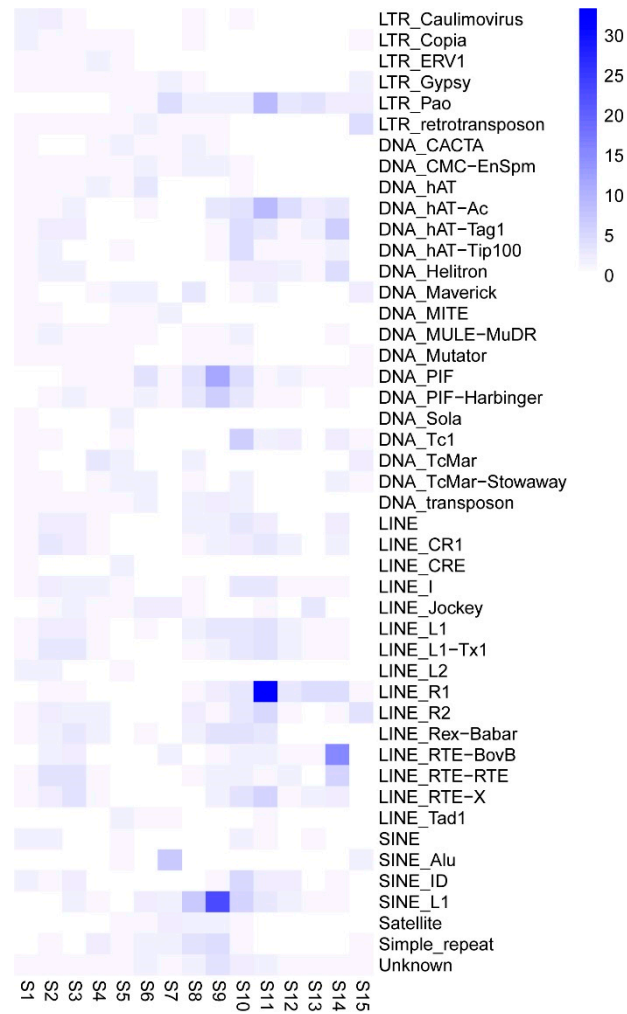
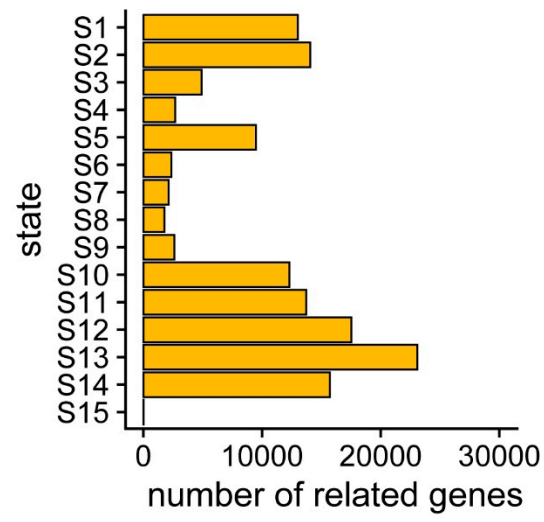


**Table S1.** List and catalog of histone antibodies used in this study.

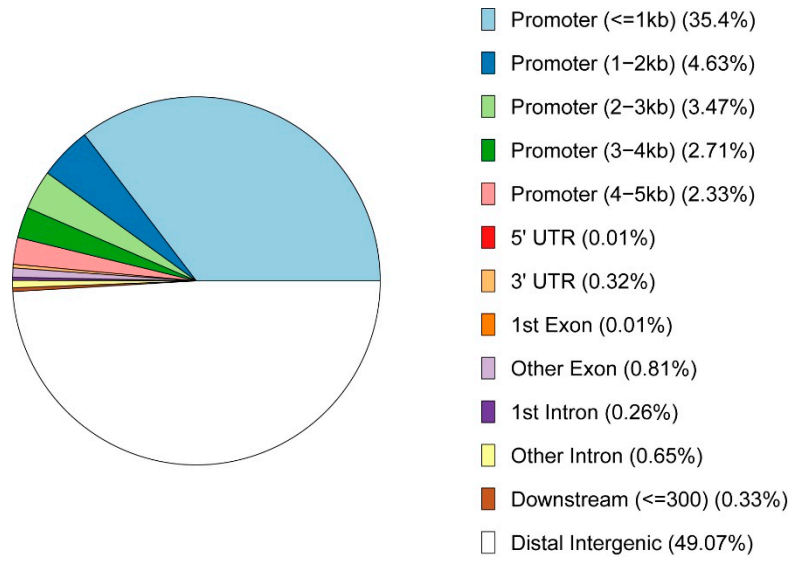
No.	Antibody	Source	Catalog N°	Host/Isotype	Clonality	Format
1	CENH3	CWBio	Zhang lab	Rabbit IgG	Polyclonal	Serum
2	H2Bub	Médimabs	MM-0029	Mouse IgG2a	Monoclonal	Purified
3	H3	Abcam	ab1791	Rabbit IgG	Polyclonal	Purified
4	H3K18ac	Abcam	ab1191	Rabbit IgG	Polyclonal	Purified
5	H3K27ac	Millipore	07-360	Rabbit IgG	Polyclonal	Serum
6	H3K27me1	Millipore	07-448	Rabbit IgG	Polyclonal	Purified
7	H3K27me2	Abcam	ab24684	Rabbit IgG	Polyclonal	Purified
8	H3K27me3	Millipore	07-449	Rabbit IgG	Polyclonal	Purified
9	H3K36me2	Abcam	ab9049	Rabbit IgG	Polyclonal	Purified
10	H3K36me3	Abcam	ab9050	Rabbit IgG	Polyclonal	Purified
11	H3K4me1	Millipore	07-436	Rabbit IgG	Polyclonal	Purified
12	H3K4me2	Millipore	07-030	Rabbit IgG	Polyclonal	Serum
13	H3K4me3	Millipore	07-473	Rabbit IgG	Polyclonal	Purified
14	H3K56ac	Abcam	ab71956	Rabbit IgG	Polyclonal	Purified
15	H3K9ac	Millipore	07-352	Rabbit IgG	Polyclonal	Serum
16	H3K9me2	Abcam	ab1220	Mouse IgG2a	Monoclonal	Purified
17	H3K9me3	Abcam	ab8898	Rabbit IgG	Polyclonal	Purified
18	H4K20me1	Millipore	07-748	Rabbit IgG	Polyclonal	Purified
19	H4K5ac	Millipore	07-327	Rabbit IgG	Polyclonal	Serum



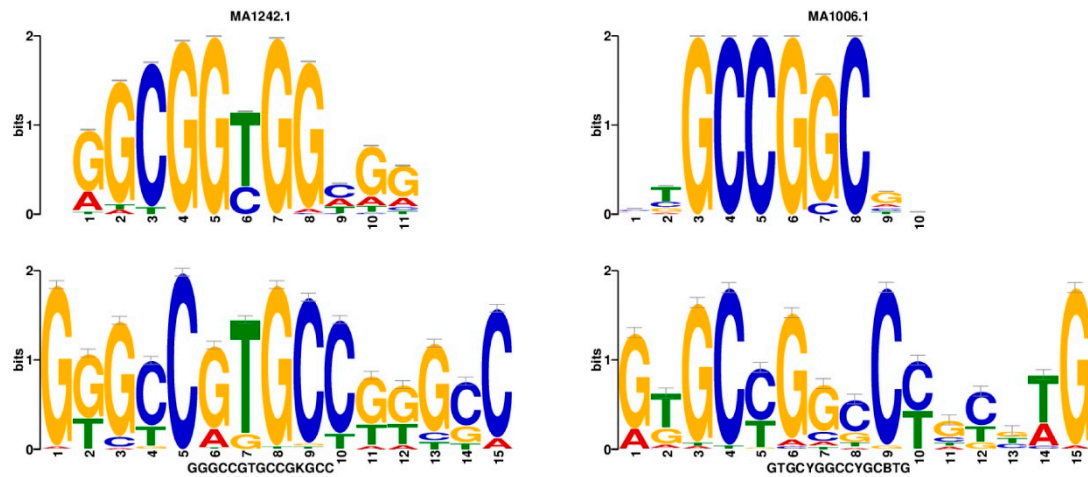
**Figure S1.** The heatmap represents the fold enrichments of TEs of different superfamilies in chromatin states.



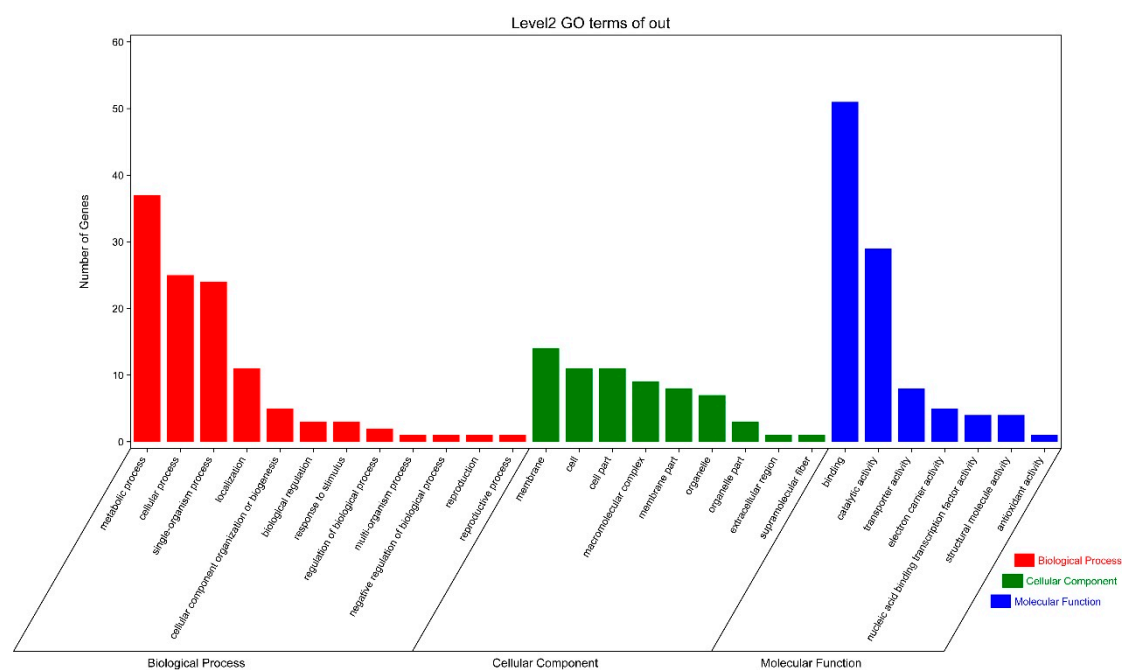
**Figure S2.** The bar chart represents the number of related genes in the chromatin states.



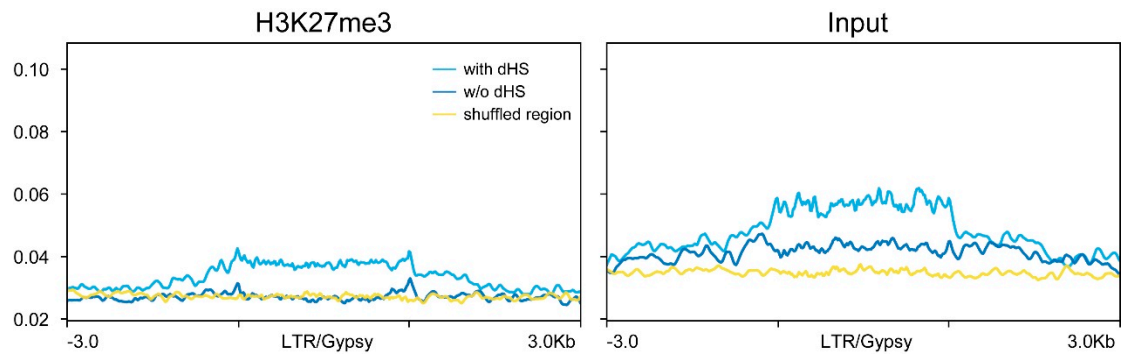
**Figure S3.** The pie chart shows the distribution of MNase HSs in the AL8/78 genome.



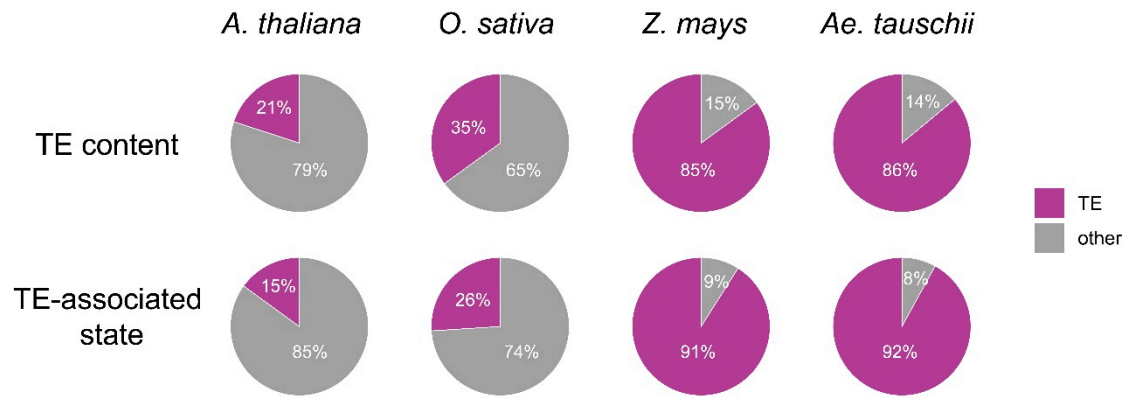
**Figure S4.** The diagrams show similarities between the known transcription factor-binding motifs of the ERF/DREB family in *Arabidopsis* (upper diagram) and the motifs found in hAT-Ac TE-HSs in *Ae. tauschii* (lower diagram). The motif similarities were searched and quantified by Tomtom software from JASPAR (NON-REDUNDANT) CORE plants database (Wasserman and Sandelin, 2004). The motifs in *Arabidopsis* were previously reported by O'Malley et al., 2016 and Weirauch et al., 2014.



**Figure S5.** The top enriched GO terms of proximal TE-HS related genes.



**Figure S6.** The profiles show H3K27me3 and Input distributions around LTR/Gypsy with or without dHS. Shuffled genomic regions are used as control.



**Figure S7.** The pie charts show the percentage of TEs in the genome (top) and the percentage of TE-associated chromatin states in all chromatin states (bottom) in *Arabidopsis thaliana*, *Oryza sativa*, *Zea mays*, and *Aegilops tauschii*, respectively. The chromatin state data used in this study for *A. thaliana*, *O. sativa*, and *Z. mays* was obtained from the Plant Chromatin State Database (PCSD) constructed by Liu et al., 2018, a study collected public and in-house plant epigenomic data sets and applied a Hidden Markov Model to define chromatin states.