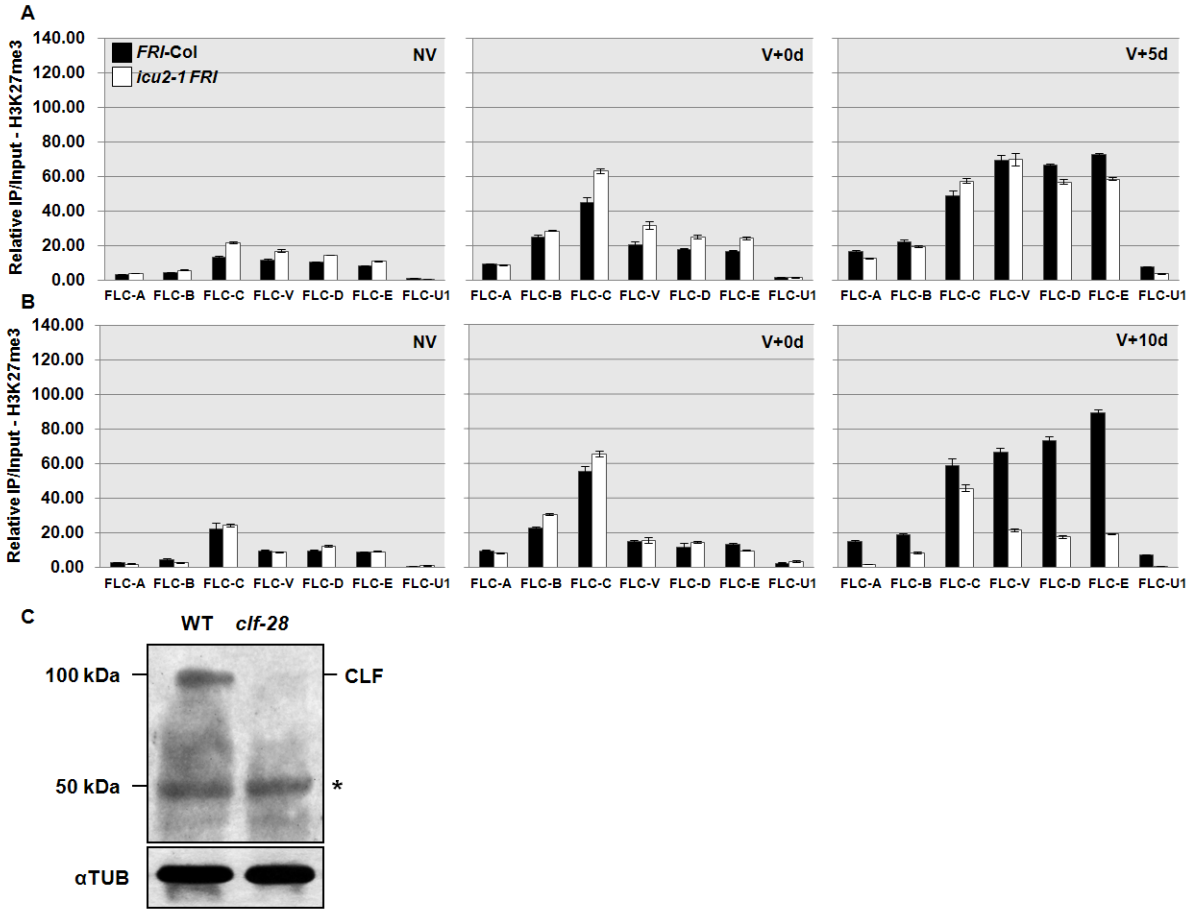

Fig. S1. Role of ICU2 in the mitotic H3K27me3 maintenance and CLF retention. (**A**,**B**) ChIP-qPCR analysis at *FLC* in *FRI*-Col and *icu2-1 FRI* plants; the levels of H3K27me3 at V+5d (A) and at V+10d (B) are shown. Two biological replicates were performed with similar results. Error bars stand for ±s.e.m. of PCR replicates (n=3). (**C**) Generation of CLF-antibody. Western blot analysis using total protein from wild-type and *clf-28* plants was performed to verify the specificity of the anti-CLF antibody. An antibody against αTUB (Sigma Aldrich) was used as a quantification control. The asterisk indicates a nonspecific band.

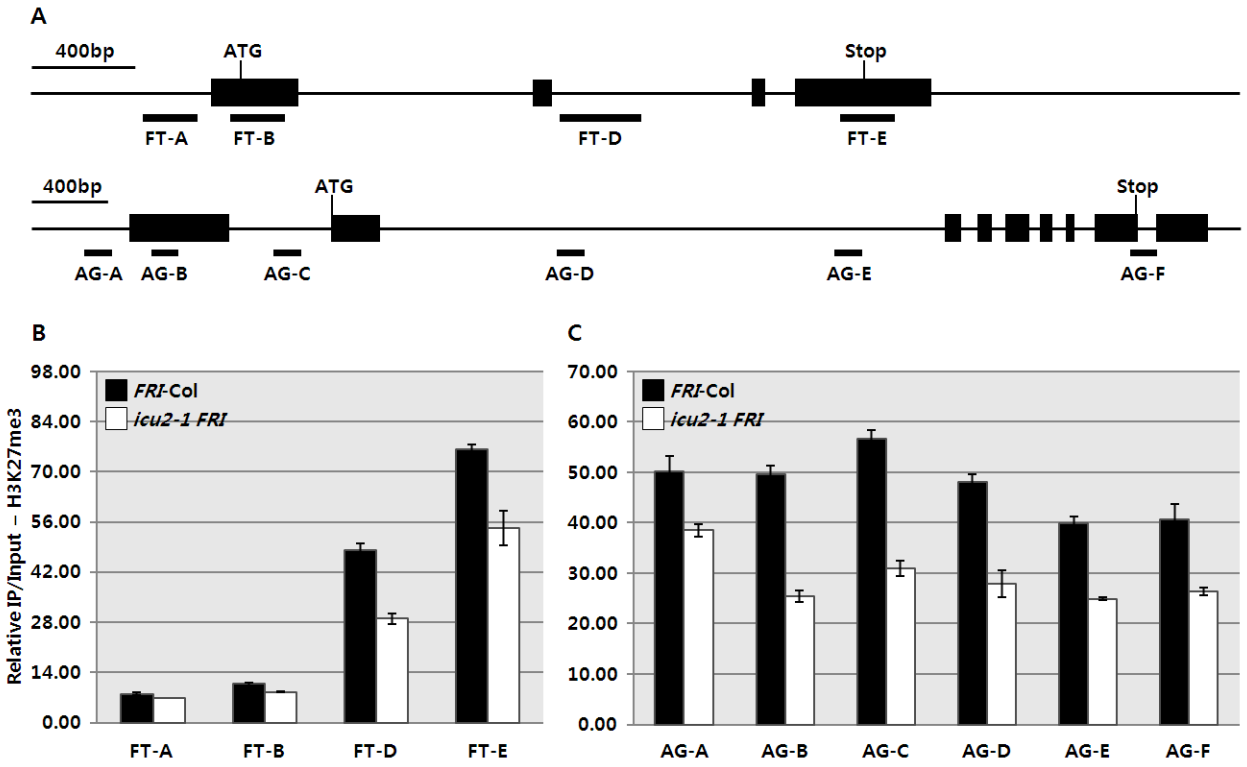

Fig. S2. Reduced levels of H3K27me3 at *FT* and *AG* in *icu2-1 FRI*. (**A**) Schematic of the *FT* and *AG* loci. (**B**,**C**) Levels of H3K27me3 at *FT* (B) and *AG* (C) in 21-day-old seedlings under the NV+LD condition. Three biological replicates were performed with similar results. Error bars stand for ±s.e.m. of PCR replicates (*n*=3).

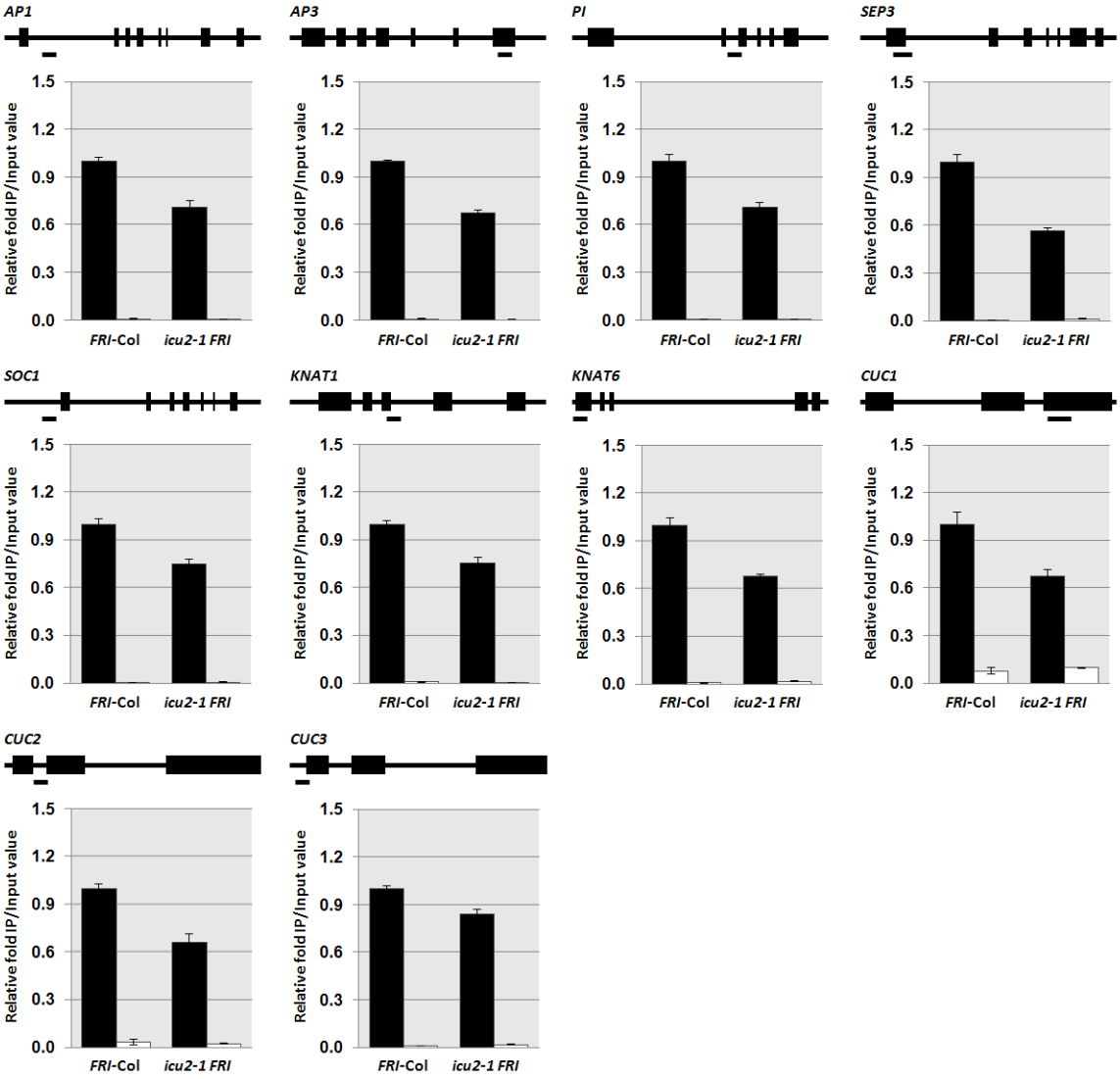

Fig. S3. Reduced levels of H3K27me3 at PRC2 target loci in *icu2-1 FRI*. ChIP-qPCR results are presented. The normalized IP/Input value of wild-type plants was set to 1 for easy comparison. The genomic structure of each gene is presented at the top of each diagram. Black boxes represent exons and PCR amplicon is indicated with black bars. Two biological replicates showed similar results. Error bars stand for ±s.e.m. of PCR replicates (*n*=3). Relative enrichment level of 'no-antibody' control is presented (white bars).

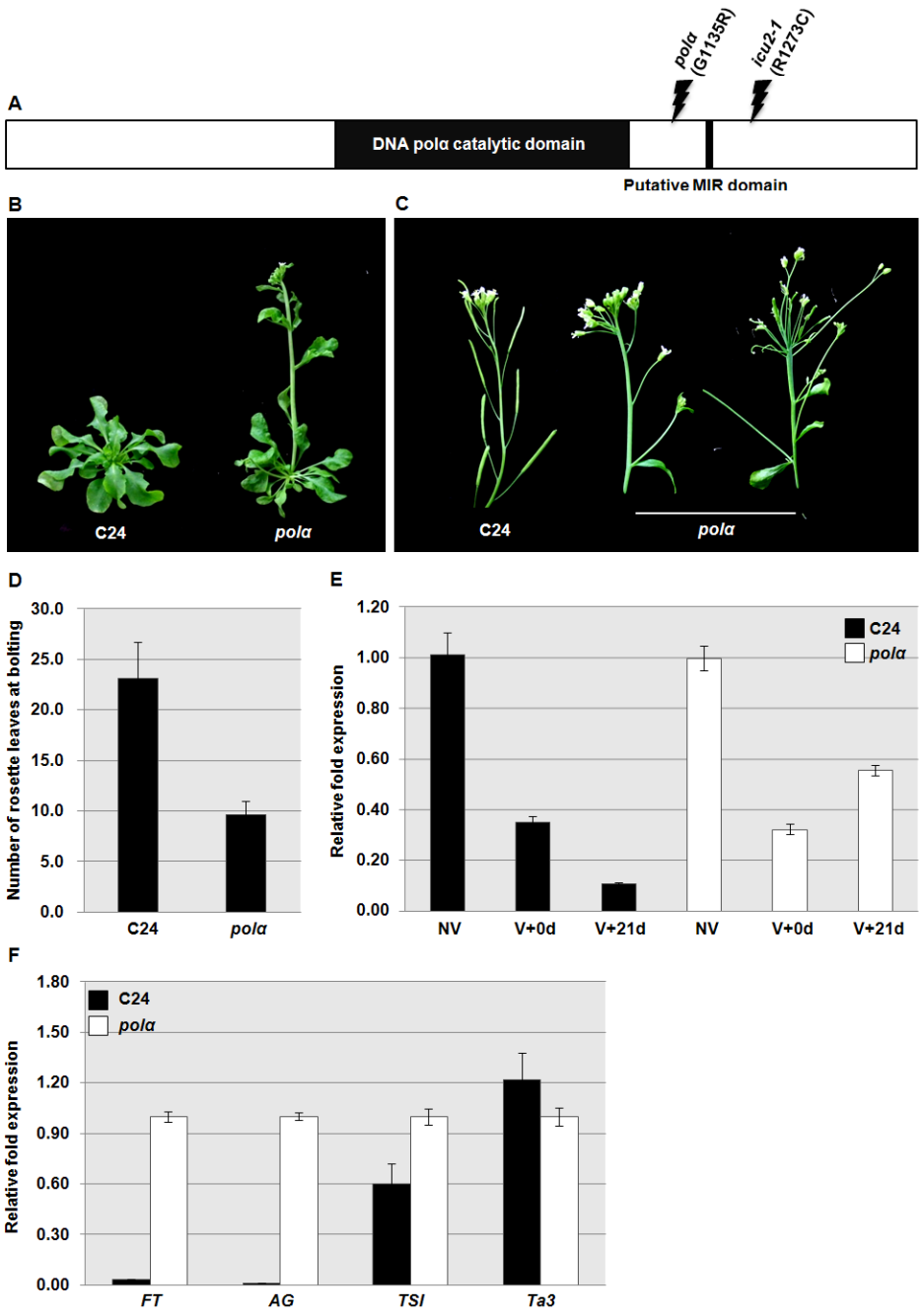

Fig. S4. Epigenetic defects in *polα*. (**A**) Schematic of the mutation sites in the *icu2-1* and *polα* mutations. The sites of mutation and the resulting amino-acid changes are shown. C, cysteine; G, glycine; R, arginine. (**B**) Early flowering phenotype of *polα*. (**C**) Defects in *polα* plants in shoot apical meristem function. Inflorescences from two independent *polα* plants showing the defects are shown. (**D**) Flowering time of *polα*. Error bars represent ±s.e.m. of flowering times from 50 plants. (**E**) Expression patterns of *FLC* at NV, V+0d and V+21d time points. The relative fold expression of *FLC* in wild-type plants grown under NV conditions was set to 1. (**F**) Expression patterns of *FT*, *AG*, *TSI* and *Ta3* in 21-day-old seedlings grown under NV+LD condition. The relative fold expression of each gene in *polα* was set to 1. Error bars stand for ±s.e.m. of PCR replicates (n=3). Two biological replicates were performed with similar results.

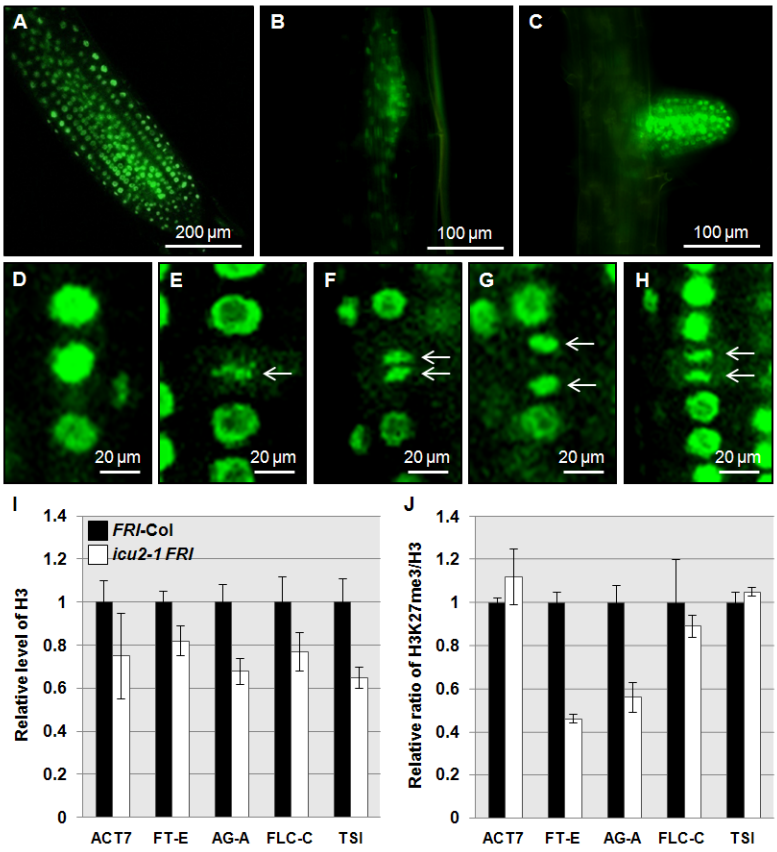

Fig. S5. *ICU2::H3.1:GFP* expression in proliferating root tissues and the nucleosome density in the *icu2-1* mutants. (**A-C**) Expression of *ICU2::H3.1:GFP* in root tips (A) and lateral root meristems (B,C). (**D-H**) Retention of H3.1:GFP fusion proteins on segregating chromosomes in wild-type (D-G) and *icu2-1* (H) root cells. Arrows indicate the segregating chromosomes. (**I**) Nucleosome density in wild-type and *icu2-1 FRI* at diverse genomic loci. Relative enrichment levels between wild-type and *icu2-1 FRI* after IP with H3 antibody are presented. Enrichment level in wild-type at each locus was set to 1 for easy comparison. (**J**) H3K27me3/H3 histone ratio in wild-type and *icu2-1 FRI* at diverse genomic loci. Relative H3K27me3 level against H3 level are compared between wild-type and *icu2-1FRI*. Relative ratio in wild-type at each locus was set to 1 for easy comparison. Error bars represent xxx.

Table S1. Primer sequences.

Purpose	Target	5'-Sequence-3'	Purpose	Target	5'-Sequence-3'
RT-qPCR	*FT*	GATACGAGTAACGAACGGTGAT	ChIP-qPCR	AG-A	CTACCCACCAATAACTCTCTC
		CCCCCTCTCATTTTTATTACAC			ACCCACCATACATCCGGACTT
	FLC	GAGAATAATCATCATGTGGGAGC		AG-B	ATCTAACATGTGTATGTTCCA
		CAACCGCCGATTTAAGGTGG			GAATGGAATCTATGAGATAAG
	ICU2	GCAACAAGCGATGAAGAAAGT		AG-C	ATAACTTGTGTATTACCATCC
		TTTAAGCCAGAATGTGGAATCA			CTGTTGCCGACACACATCTTA
	AG	TCTCAACCGTTTGATTCACGG		AG-D	CGTACATGTAGGACAATTTAG
		GCCTATATTACACTAACTGGA			CTTCTAAACTAATCTTAGCTC
	TSI	ATCCAGTCCGAAGAACGCGAACTA		AG-E	CATTTAGTTACATCCATCACG
		TCACTTGTGAGTGTTCGTGAGGTC			CAGACATGTGACATGTGTCAA
	Ta3	AAGAGAGCTGGCAGAAGCAGTTGA		AG-F	CTCCAGTTAGTGTAAGGACAC
		ACGCCCTTTACCTTGACCTCCTTT			GACCAAATCCATGCTGTCAAG
	H3.1:GFP	GTCTATATCATGGCCGACAA		AP1	CGAAAGACATGGCTATTGGAGAAC
		CTTGTACAGCTCGTCCATGCC			TGAACCCTAGAACACACTAATTAT
	TUB2	ATCGATTCCGTTCTCGATGT		AP3	AGAAGATGGAAGGTAATGATGTCA
		ATCCAGTTCCTCCTCCCAAC			AGGAGATTACGACTCAGTTCTTGG
ChIP-qPCR	FLC-A	TGTAGGCACGACTTTGGTAACA		PI	CATTATTCTTCACCCTTCATTGCC
		GCAGAAAGAACCTCCACTCTAC			AGACTGTATATCTTCTCCCTTCAA
	FLC-B	TATCTGGCCCGACGAAGAAAAA		SEP3	CACAGAGAGACCCATACATACAAG
		TTTGGGTTCAAGTCGCCGGAGA			AAGAGGATAGAGAACAAGATCAAT
	FLC-C	ACCTGGGTTTTCATTTGTTCCC		SOC1	GGTTGCACCATTGATCTACCG
		GAAACAACAAGAGATCCGCCGG			TTAGTTAATTTCCCTTGCACA
	FLC-V	CACACAACCTTTGTATCTTGTG		KNAT1	ATTAGCCCTACCTTGCCACTACAC
		CATGAAGACAAGTGTTGTGGGA			GTCCCATTCACATCCTCAACAATC
	FLC-D	CGCTTTGTAAAGGATATAGGTG		KNAT6	GTGACATCATCAGAACCGACTTAT
		GACTGCTTCCAATTCATTTGCA			ACAATTCAAGAAAGCGATTTAGAA
	FLC-E	CTCTCCACCTTTGATTACAAAG		CUC1	AAAGCGGCGTAGTTAGTAGAGAGA
		CAAGGTGTTCCTCCAGTTGAAC			TCGGTATGAGCAGCAGAGTTATTG
	FLC-U1	GACAAAAGGTTGATGAACTTTG		CUC2	ACCATTCTTTCTCTCCCATCTTAG
		TGTTGCAAAATAAGCCGTAGGC			GTGTGAGCCTTGGCAACTTCC
	FT-A	GTGGCTACCAAGTGGGAGAT		CUC3	AATCCTCTCTCGTTCCTTTCTTCT
		TAACTCGGGTCGGTGAAATC			TATCATTGCTATCTTTGTTCTTCC
	FT-B	TCAACACAGAGAAACCACCTG		ACT7	CGTTTCGCTTTCCTTAGTGTTA
		TCCACCAATCTCAACTCTTGG			AGCGAACGGATCTAGAGACTCA
	FT-D	GCTCAAACATGTTGCTCGAA	Cloning	*ICU2* promoter	GTCGACCAACGCTGCCAGATT
		TGCGATCAGTAAAATACACAGACA			GGATCCTTTTACAAATCCGGTCAATT
	FT-E	GATCTACAATCTCGGCCTTCC		*H3* CDS	GGATCCATGGCTCGTACCAAGCAGACG
		ATCATCACCGTTCGTTACTCG			GGATCCAGCTCGTTCTCCTCTGATTCT