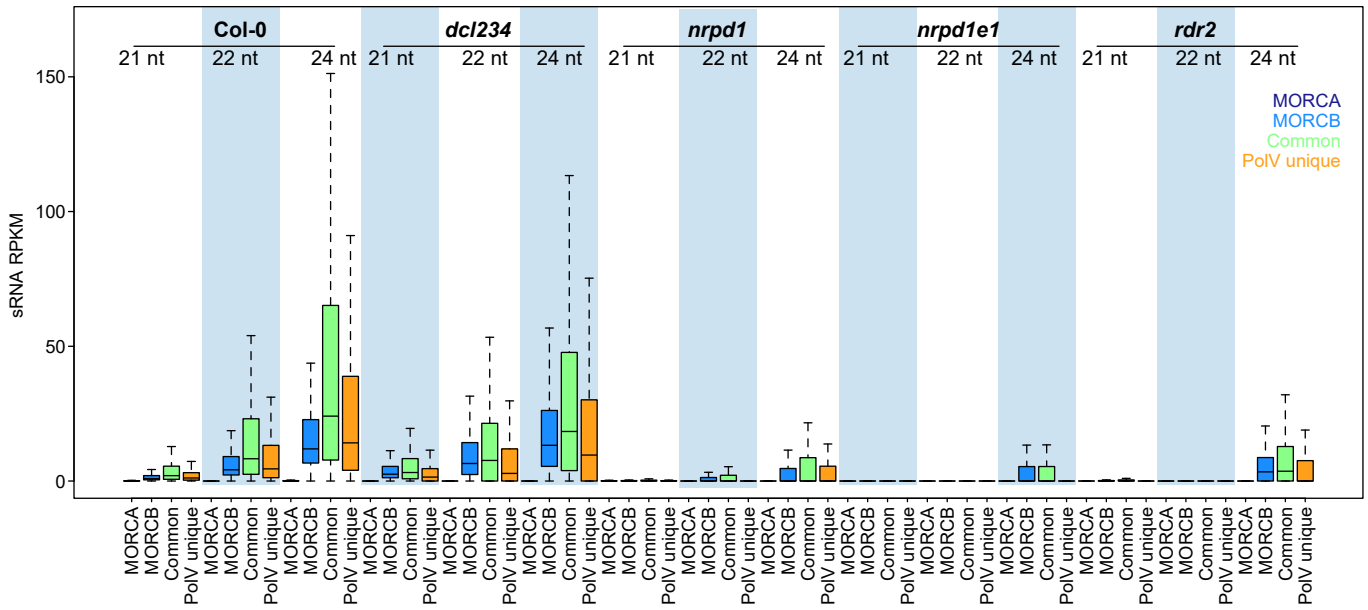
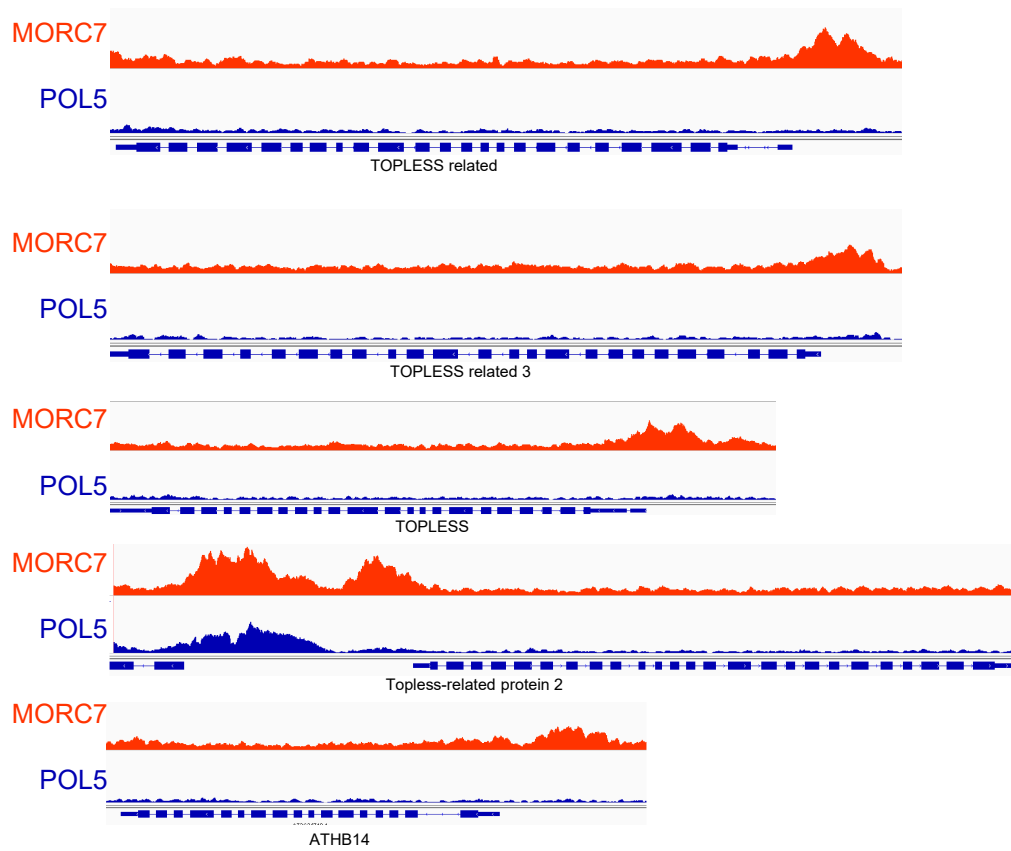


**Fig. S1 Chromatin states of MORC7.** ChIP-seq analysis was performed for H4K16ac, H3K4me3, H3K27ac, H3K9ac, H3Ac, H3K36me3, H3K4me1, H3K36me2, H3K9me2, H3K27me3, Pol II, Pol V, and MORC7.

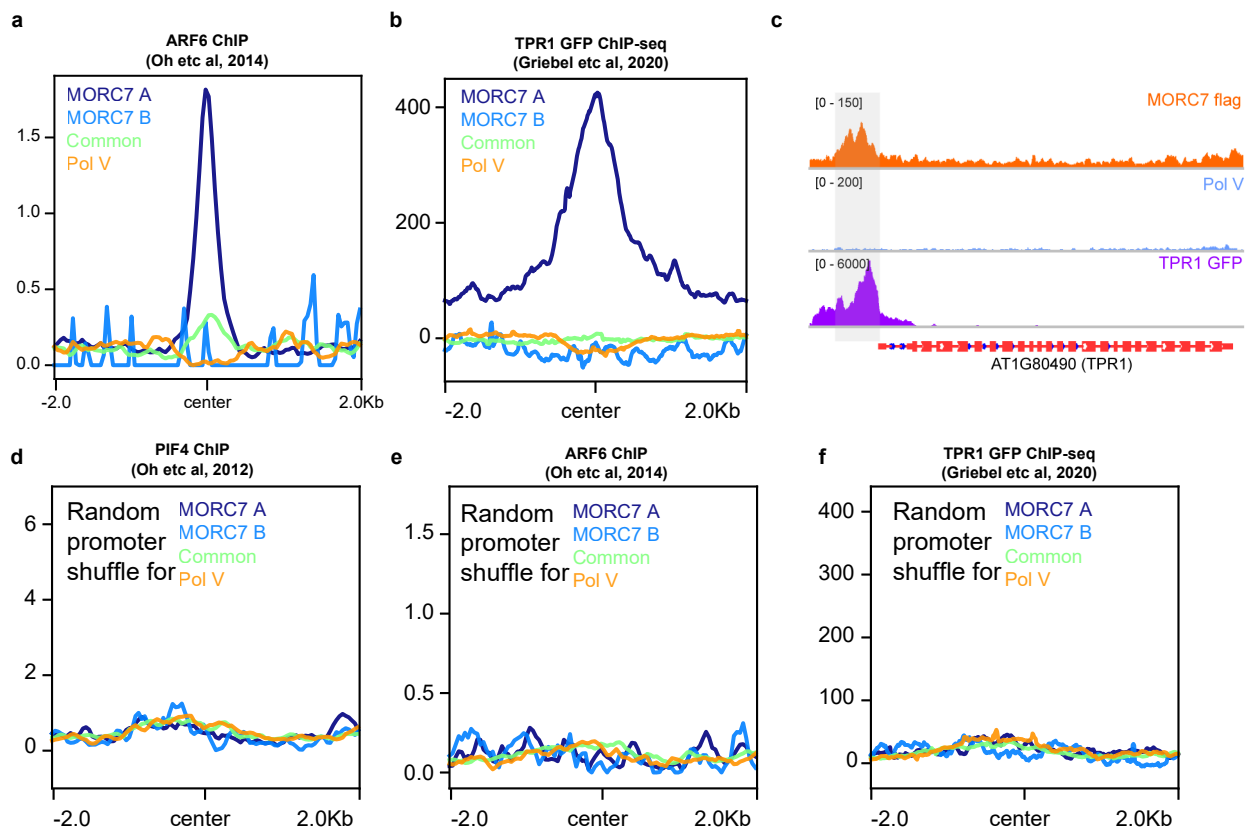
### small RNA (Zhai, 2015)



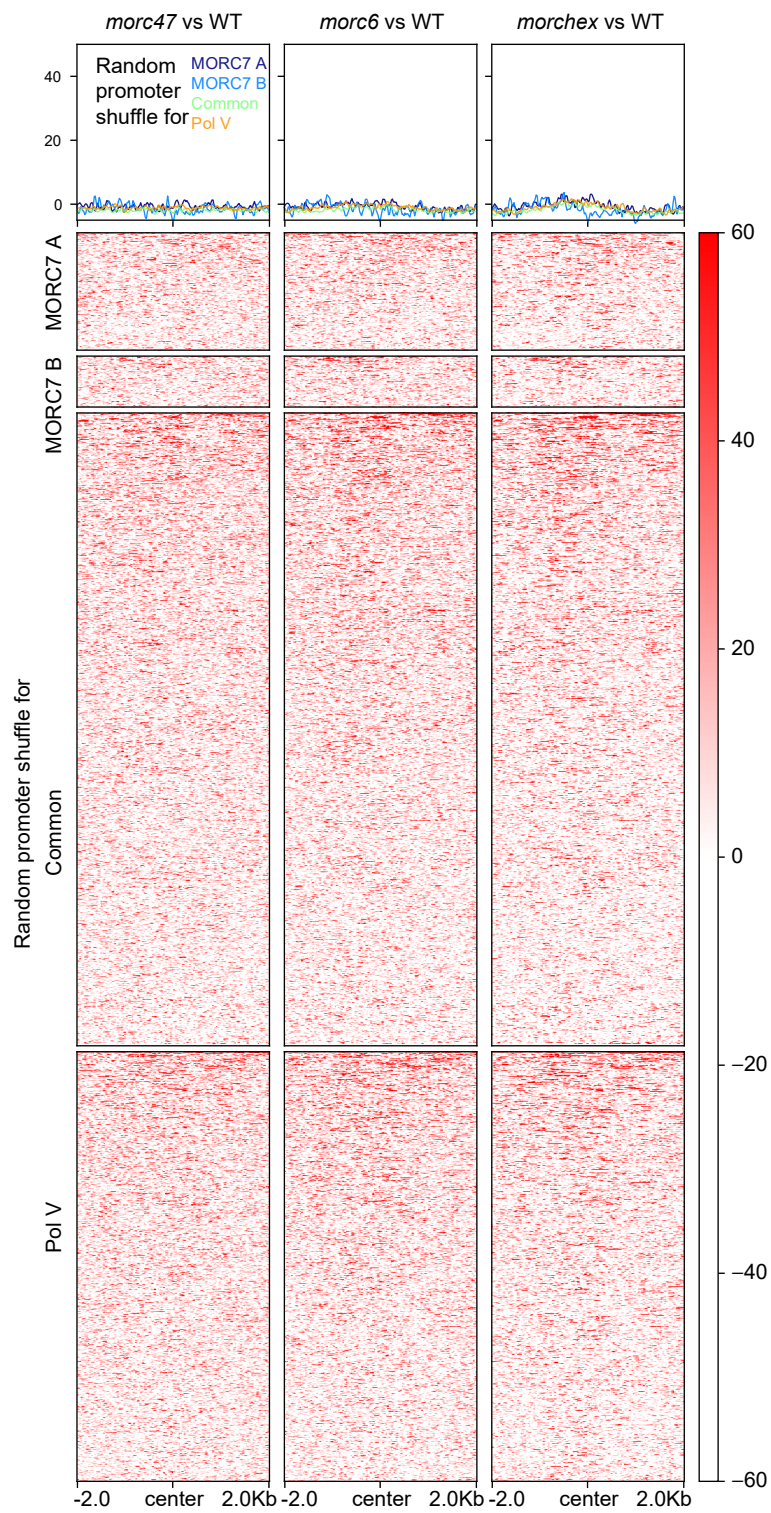
**Fig. S2 Small RNA data over MORC7 peaks.** Boxplot showing 21-nt, 22-nt, and 24-nt siRNA in Col-0, *dcl234*, *nrpd1*, *nrpd1 nrpe1*, and *rdr2* mutants [31] over MORC7A-unique, MORC7B-unique, MORC7-Pol V Common, and Pol V-unique regions.



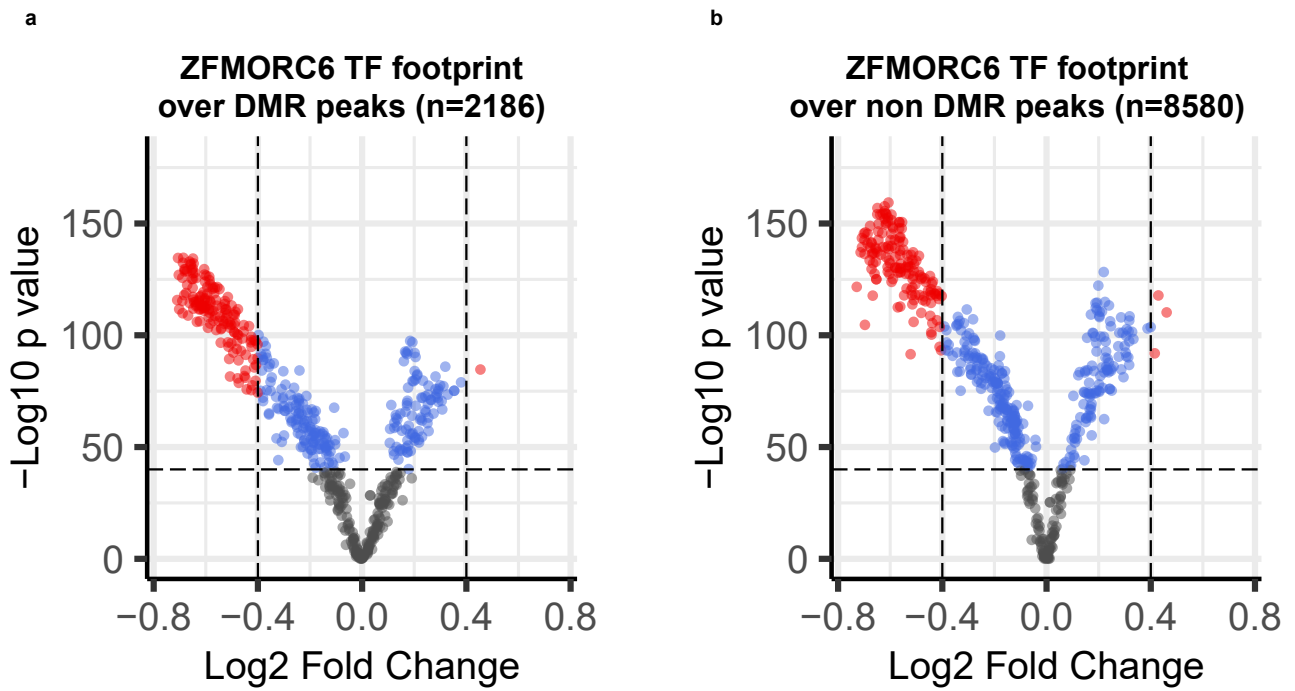
**Fig. S3** Examples showing MORC7 enrichment over the promoter regions of the TOPLESS genes.



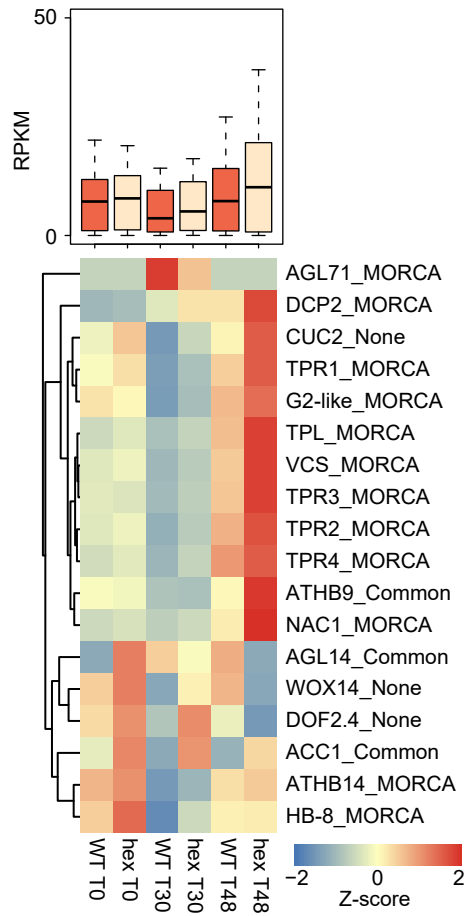
**Fig. S4 MORC7 associates with some TFs.** **a.** Metaplot of ARF6 ChIP-seq data [20] over MORC7A-unique, MORC7B-unique, MORC7-Pol V Common, and Pol V-unique regions. **b.** Metaplot of TPR1 ChIP-seq data [21] over MORC7A-unique, MORC7B-unique, MORC7-Pol V Common, and Pol V-unique regions. **c.** A screenshot showing MORC7A co-localization with TPR1. **d.** Metaplot of PIF4 ChIP-seq data over MORC7A-unique, MORC7B-unique, MORC7-Pol V Common, and Pol V-unique random promoter shuffle regions. **e.** Metaplot of ARF6 ChIP-seq data over MORC7A-unique, MORC7B-unique, MORC7-Pol V Common, and Pol V-unique random promoter shuffle regions. **f.** Metaplot of TPR1 ChIP-seq data over MORC7A-unique, MORC7B-unique, MORC7-Pol V Common, and Pol V-unique random promoter shuffle regions.



**Fig. S5** Metaplot and heatmap showing chromatin accessibility changes in MORC7A-unique, MORC7B-unique, MORC7-Pol V Common, and Pol V-unique promoter random shuffle regions profiled by ATAC-seq.



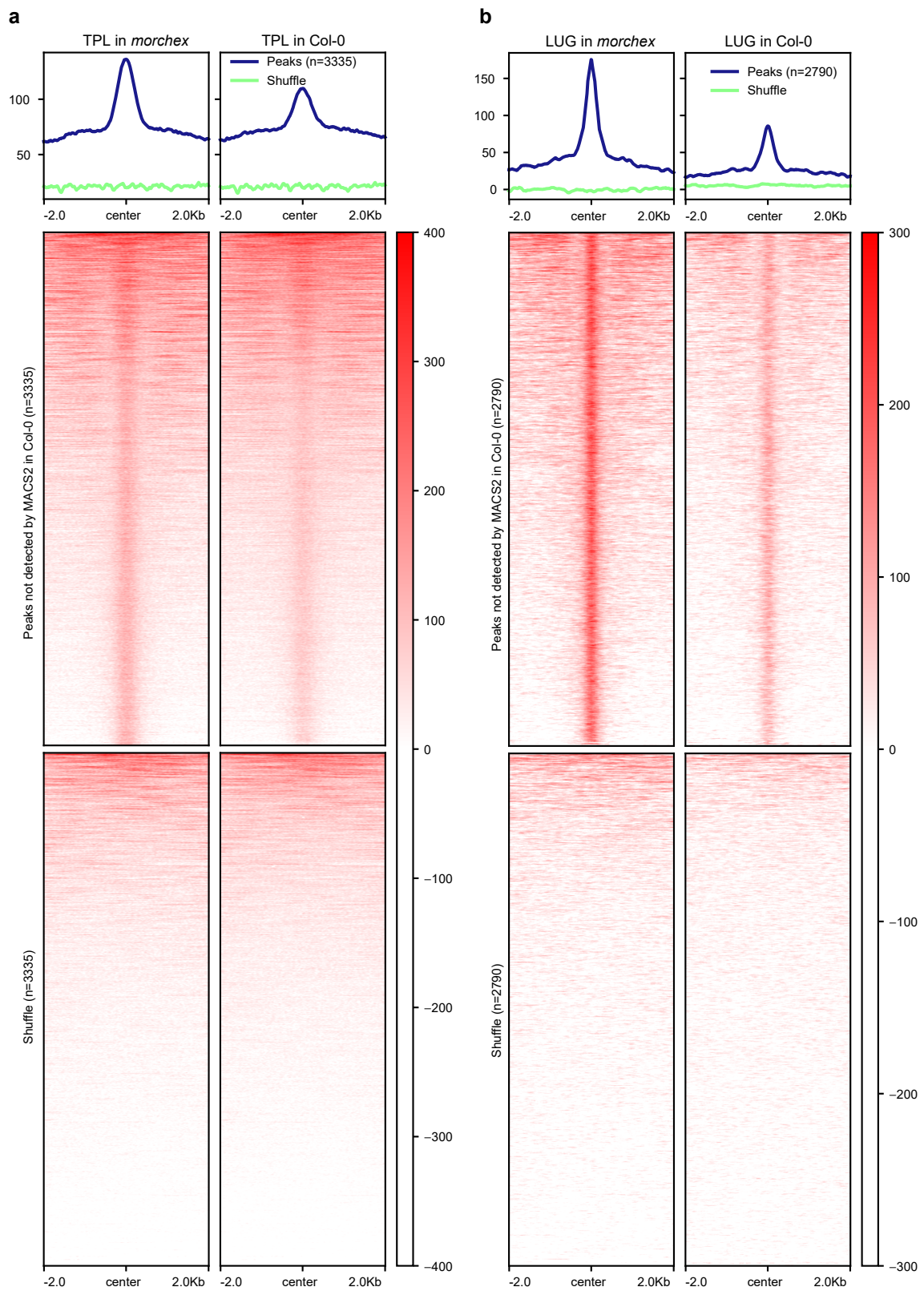
**Fig. S6 a.** Volcano plot showing TF changes for ZF off-target sites (n=2186) that gained DNA methylation comparing ZF-MORC6 and *fwa-4* plants. **b.** Volcano plot showing TF changes for ZF off-target sites (n=8560) that did not gain DNA methylation comparing ZF-MORC6 and *fwa-4* plants. P values were calculated by the two-sided Student's t-test.



**Fig. S7** Expression levels of genes in the primary shoot apical meristem specification pathway, with and without heat treatment, in Col-0 and *morchex* mutants.







**Fig. S9 a.** Metaplot and heatmap showing TPL ChIP-seq signals over peaks detected in *morchex* mutant but not Col-0 by MACS2 (n=3335). **b.** Metaplot and heatmap showing LUG ChIP-seq signals over peaks detected in *morchex* mutant but not Col-0 by MACS2 (n=2790).