

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, MORC7-Pol V Common, and Pol V-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, MORC7A-unique, MORC7B-unique, MORC7A-unique, MORC7A-UNEXA-UNIQUE, MORC7A-UNEXA-UNEXA-UN



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.

TPL in WT					TPL in <i>morchex</i>		
Motif	E-value	Site n	umber		Motif	E-value	Site number
	6.8e-119	1910)		*] 	3.6e-128	3842
	9.7e-092	4229)			4.9e-108	1286
	6.5e-066	1355	5			1.2e-015	11973
	7.8e-031	1142	2			7.8e-024	1279
e AaACACA	1.8e-001	664				1.6e-010	9816
LUG in WT					LUG in <i>morchex</i>		
Motif		E-value	Site numb	ber	Motif	E-value	Site number
	2	4.5e-050	702			1.2e-095	1320
		l.8e-025	1198			4.9e-069	2017
]	l.6e-018	534			7.0e-056	1228
GGAAACAstacTTAgQ		3.6e-004	33			3.8e-019	282
a <mark>CTTTACCC</mark>	2	2.9e-003	49			2.2e-005	1189

Fig. S8 Motif enrichment of TPL and LUG peaks identified in Col-0 or morchex mutant.



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).