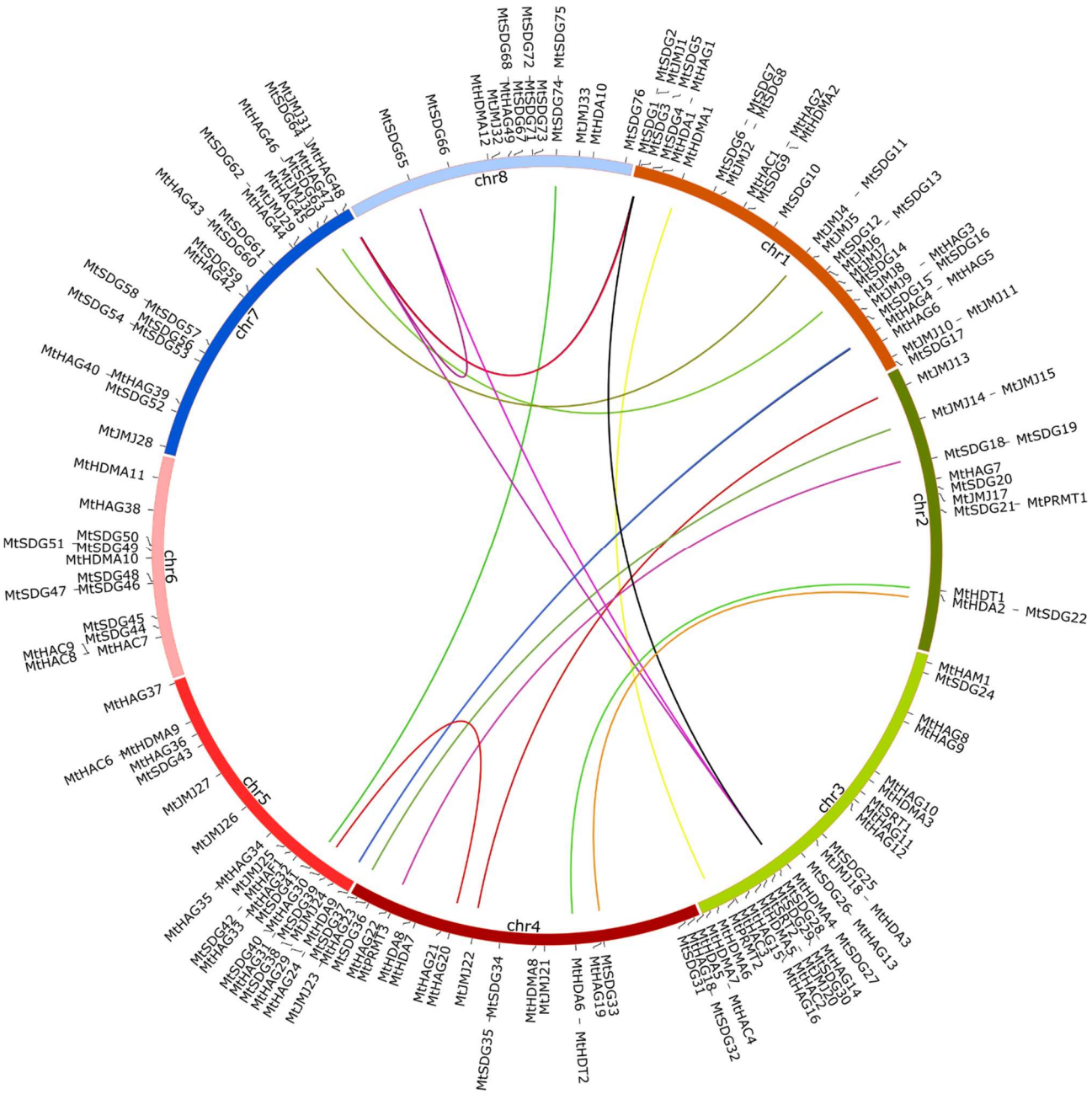


Figure S1. Synteny analysis and chromosomal distribution of MtHMGs.

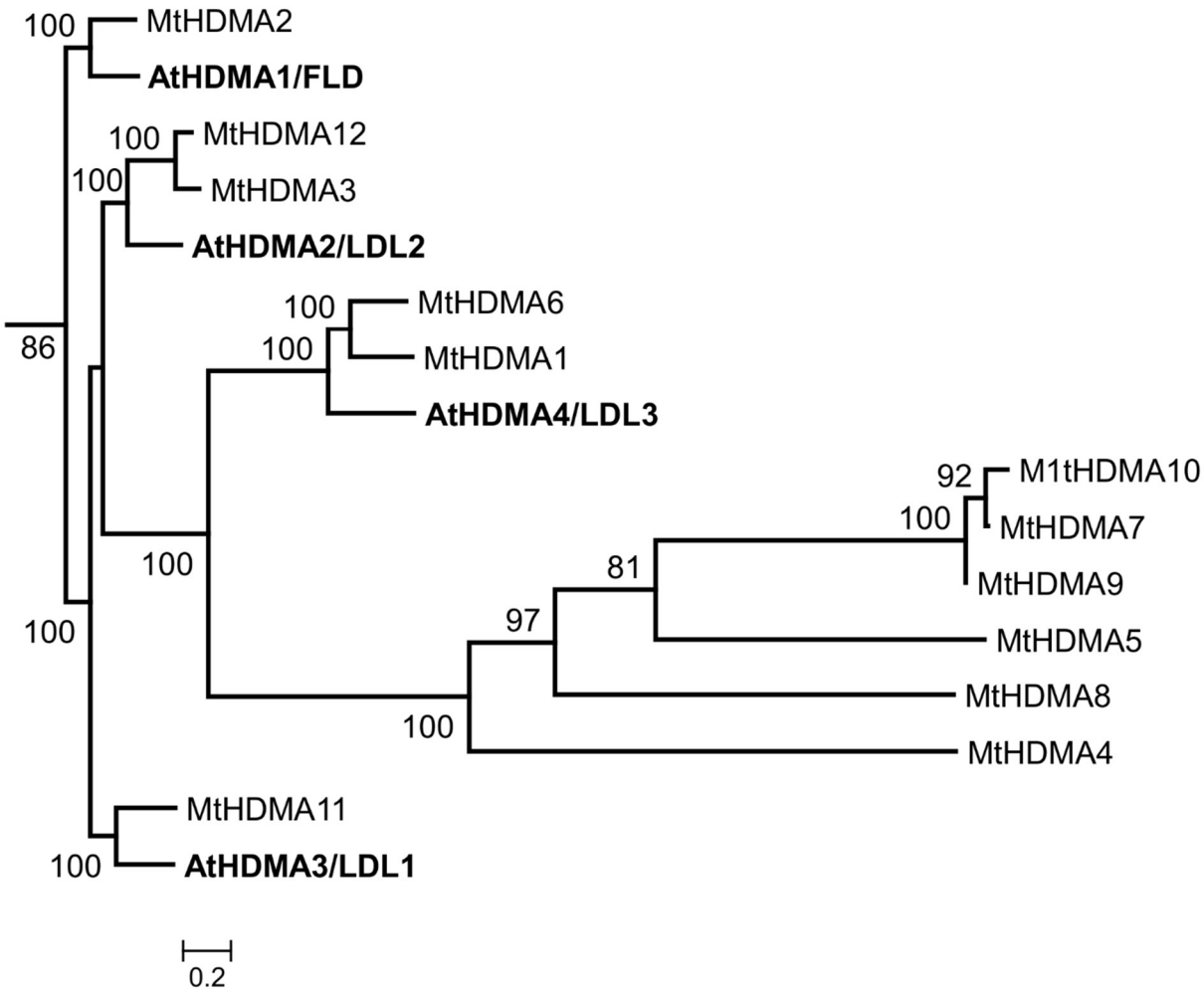


Figure S2. Phylogenetic tree of HDMA proteins of *M.truncatula* and *Arabidopsis* (in bold). Numbers near the tree branches represent bootstrap values.

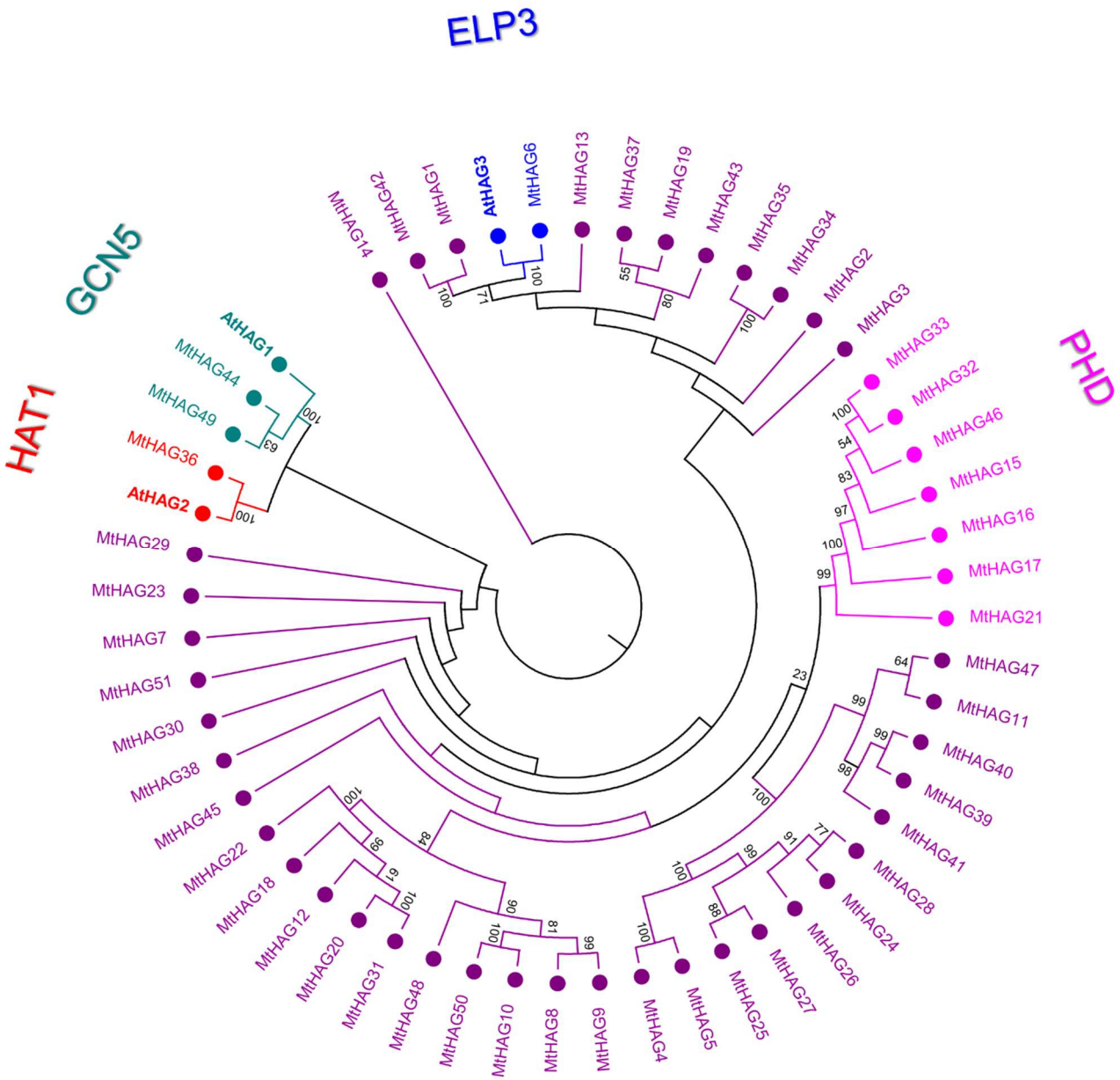


Figure S3. Phylogenetic tree of HAG proteins of *M.truncatula* and *Arabidopsis* (in bold). Numbers near the tree branches represent bootstrap values.

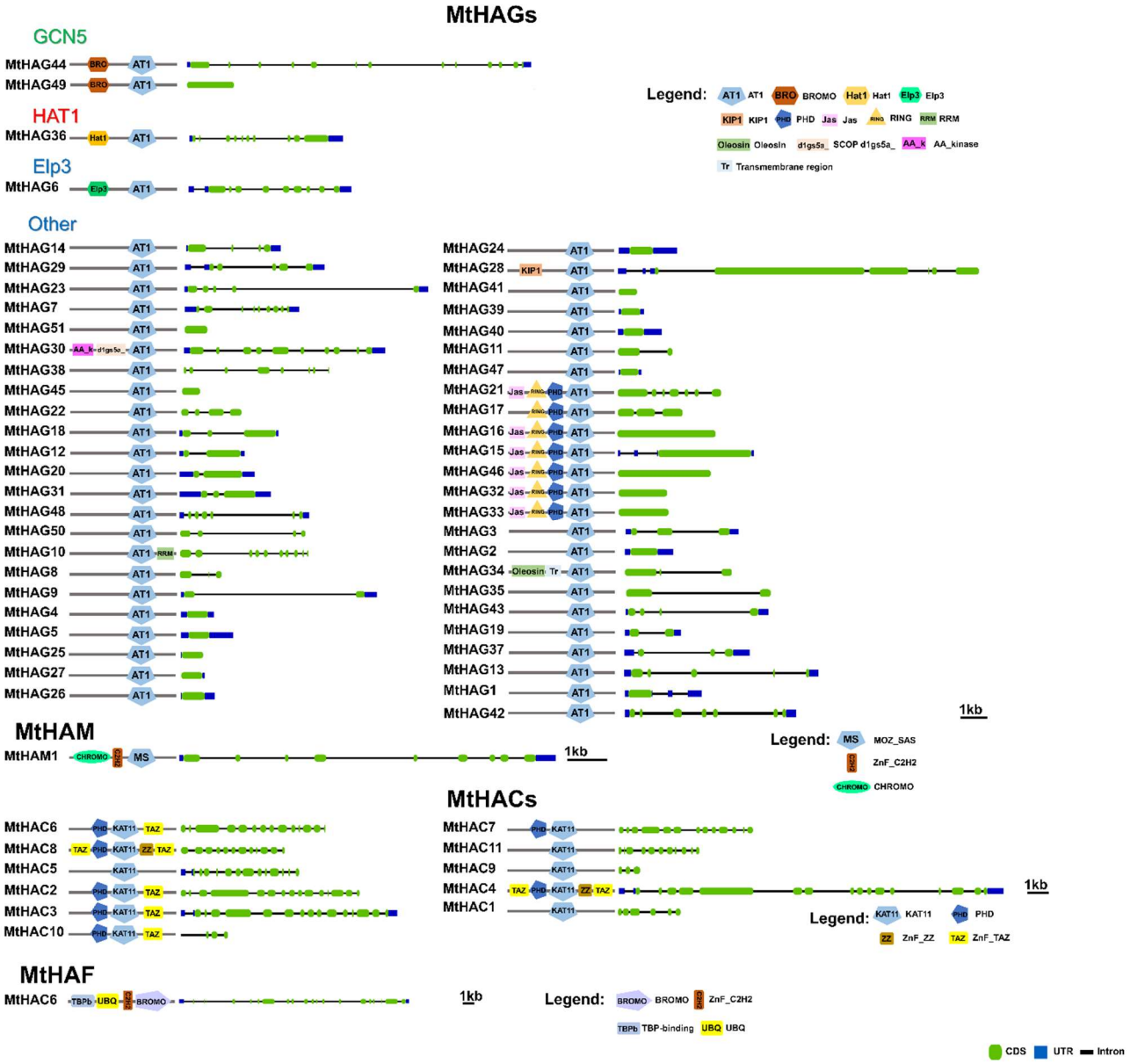


Figure S4. Domain composition and intron-exon structure of *M.truncatula* HATs.

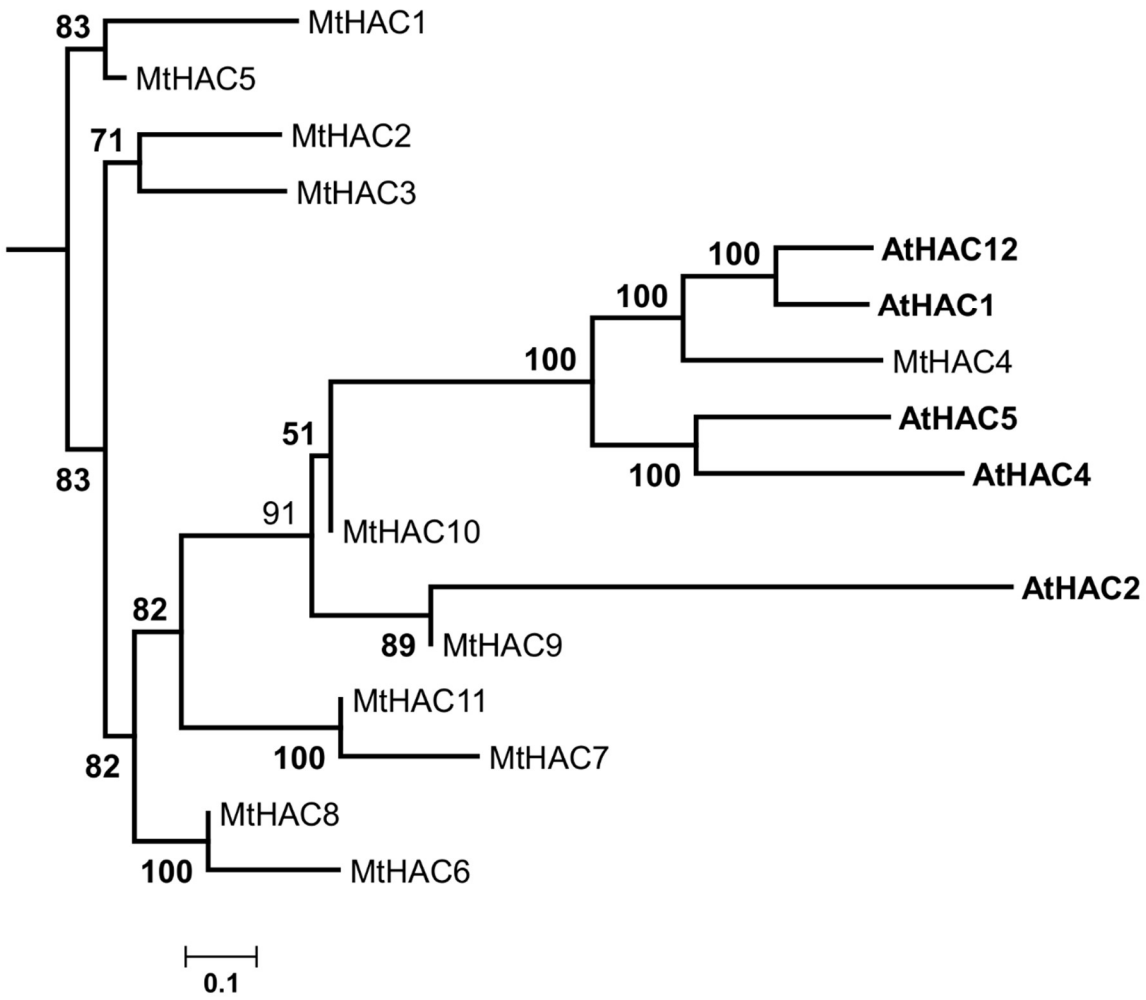


Figure S5. Phylogenetic tree of HAC proteins of *M.truncatula* and *Arabidopsis* (in bold). Numbers near the tree branches represent bootstrap values.

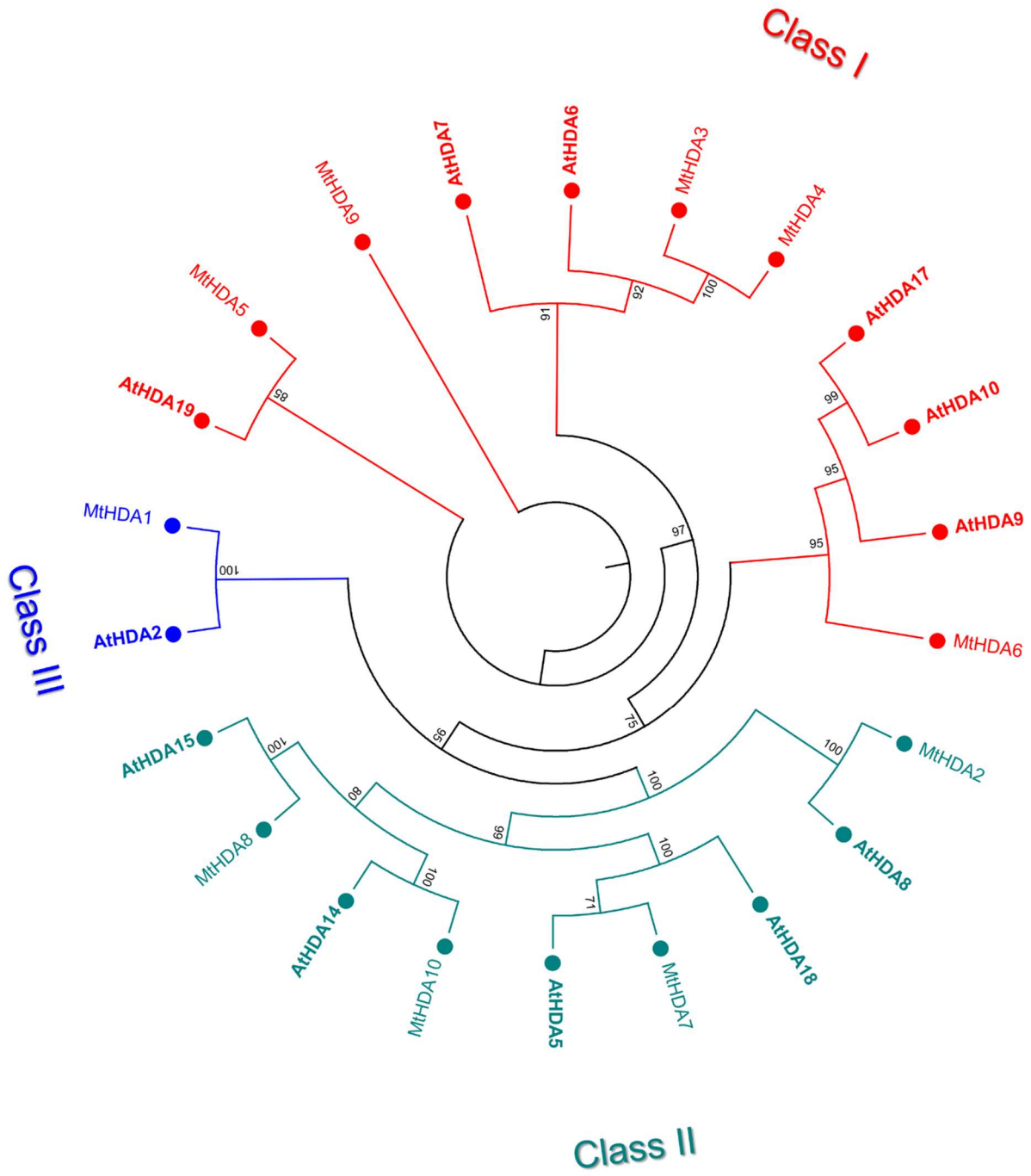


Figure S6. Phylogenetic tree of HDA proteins of *M.truncatula* and *Arabidopsis* (in bold). Numbers near the tree branches represent bootstrap values.

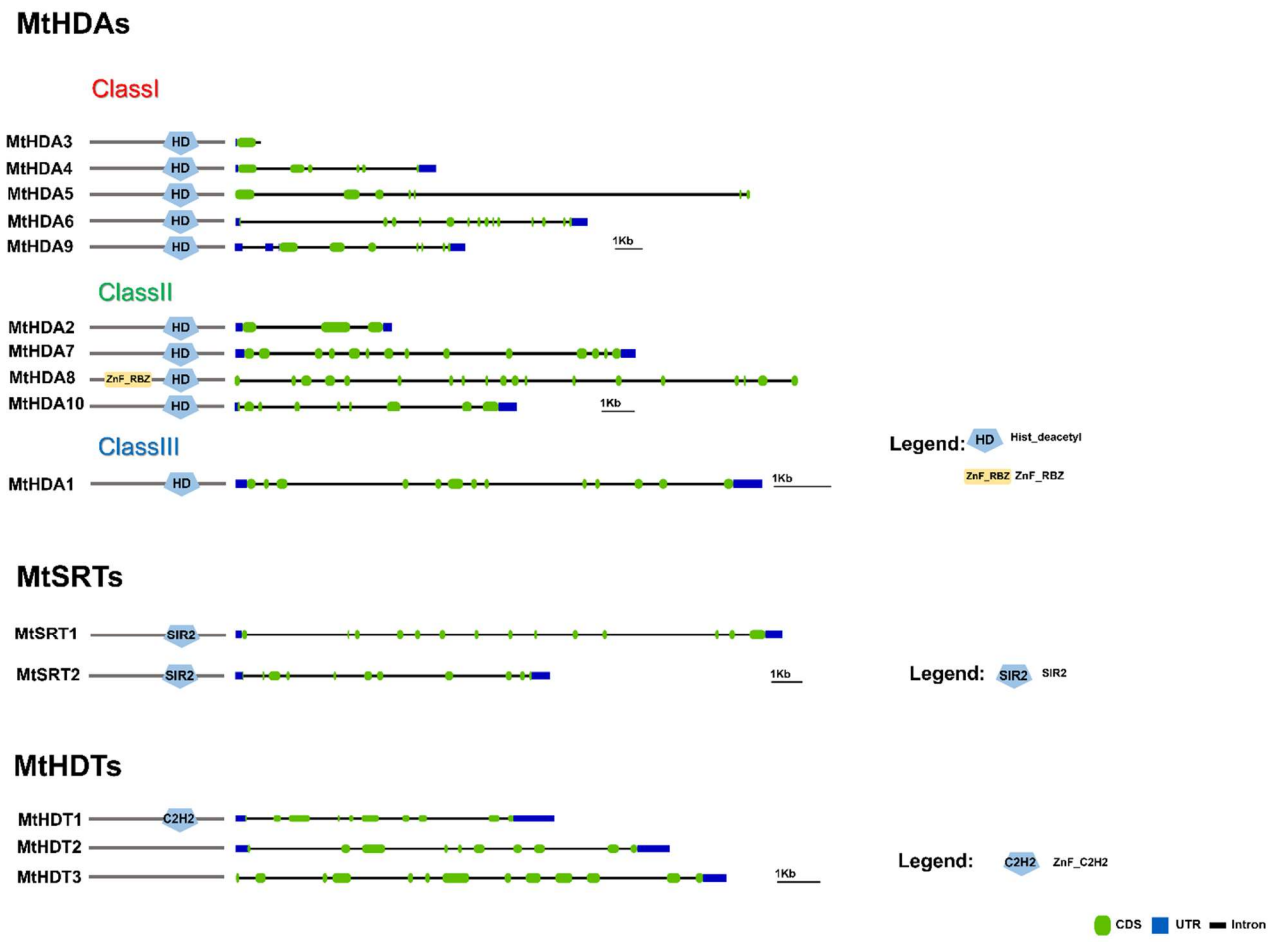


Figure S7. Domain composition and intron-exon structure of *M.truncatula* HDACs.

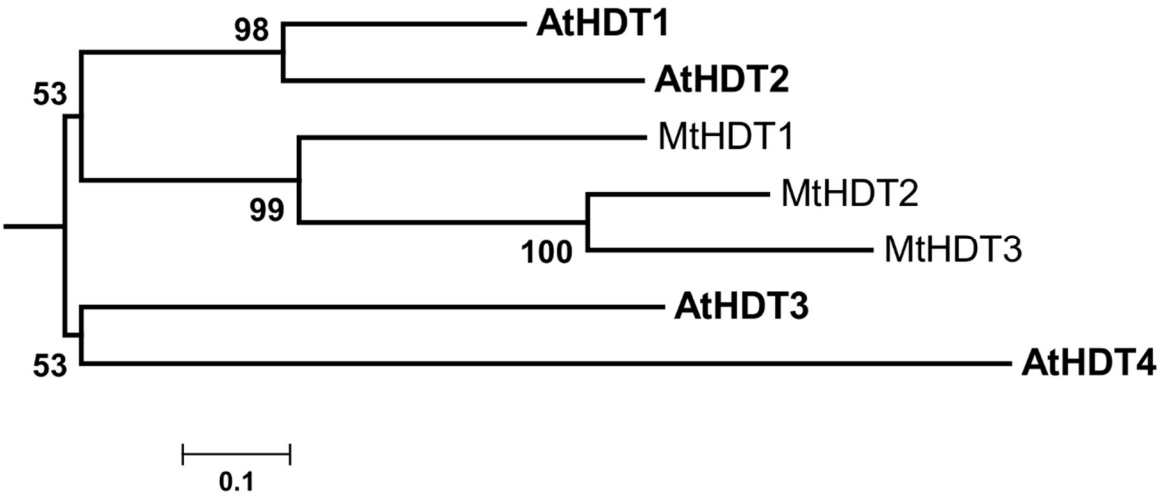


Figure S8. Phylogenetic tree of HDT proteins of *M.truncatula* and *Arabidopsis* (in bold). Numbers near the tree branches represent bootstrap values.