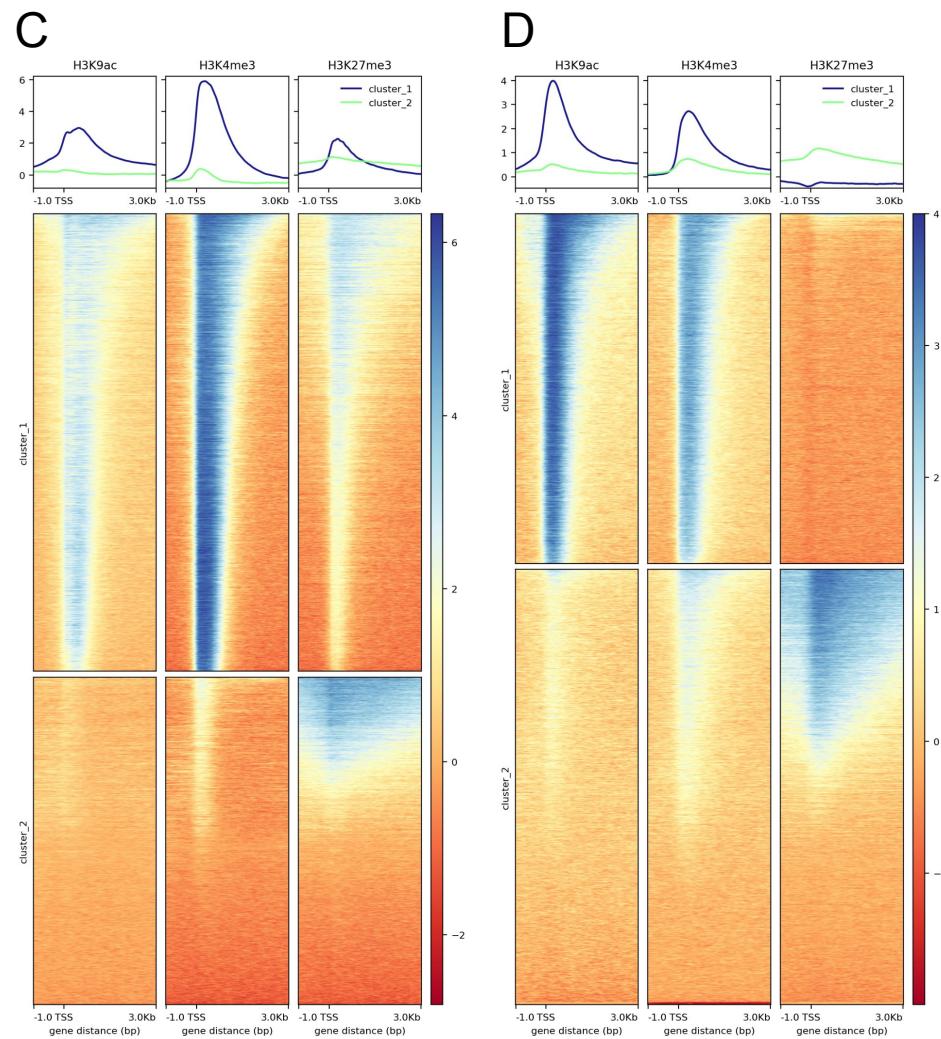
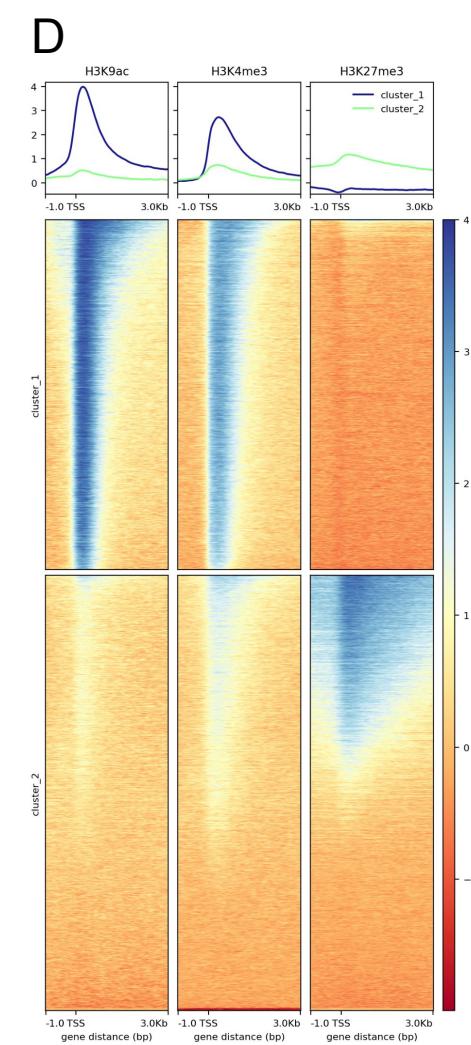
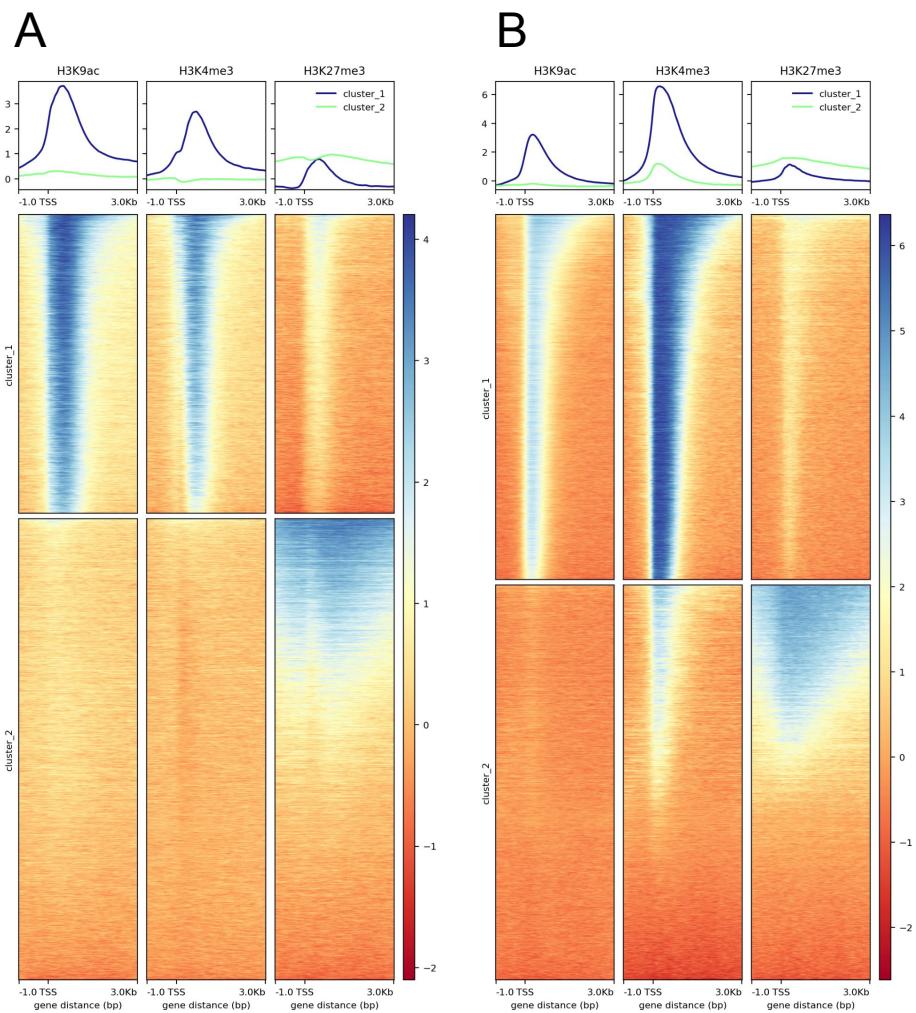
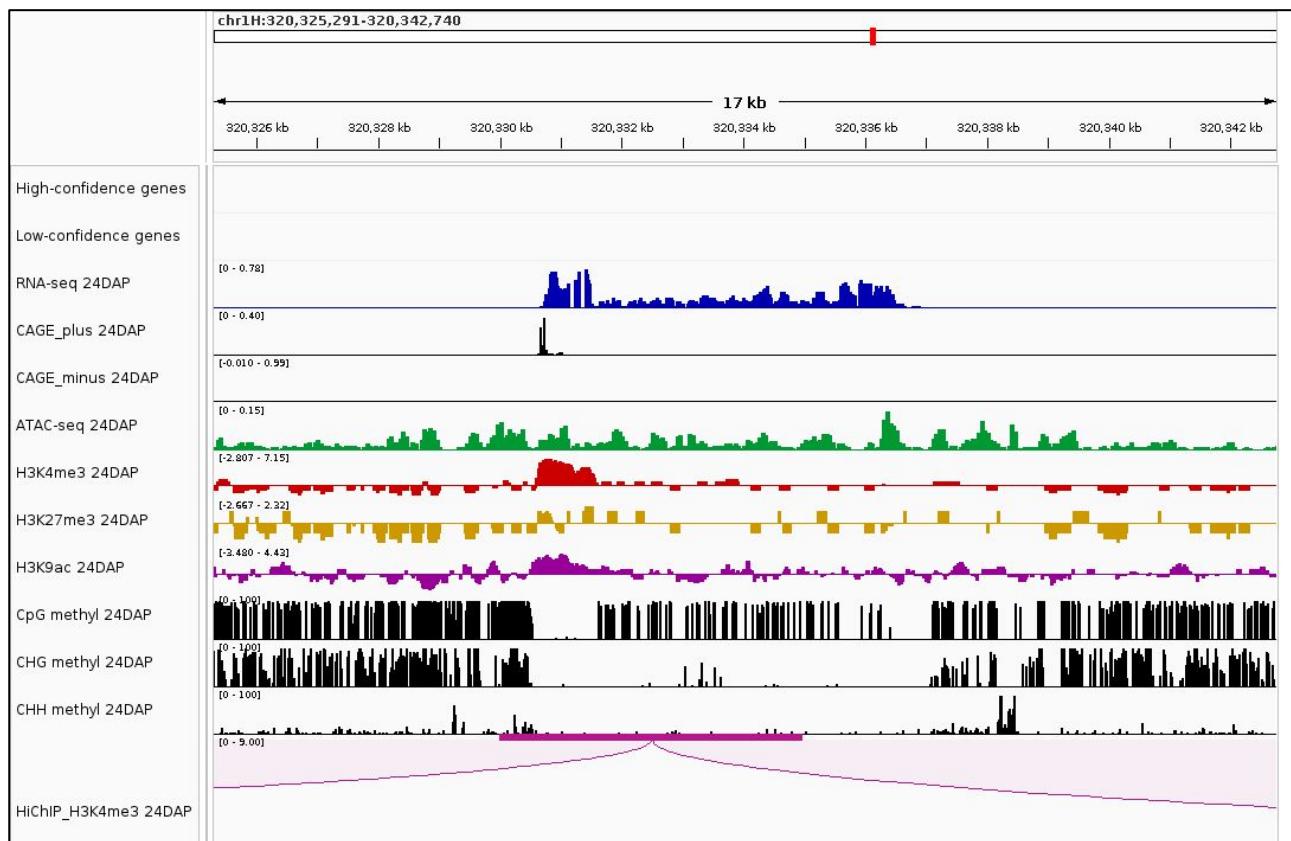


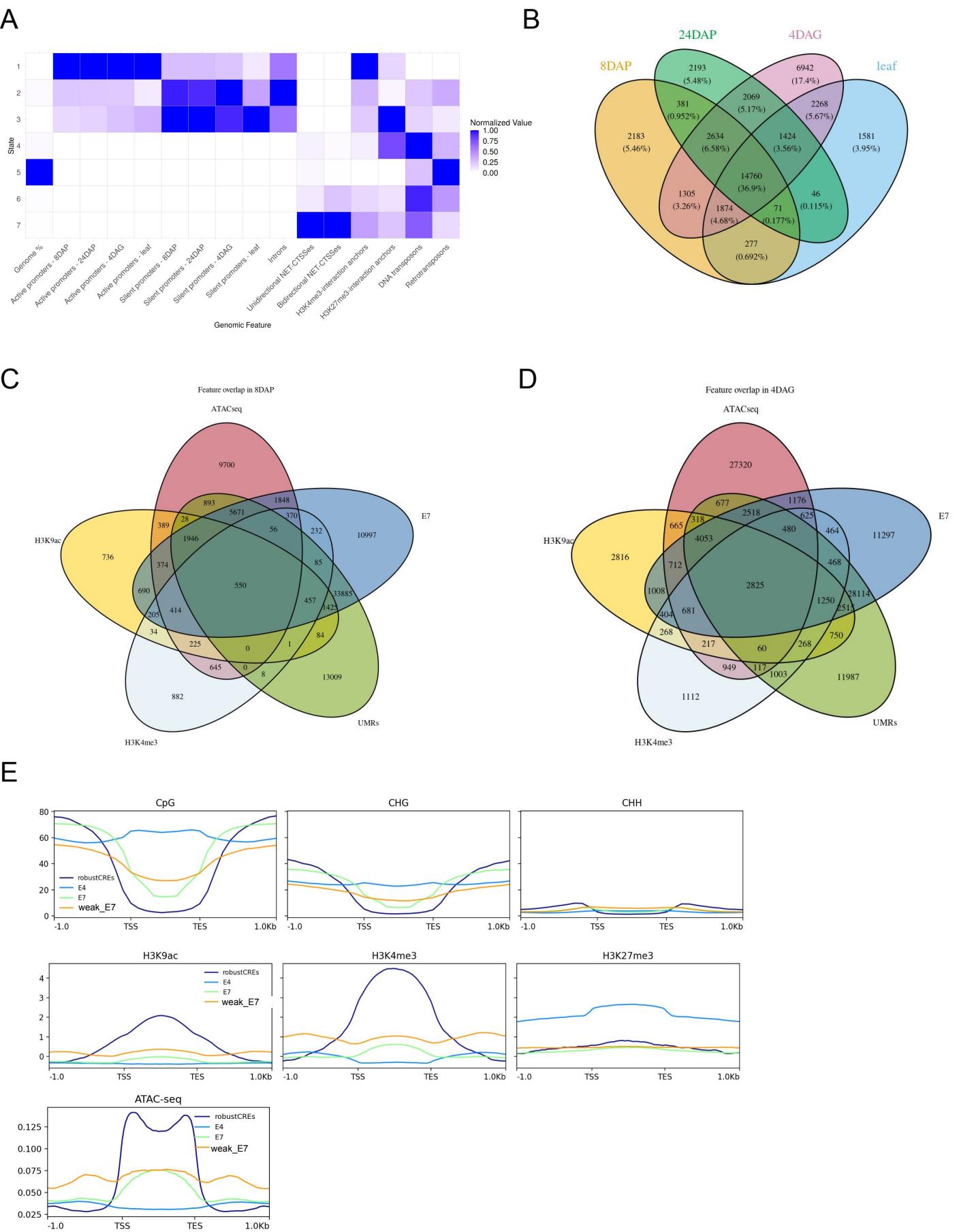
Suppl. Fig. 1. Profiles and heatmaps showing read coverages for two epigenetic features across MorexV3 high-confidence genes. Data from bisulfite sequencing show cytosine methylation in three sequence contexts in (A) 24DAP embryo and (B) leaf. (C) Profiles of ATAC-seq coverages around transcription start sites (TSSs) in the four developmental stages used in the study.



Suppl. Fig 2: K-means clustered profiles of histone modifications around HC gene TSSs from ChIP-seq. (A) in 8DAP embryo. The cluster 1 (top) represents active genes while the cluster 2 (bottom) shows profile of silent genes. (B) represents data from 24DAP, (C) 4DAG and (D) leaf.

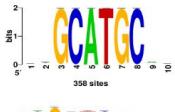
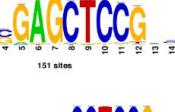
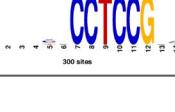


Suppl. Fig. 3: Example of a putative unannotated gene. The presence of transcripts and features of active chromatin indicate presence of an unannotated gene. To prevent misinterpretation of its promoter as an intergenic CREs, we excluded this and similar regions from the analysis of the non-coding genome.

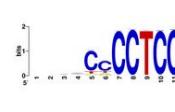
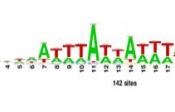


Suppl. Fig. 4: Chromatin state analysis is a sensitive method of cCREs detection. (A) Overlap enrichment of genomic features across 7 chromatin states in 4DAG showing state dynamics following transcription dynamics between individual stages. (B) Dynamics of chromatin state E4 segments, potentially representing silenced cCREs. (C) Overlaps of the intergenic epigenetic features, as detected by ChIP-seq/ATAC-seq peak calling or DNA methylation analysis, with the E7 chromatin state in 8DAP and (D) 4DAG. (E) Comparison of main chromatin feature profiles across robust CREs, states E4, E7 and the E7 state segments not overlapped with a robust CRE (weak E7).

A

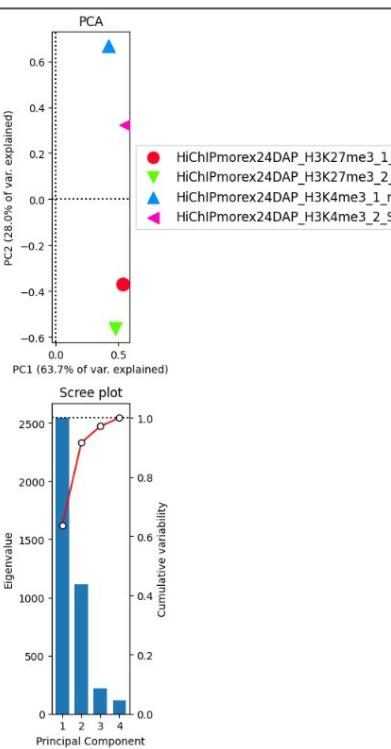
8DAP robust CRE motif	significance	Transcription factor
	9.3e-10	B3 transcription factor ABI3-like
	9.8e-09	Tryptophan cluster factor
	9.8e-09	ERF family protein

B

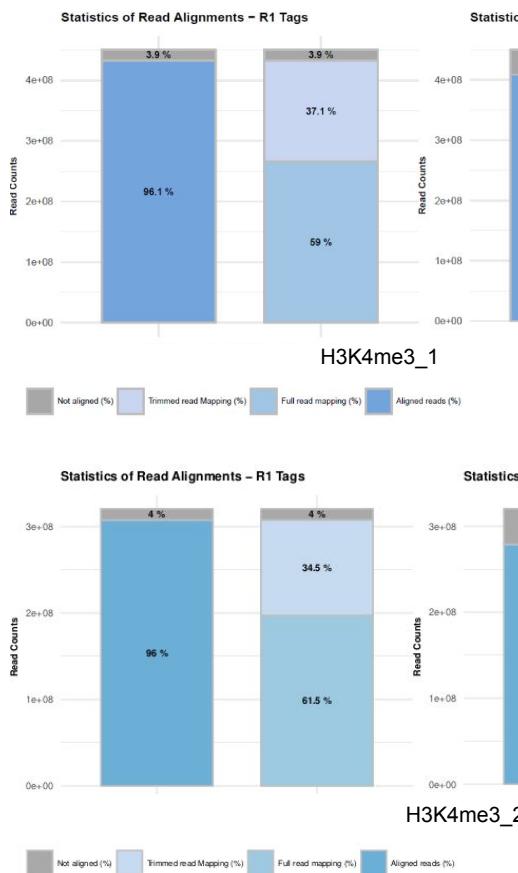
4DAG robust CRE motif	significance	Transcription factor
	9.94	ZnF (SP5-related) or Myb-like transcription factor
	1.3e-37	ATHB Homeo-domain factors
	3e-54	Ethylene-responsive transcription factors ERF115

Suppl. Fig. 5: Transcription factor binding sites enriched in the (A) 8 DAP- and (B) 4 DAG-specific robust cCREs datasets.

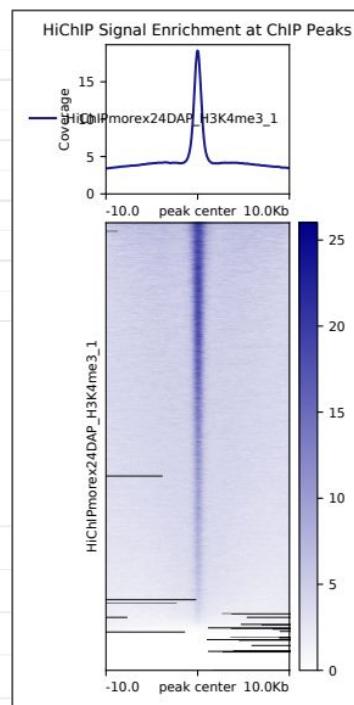
A



B

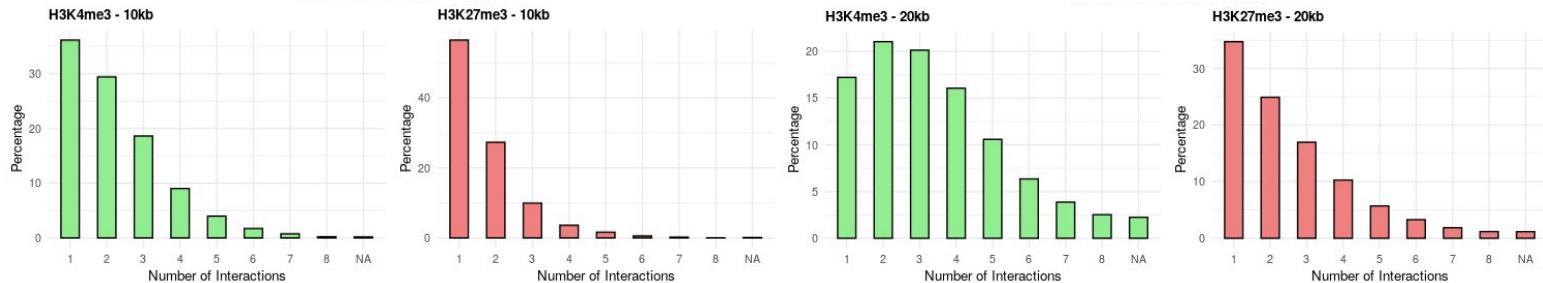


C

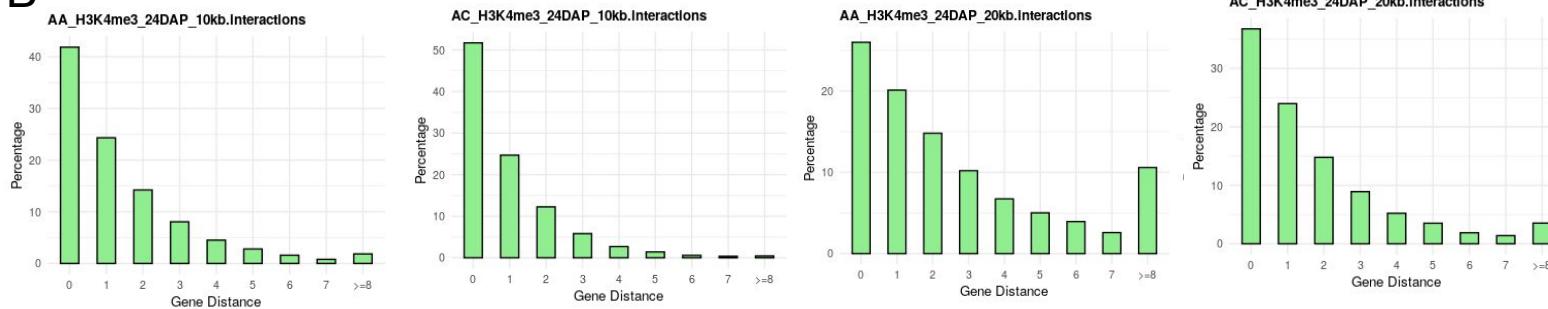


Suppl. Fig. 6. Quality Control of the 24DAP H3K4me3 HiChIP sequencing datasets. (A) HiChIP replicate correlation - PCA of the 24DAP mapped datasets. (B) Mapping statistics of the two 24DAP H3K4me3 HiChIP replicates. (C) HiChIP signal enrichment at the H3K4me3 ChIP peaks as called from previously performed native ChIP-seq experiment.

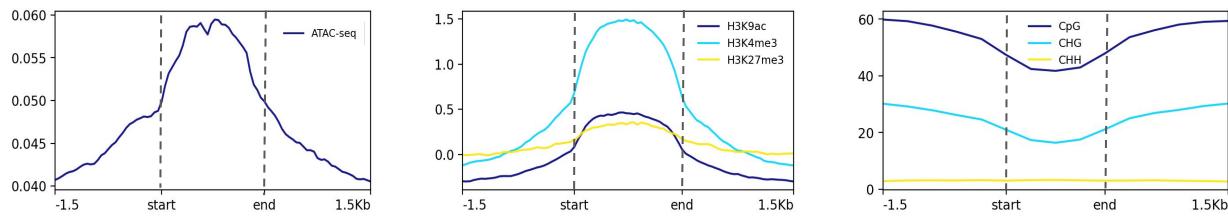
A



B

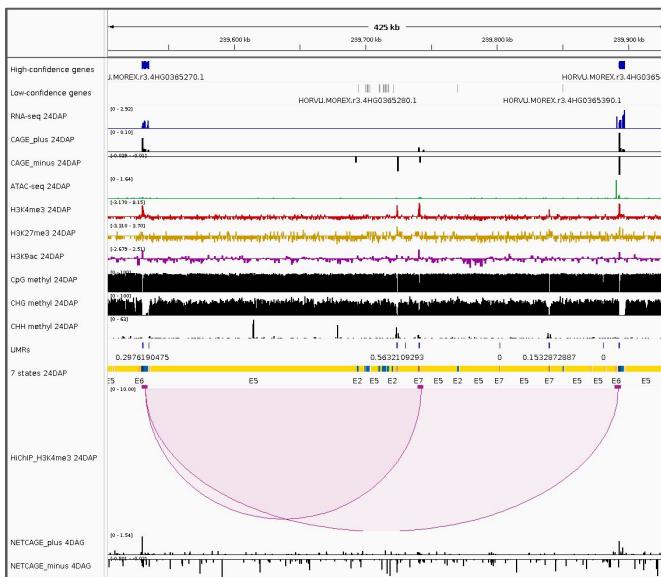


C

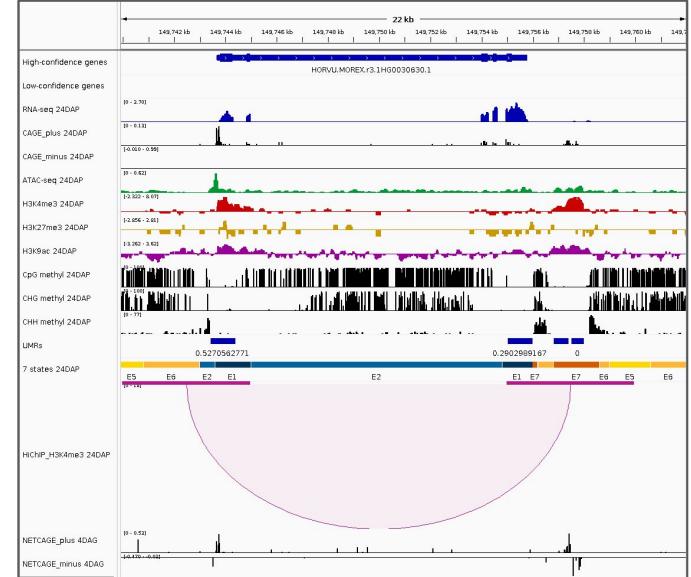


Suppl. Fig. 7: (A) Numbers of H3K4me3 and H3K27me3 HiChIP interactions per promoter at lower resolutions (10- and 20-kb). (B) Numbers of genes spanned by H3K4me3 and H3K27me3 HiChIP interactions at lower resolutions (gene distances). (C) Increased enrichments of the epigenetic features across H3K4me3 HiChIP anchors in the 5-kb resolution 24DAP indicates that they are transcriptionally dense regions.

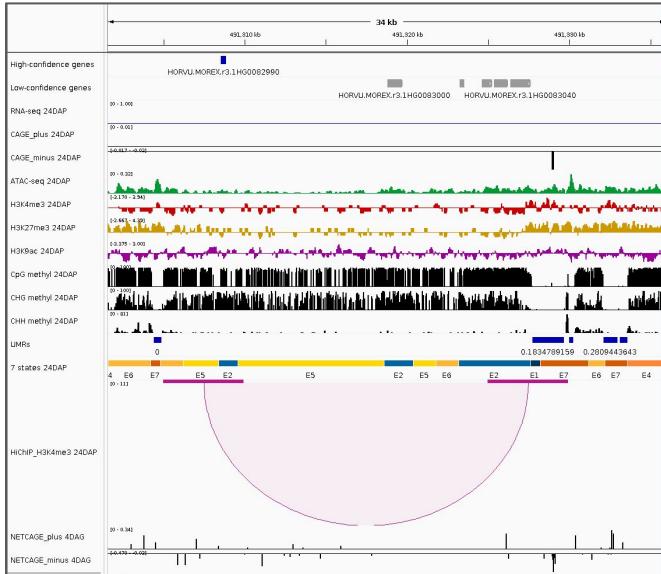
A



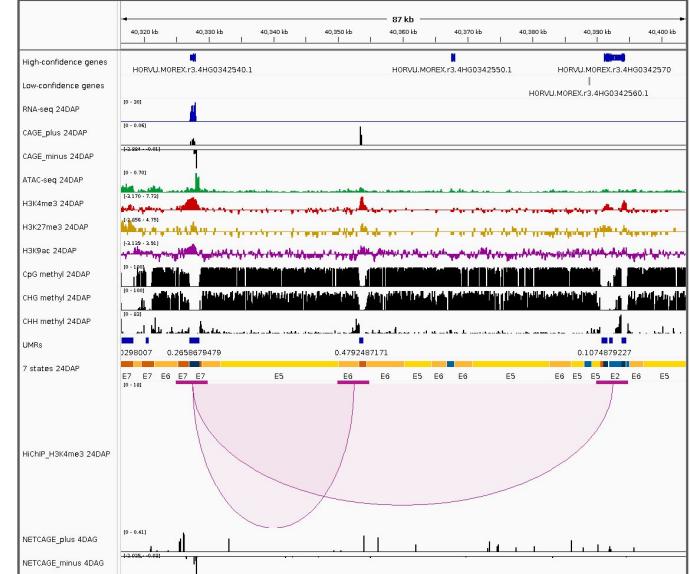
B



C



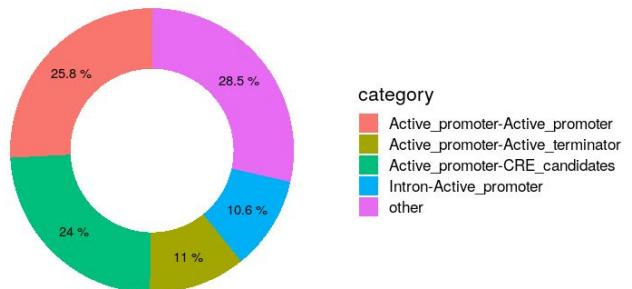
D



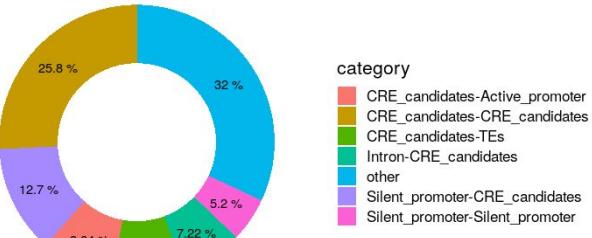
Suppl. Fig. 8: Examples of distinct interaction classes together with epigenomic features, visualized in the IGV genome browser. (A) Active promoter-active promoter (B) Active self-gene loop (C) Silent promoter-CREc (D) Active promoter-CREc and Active promoter-silent gene.

A

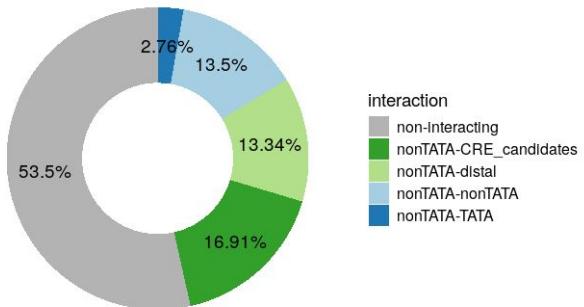
H3K4me3_24DAP_5kb.interactions_Q0.1

**B**

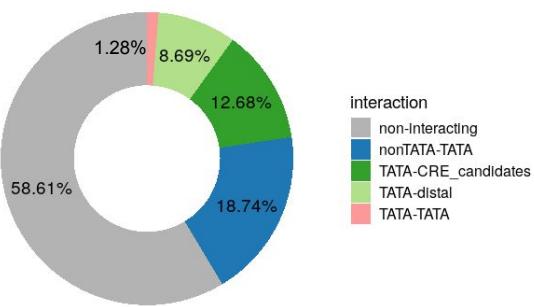
H3K27me3_24DAP_5kb.interactions_Q0.1

**C**

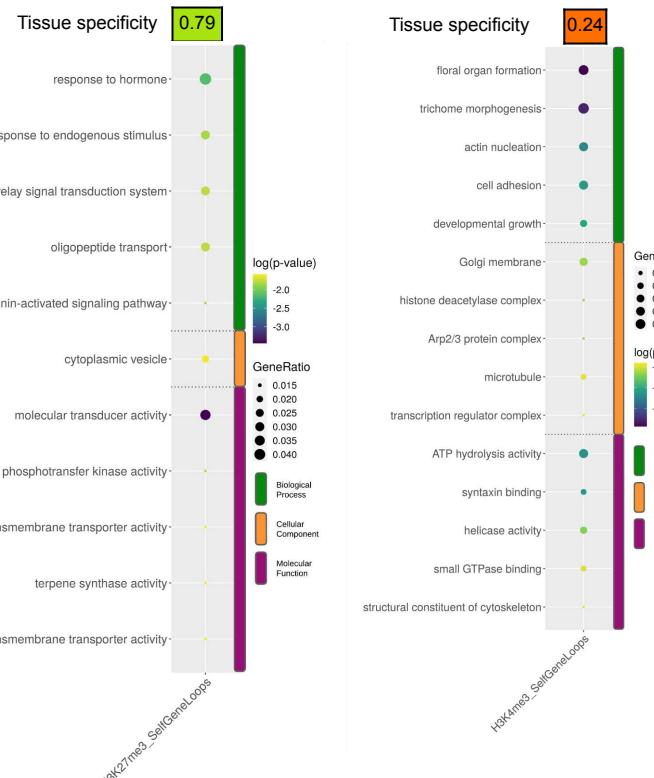
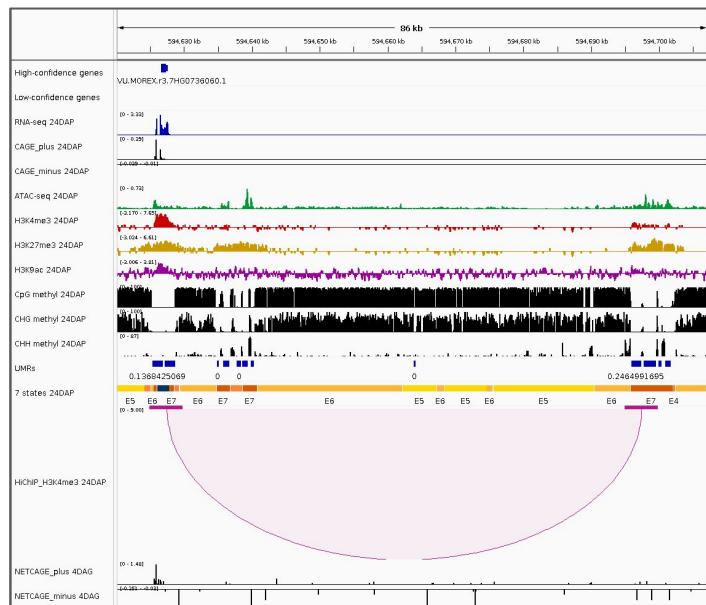
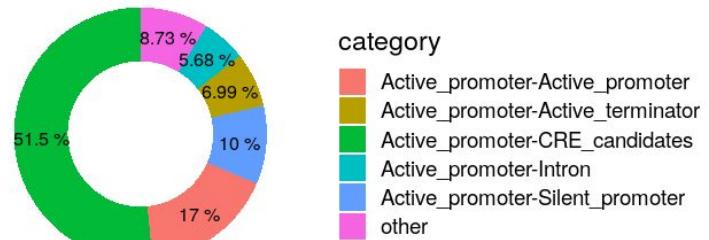
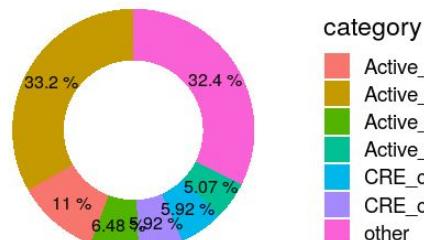
Normalized Proportions of non-TATA Interactions

**D**

Normalized Proportions of TATA Interactions



Suppl. Fig. 9: Proportions of interaction classes identified by HiChIP at 5kb resolution in 24DAP, focusing on high-confidence genes. Annotation of all significant interactions associated with (A) activating (H3K4me3) histone mark and (B) repressive (H3K27me3) mark. Proportions of promoter interaction classes in 24DAP, focusing on distinction between (C) TATA and (D) non-TATA high confidence gene promoter. The proportion of non-TATA promoter-CRE interactions is higher than that of TATA promoter-CRE interactions.



Suppl. Fig. 10: Features of bivalent interactions and gene self-loops (A) Annotation of all bivalent interactions and the same set (B) from the Active promoter-centric view. (C) An example of a bivalent interaction. (D) GO and tissue specificity analysis of genes involved in H3K4me3 self-gene loops involves particularly long genes, therefore the set of genes matching the length range of the analyzed set of genes was used as a background. (B) Same analysis of the H3K27me3 self-gene loops with all genes as a background set demonstrating high tissue-specificity and apparent developmentally-regulated function unused in the embryonic tissues (floral organ development, trichome morphogenesis).