Genome-wide association studies for yield-related traits in soft red winter wheat grown in Virginia

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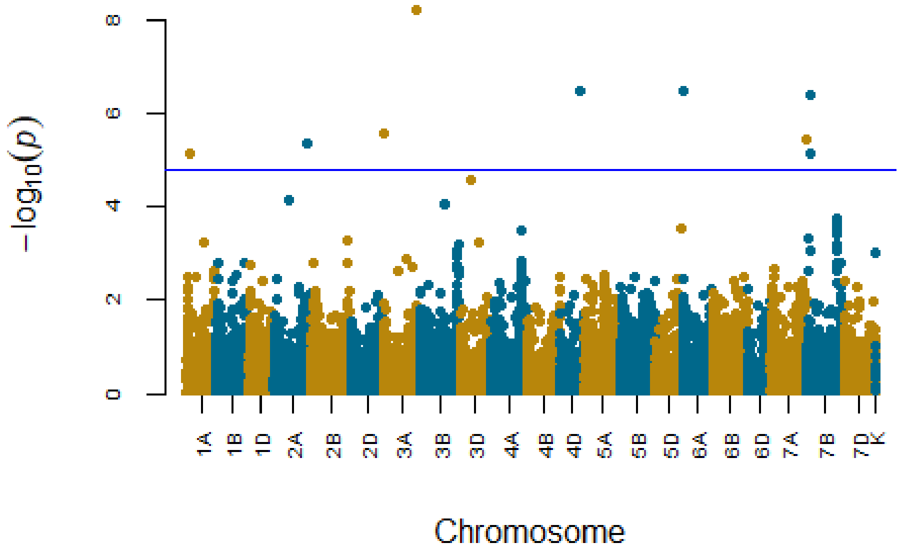
S2 File. Manhattan and QQ plots for SNP p-values generated by the FarmCPU algorithm.

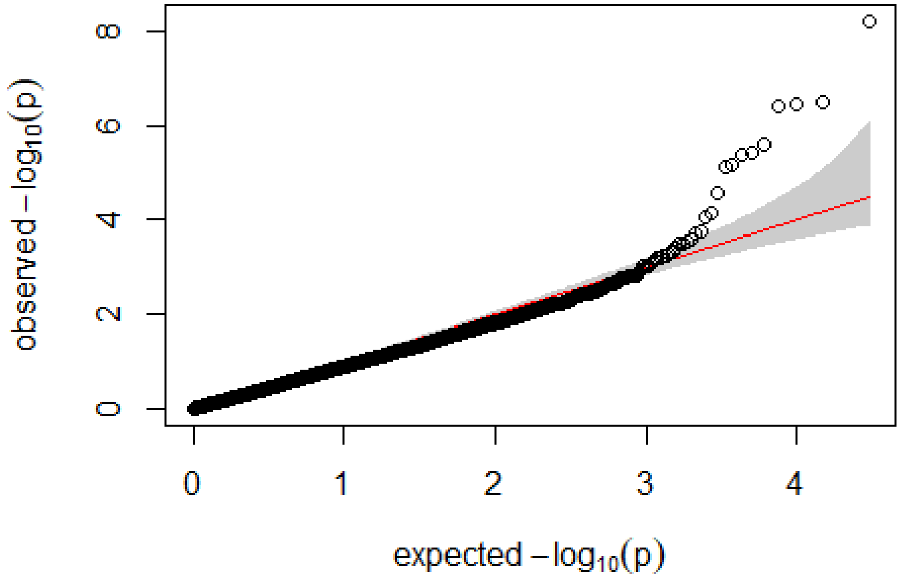
Below are Manhattan and uniform distribution quantile-quantile (QQ) plots produced from the output of a GWAS analysis performed using the FarmCPU algorithm.

A total of 29,949 genotyping-by-sequencing (GBS) generated markers were included in the analysis.

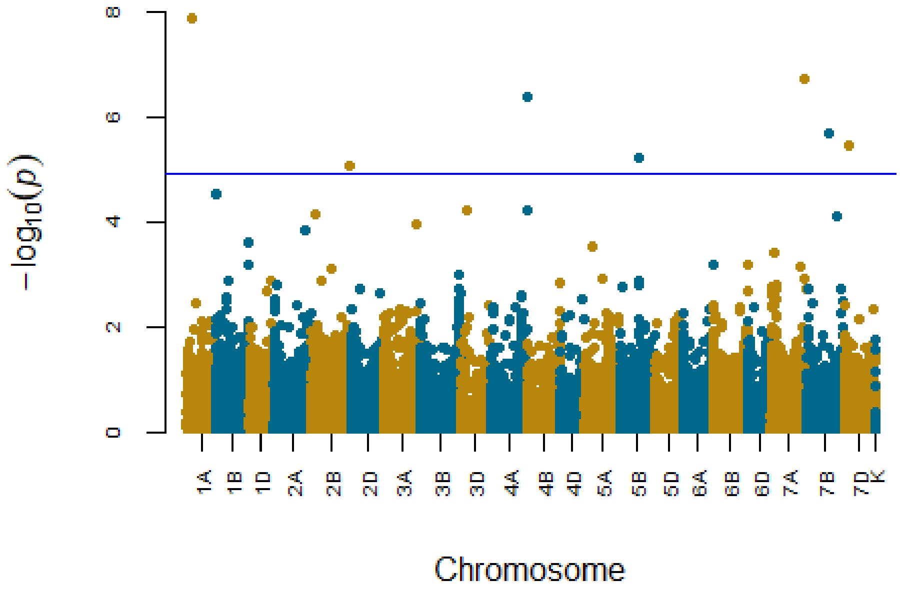
A false-discovery rate (FDR) threshold was used to determine signficance for individual SNP p-values. A horizontal line is placed on the Manhattan plot only if at least one SNP’s -log(p) value exceeds the FDR threshold.

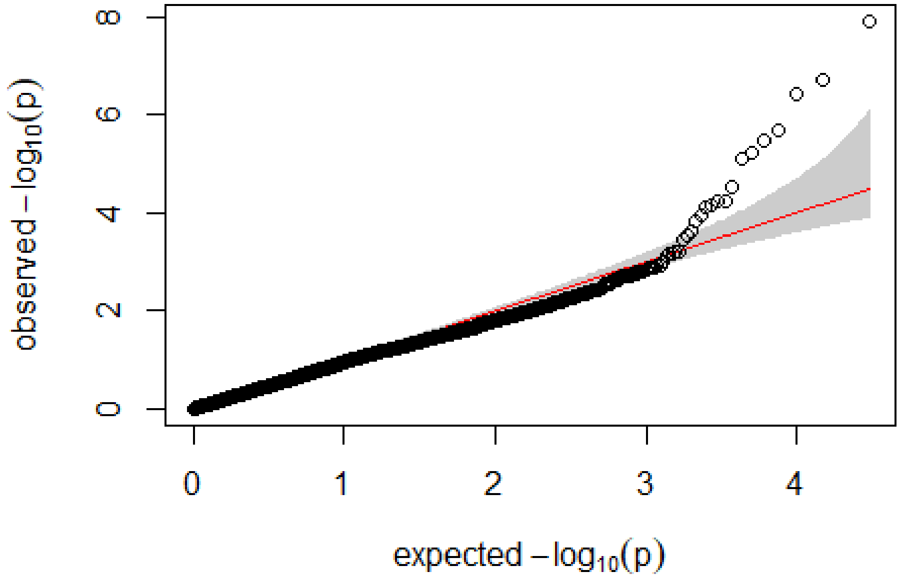
Manhattan and QQ plots for trait FLSG



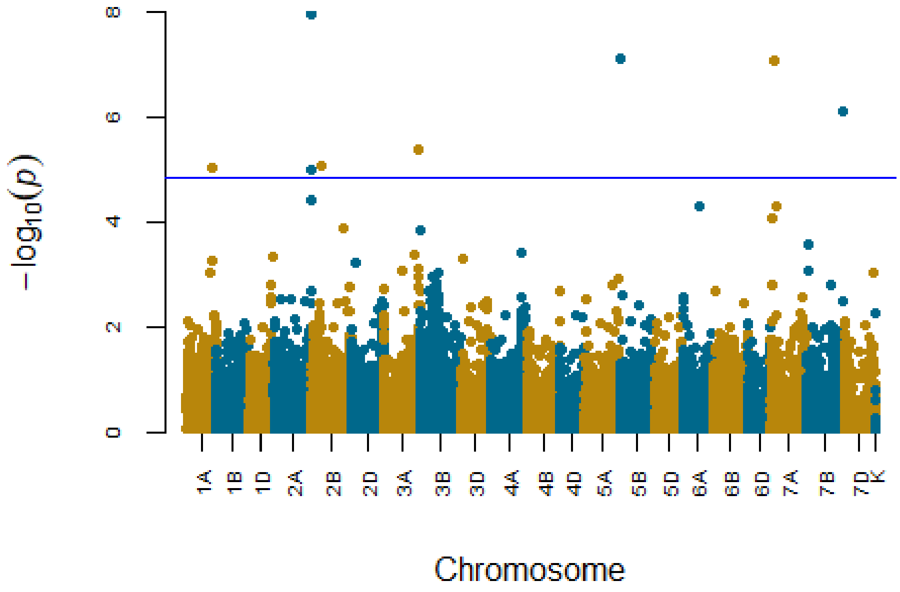


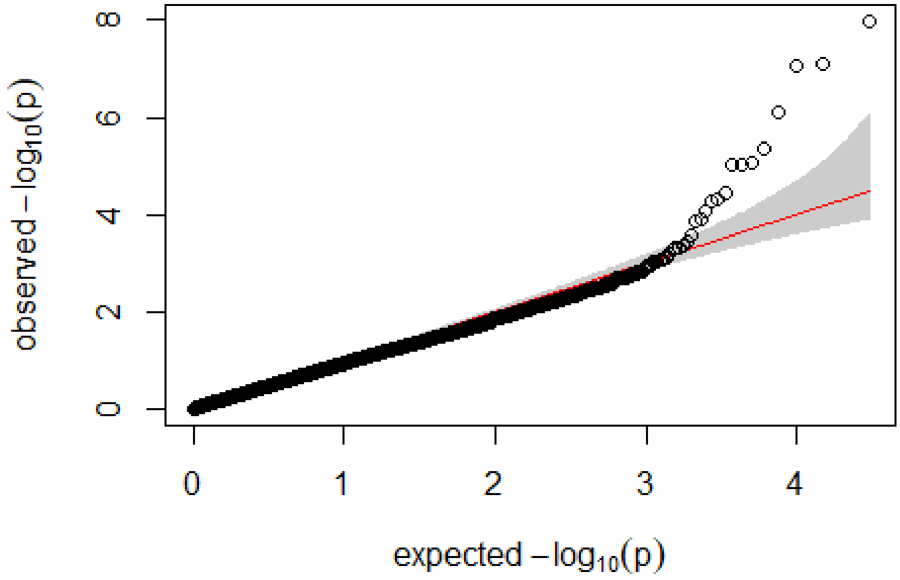
Manhattan and QQ plots for trait GSQM



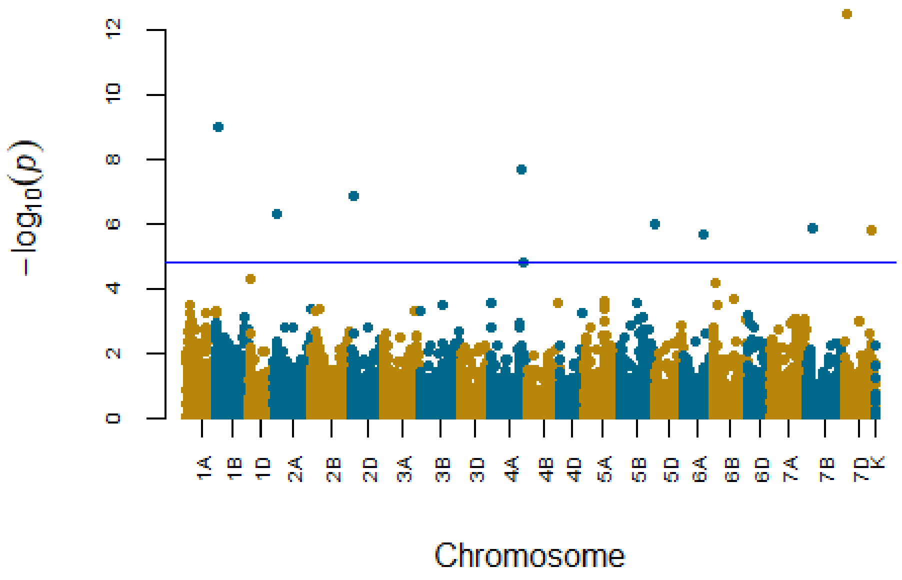


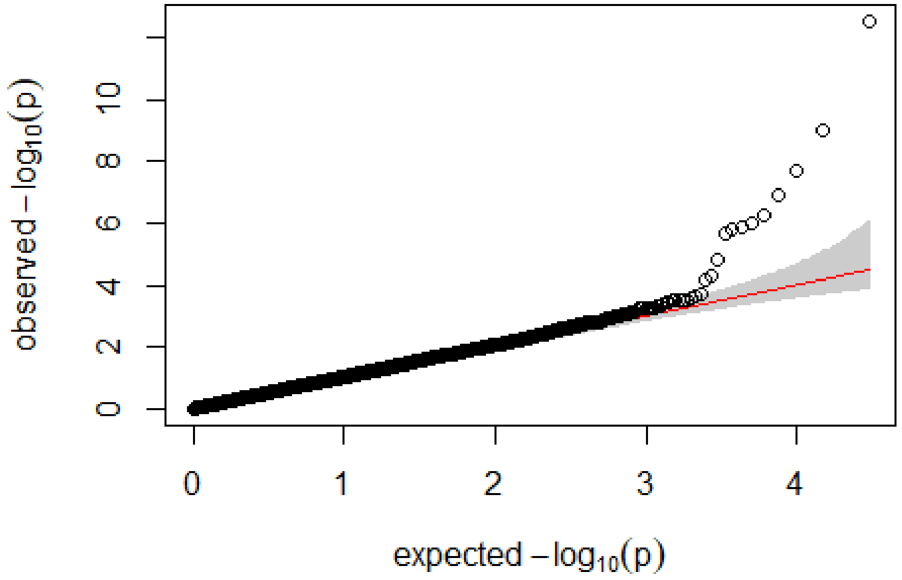
Manhattan and QQ plots for trait GW



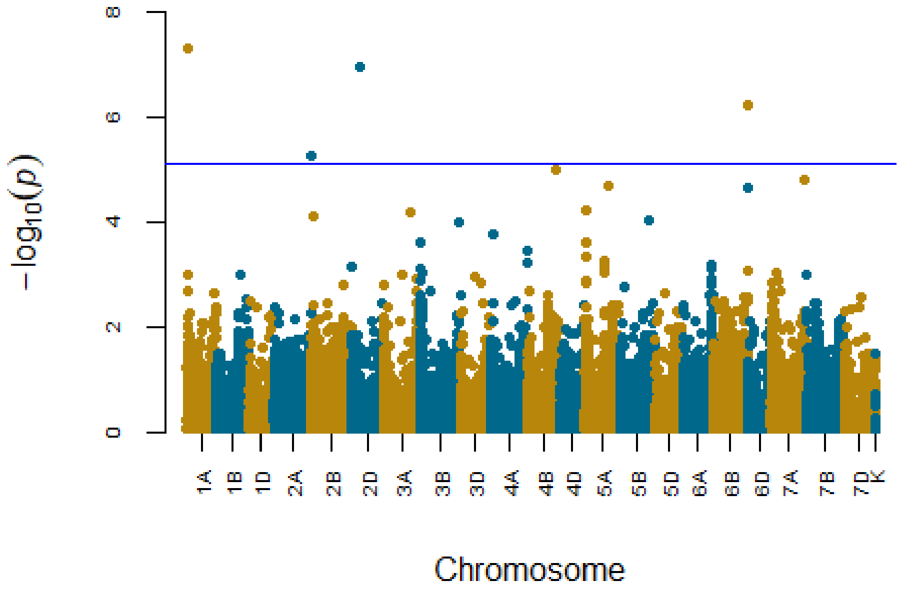


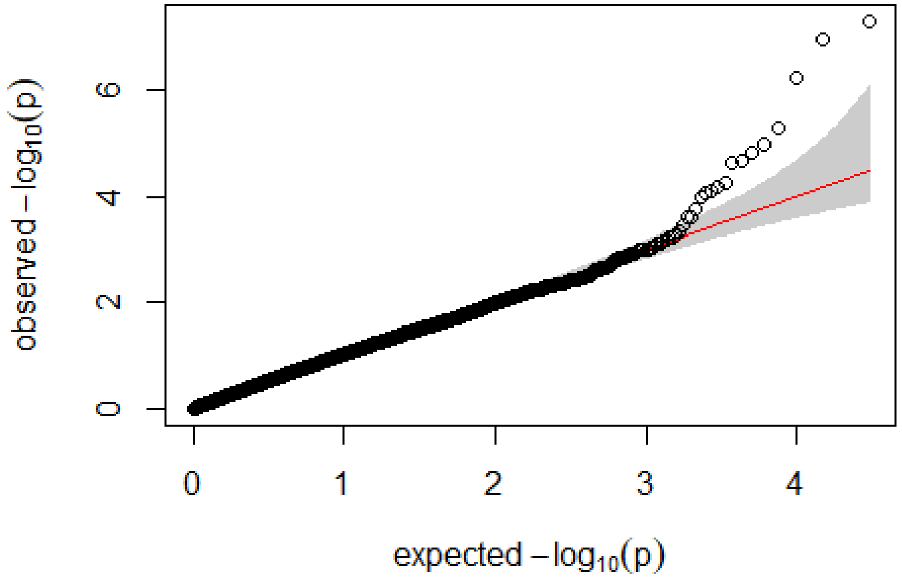
Manhattan and QQ plots for trait HD



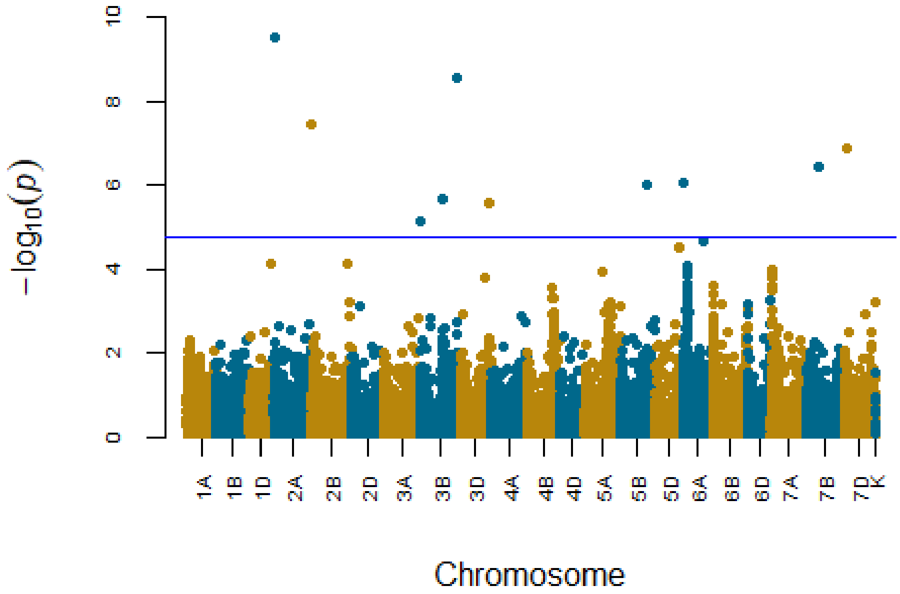


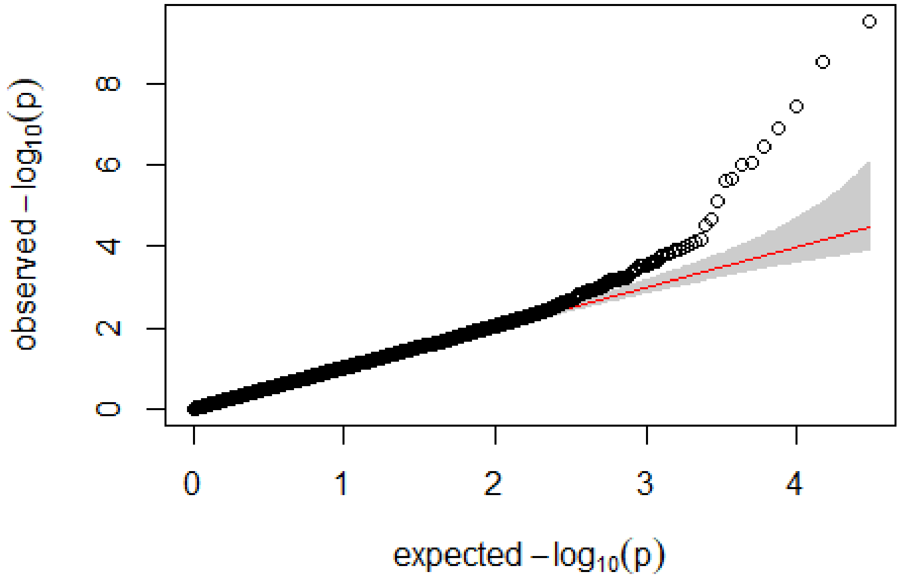
Manhattan and QQ plots for trait HT



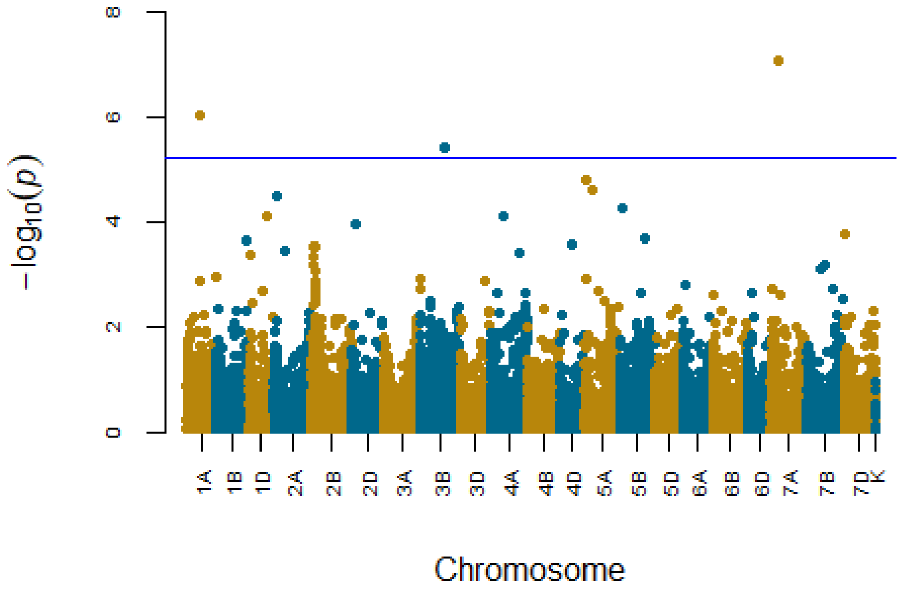


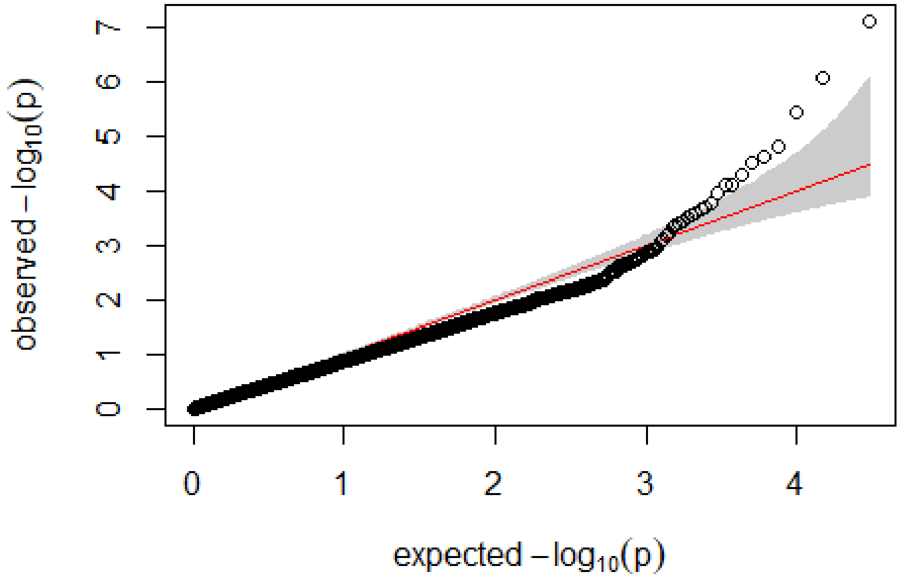
Manhattan and QQ plots for trait MAT



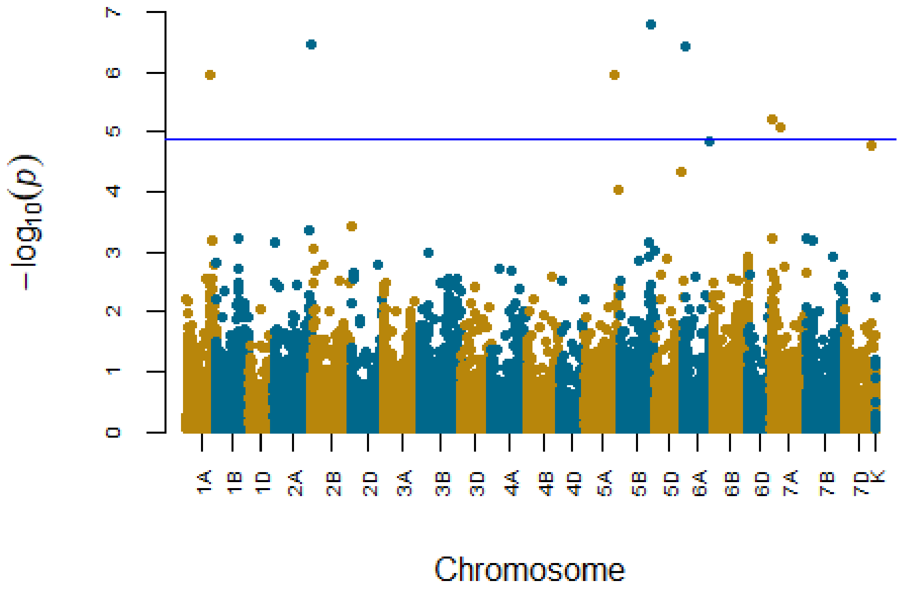


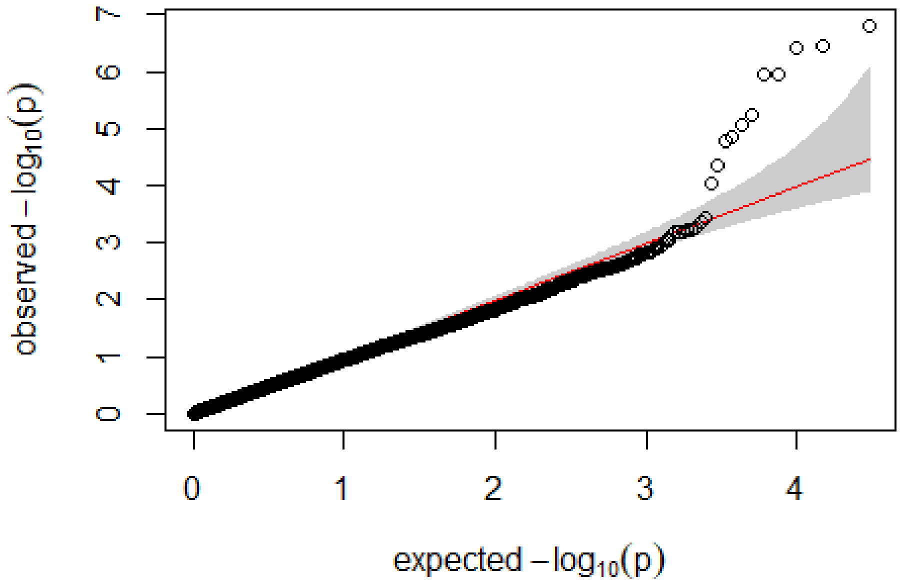
Manhattan and QQ plots for trait NDVI



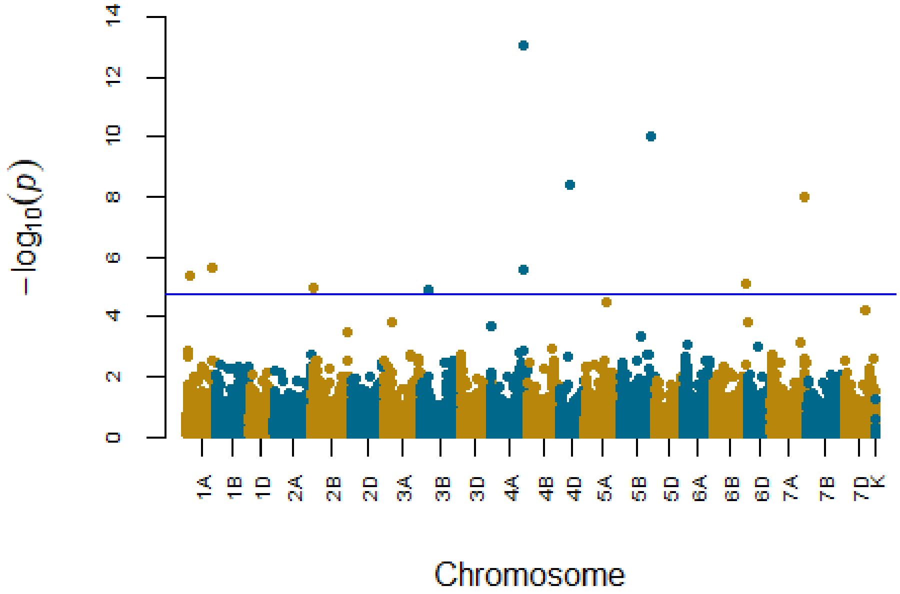


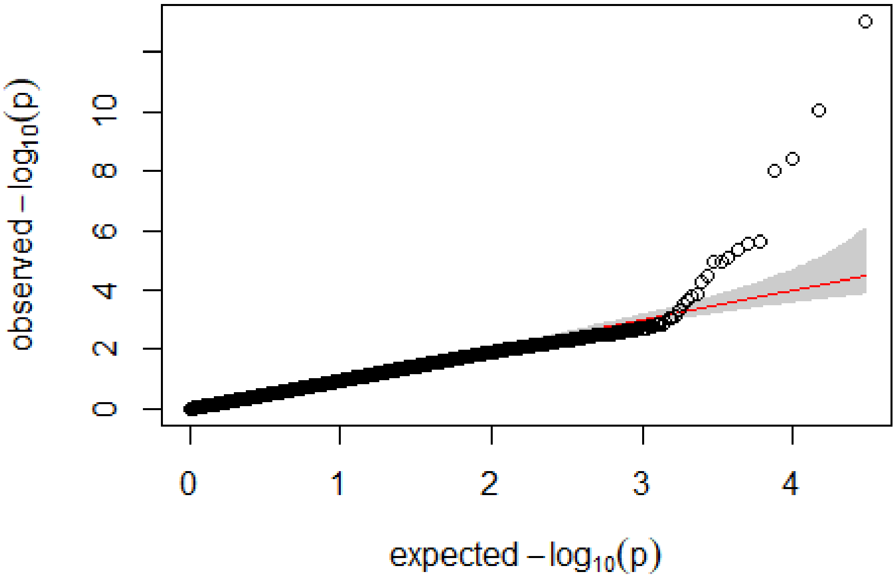
Manhattan and QQ plots for trait PROT



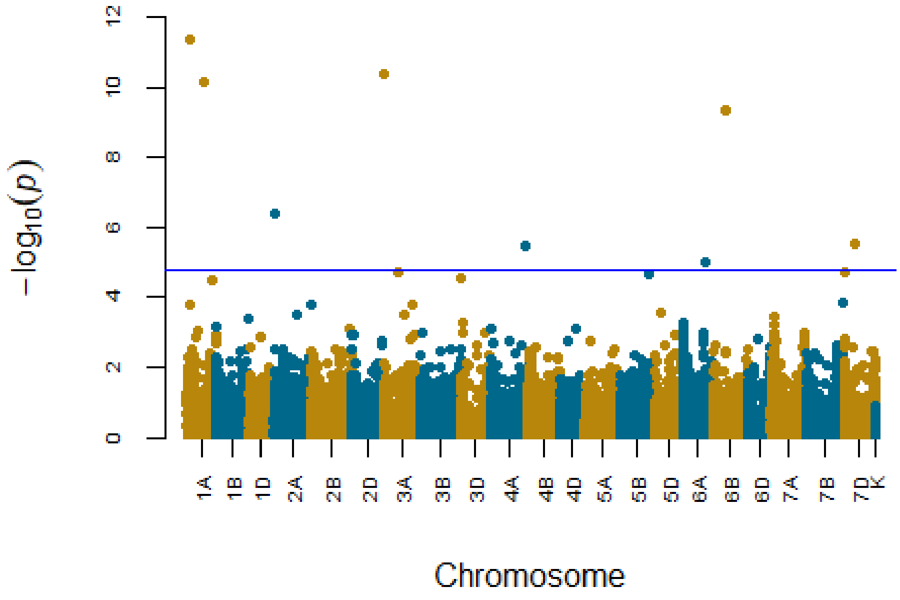


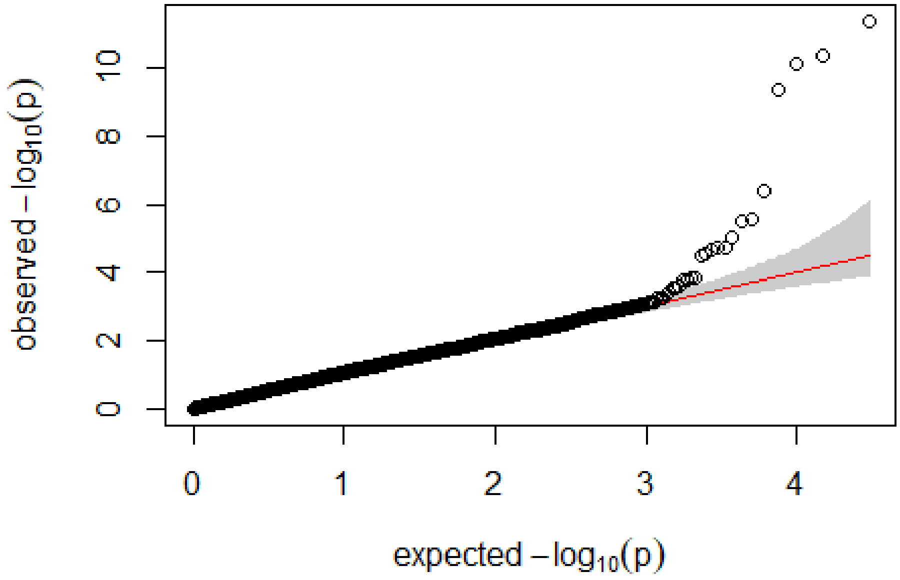
Manhattan and QQ plots for trait SPH



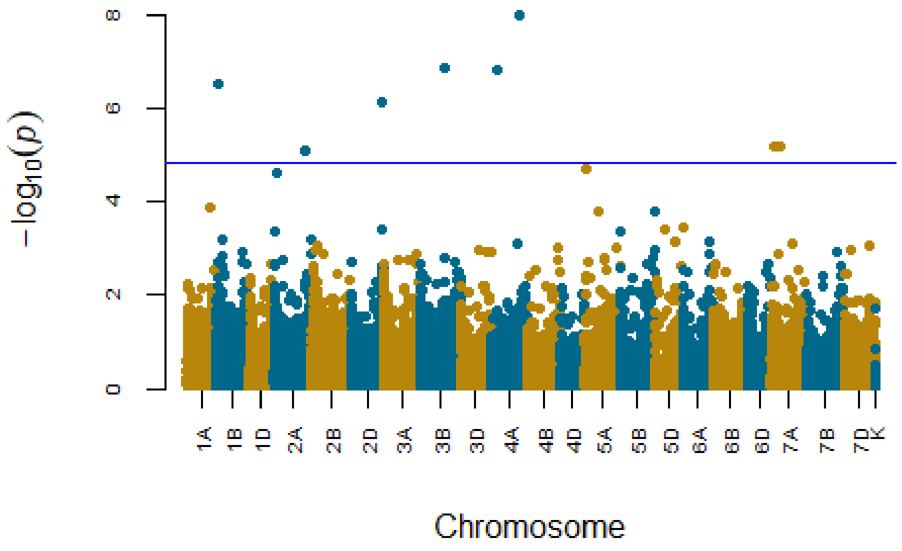


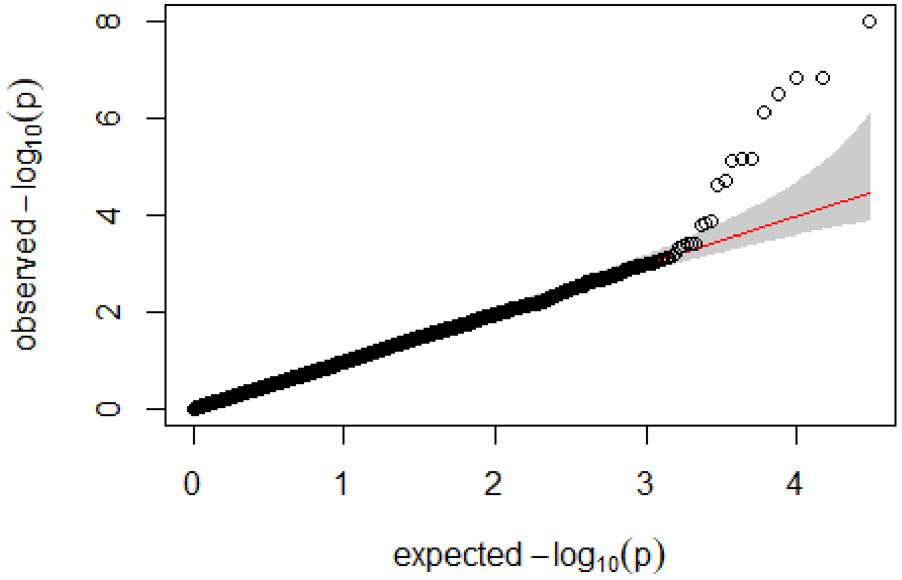
Manhattan and QQ plots for trait SSQM



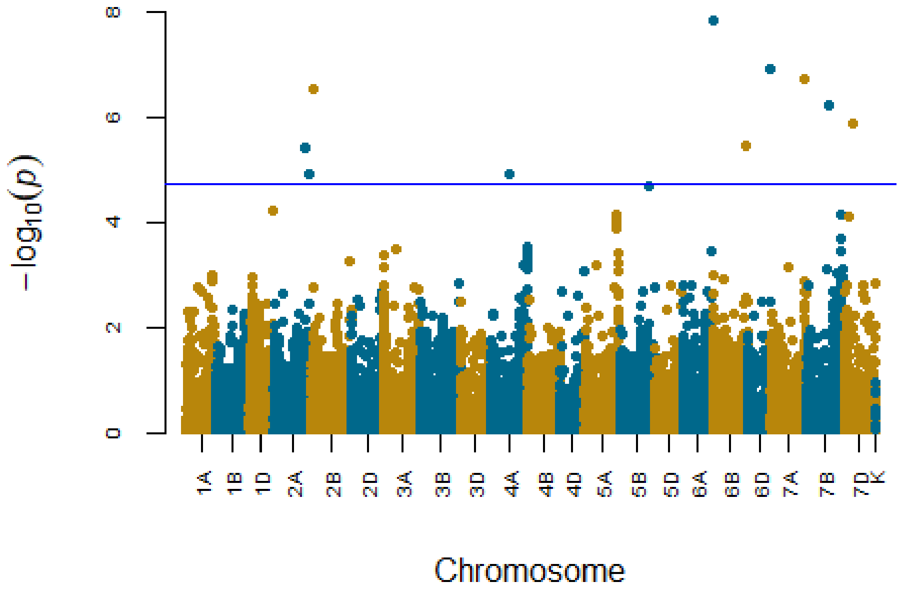


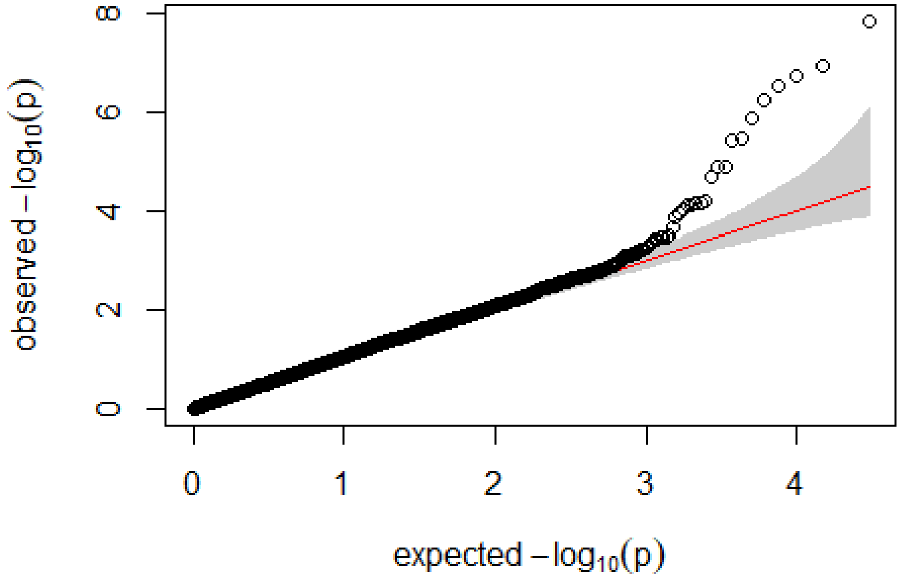
Manhattan and QQ plots for trait STARCH



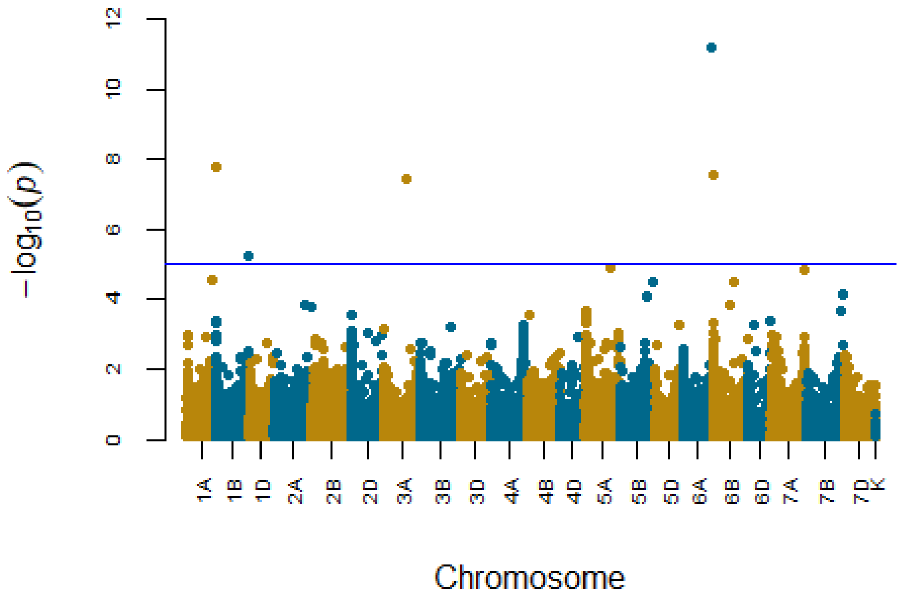


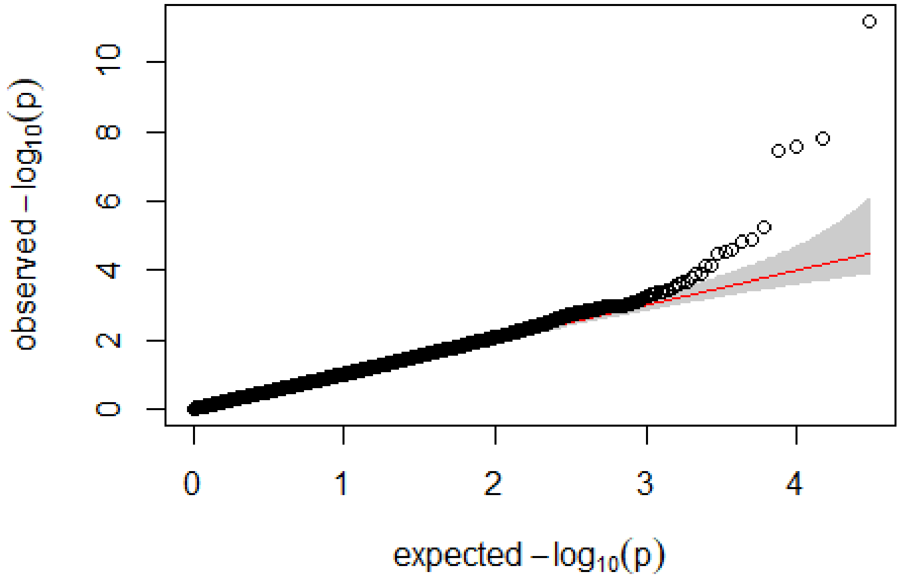
Manhattan and QQ plots for trait TKW





Manhattan and QQ plots for trait TWT





Manhattan and QQ plots for trait YLD