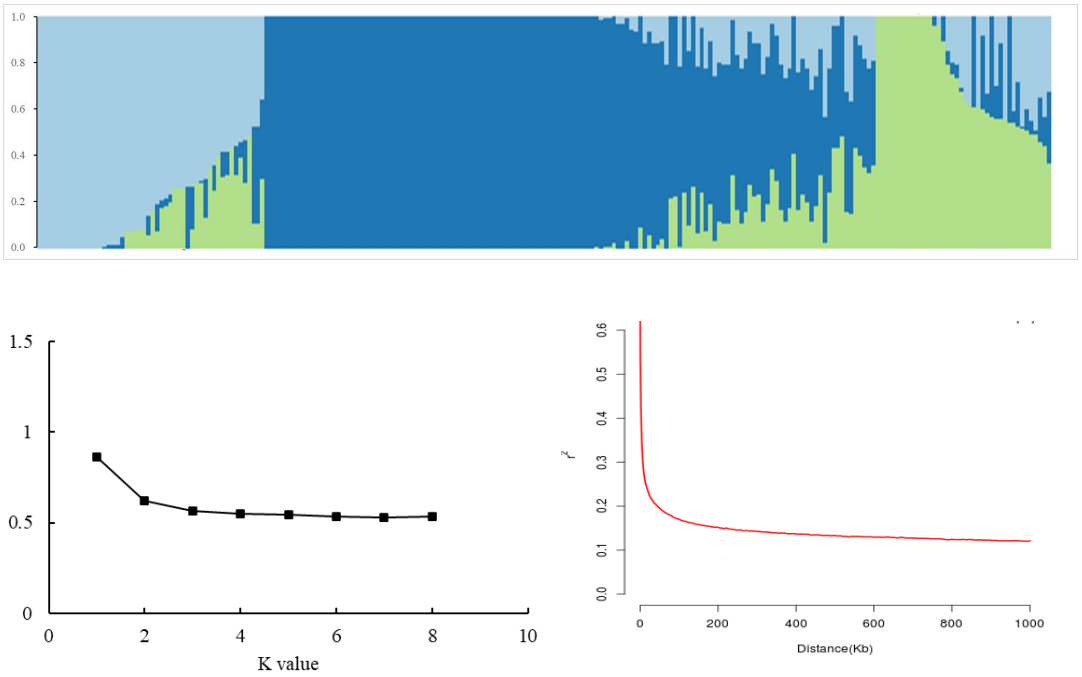


Figure.S1-Population structure of an association panel of 232 sorghum accessions

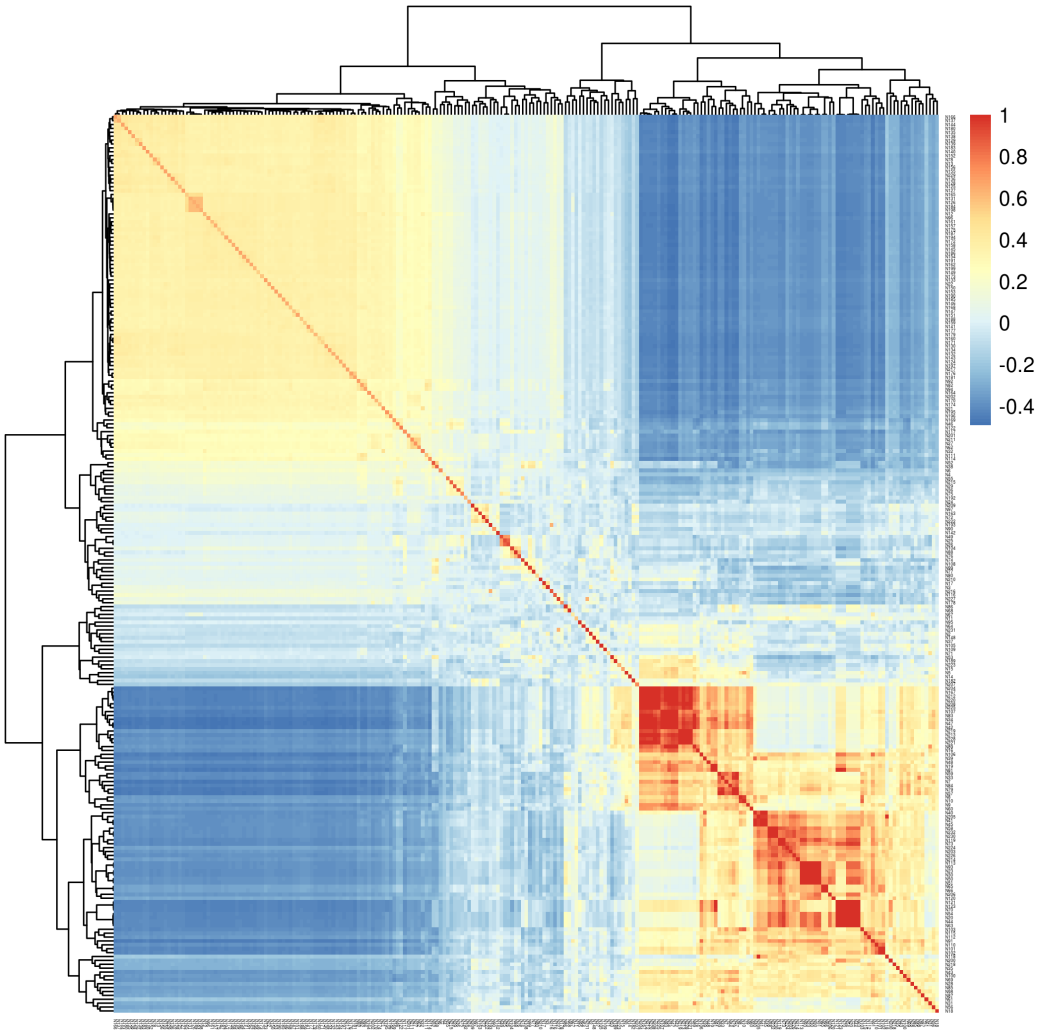


Figure.S2-Heatmap of the genome-wide relationship matrix (GRM) based on genetic similarity.

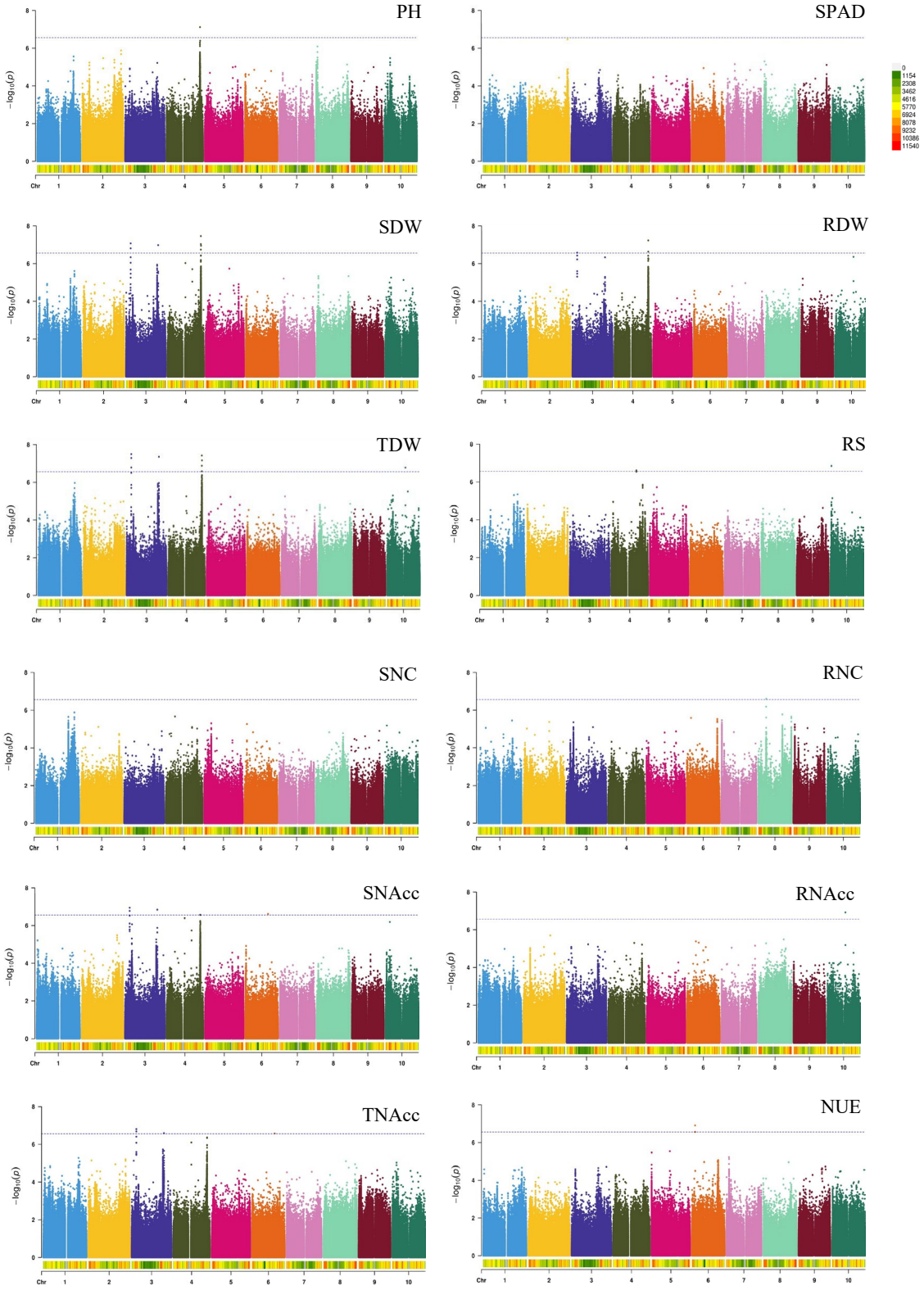


Figure. S3- Manhattan plots for the genome-wide association analysis.

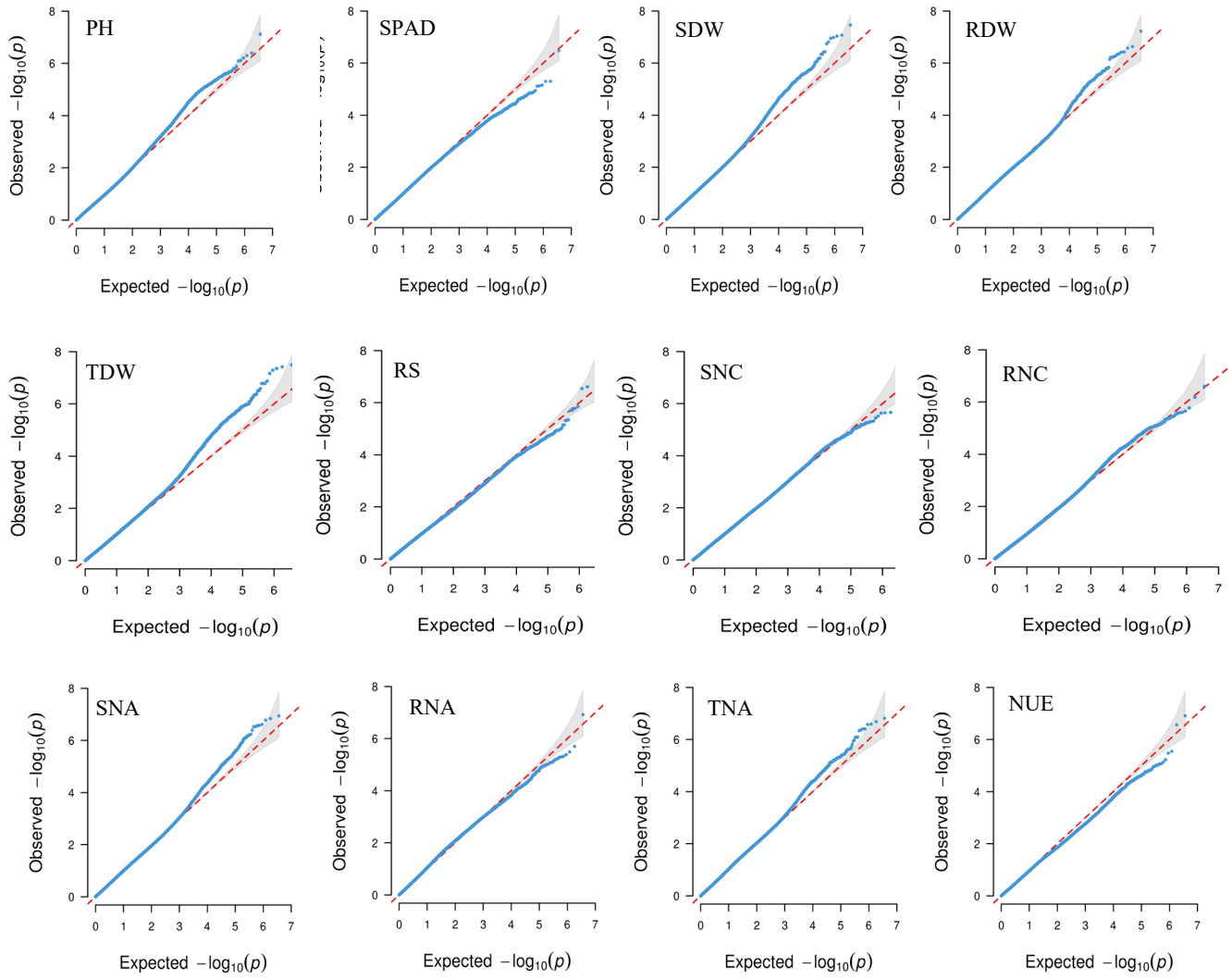


Figure. S4-Q-Q plots for genome-wide association analysis

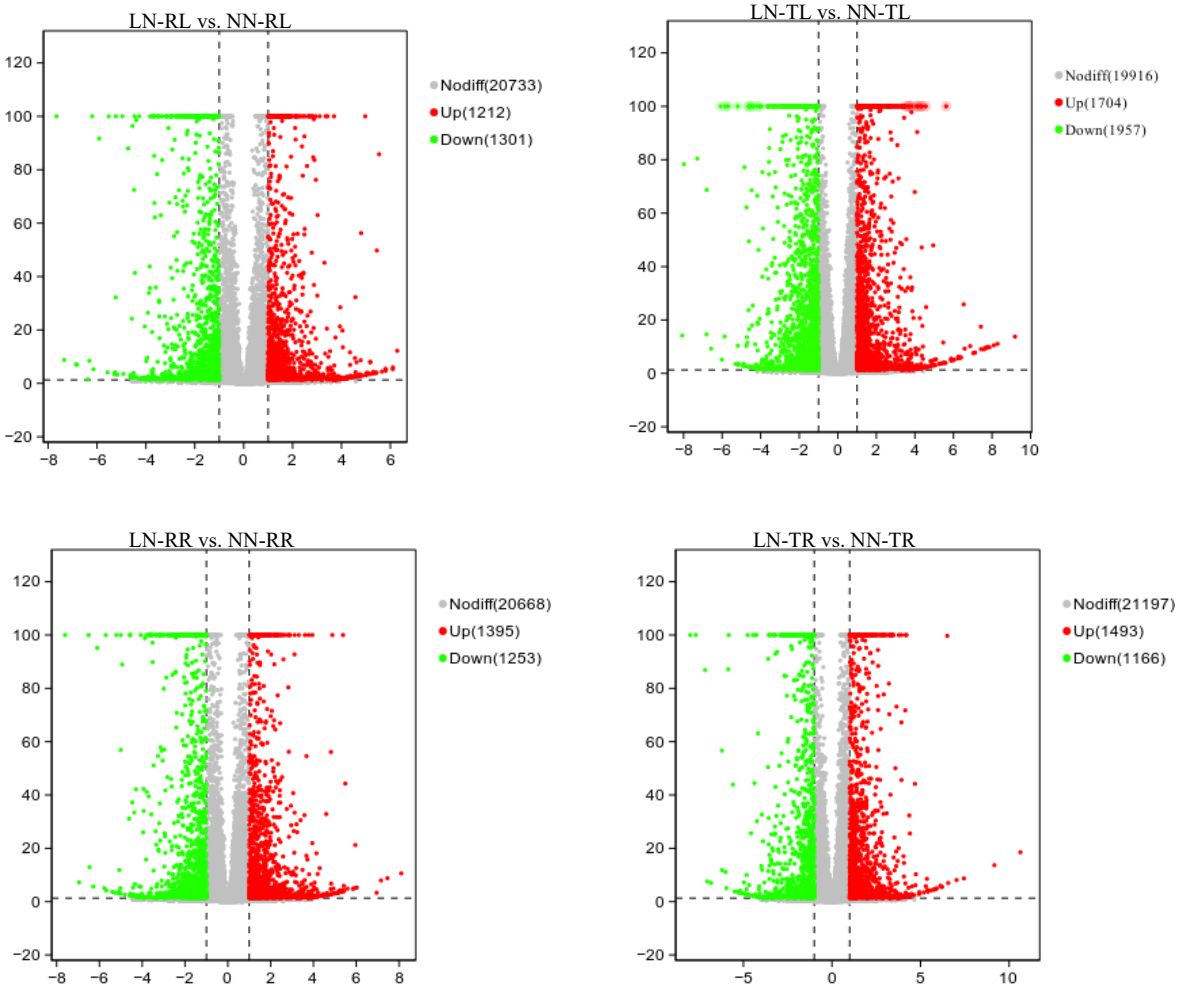
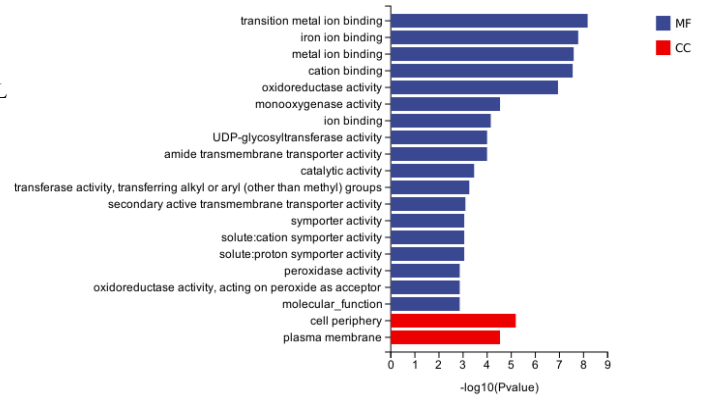
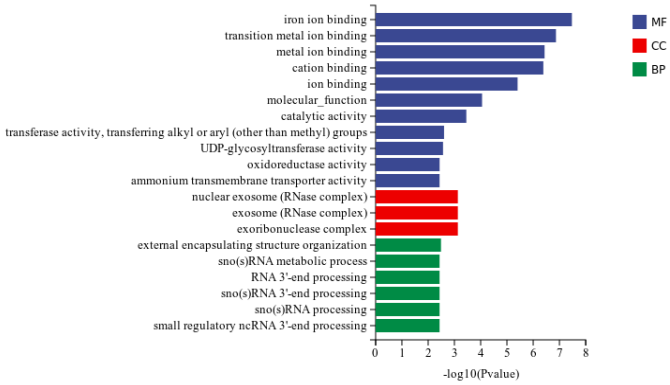


Figure. S5-Volcano plot of DEGs between the transcriptome sequencing samples of LN-responsive sorghum accessions and LN--tolerant sorghum accessions

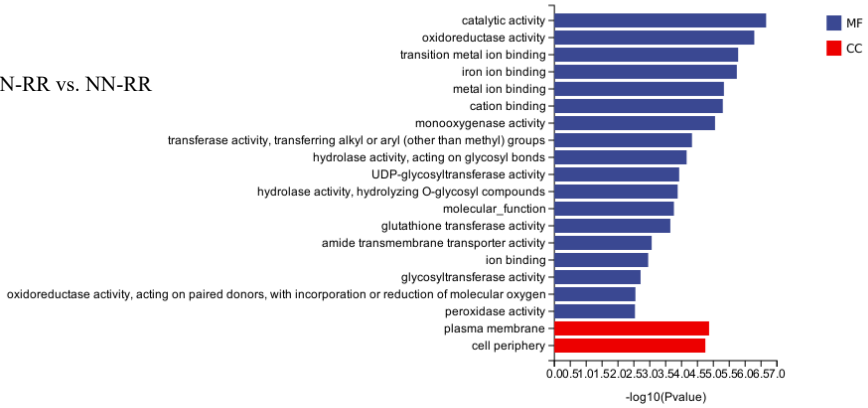
LN-RL vs. NN-RL



LN-TL vs. NN-TL



LN-RR vs. NN-RR



LN-TR vs. NN-TR

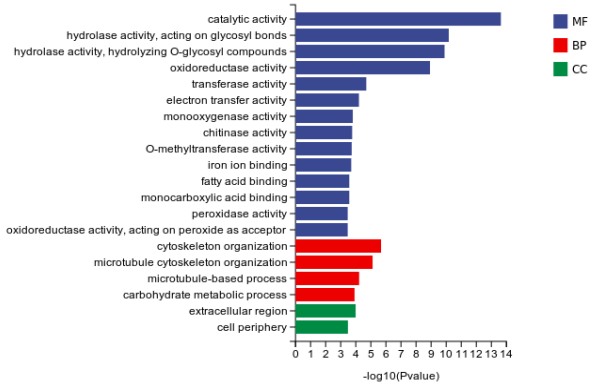


Figure. S6-GO enrichment analysis of LN-responsive sorghum accessions and LN--tolerant sorghum accessions