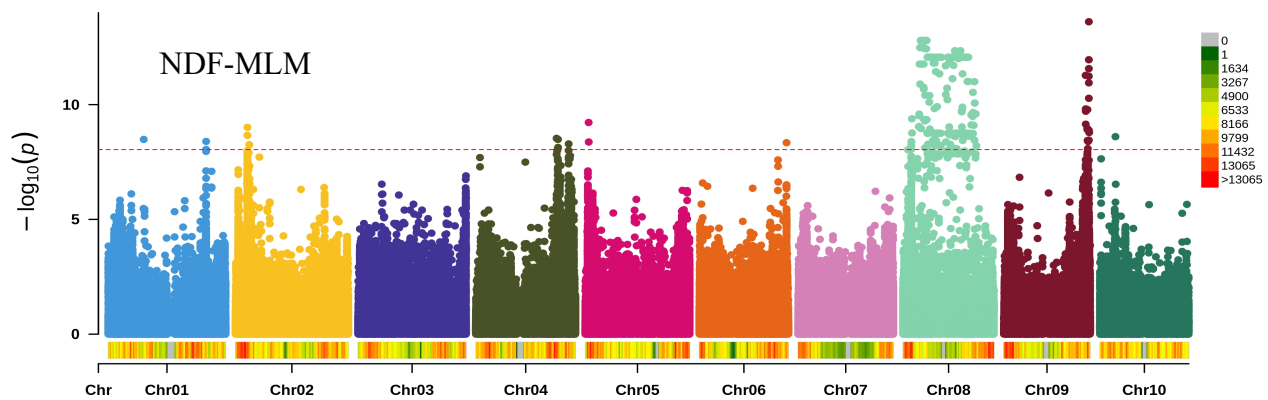


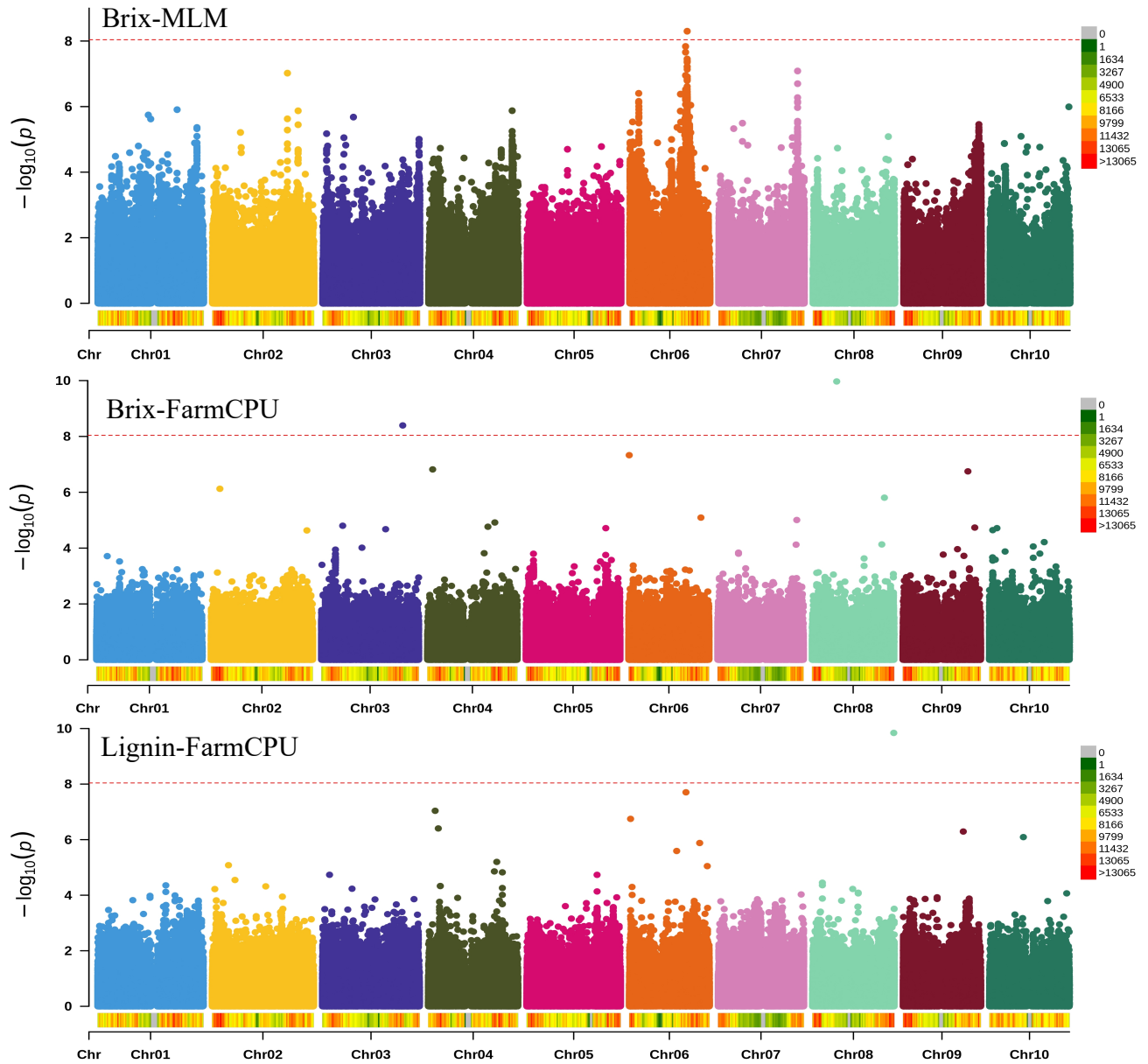
Supplementary Figure S2. Genome-wide signatures of selection. (a) The mean F_{st} across the sorghum genome between photoperiod sensitive and insensitive accessions. (b) Expected heterozygosity in the photoperiod sensitive and insensitive group. (c) Genome-wide Tajima's D estimates. The horizontal lines show the mean and standard deviations of the estimates; solid black lines show the genome-wide average Tajima's D; dotted lines show the mean plus 1 standard deviation (SD); and long dashed lines show the mean plus 2 SD of the estimates. Vertical dotted lines show genes and loci related to height, maturity, and other domestication-related traits.



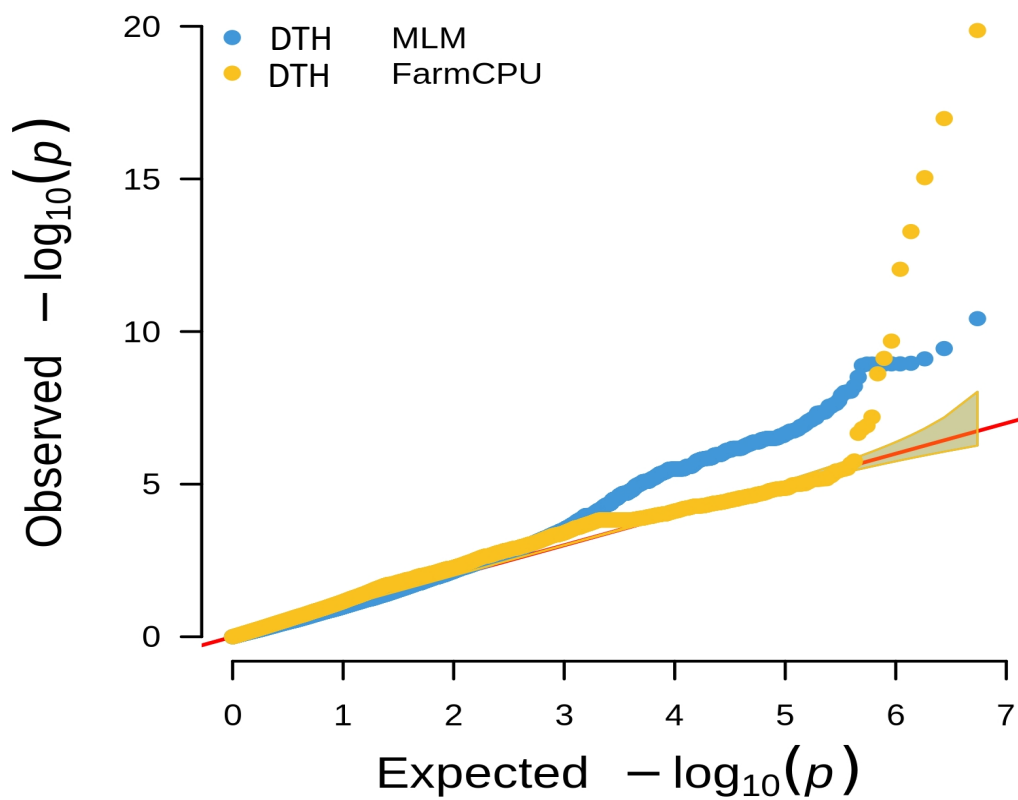
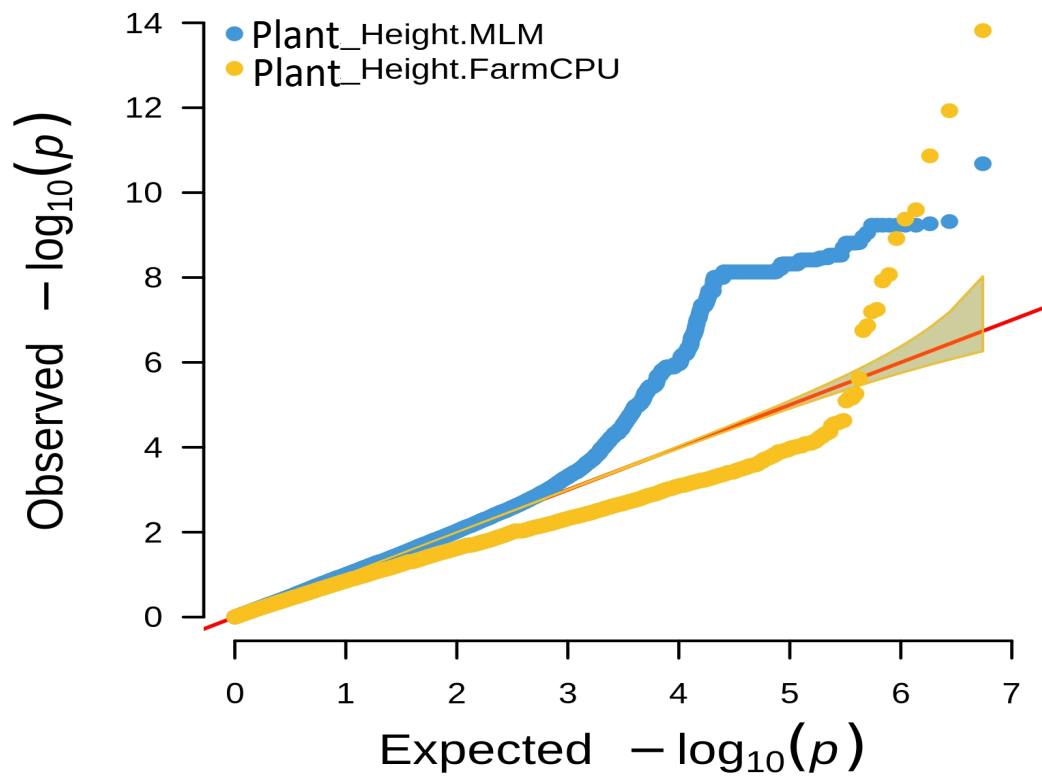


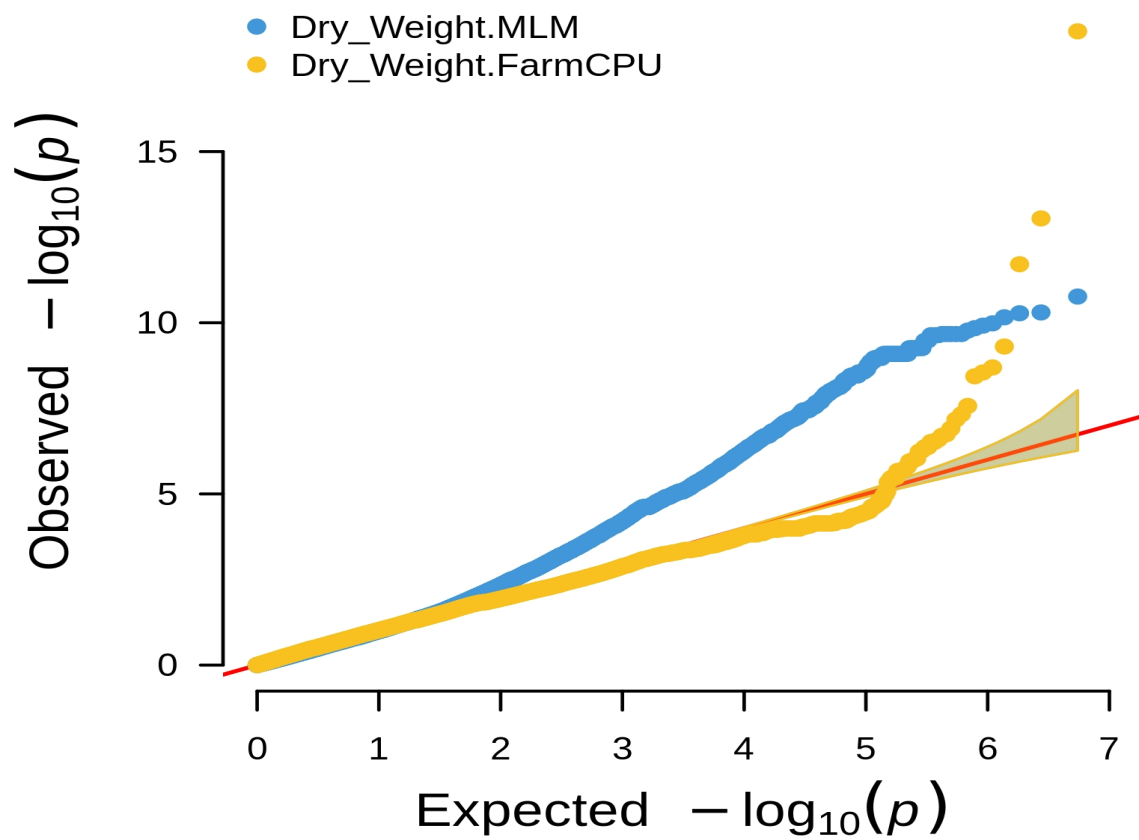
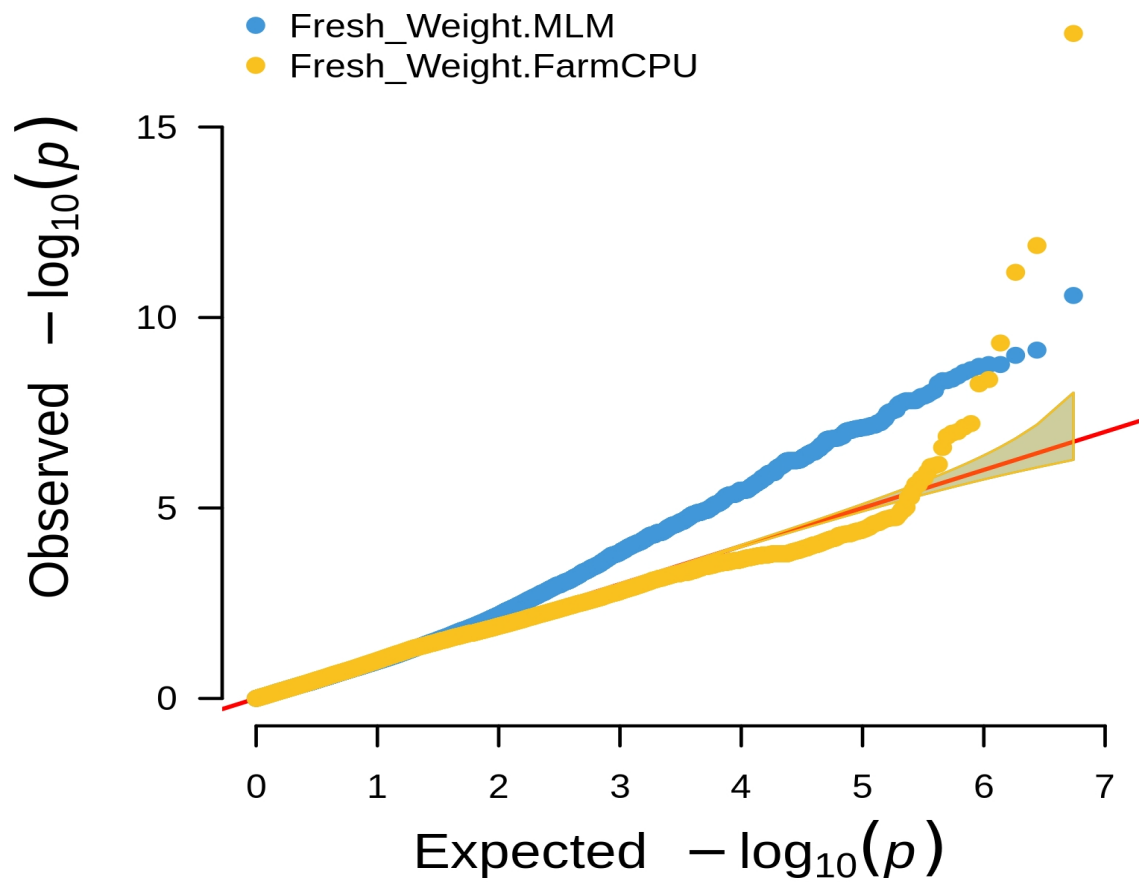


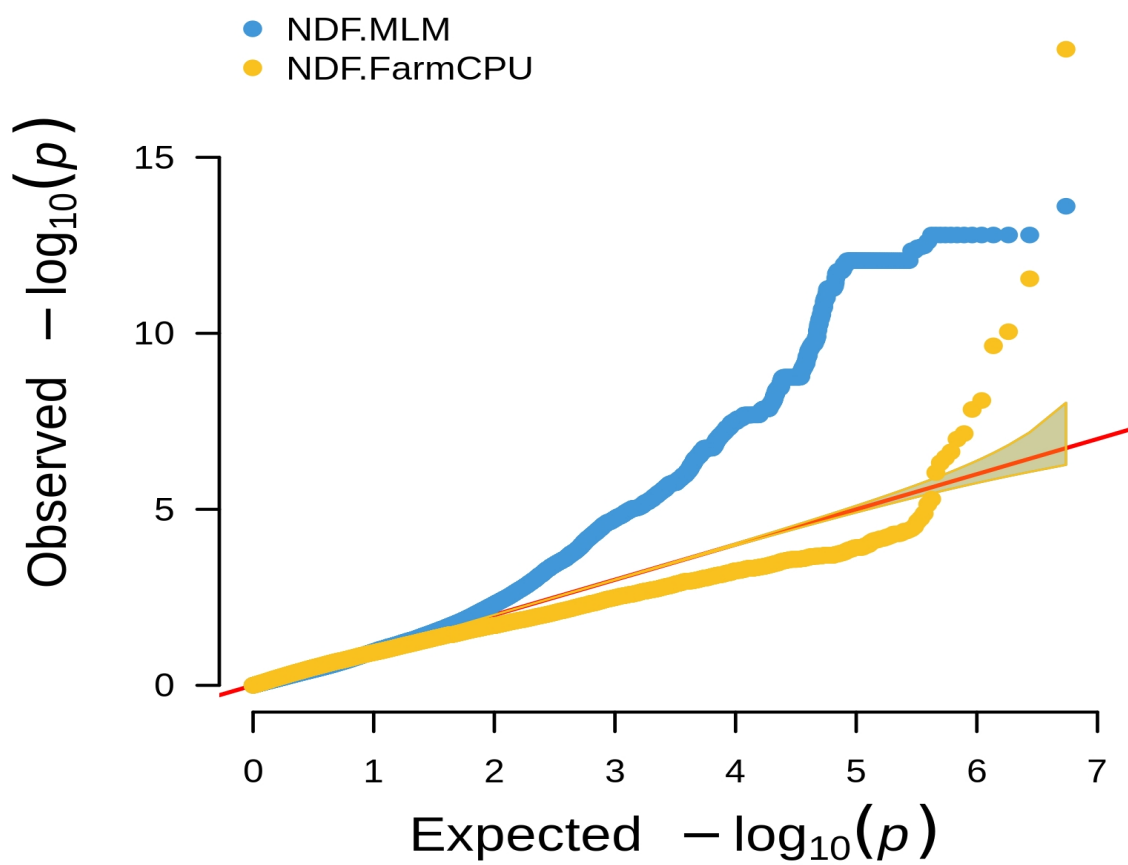
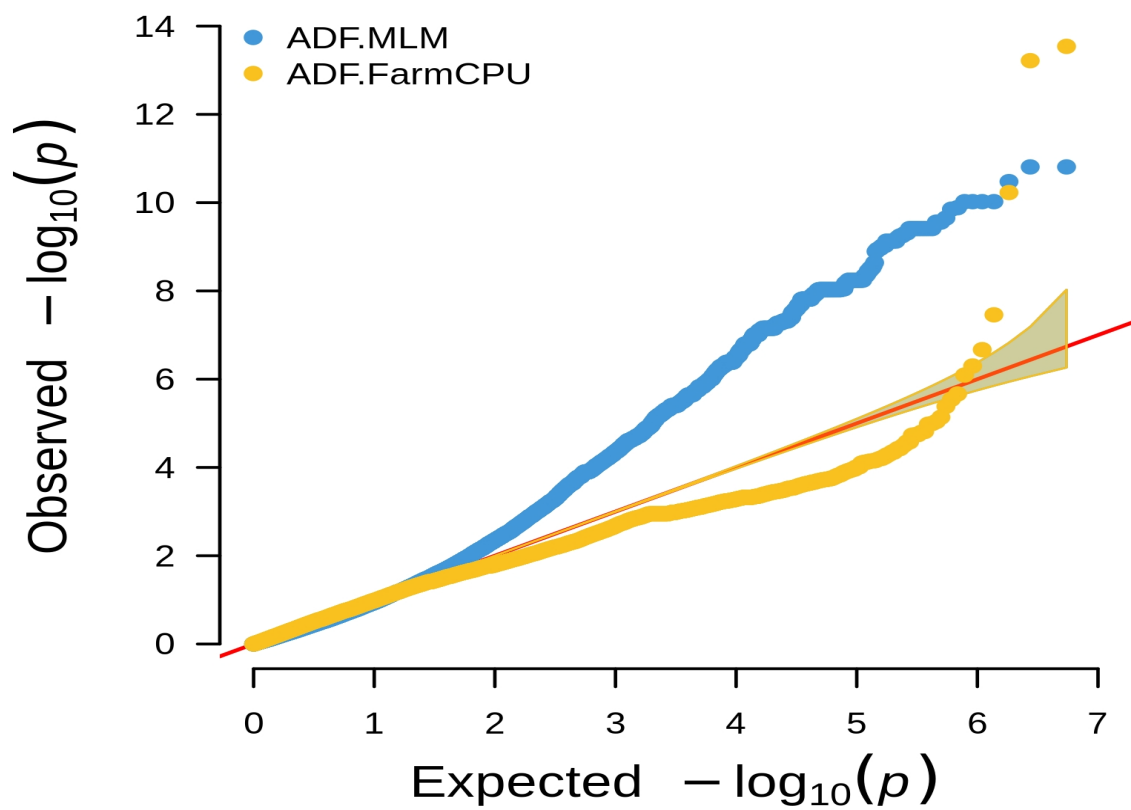


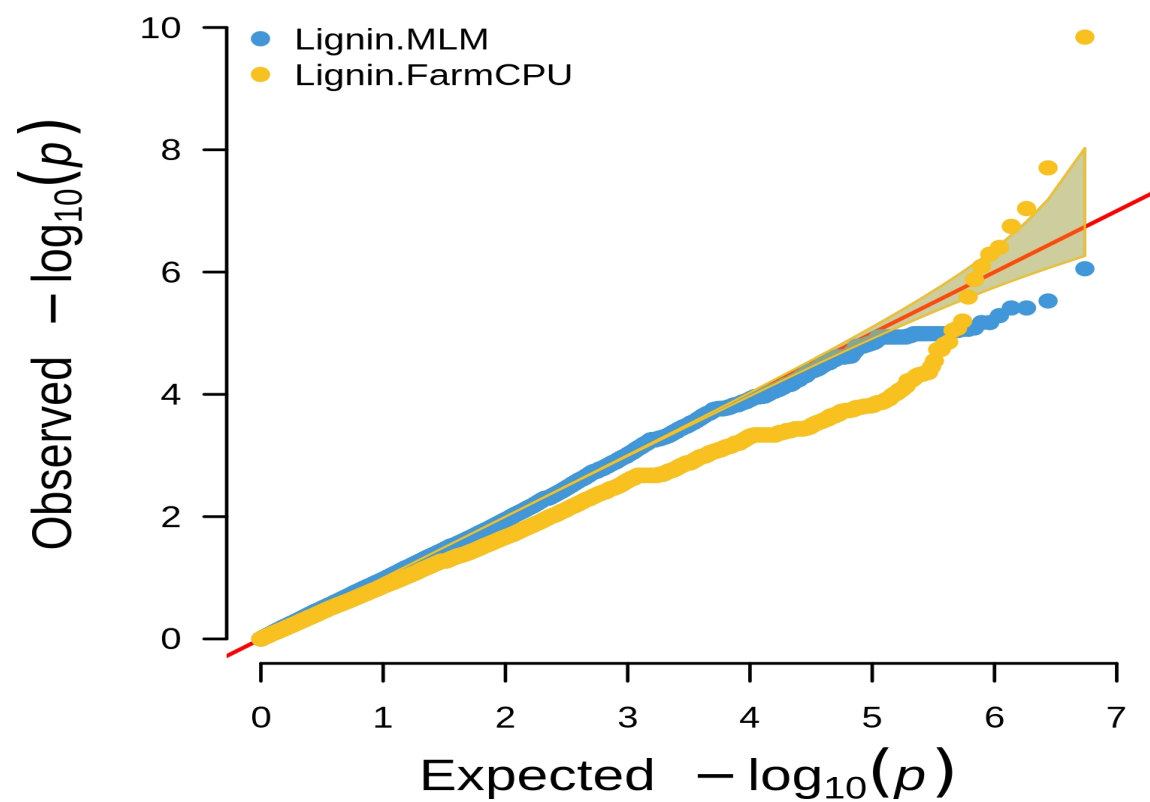
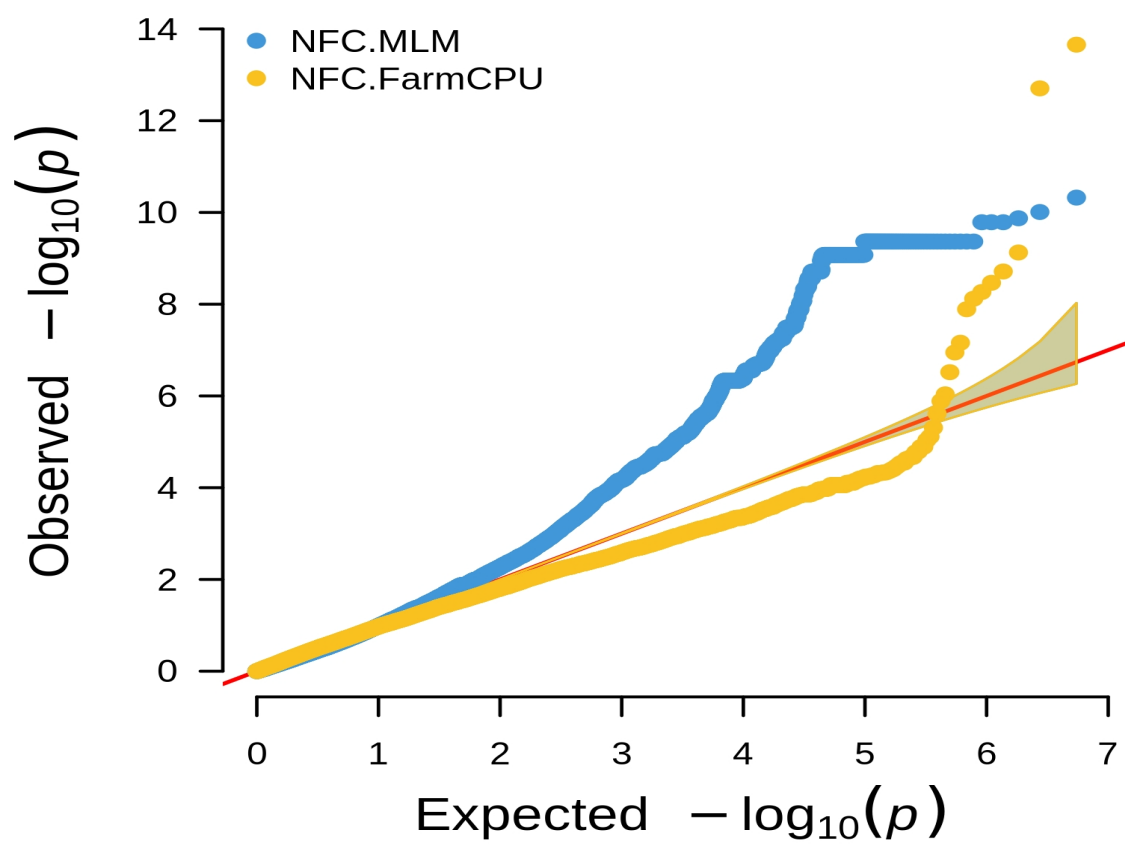


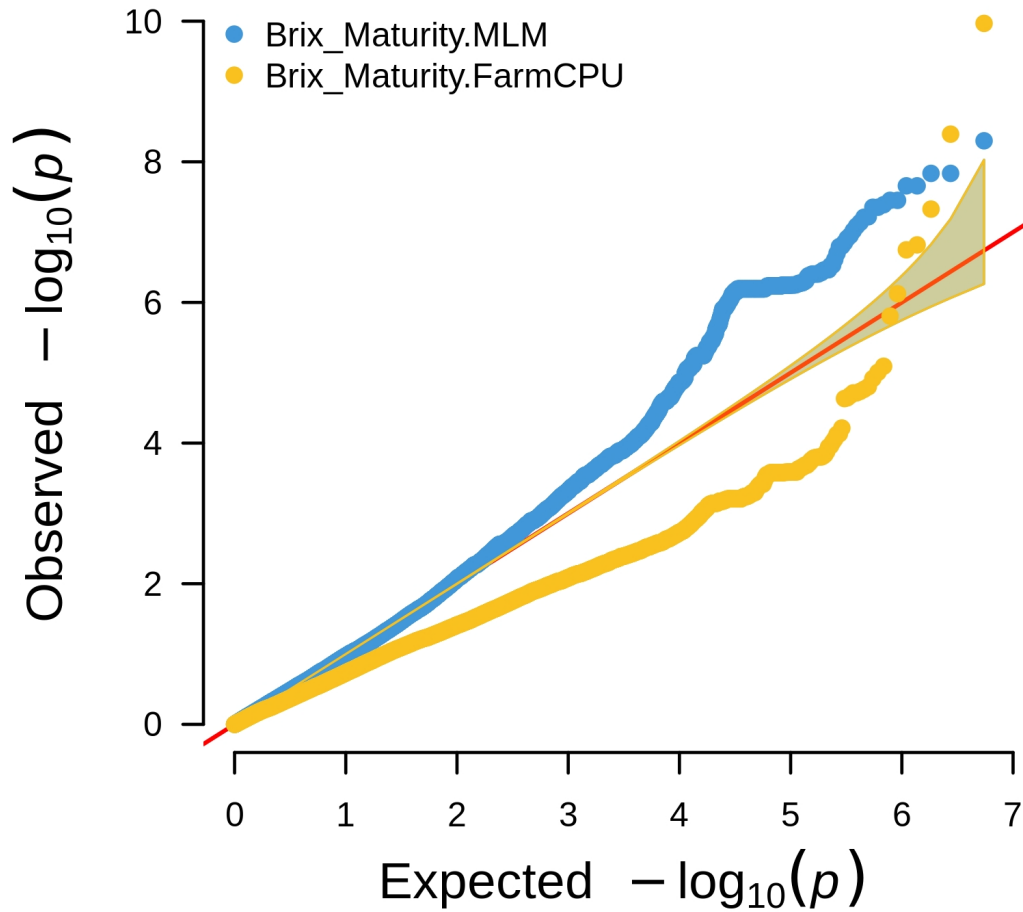
Supplementary Figure S3. Manhattan plots of genome-wide association for various traits using two models (MLM and FarmCPU). (A) Seed color (SC), plant height (PH), days to harvest (DTH), fresh weight (FW), and dry weight (DW). (B) acid detergent fiber (ADF), neutral detergent fiber (NDF), non-fibrous carbohydrate (NFC), Brix, and lignin. The $-\log_{10}(p)$ values (y -axis) are plotted against the position on each chromosome (x -axis). Each solid circle represents a SNP, and the red dashed line represents the Bonferroni-corrected threshold ($p \leq 0.05$).



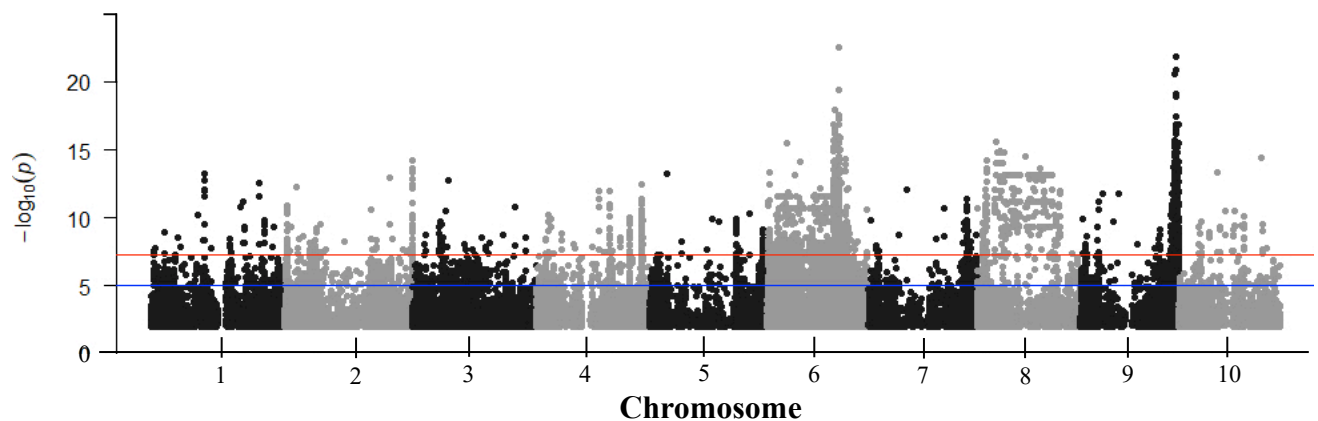








Supplementary Figure S4. Quantile-quantile (QQ) plot of each trait using two models (MLM and FarmCPU) in GWAS analysis of BAP. Each plot represents the expected $-\log_{10}(p)$ values on the x -axis, whereas the observed p -values are on the y -axis for both these models.



Supplementary Figure S5. Manhattan plots showing genome-wide measures of pleiotropic effects associated regions for various traits of bioenergy association panel. The horizontal blue line represents a Bonferroni-adjusted threshold of 0.05, and the horizontal red line represents a Bonferroni-adjusted threshold of 0.01.