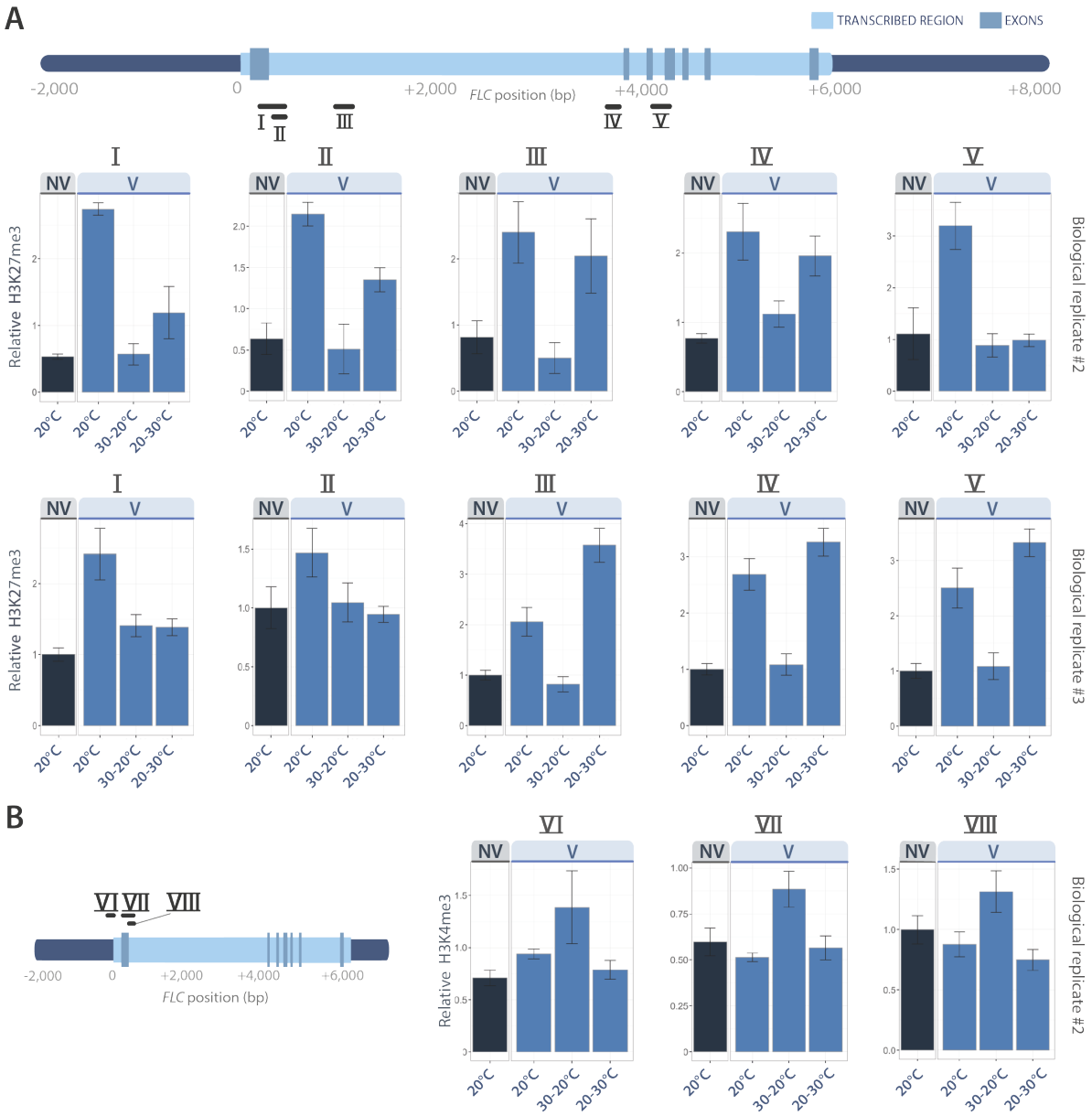

Figure S1. Biological replicates of H3K27me3 and H3K4me3 ChIP experiments. A, H3K27me3 relative abundance (± SE of 3 qPCR technical replicates) at different positions of the *FLC* locus for non vernalized seedlings (NV) and after 6 weeks of vernalization (V) followed by 3 weeks of warm (20°C), or 1 week of heat (30°C) given before (30-20°C) or after (20-30°C) 2 weeks of warm. H3K27me3 quantifications are relative to constitutive marks at *AGAMOUS* and *SHOOT MERISTEMLESS* genes. Data are from 2 independent experiments. B, H3K4me3 quantifications (± SE of 3 qPCR technical replicates) relative to constitutive marks at *ACTIN7* and *UBIQUITIN10* genes. Primers used are listed in tables S1 and S2.

Table S1. List of primers used for H3K27me3 marks quantification.

	Targeted region	Locus	Name in figure 1A	Primer	Primer binding (relative to the transcription start site)	Amplicon size	Tm (°C)	Sequence	Calculated efficiency	Hydridization temperature	Refs.
FLOWERING LOCUS C	Nucleation region	*FLC* (AT5G10140)	I	FOR	157	177	58.17	CGACAAGTCACCTTCTCCAAA	112,9 % (R^2=0,990).	60	1
				REV	333		56.09	AGGGGGAACAAATGAAAACC			
		FLC (AT5G10140)	II	FOR	235	99	60.25	GTCGCTCTTCTCGTCGTCTC	93,5% (R^2=0,995)	60	2
				REV	333		56.09	AGGGGGAACAAATGAAAACC			
		FLC (AT5G10140)	III	FOR	936	181	59.09	TTCCTATCTTTGCTGTGGACCT	125 % (R^2=0,99).	60	1
				REV	1106		56.24	GAATCGCAATCGATAACCAGA			
	Nucleation distal region	*FLC* (AT5G10140)	IV	FOR	3710	84	56.73	GTTTCCAGTGGCCTTTTCAA	97,4 % (R^2=0,995)	60	3
				REV	3793		59.54	GACCAGGCTGGAGAGATGAC			
		FLC (AT5G10140)	V	FOR	4008	190	55,98	CTTTTTCATGGGCAGGATCA	99,8 (R^2=0,988)	60	1
				REV	4197		56,31	TGACATTTGATCCCACAAGC			
H3K27me3 positive controls	First exon	*STM* (AT1G62360)	NA	FOR	92	104	56.63	GCCCATCATGACATCACATC	112 % (R^2=0,996)	60	1
				REV	195		59.38	GGGAACTACTTTGTTGGTGGTG			
	Coding region	*AGAMOUS* (AT4G18960)	NA	FOR	1112	129	55.86	TGGGAGAGGAAAGATCGAAA	101,3 % (R^2= 0,996)	60	4
				REV	1240		57.76	GCGACTTCAGCATCACAAAG			

Table S2. List of primers used for H3K4me3 analysis.

	Targeted region	Amplfied locus	Name in figure 1B	Primer	Primer binding (relative to the transcription start site)	Amplicon size	Tm	Sequence	Calculated efficiency	Hydridization temperature	Refs.
FLOWERING LOCUS C	Promoter & beginning of the transcribed region	*FLC* (AT5G10140)	VI	FOR	-34	80	56.44	GTAGATAGGCACAAAAAATAGAAAGAA	113,8 % (R^2=0,992).	60	1
				REV	23		52.86	GAGATACTAAGCGTTTTCTCT			
		FLC (AT5G10140)	VII	FOR	157	177	58.17	CGACAAGTCACCTTCTCCAAA	112,9 % (R^2=0,990).	60	1
				REV	333		56.09	AGGGGGAACAAATGAAAACC			
		FLC (AT5G10140)	VIII	FOR	235	99	60.25	GTCGCTCTTCTCGTCGTCTC	93,5% (R^2=0,995)	60	2
				REV	333		56.09	AGGGGGAACAAATGAAAACC			
H3K4me3 positive controls	First exon	*UBQ10* (AT4G05320)	NA	FOR	1934	62	63.5	GGGCCTTGTATAATCCCTGATGAATAAGTG	100,5 % (R^2=0,996)	60	5
				REV	1895		60.74	AAAGAGATAACAGGAACGGAAACATAGT			
	Coding region	*ACT7* (AT5G09810)	NA	FOR	728	108	57.13	GATATTCAGCCACTTGTCTGTG	107,5% (R2=0,991)	60	6
				REV	835		56.23	CTTACACATGTACAACAAAGAAGG			

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