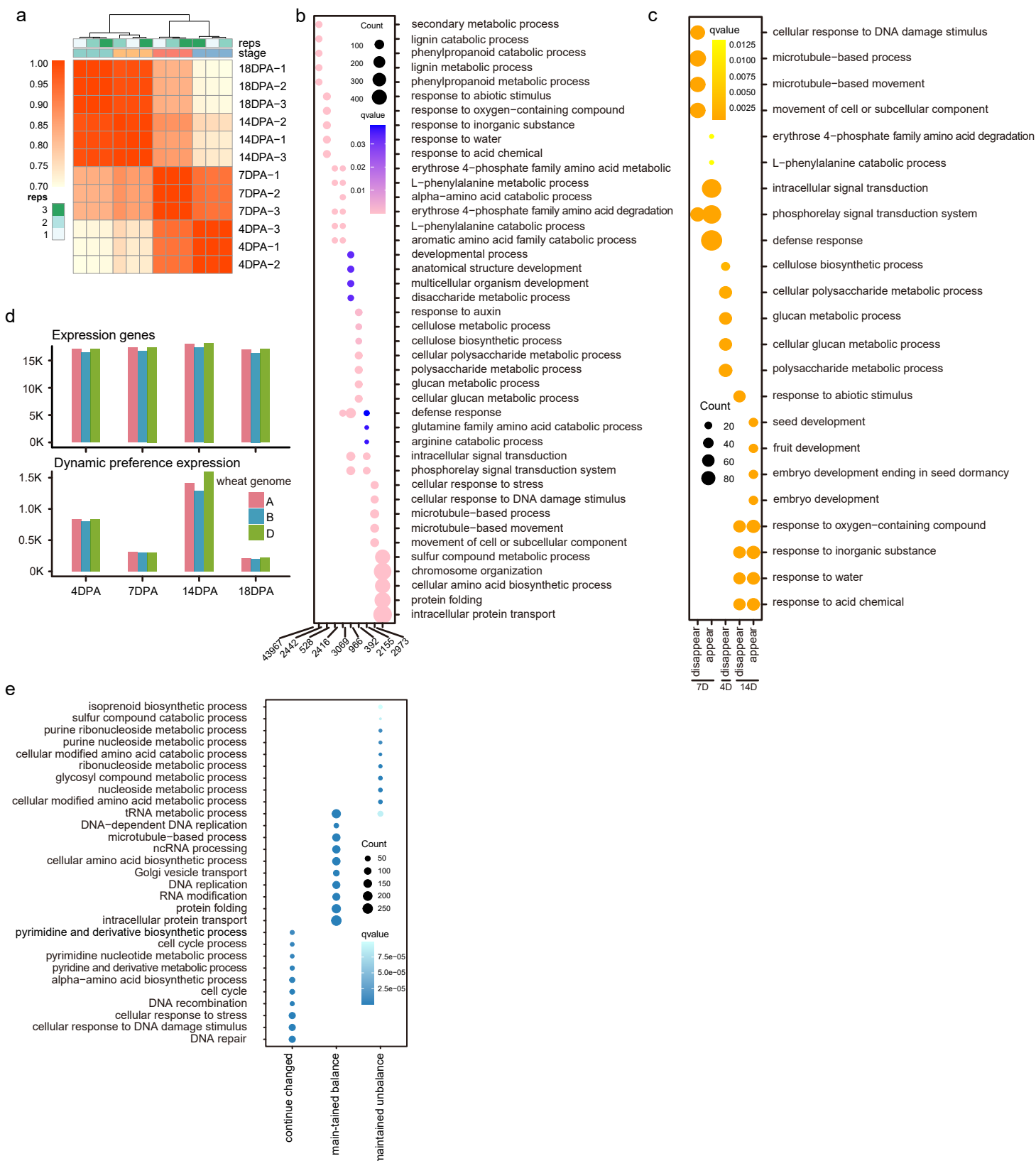
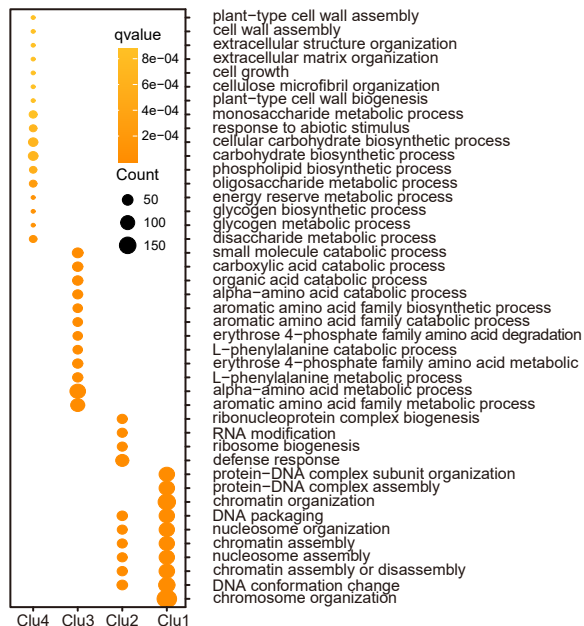


Supplementary Figures

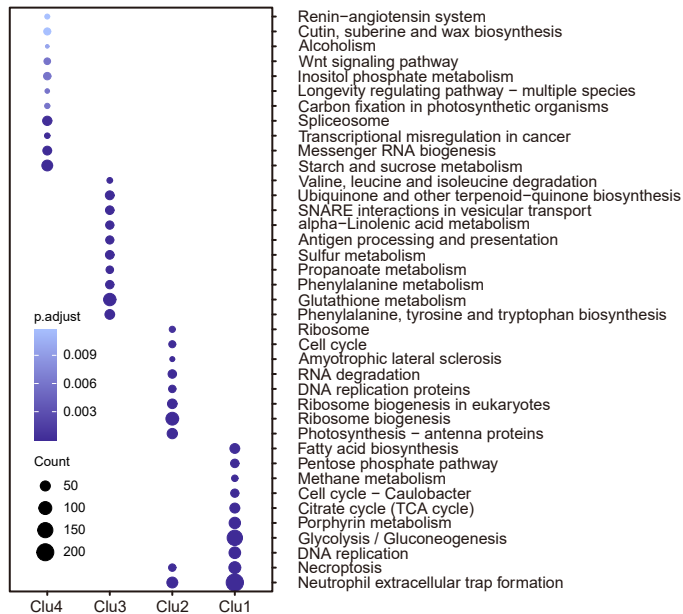


Supplementary Figure 1 Quality control of the RNA-seq data and GO analysis of expressed genes. a) Correlation analysis showing the reproducibility of the data. b) GO enriched terms of the expressed genes in each endosperm development stage. The values at the bottom refer the number of genes in Figure 1c. c) GO enrichment of the appear and disappear expressed genes in each endosperm development stage. d) Number of expressed genes in A, B and D sub-genomes in different endosperm development stages. e) GO enrichment for homoeologous triads that maintain unbalanced or balanced expression patterns at different stages of endosperm development in Figure 1e.

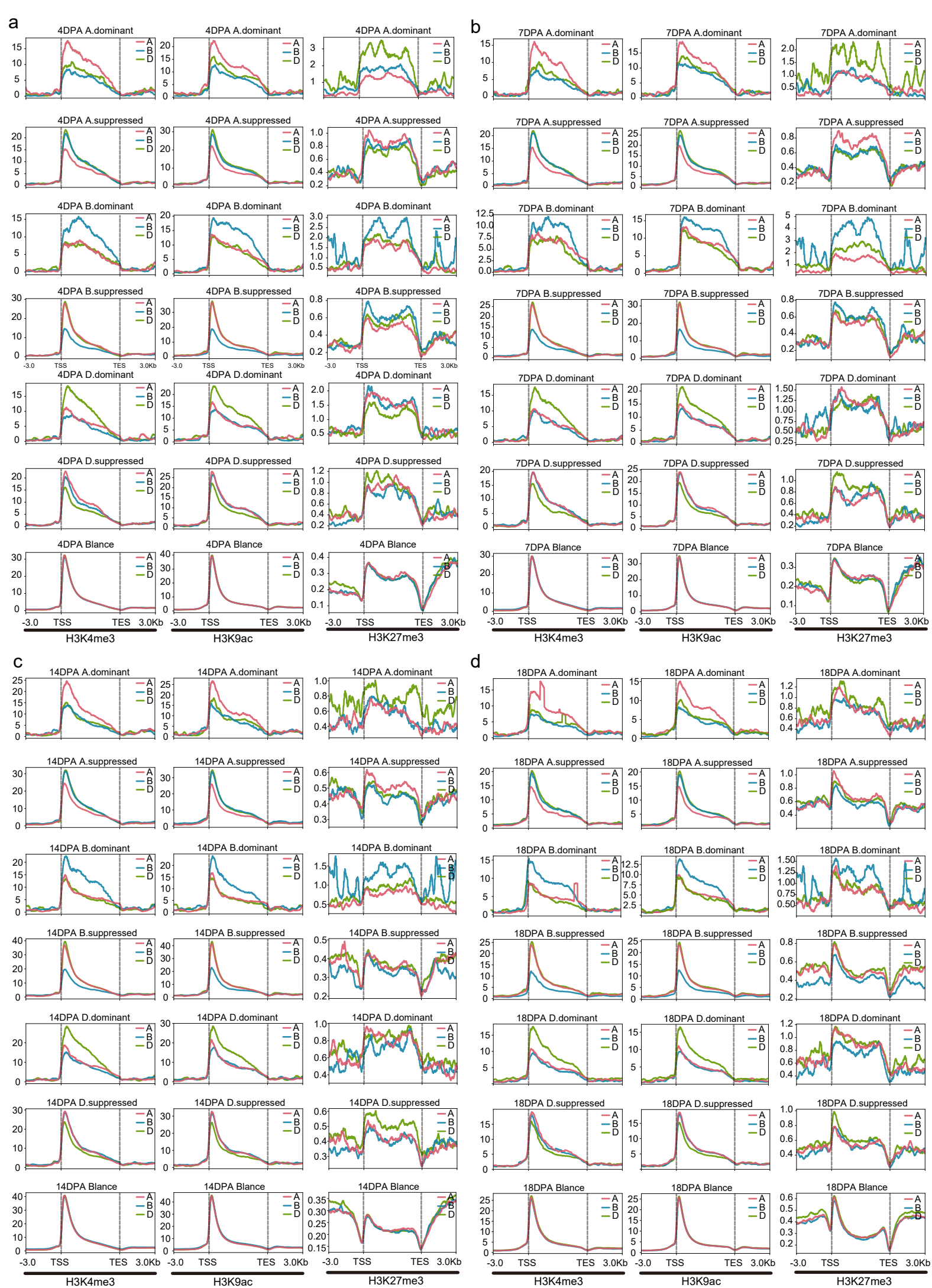
a



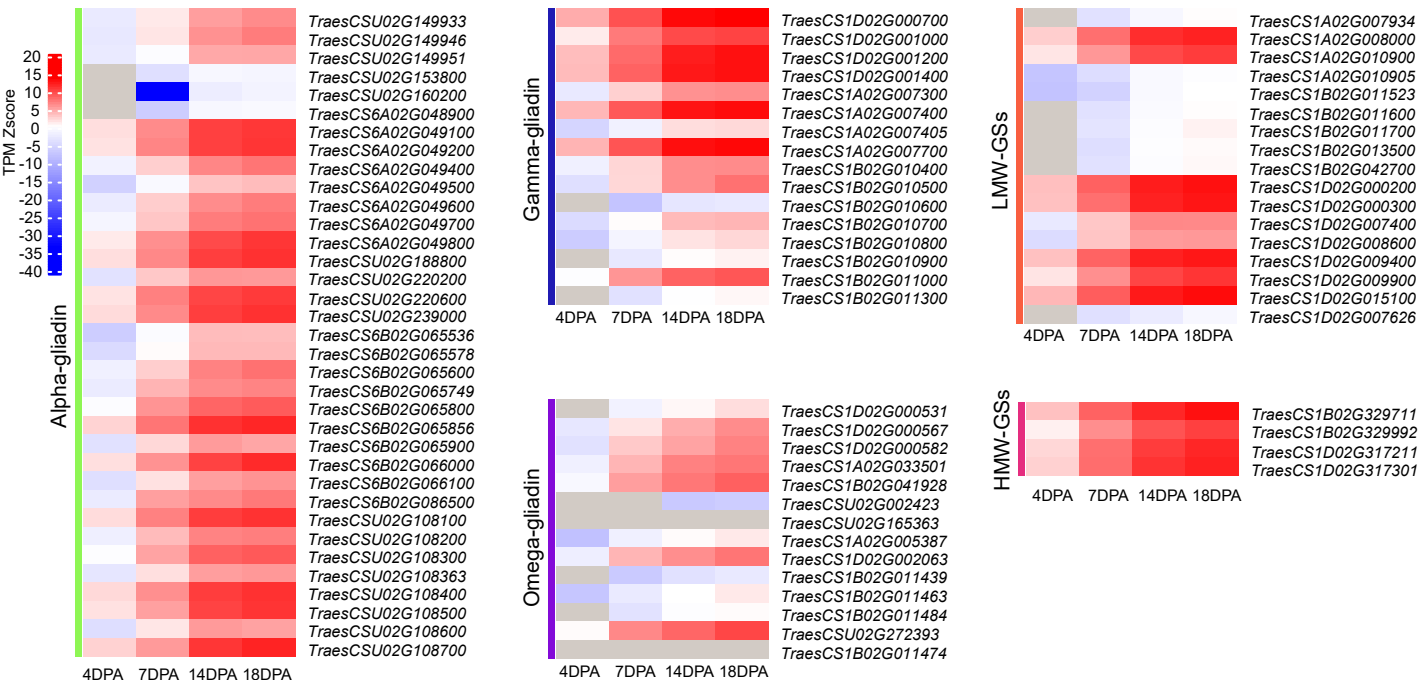
b



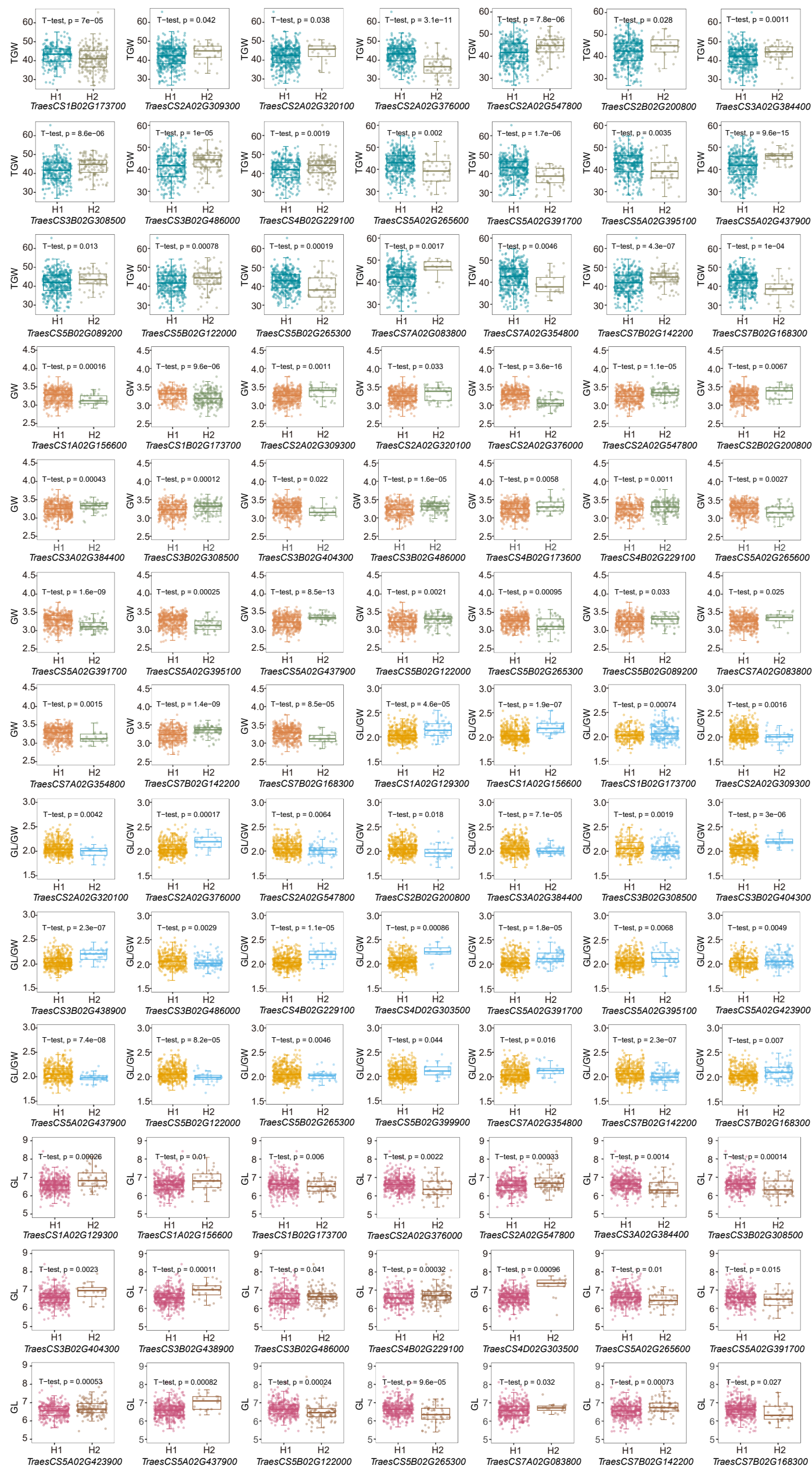
Supplementary Figure 2 Function annotations of stage specifically expressed genes. a) GO and b) KEGG enrichment of stage specifically expressed genes (related to Figure 1j).



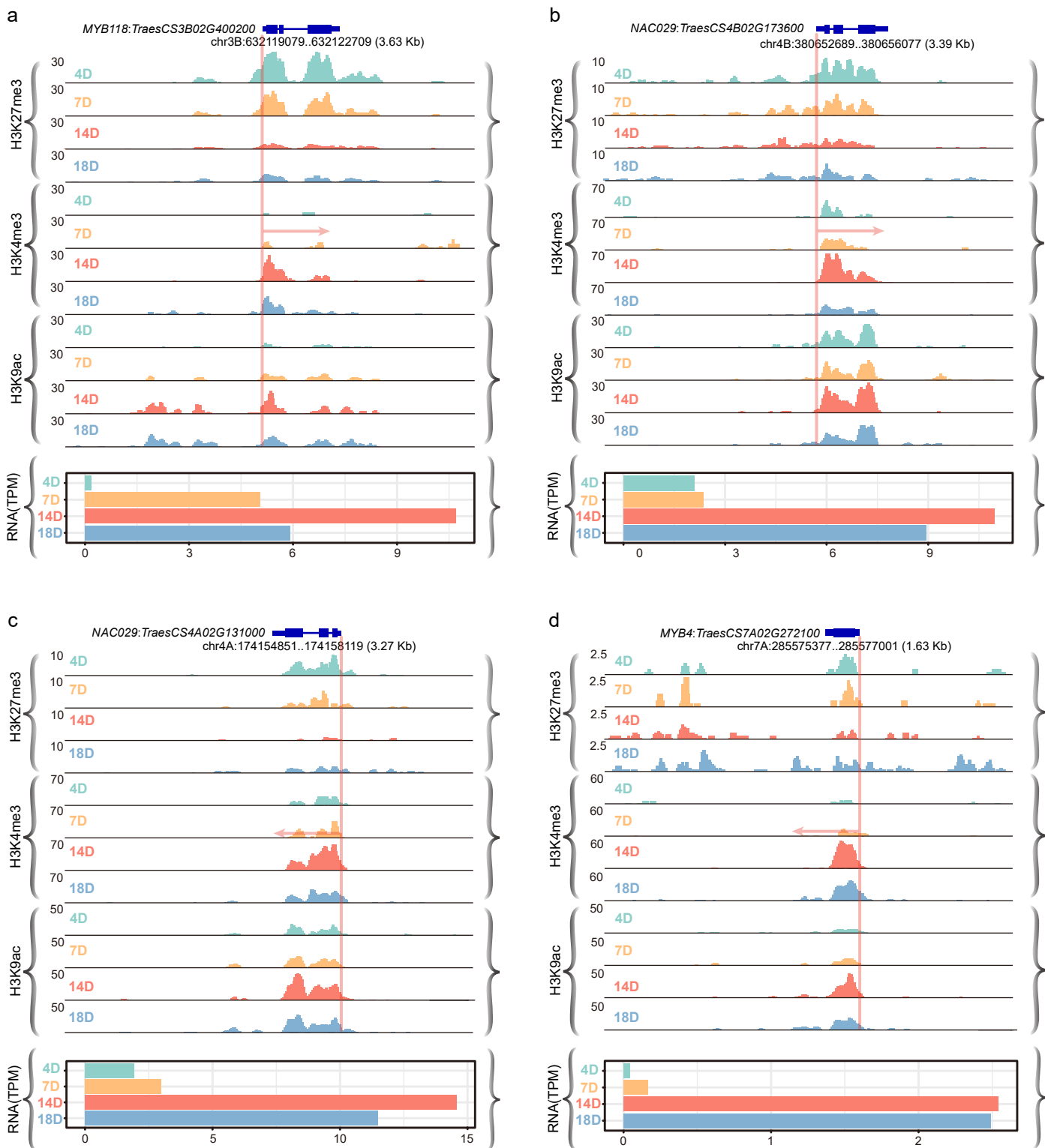
Supplementary Figure 4 The histone modifications on different types of asymmetrically expressed genes at a) 4DPA, b) 7DPA, c) 14DPA and d) 18DPA.



Supplementary Figure 5 The expression patterns of all the expressed seed storage protein encoded genes in endosperm.



Supplementary Figure 6 The effects of different haplotypes of candidate hub genes identified from the regulatory network. The GW, GL, TGW and GL/GW indicate the grain width, grain length, grain thousand weigh and ratio of grain length to grain width, respectively.



Supplementary Figure 7 IGV view of histone modifications and mRNA abundance on a) *MYB118*, b) *NAC029-4A*, c) *NAC029-4B* and d) *MYB4*.