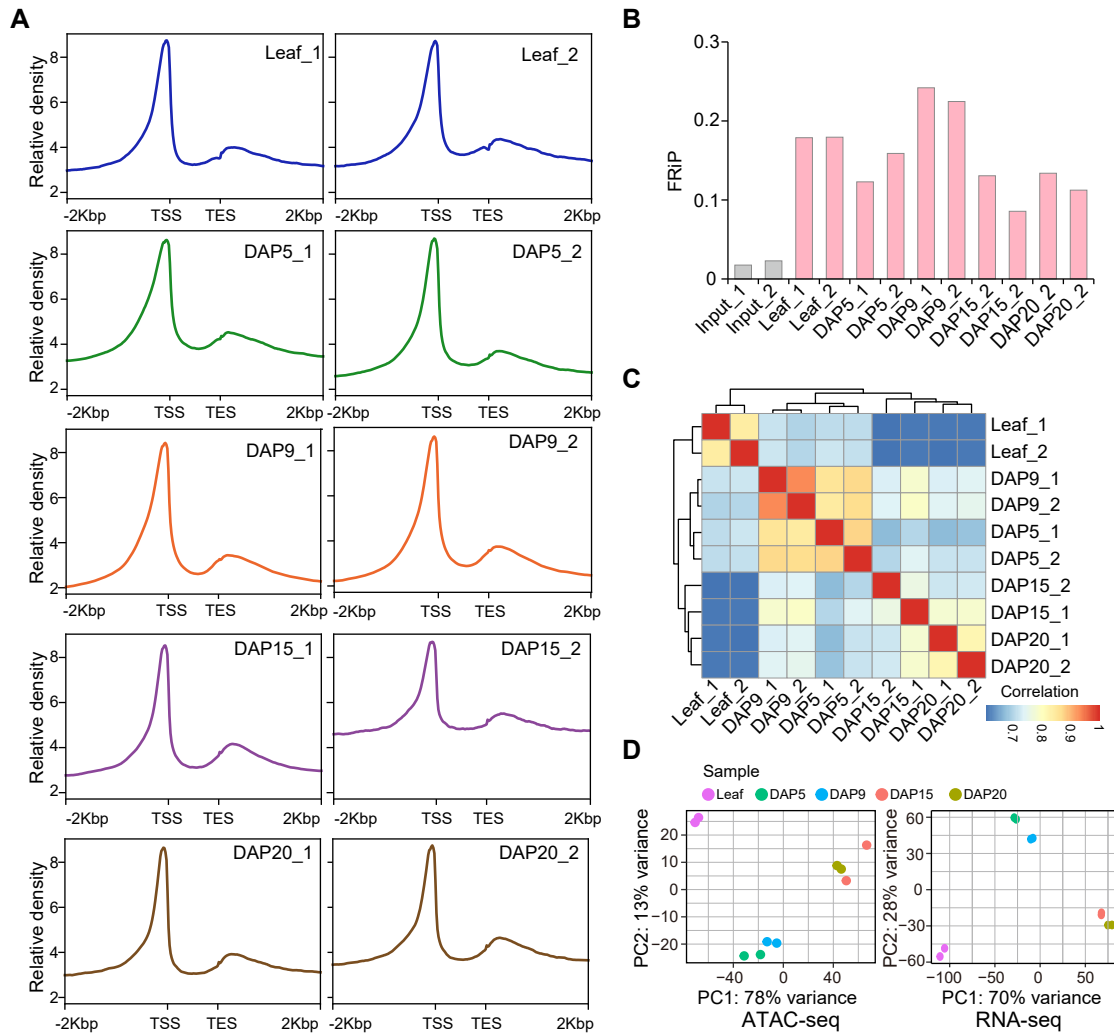
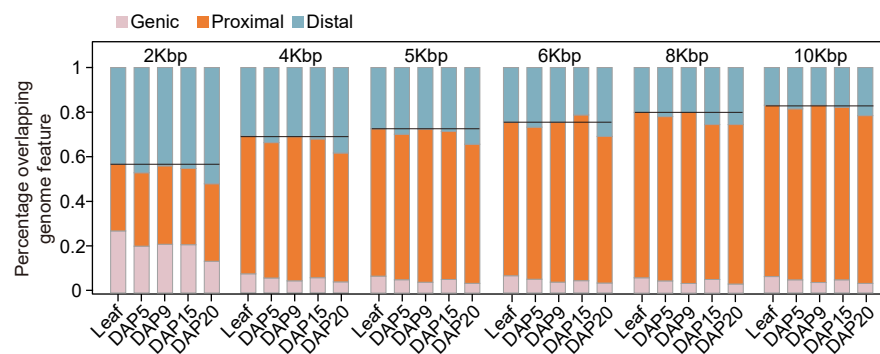


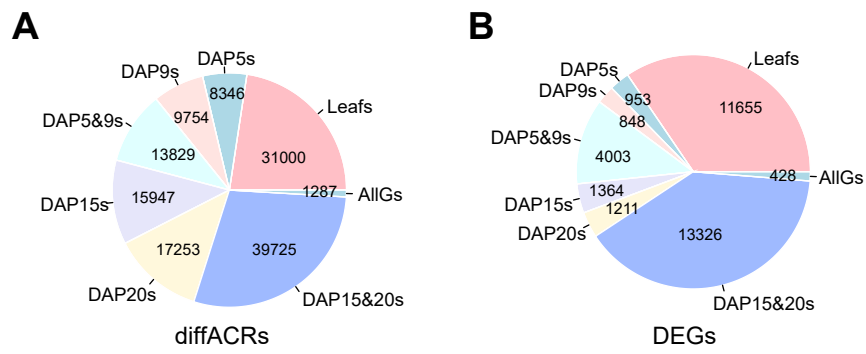


Supplemental Fig. 1 Quality control of ATAC-seq and RNA-seq samples.

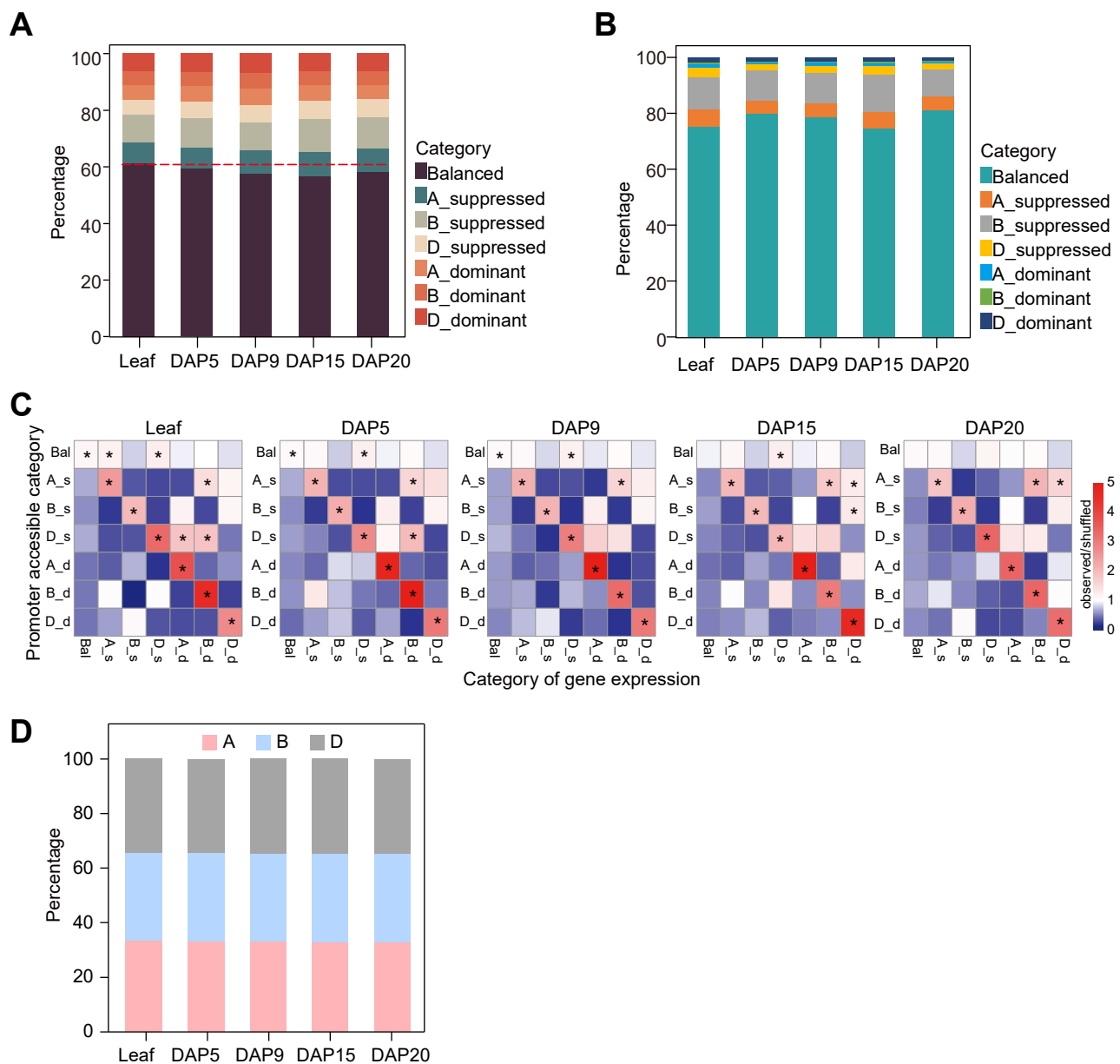
A Distribution of ATAC-seq reads around Transcriptional Start sites (TSSs) and Transcriptional End Sites (TESs) in the five wheat samples. **B** Fraction of Reads in Peaks (FRiP) for all ATAC-seq data used in this study. **C** Heatmap showing the correlation among all ATAC-seq samples. **D** PCA analysis of ATAC-seq and RNA-seq data.



Supplemental Fig. 2 Distribution of ACRs on different genomic features with different cutoffs. Genic, ACRs with their centers in gene bodies; The proportion of ACRs located in proximal and distal were categorized with different cutoffs. Proximal, ACRs with their centers $\leq n$ Kbp upstream of TSS or $\leq n$ Kbp downstream of TES; Distal, ACR with their centers $> n$ Kbp away from genes.

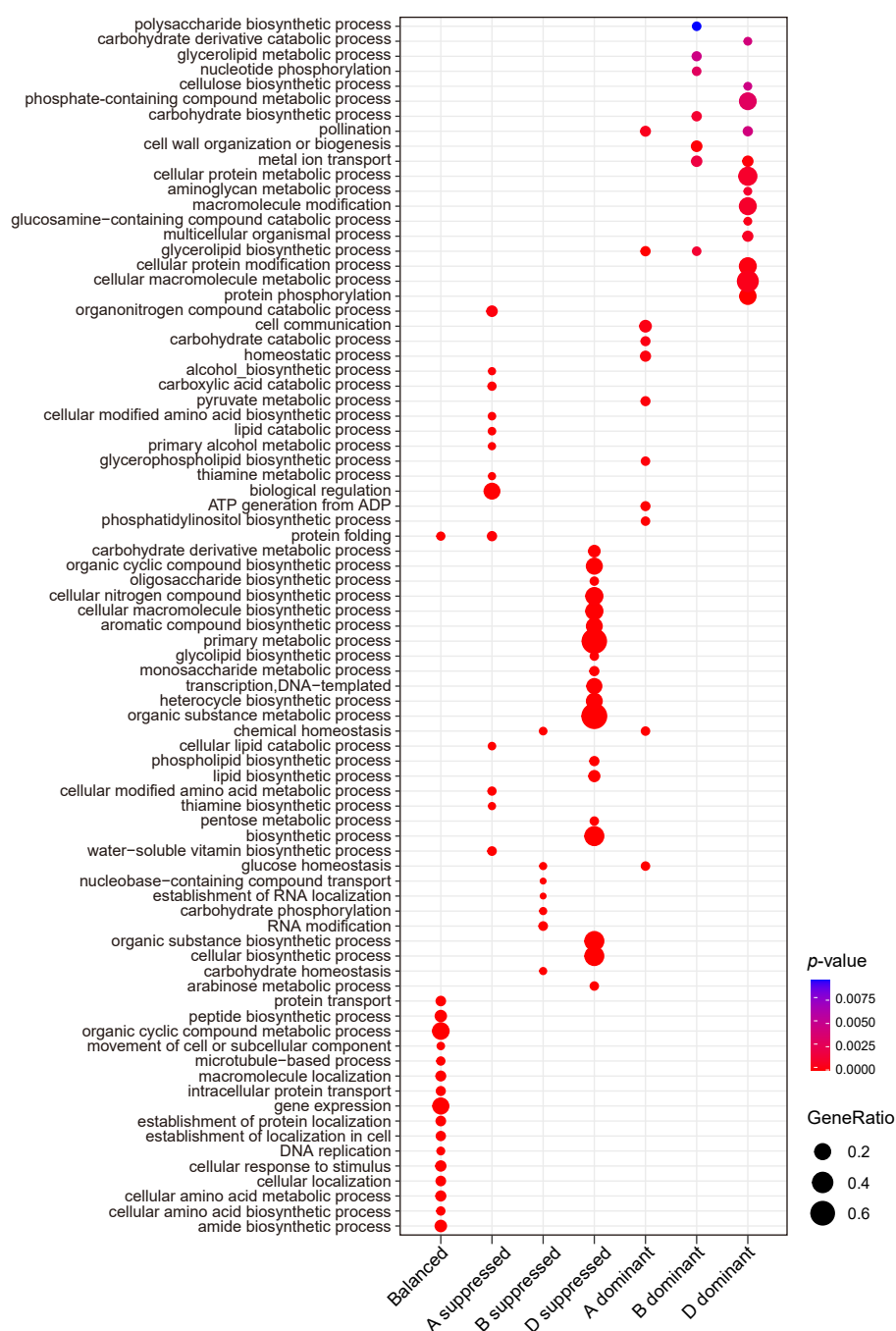


Supplemental Fig. 3 The number of diffACRs (A) and DEGs (B) in each cluster.

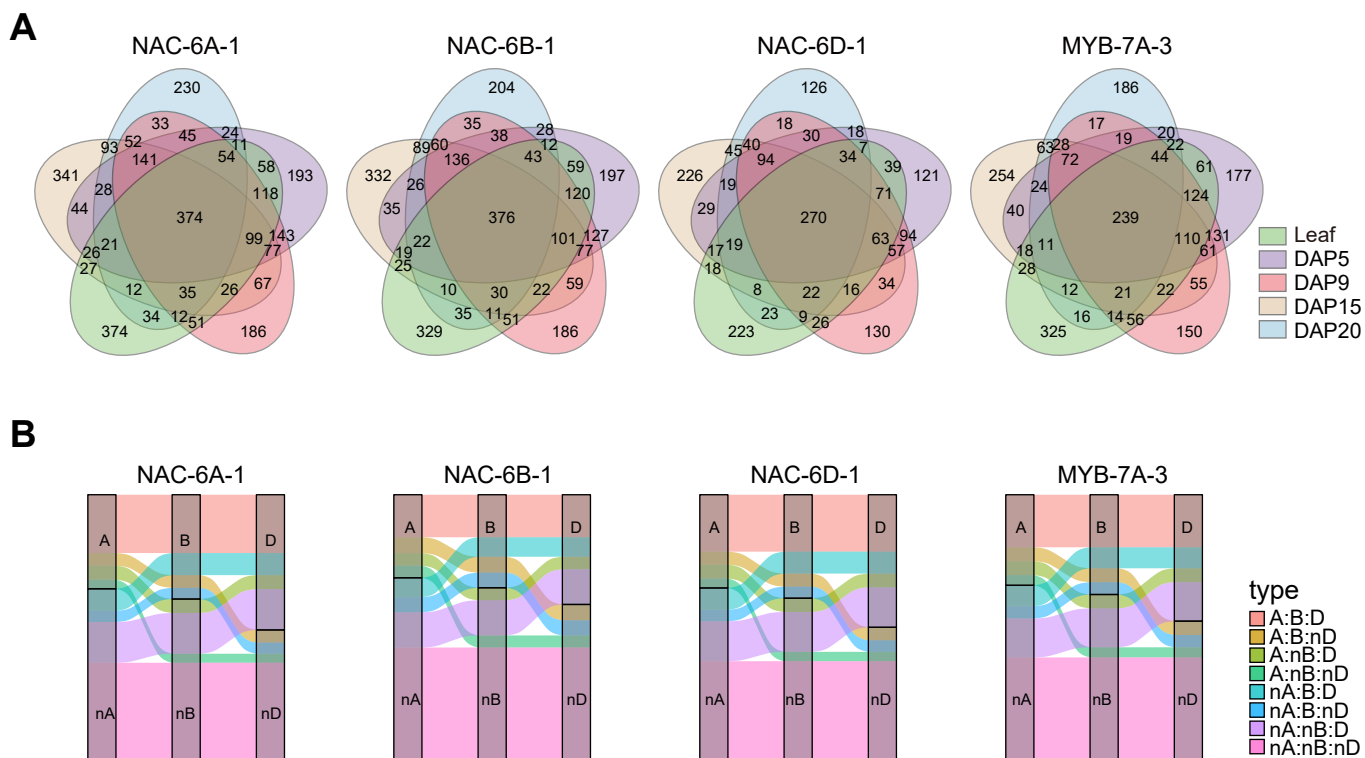


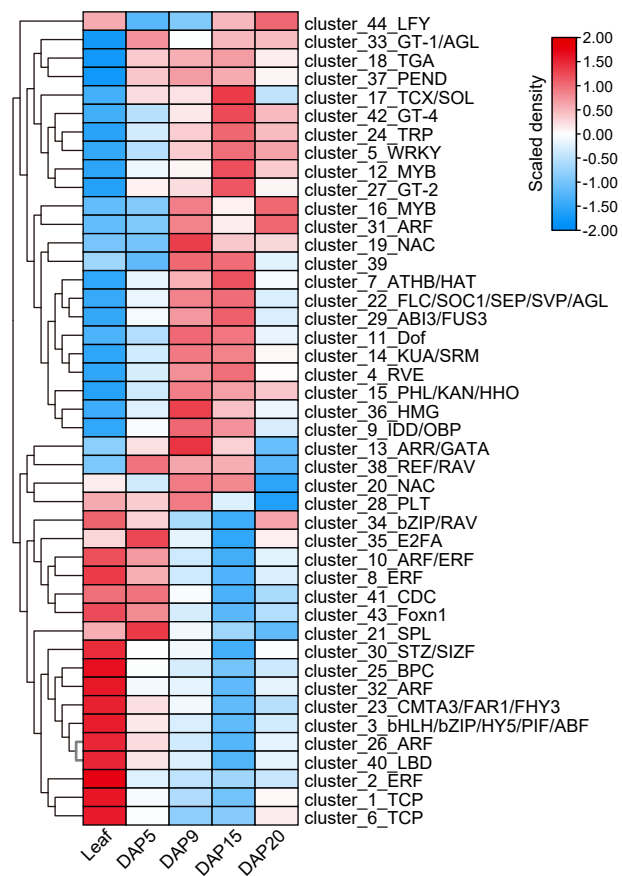
Supplemental Fig. 4 Subgenome-divergence of genes' expression levels and promoter accessibilities.

A The percentage of balanced and unbalanced expressed triad genes according to Fig 2B. **B** The percentage of different promoter accessibility type of triad genes. **C** Correlation analysis of unbalanced expressed genes and differential promoter accessible regions. Bal: Balanced, A_s: A suppressed, B_s: B suppressed, D_s: D suppressed, A_d: A dominant, B_d: B dominant, D_d: D dominant. **D** The distribution of diff ACRs on the three subgenomes.

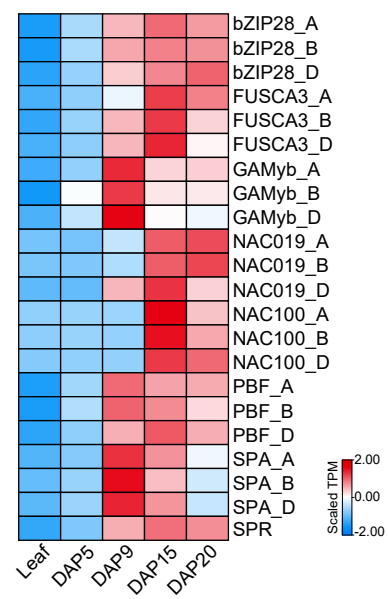


Supplemental Fig. 5 Gene ontology (GO) enrichment analysis for the balanced and unbalanced expressed genes during seed development.





Supplemental Fig. 7 Motif density of ACRs in the promoters of genes related with gluten accumulation and starch biosynthesis.



Supplemental Fig. 8 Heatmap displays the expression pattern of key TFs.