

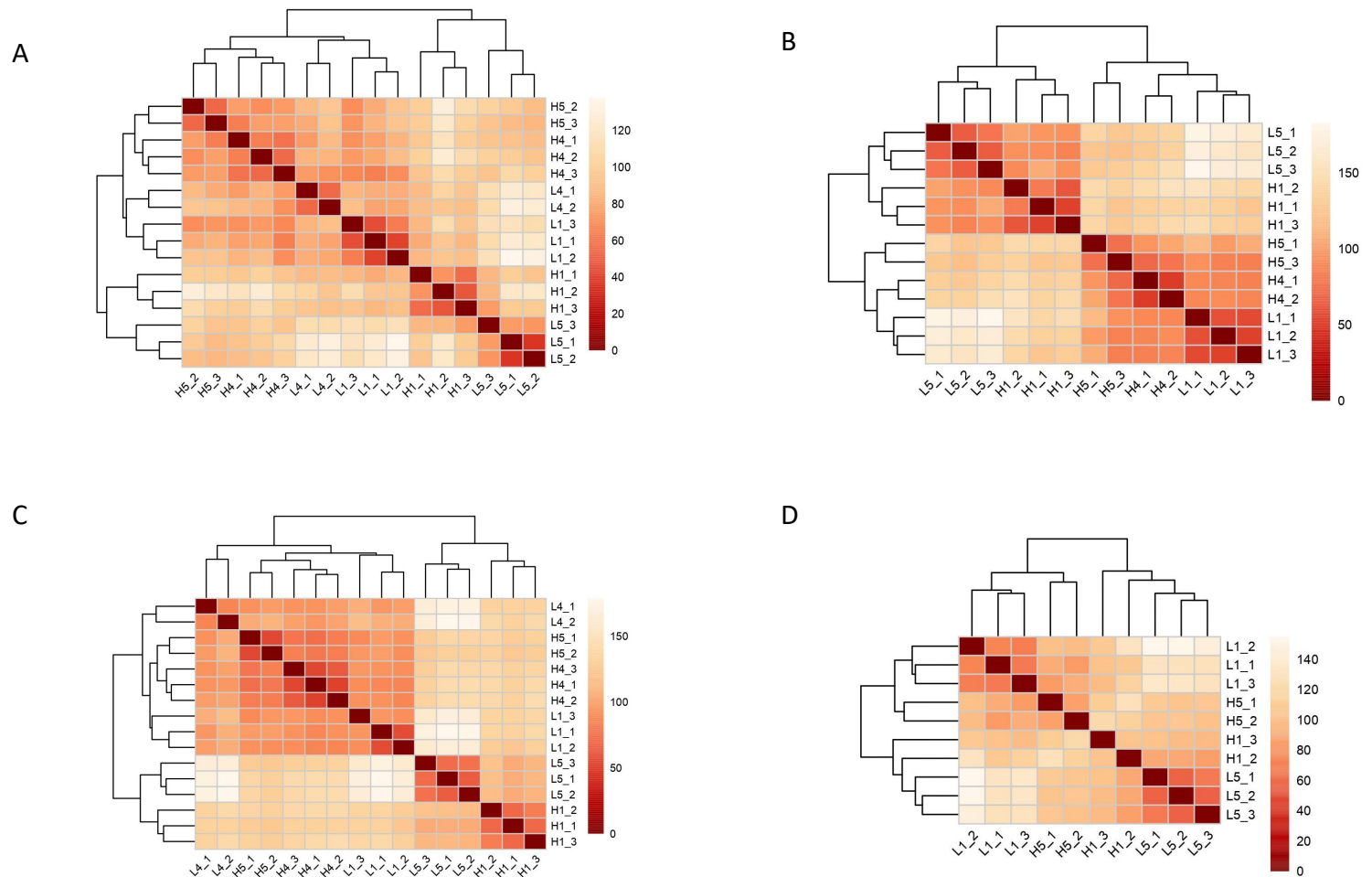
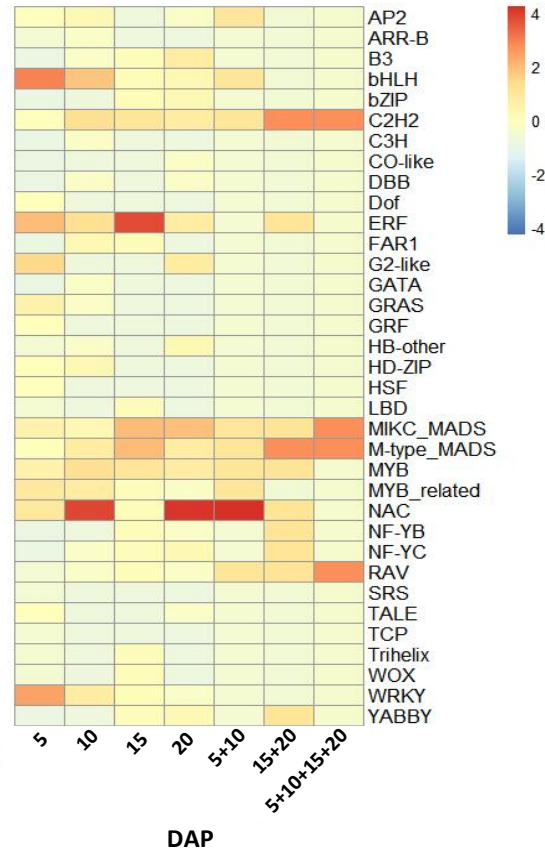


Fig. S1-Cluster dendrogram of gene expression profiles among biological replicates with high-quality RNA-seq data at four different time points. A), B), C) and D) stand for the for different time points of 5DAP, 10DAP, 15DAP and 20DAP, respectively.

A



B

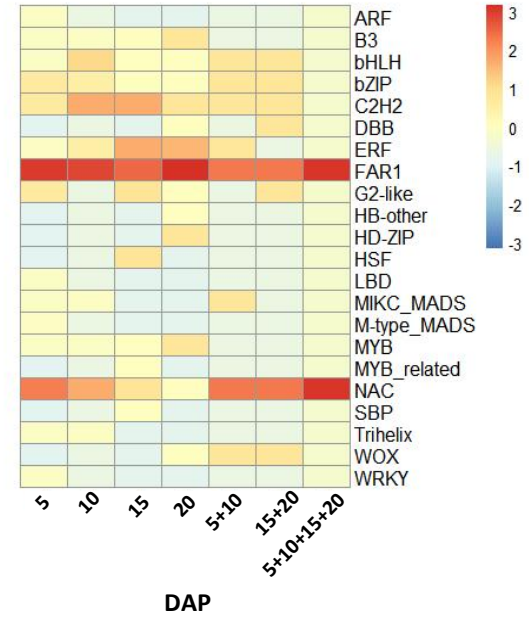
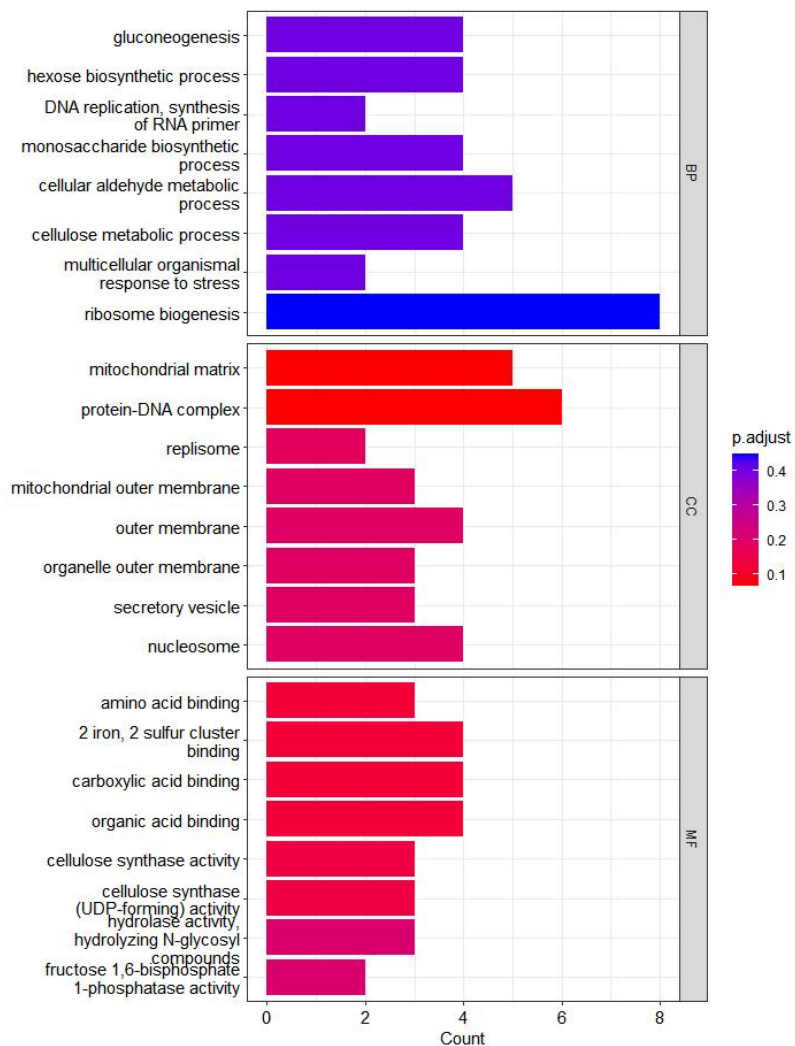


Fig. S2-Heatmap of the scaled number of TF genes for up-regulated DEGs (A) and down-regulated DEGs(B) at different development stages.

A



B

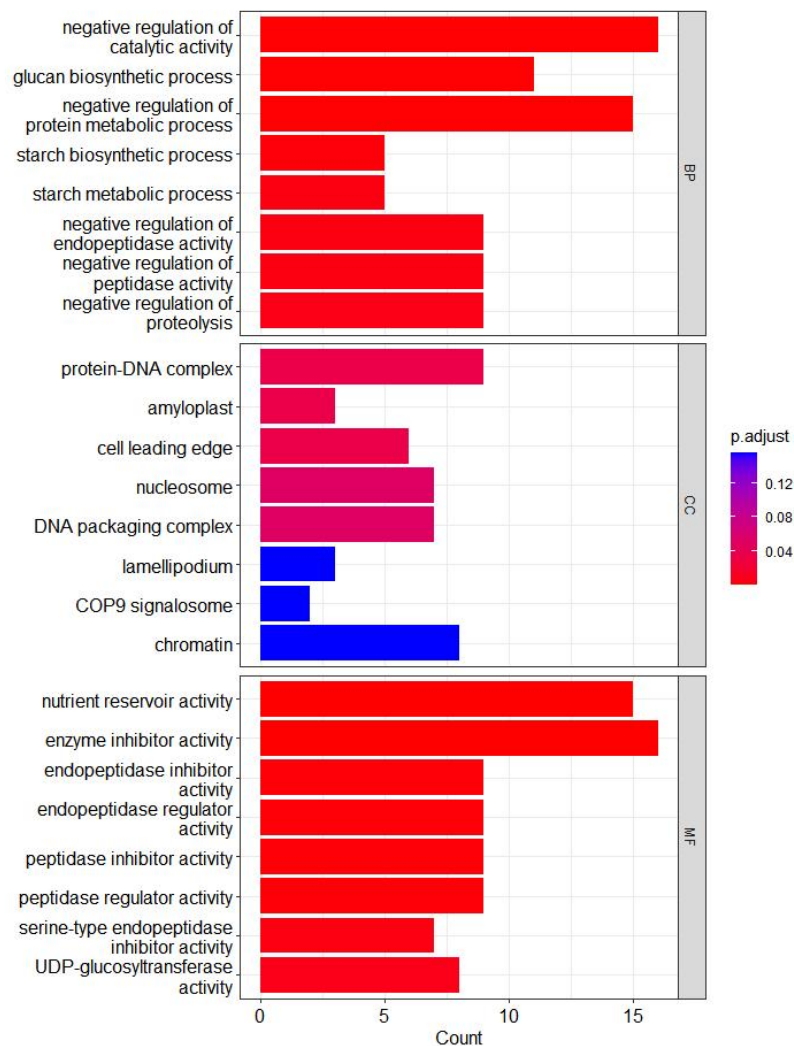
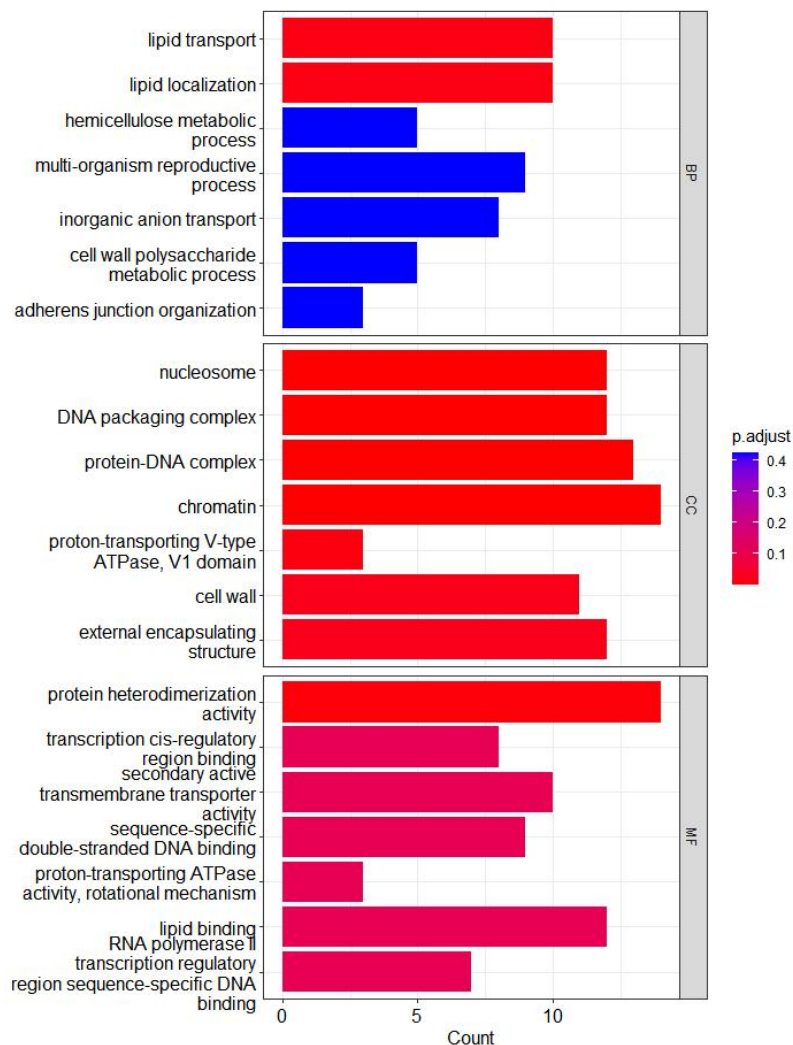


Fig. S3 -GO enrichment analysis of DEGs at 5 DAP between the thick-aleurone group and thin-aleurone group. (A) and (B) are for the up-regulated DEGs and down-regulated DEGs respectively. BP=biological process, CC=cellular component, MF=molecular function.

A



B

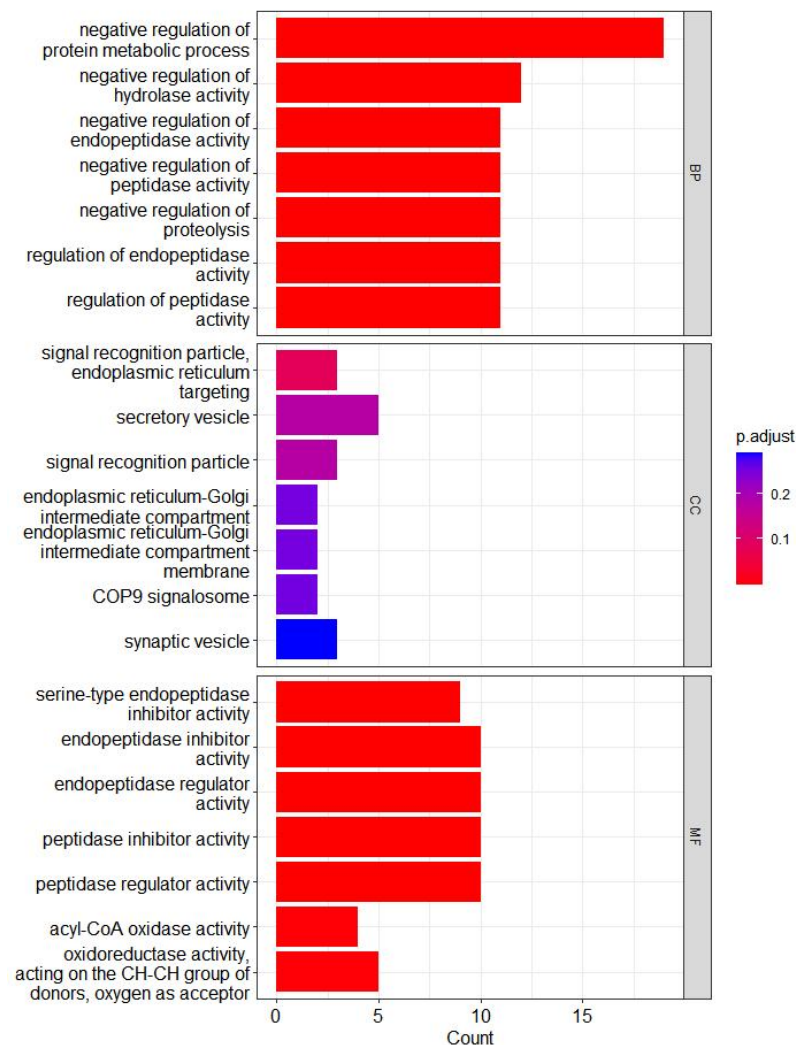
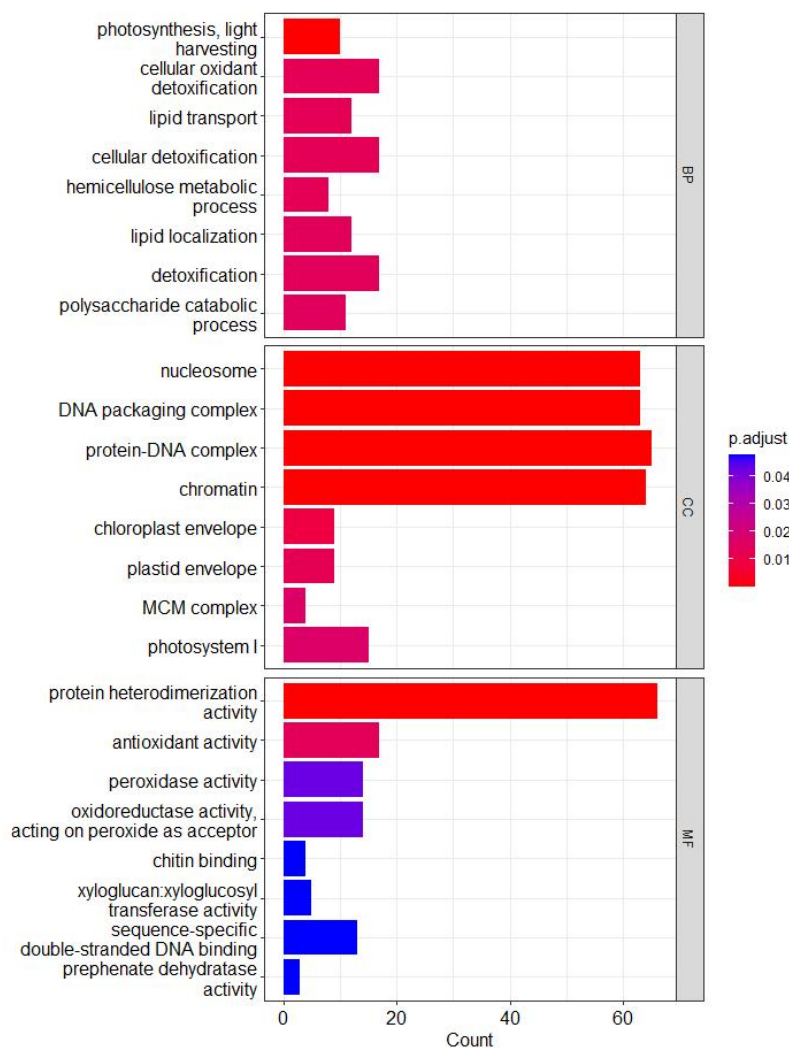


Fig. S4-GO enrichment analysis of DEGs at 15 DAP between the thick-aleurone group and thin-aleurone group. (A) and (B) are for the up-regulated DEGs and down-regulated DEGs respectively. BP=biological process, CC=cellular component, MF=molecular function.

A



B

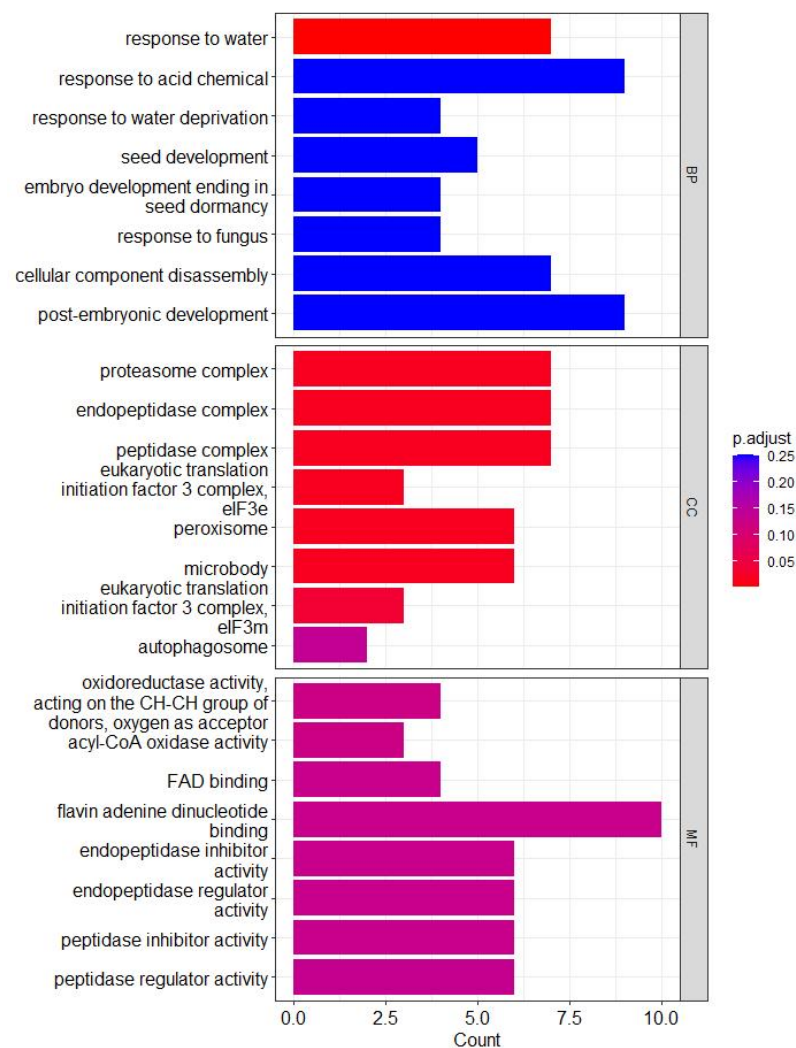


Fig. S5-GO enrichment analysis of DEGs at 20 DAP between the thick-aleurone group and thin-aleurone group. (A) and (B) are for the up-regulated DEGs and down-regulated DEGs respectively. BP=biological process, CC=cellular component, MF=molecular function.

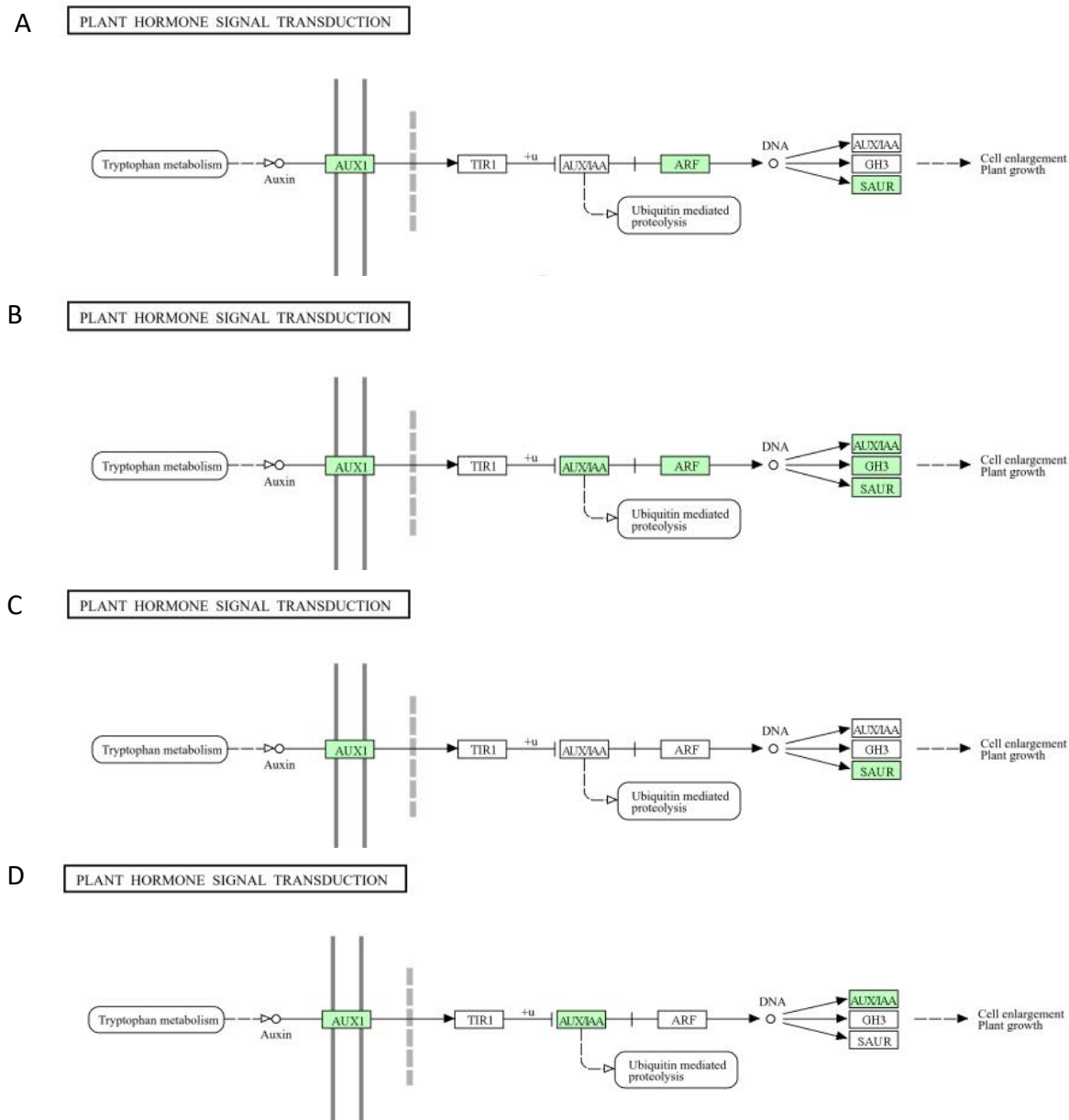
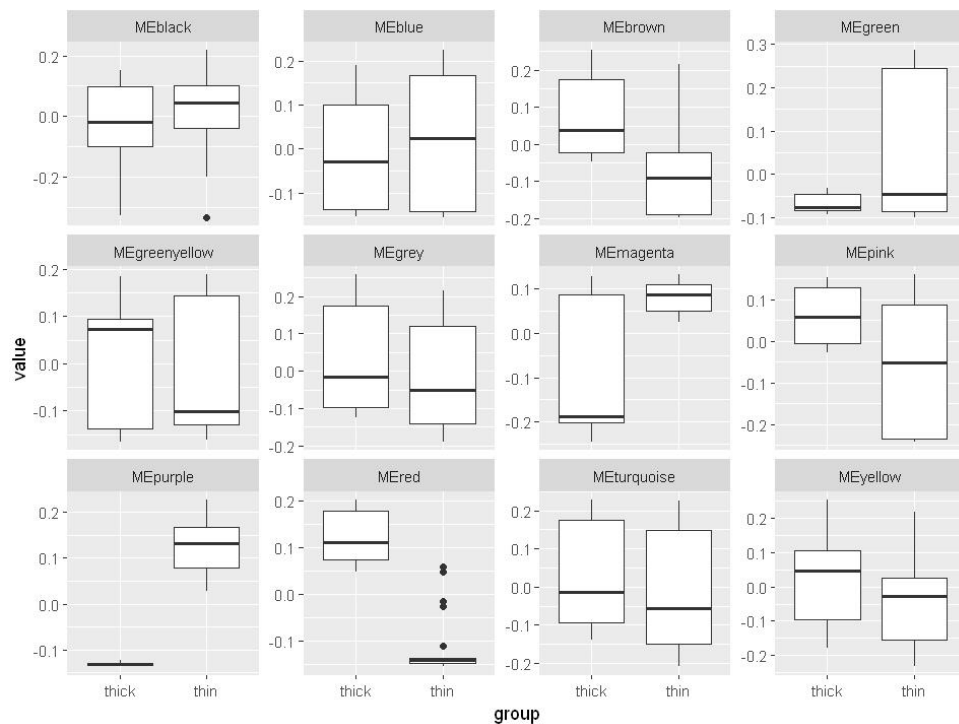


Fig. S6-KEGG analysis of plants hormone signal transduction pathway for up-regulated DEGs at A)5DAP, B)10DAP, C) 15DAP and D) 20DAP.

A



B

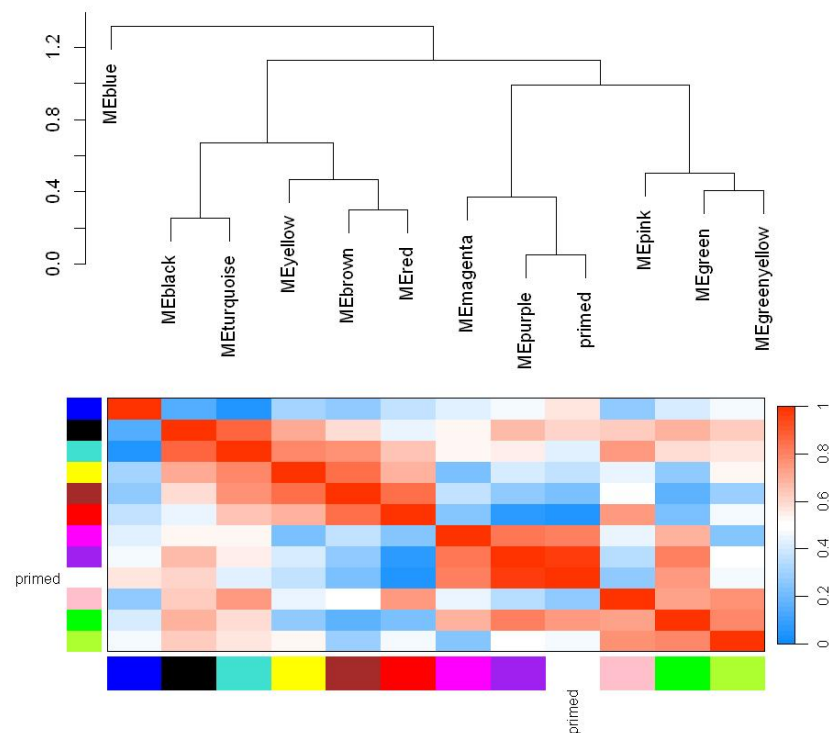


Fig. S7-The module-traits relationship and cluster dendrograms of modules detecting for WGCNA. (A) Boxplots showing the relationship between different gene modules and the aleurone thickness traits. The values of Y axis stand for the scaled TPM value for genes in each module. (B) Dendrogram and heatmap of gene modules. The upper tree diagram shows that the purple module is highly correlated with aleurone thickness trait (primed).

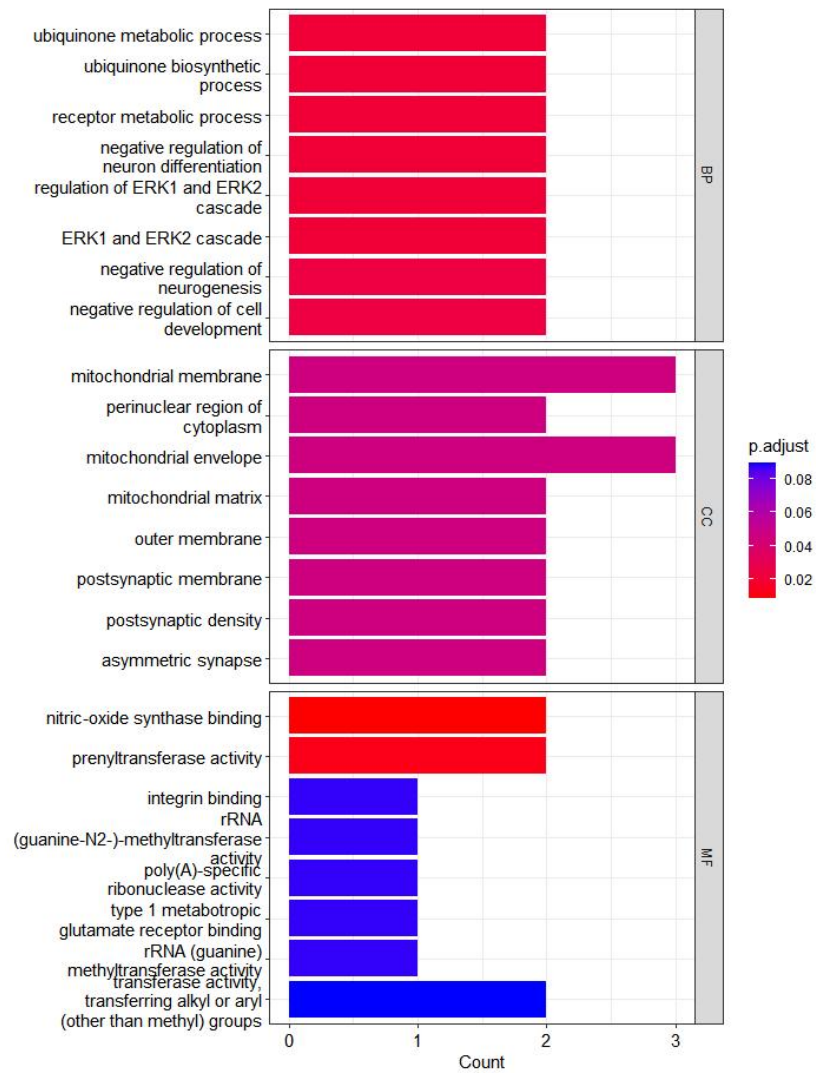
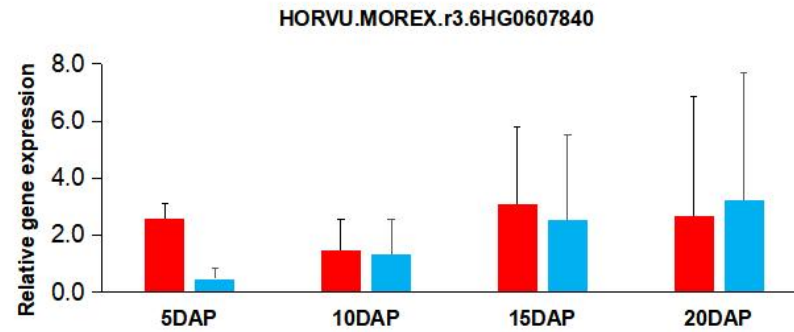
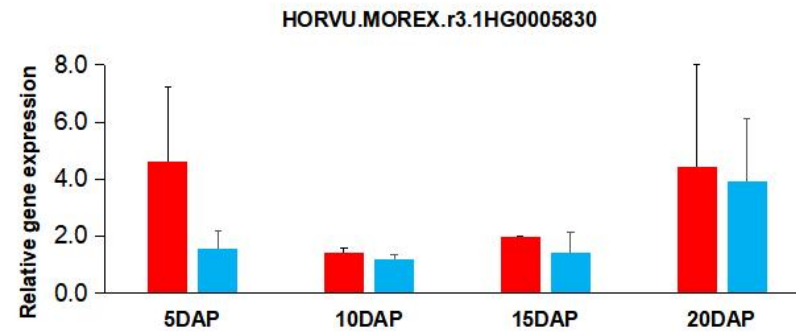


Fig. S8-GO enrichment analysis of key genes in purple module.

A



B



C

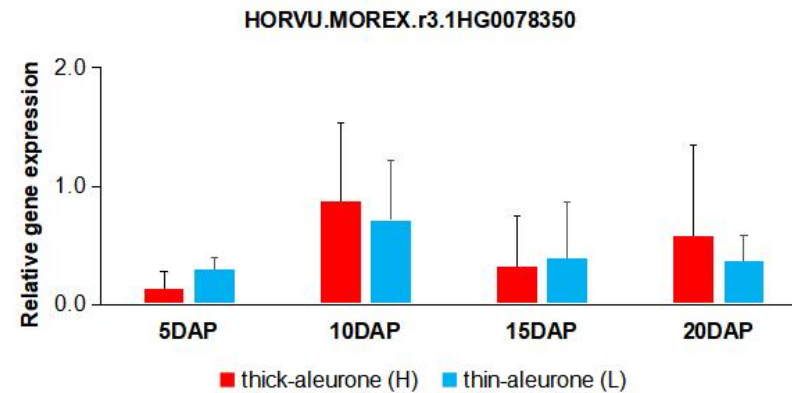


Fig. S9-Validation of gene expression by qRT-PCR. A), B) and C) represent for the barley homolog gene of *RPBF*(*OsDof3*), *ZmDof3* and *RISBZ1*(*OsSMF1*), respectively.