

Figure S1

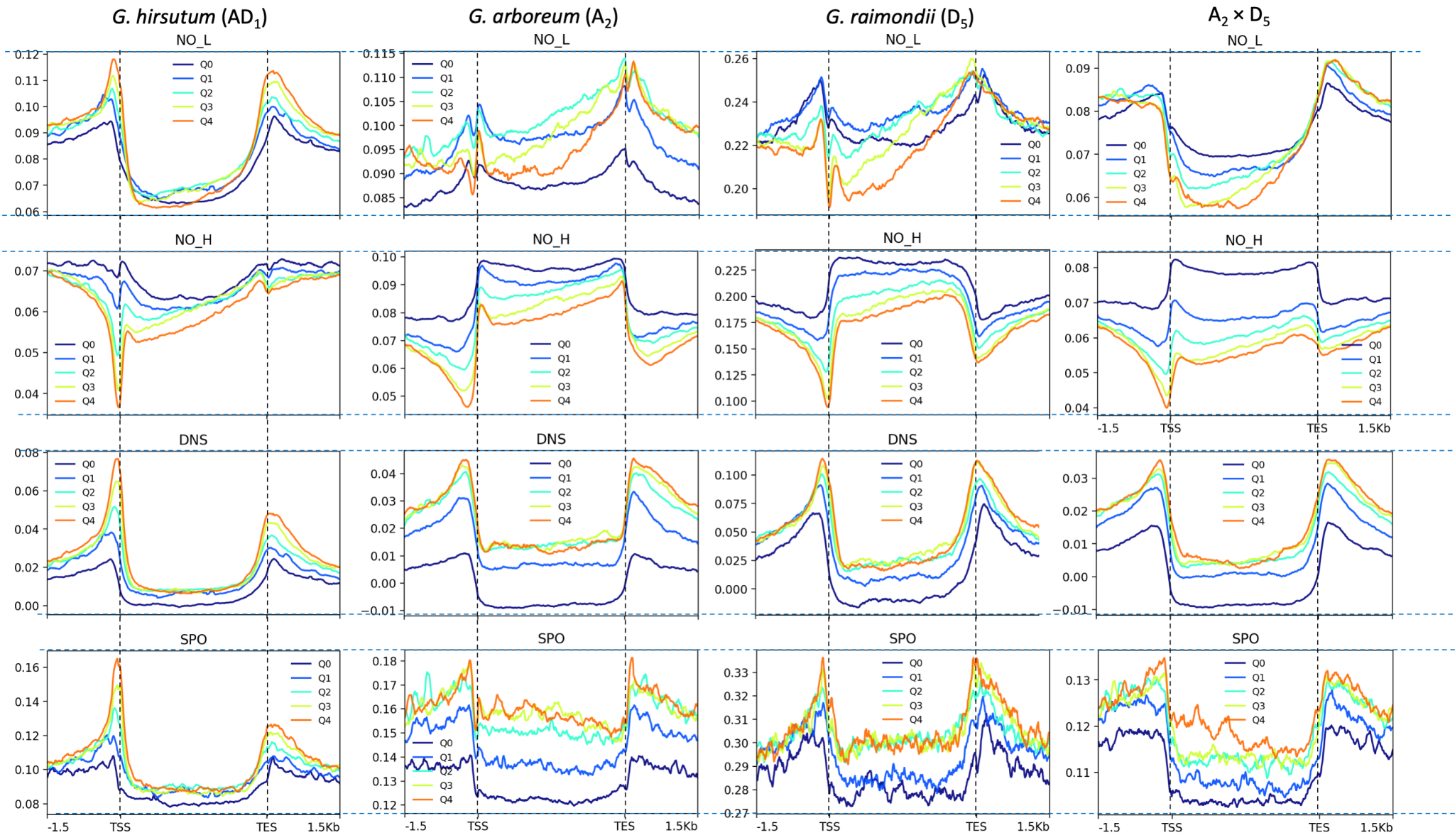


Figure S1. Aggregate plots of chromatin features profiled by differential sensitivity MNase-seq. For each species, genome-wide nucleosome occupancy by heavy (NO_H) and light (NO_L) MNase digestion, differential nuclease sensitivity (DNS), and subnucleosomal particle occupancy (SPO) were plotted over scaled gene regions. The scaled gene region encompasses 1.5 kb upstream of the transcription start site (TSS), the metagene scaled to 3 kb, and 1.5 kb downstream of the transcription end site (TES). Gene groups Q1 to Q4 represent the increasing expression quantiles, and Q0 represents the group of non-expressed genes.

Figure S2

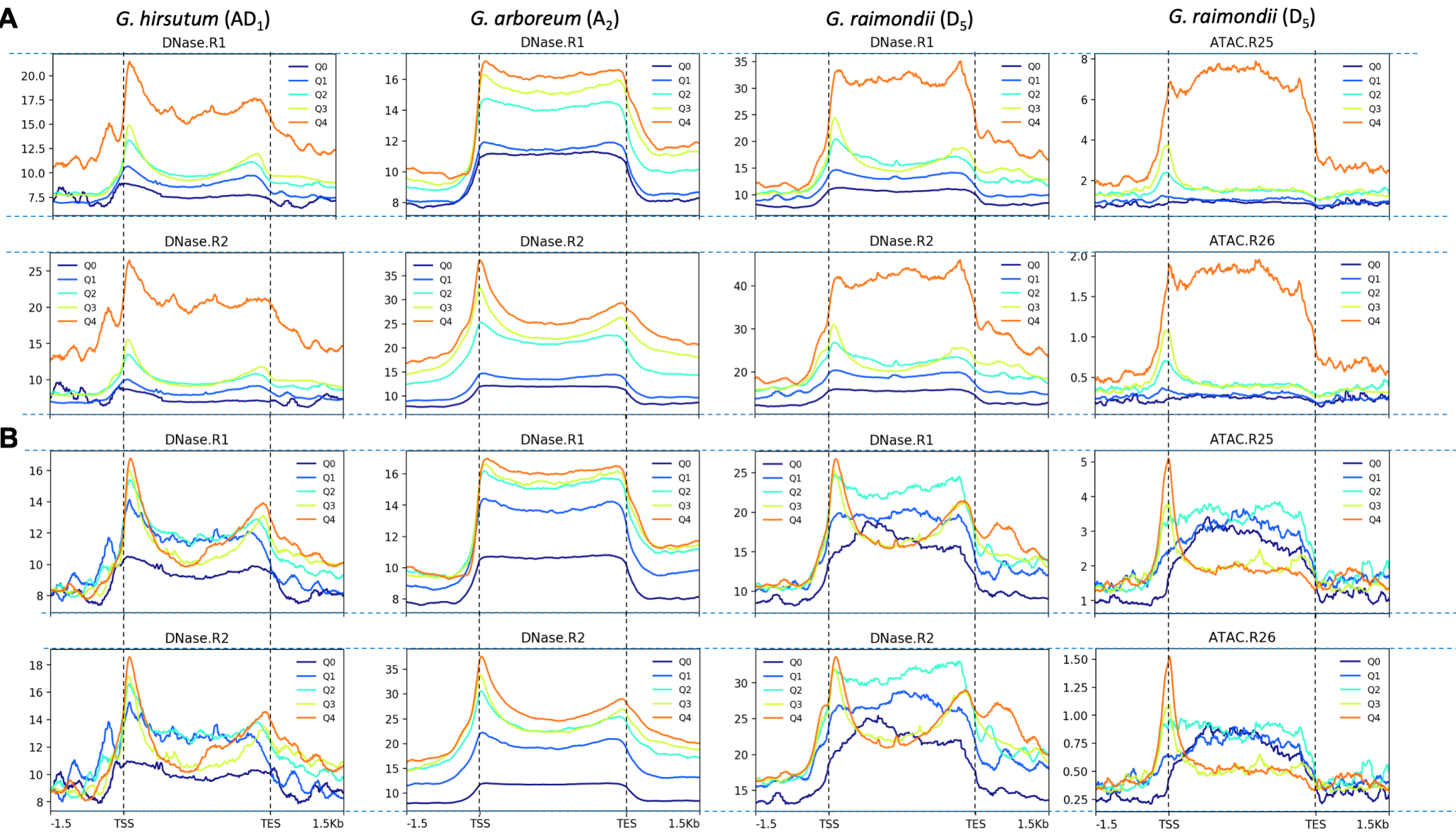


Figure S2. Aggregate plots of chromatin features profiled by ATAC-seq and DNase-seq. A. Gene groups Q0-Q4 were categorized using young leaf expression data. B. Gene groups Q0-Q4 were categorized using mature leaf expression data.

Figure S3

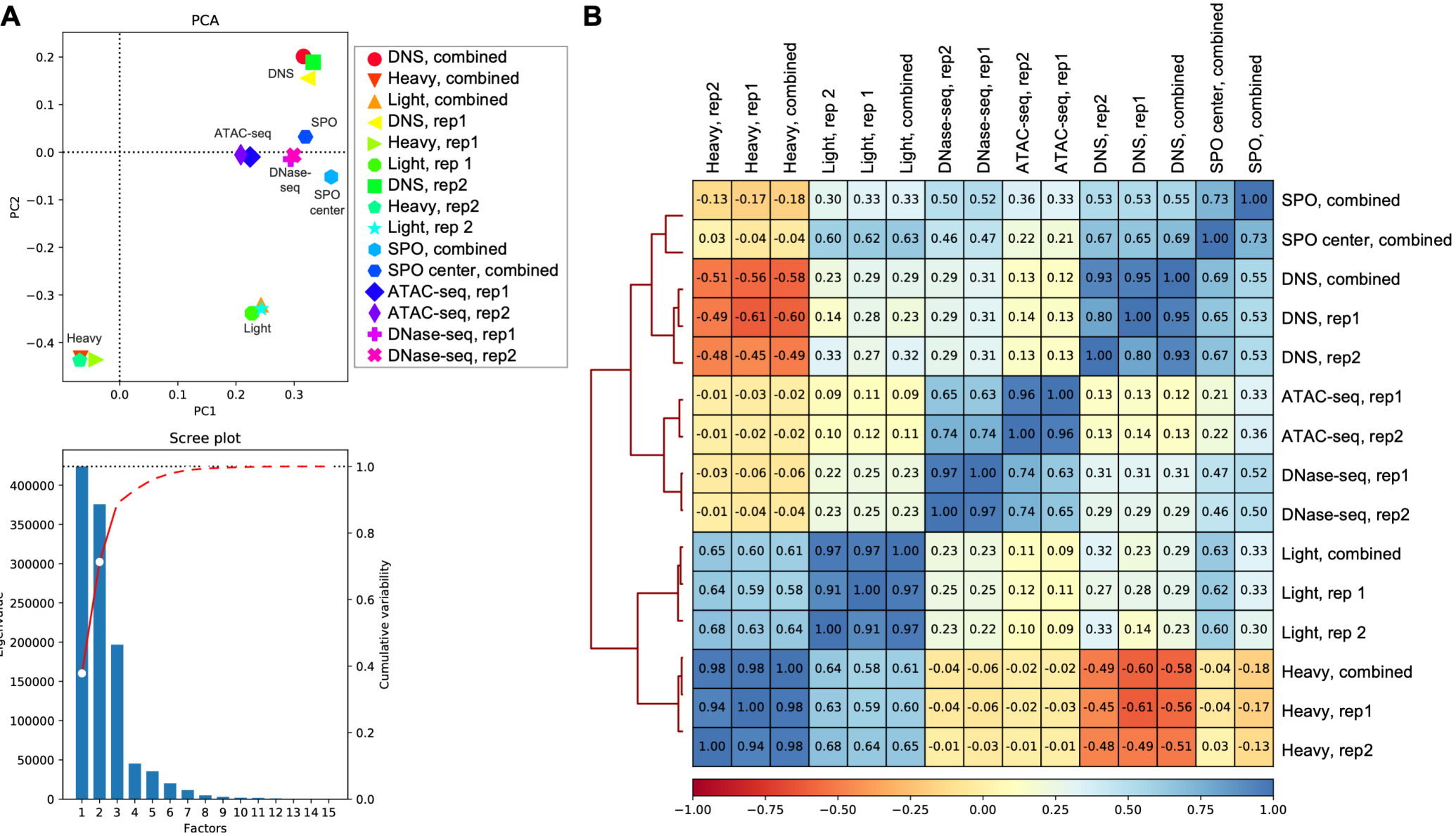


Figure S3. Comparing various chromatin profiles in *G. raimondii*. A. PCA analysis and eigenvalues. B. Heatmap and clustering based on Pearson's correlation coefficients. ATAC-seq and DNase-seq were most correlated with each other (Pearson's $r = 0.63-0.74$), followed by DNS versus SPO ($r = 0.53-0.69$). Despite the tissue difference, SPO signals were also well correlated with the DNase-seq results ($r = 0.46-0.52$). The lowest correlation was observed between DNS and ATAC-seq ($r = 0.12-0.14$).

Figure S4

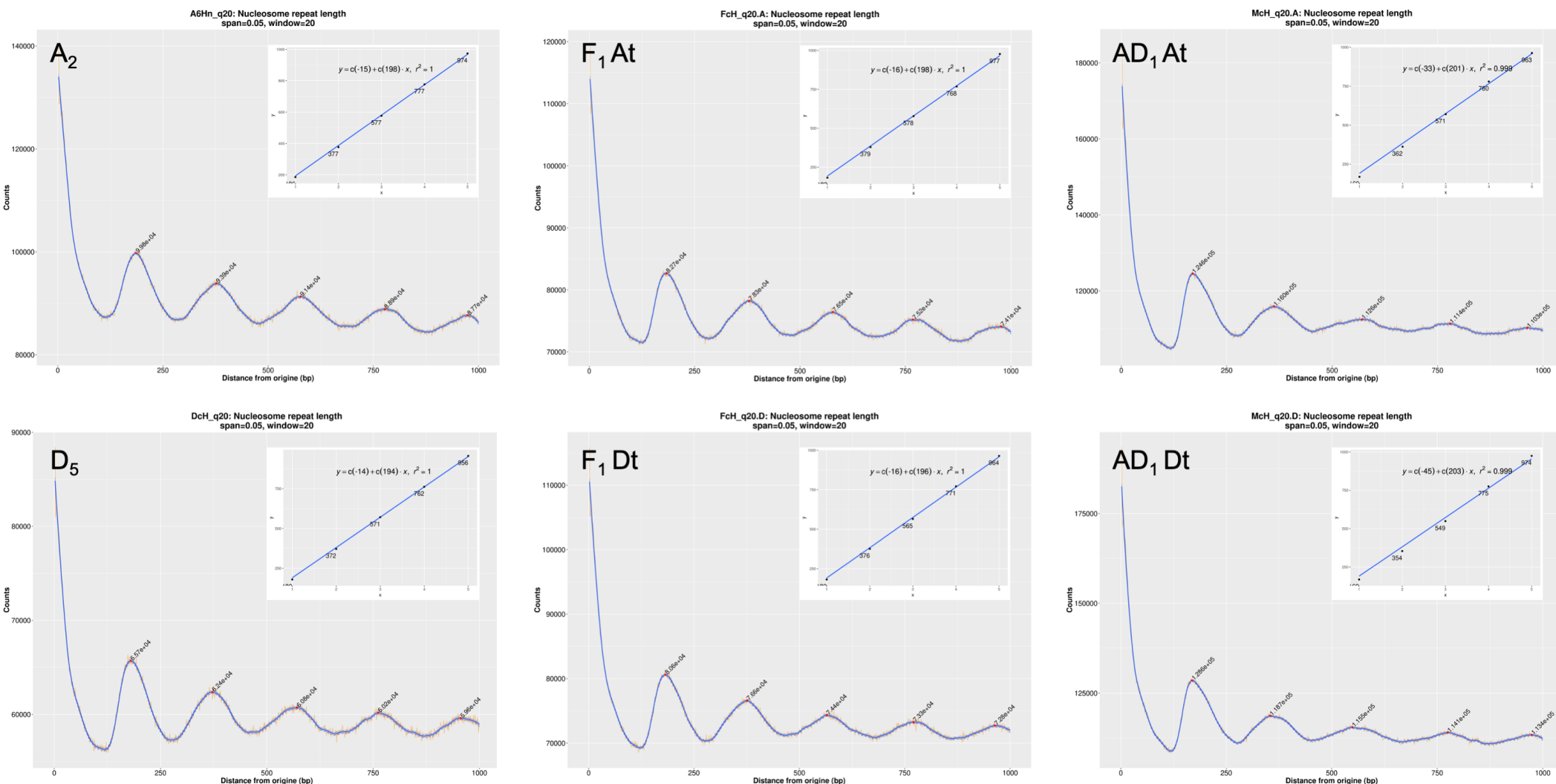


Figure S4. Phasograms of nucleosomes in diploid, hybrid, and allopolyploid cotton. Phasograms are histograms of distances between the midpoints of neighboring nucleosome cores (i.e., center of paired-end reads), which reveal consistent spacing of positioned nucleosomes by exhibiting a wave-like pattern with a period that represents genome-average internucleosomal spacing. The x-axis shows the range of recorded phases in base pair (bp). The y-axis shows frequencies of corresponding phases by read counts. Inset presents a linear fit to the positions of the phase peaks, where the slope represents the estimated nucleosome repeat length (NRL). For example, in the upper left panel, the NRL was estimated 198 bp in A2.

Figure S6

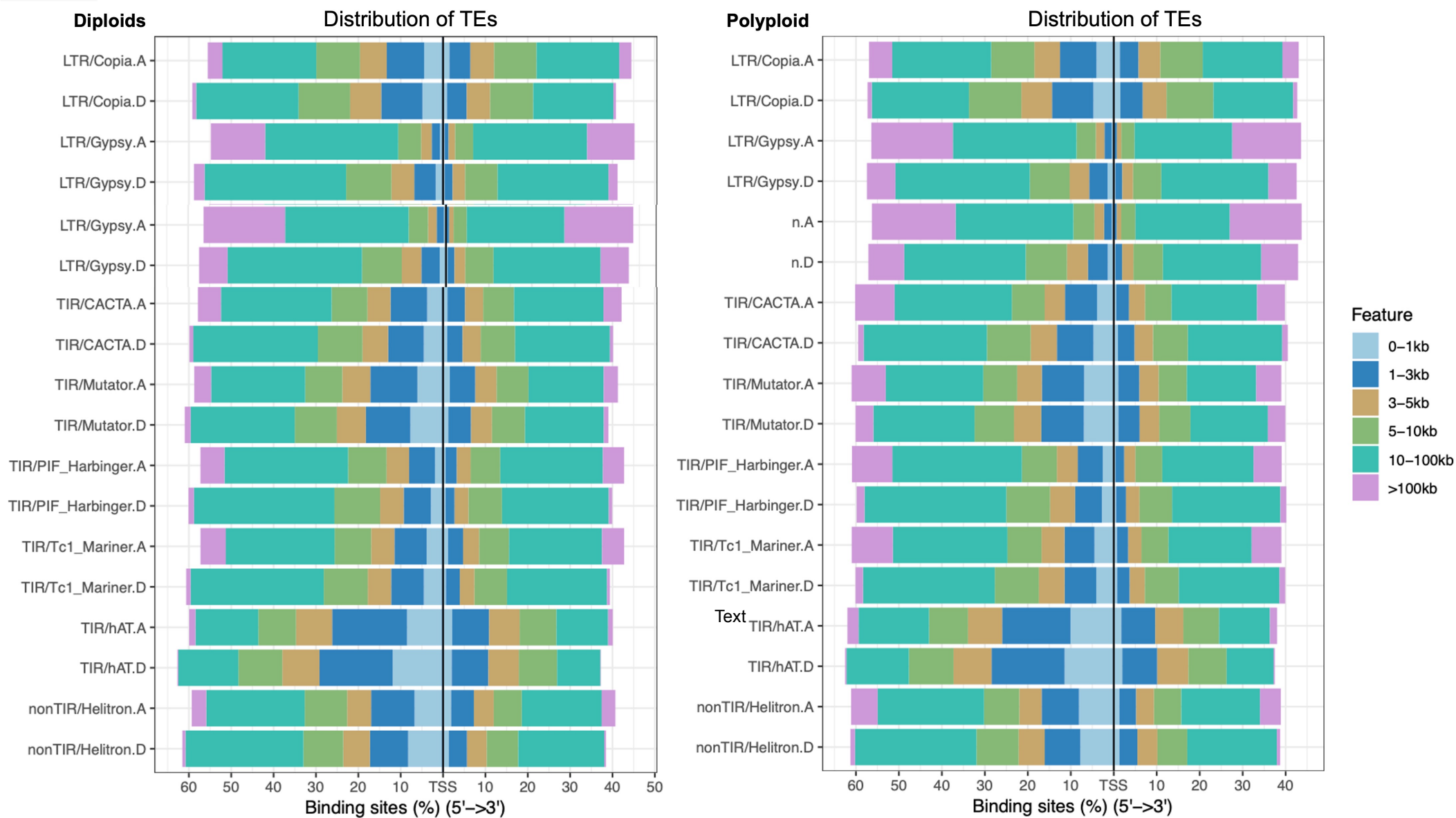


Figure S6. Distribution of TEs relative to transcription start sites in A- and D- cotton genomes.

Figure S7



Figure S7. Sizes of TE superfamilies in different genomic regions.

Figure S8

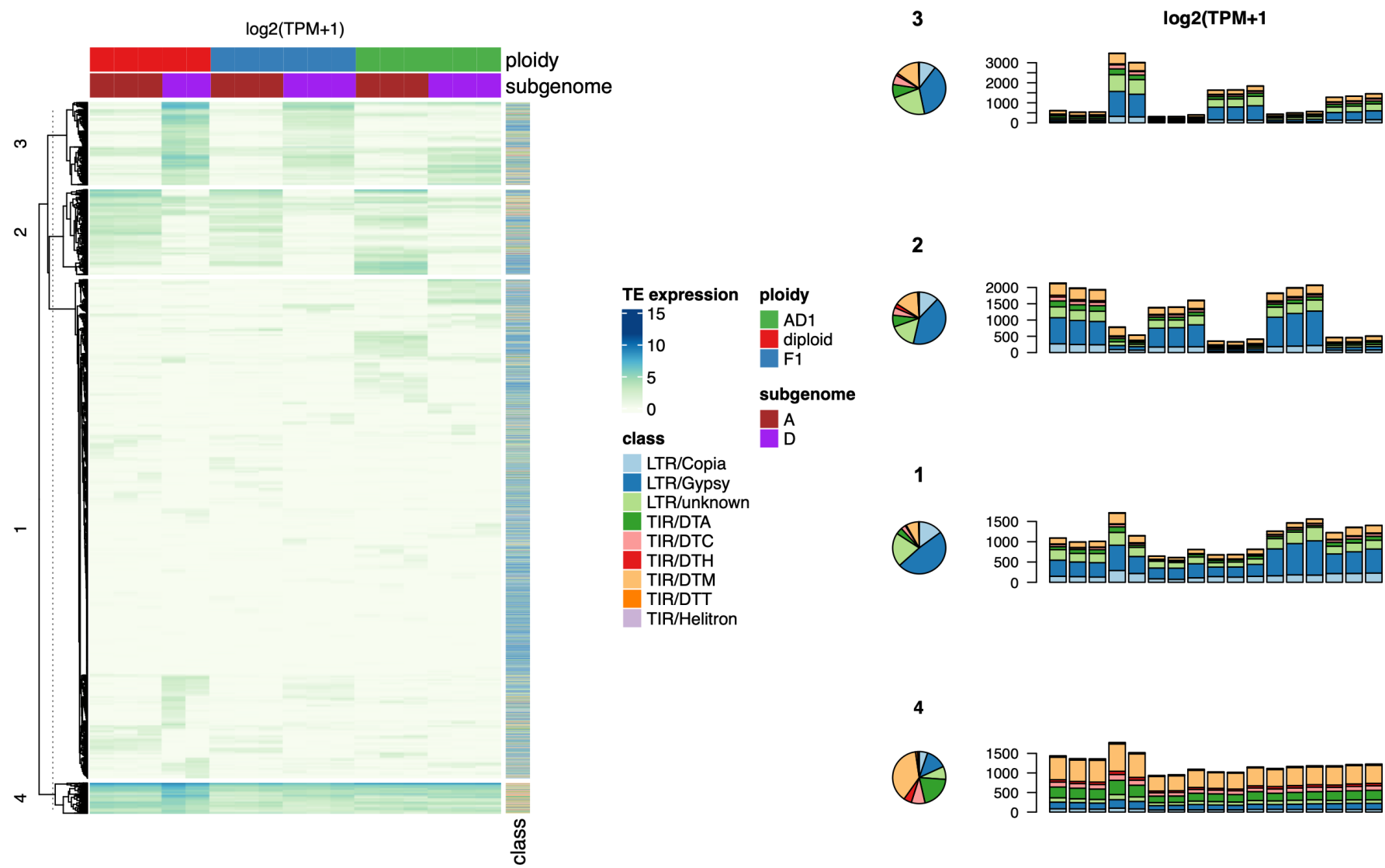


Figure S8. Heatmap and clustering of expressed TE families.

Figure S9

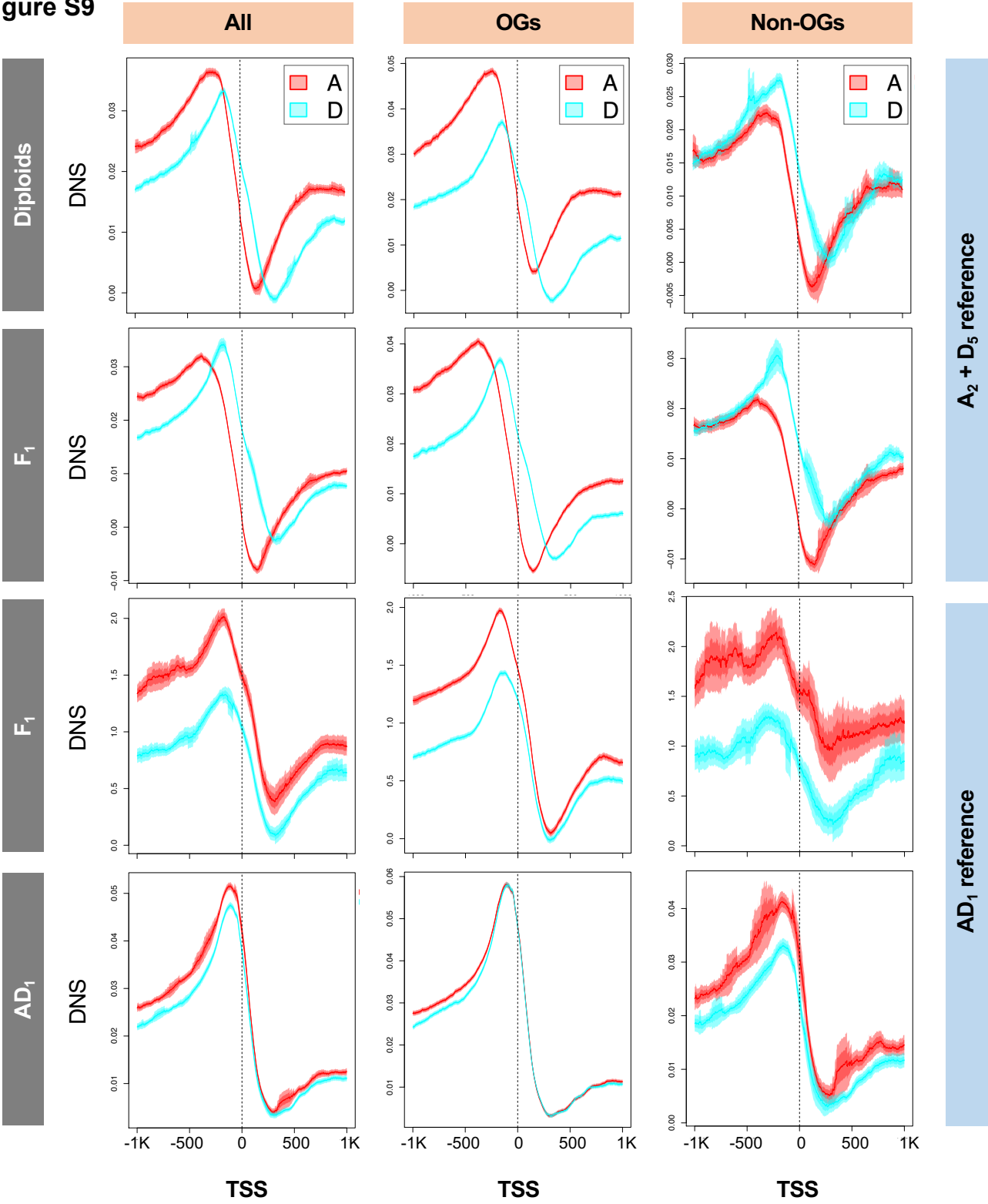


Figure S9. Promoter accessibility of all, OG, and nonOG genes in diploid and allopolyploid cottons. Aggregation plots of DNS signals around TSS were present in diploids (top row), F1 (middle two rows), and AD1 (bottom row).

Figure S10. p1/2

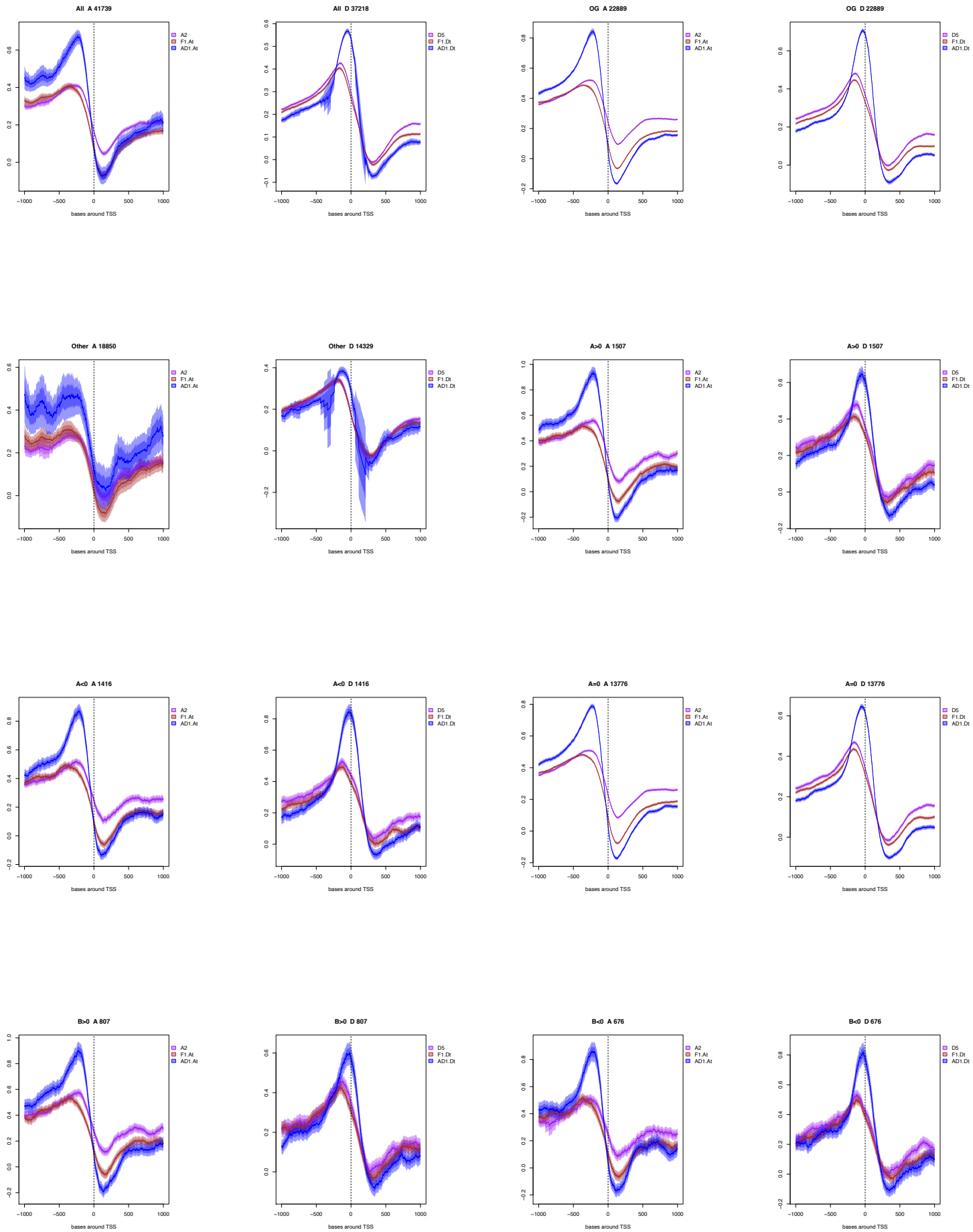


Figure S10. p2/2

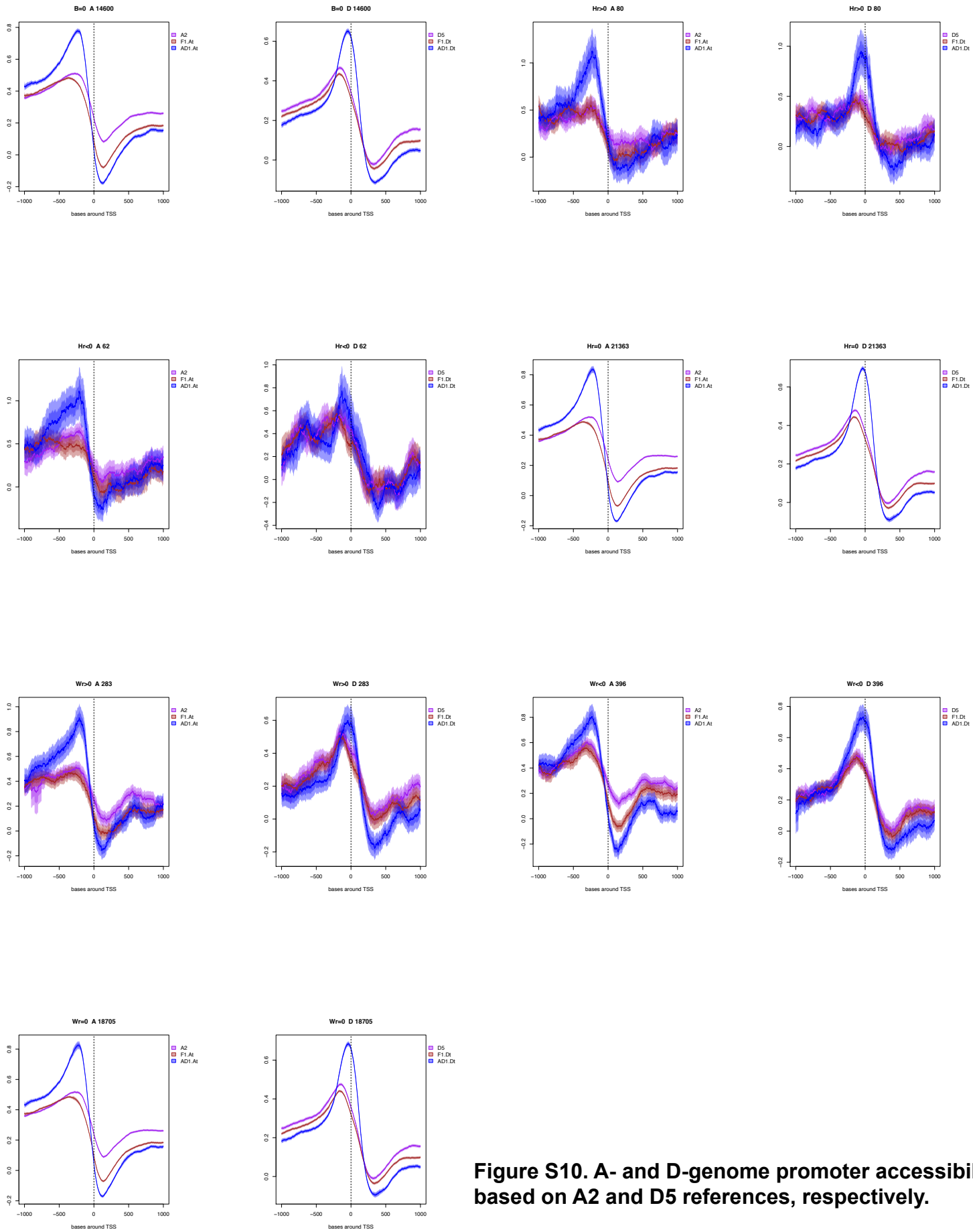


Figure S10. A- and D-genome promoter accessibility based on A2 and D5 references, respectively.

Figure S11A. p1/3

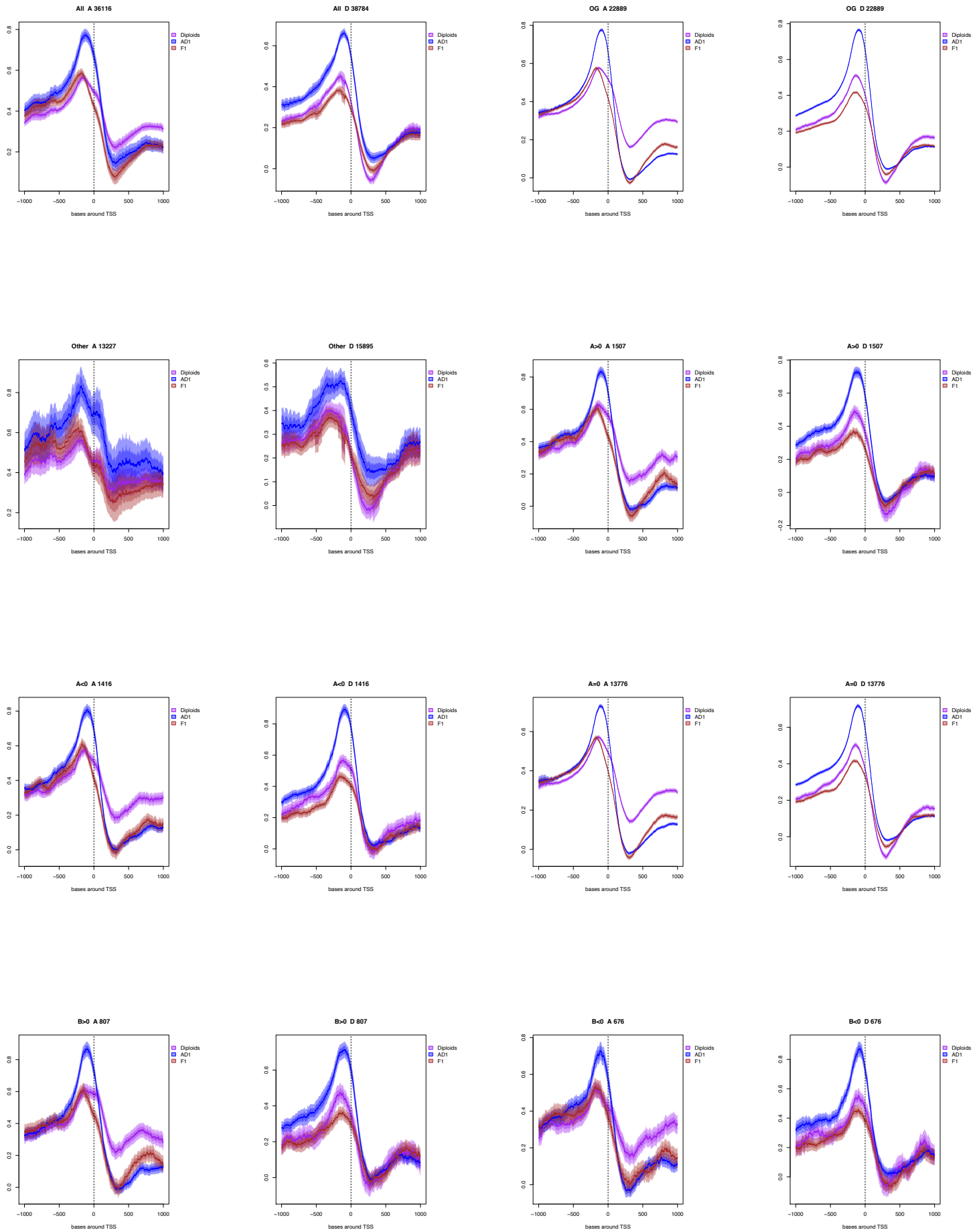


Figure S11A. p2/3

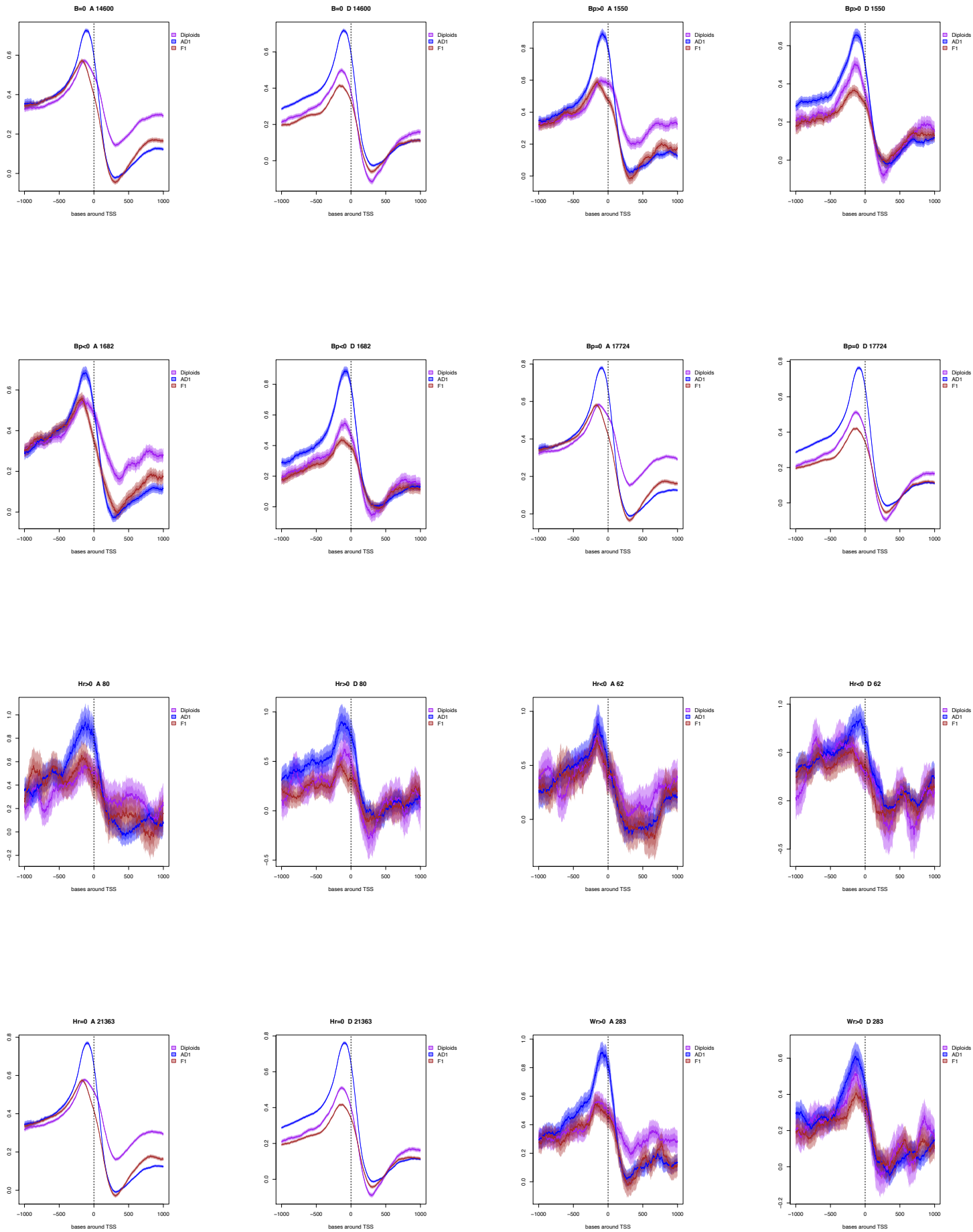


Figure S11A. p3/3

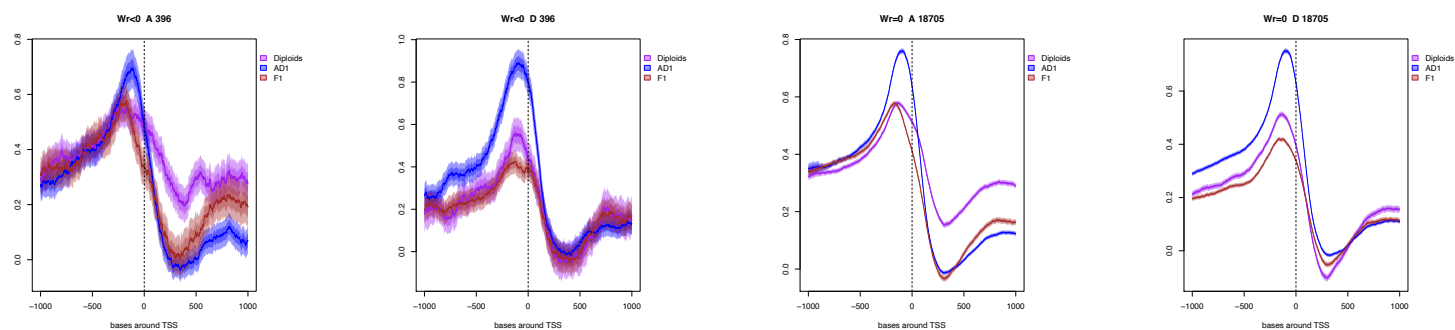


Figure S11. A- and D-genome promoter accessibility based on AD1 references, respectively.

A. HEB and impacts of genome evolution.

B. nonadditive expression in F1.

C. nonadditive expression in AD1.

Figure S11B

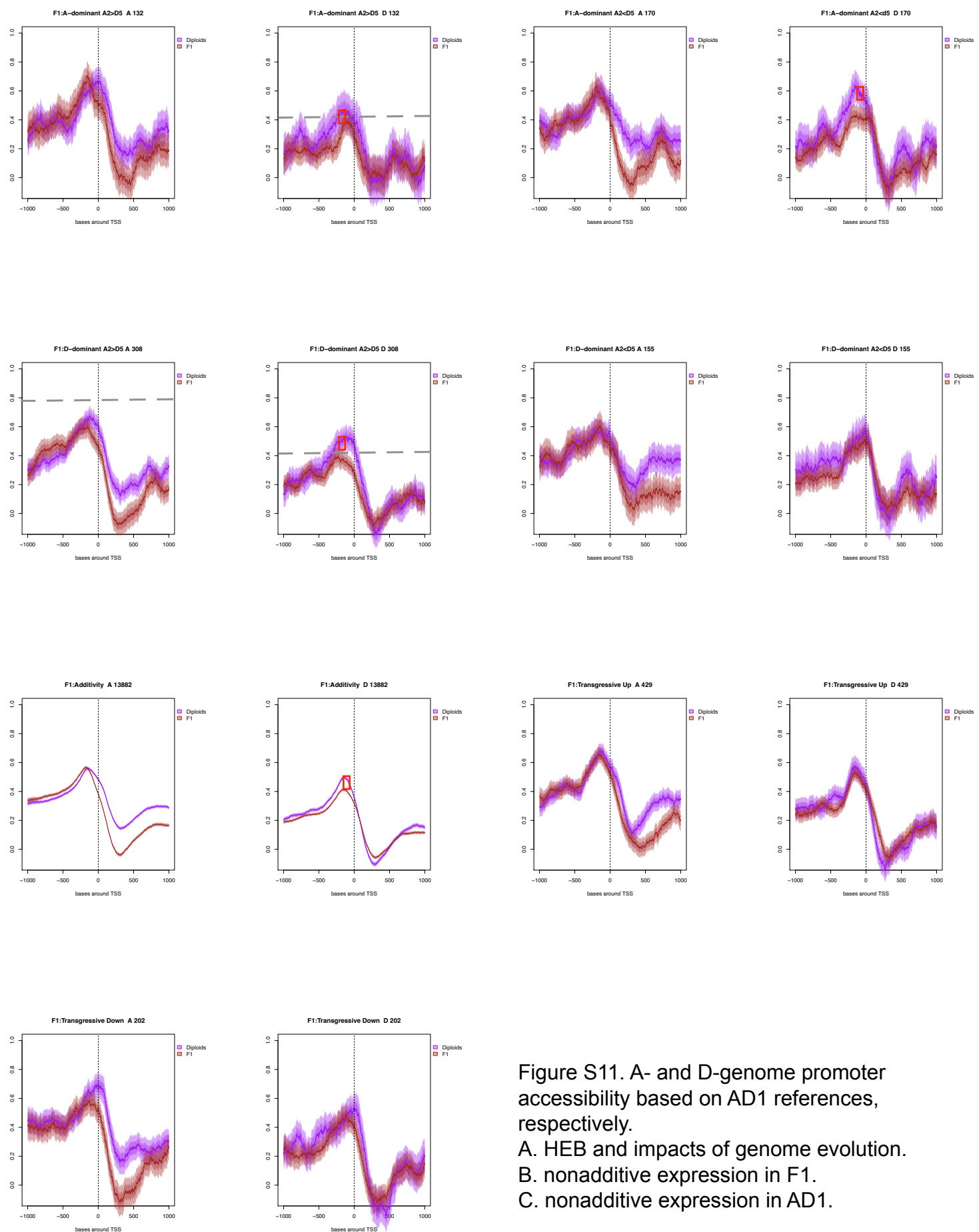


Figure S11. A- and D-genome promoter accessibility based on AD1 references, respectively.
A. HEB and impacts of genome evolution.
B. nonadditive expression in F1.
C. nonadditive expression in AD1.

Figure S11C

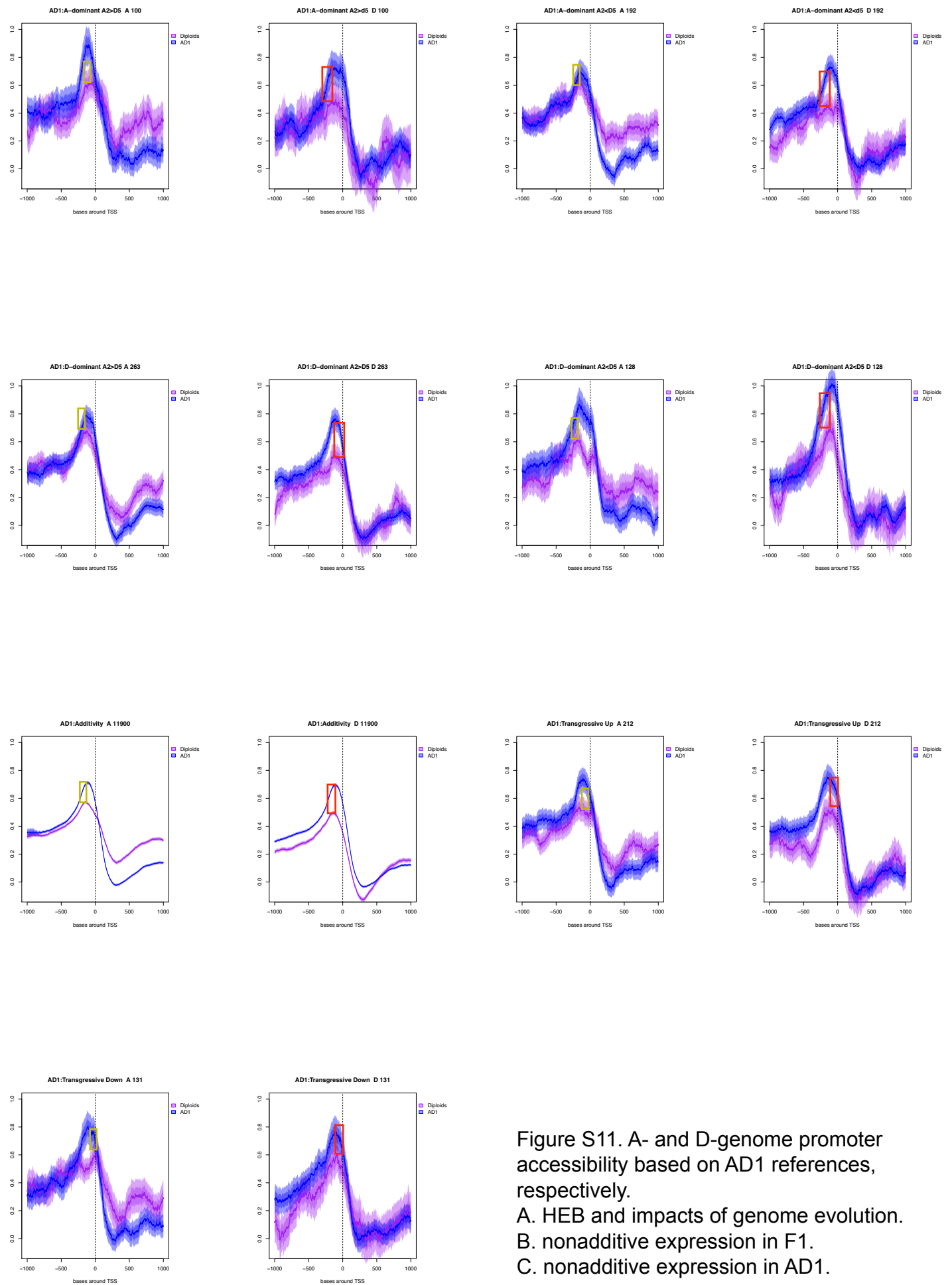
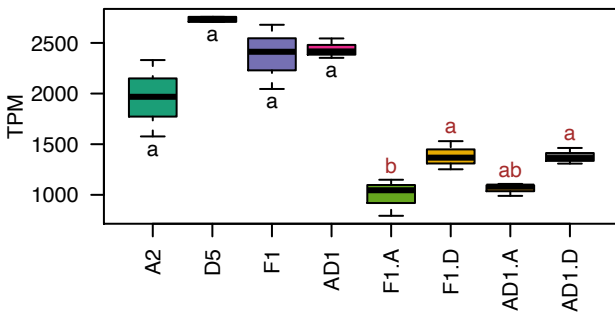


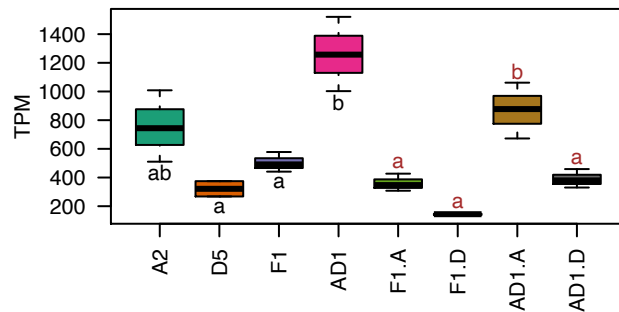
Figure S11. A- and D-genome promoter accessibility based on AD1 references, respectively.
A. HEB and impacts of genome evolution.
B. nonadditive expression in F1.
C. nonadditive expression in AD1.

Figure S12. p1/2

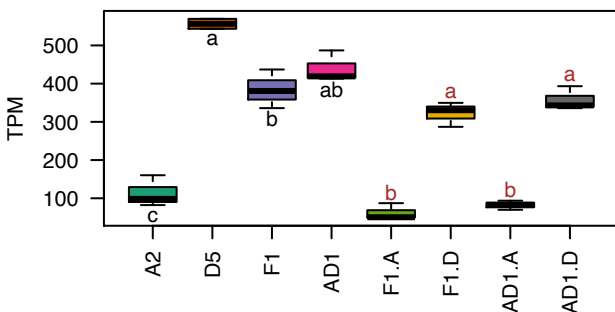
canonical core histones



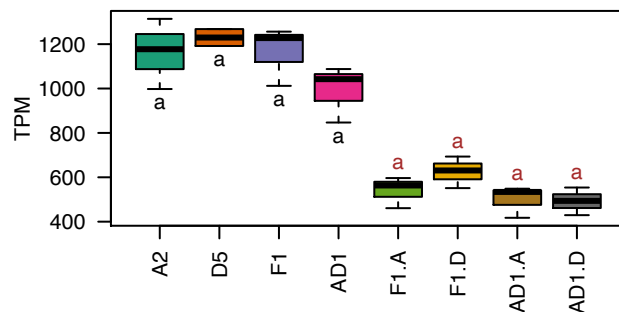
canonical_H1



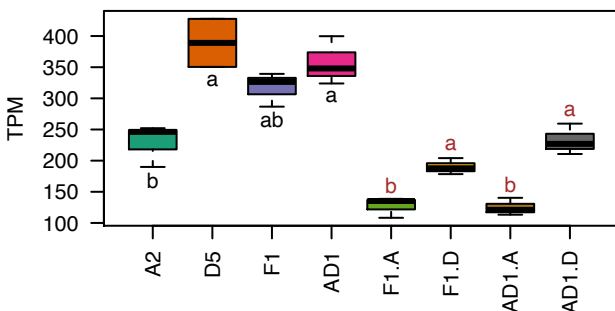
canonical_H2A



canonical_H2B



canonical_H3



canonical_H4

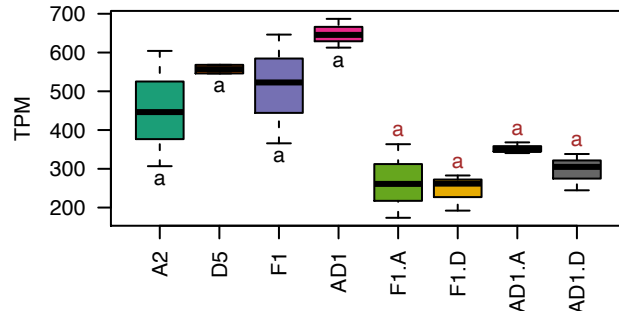
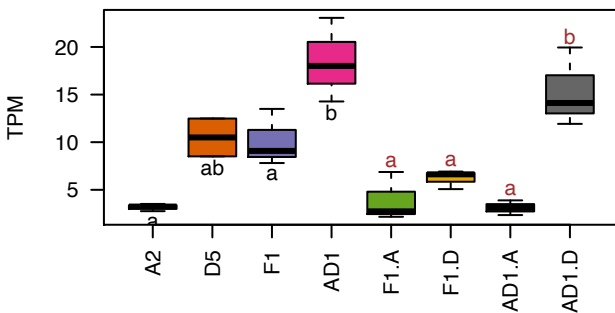
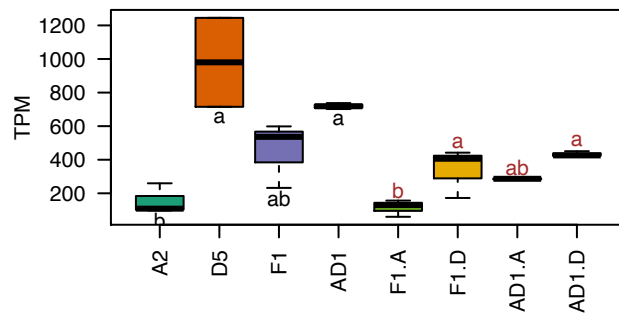


Figure S12. p2/2

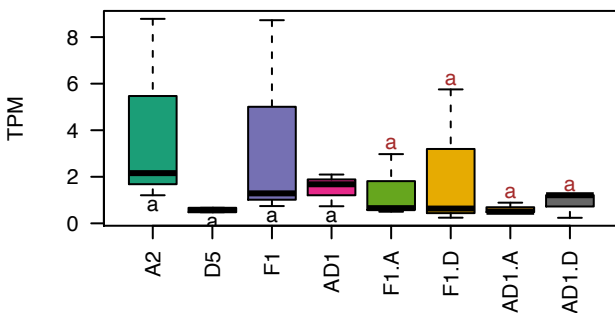
cenH3



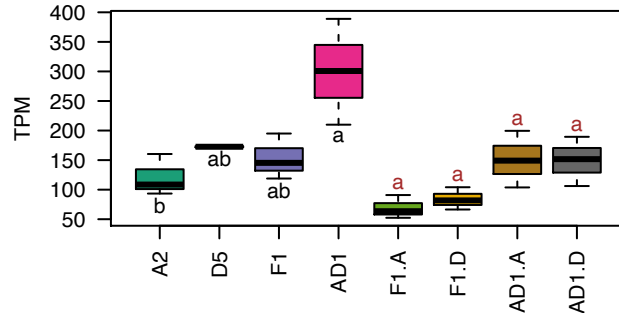
H1.3



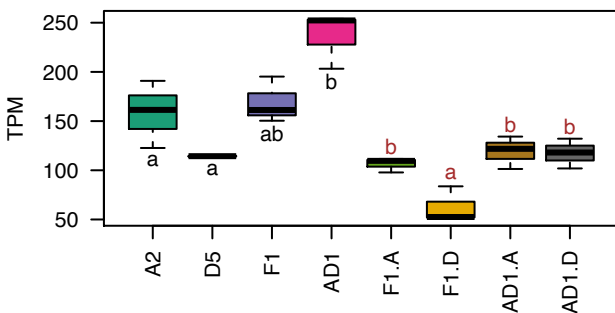
H2A.W



H2A.X



H2A.Z



H3.1

