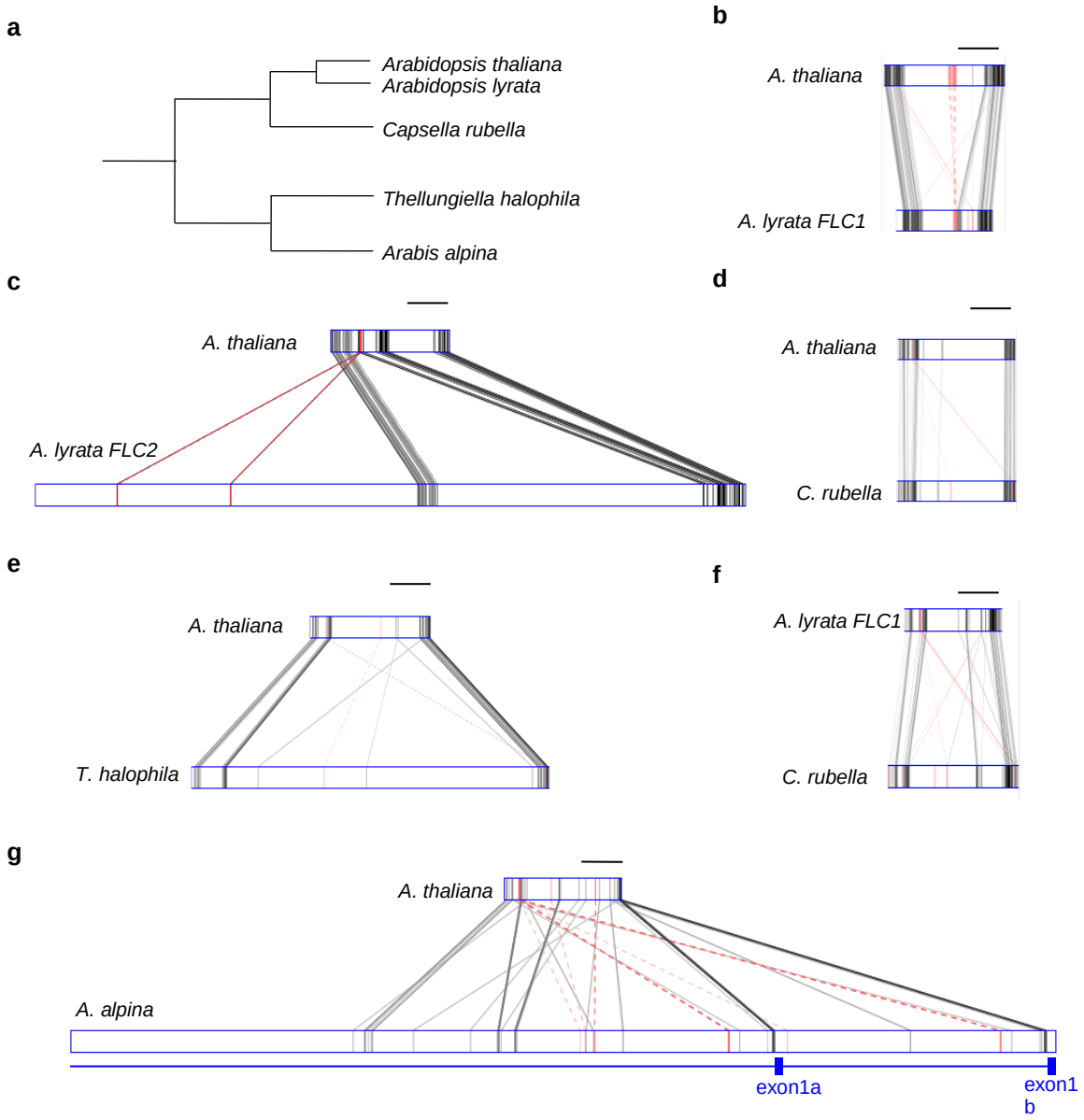
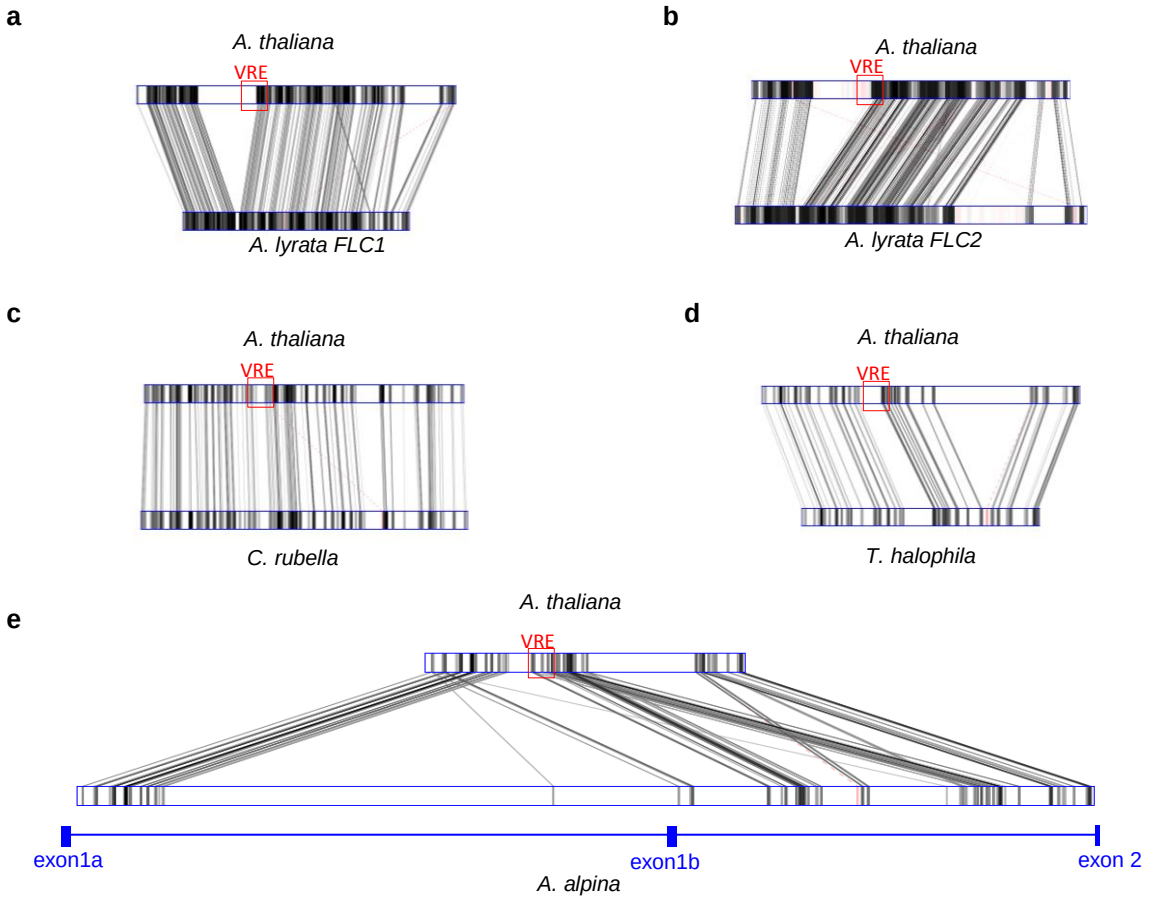


Supplementary Figure 1: 5′ promoter conservation among *FLC* orthologues
Schematic representation of phylogenetic relationship of Brassicaceae species used in this study **(a)**. GATA alignment of *A. thaliana* to *A. lyrata FLC1* 5′ intergenic region **(b)**, to *A. lyrata FLC2* 5′ intergenic region **(c)**, to *C. rubella FLC* 5′ intergenic region **(d)** and to *T. halophila FLC* 5′ intergenic region **(e)**. GATA alignment of *A. lyrata FLC1* to *C. rubella FLC* 5′ intergenic regions **(f)** showing that the low level of homology observed in **b**, **c**, **d**, **e** and **g** is not due to *A. thaliana* containing a unique *FLC* 5′ intergenic region. GATA alignments of *A. thaliana FLC* 5′ intergenic region to the full *PEP1*a and b 5` intergenic regions **(g)**. The position of *PEP1* exon 1a and 1b on the *A. alpina* alignment is indicated by blue boxes on a blue line under the alignment.
Grey boxes are homologous regions whereas the red boxes indicate homologous inverted regions (the darker the box, the higher the similarity). Scale bars, 1 kb.



f

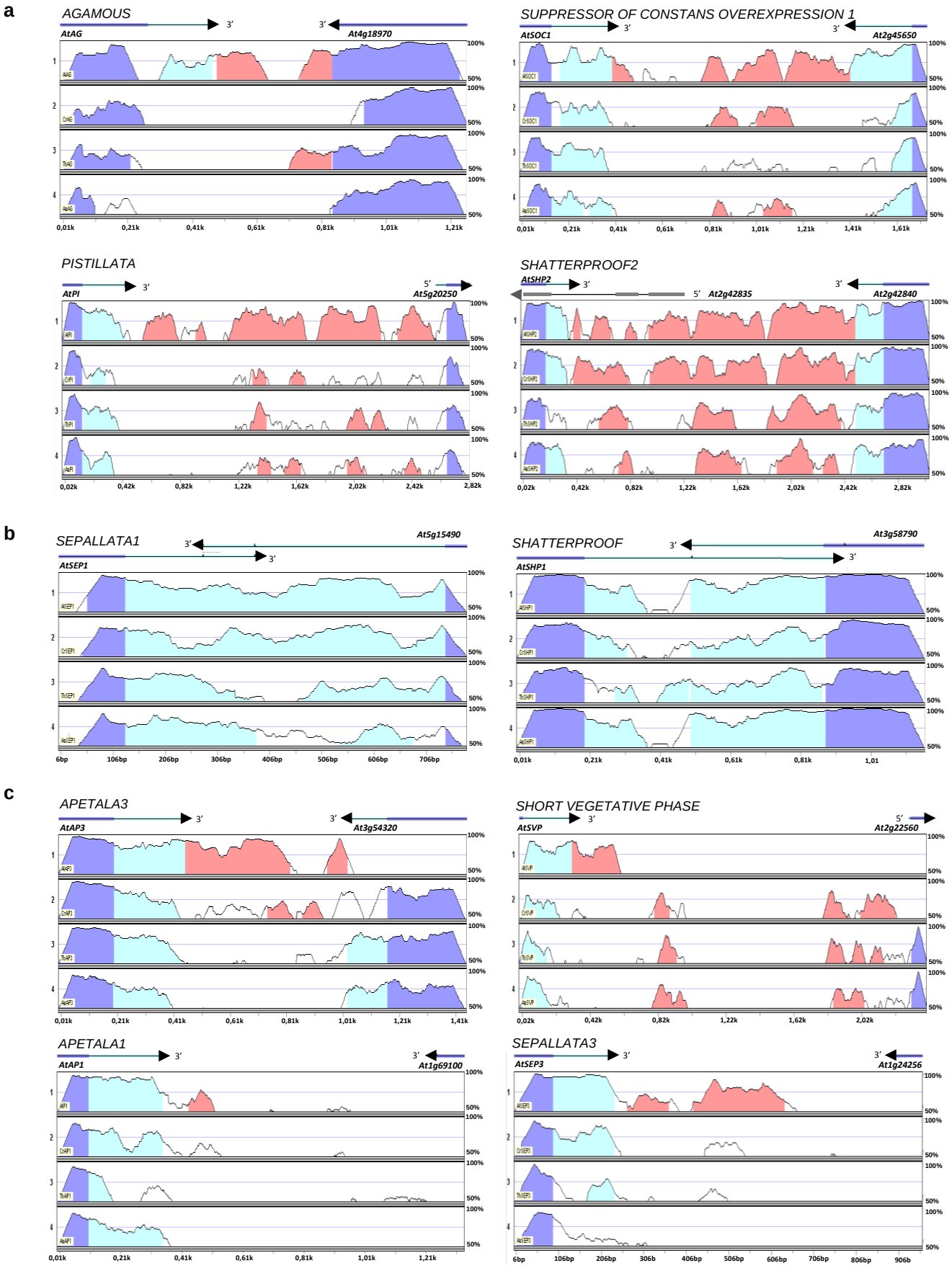
```
AlVRE-Like_FLC1  ----------------------------------------------------------------------------------------------------------------------
AlVRE-Like_FLC2  ----------------------------------------------------------------------------------------------------------------------
AtVRE            --ATAGATTTGCCTCATATTTATGTGATTGTATATCAATTATCGCCCTTAATCTTATCATCGTTGTGTTCATT-TATGACTTTGTTCCTATTCGTTAAAATTGACAATCCACAACCTCAA
ThVRE-Like       ----------------------------------------------------------------------------------------------------------------------
CrVRE-Like       ACATAGATATGCTACATATCTATGTGTTTGTTTATCAATTATCACTCTTCGTCTTATAAGGCATATGTGCATTATAAGACTTTGTCCCTATT------ATTTTACTATGTATTAATTTGA
AaVRE-Like1      ------------TAAATATTTAAGTGATTGGATATCAATTATAACCCTTAATCT-ATATCTGTTGTGTGCAATGTATGAATTT----------------------AACTGGTAGCTTTGG
AaVRE-Like2      ------------------------------GGTA--AATTTTCACCCTTAATCTTATATCT---GTGTGCAATGCATAAATT----------------------AGCTTGTAGCTTTGG


AlVRE-Like_FLC1  ----------------------------------------------------------------------TCACACAACCTTTGTATCTTGTG-TCTTTTGTCATAGAAATTGTCAA
AlVRE-Like_FLC2  ----------------------------------------------------------------------TCACACAACCTTTGTATCTTGTG-TCTTTTGTCATAGAAATTGTCAA
AtVRE            TCTTTTGTTGTGAA-----------------AATCGACAATCACACAACCTTTGTATCTTGT---GTCTTTTGTCACACAACCTTTGTATCTTGTG-TCTTTTGTCATGGAAATTGTCAT
ThVRE-Like       ----------------------------------------------------------------------ATCACACAAC-TTTGTATCTTGTG-TCTTATGTCATGGAAATTGGCAA
CrVRE-Like       CATTGTAGTGTTGATCATTGGAATCAACATGAATCCACAACCTTGTAACTTTTGTTGTGTAA---ATCAACAATCATACAAGCTTTGTATCTTGGGGTCTTTTGTCATGATTATTGTCAA
AaVRE-Like1      TCGTTGGAAATGACA----------------ATCACACAACCTTGTGTCTATTCCCCATCAACCAATCGATAATTACACTAC-CTTGTATCTTGCG--TTTTTTTCATGGAAATGGACAA
AaVRE-Like2      TCACTAAAACCGACC----------------ACCACACAACCTTGTATCTATTGCA-GTGAA--AATAGACAATTACGCAAC-CTTTTGTCTTGCG--TCTTTGTCATGGAAATGGACAA
                                                                                                     * *  * *   ** * ***** *    * * ****    ** * **

AlVRE-Like_FLC1  TAACACA--GCC-TTGTTTCTTTGGTGCCTCTAG-GAAATTGGAAATCCCTCAAAA------CTTGTCTTCATATAAGAAATA--
AlVRE-Like_FLC2  TAACACA--GCC-TTGTTTCTTTGGTGCCTCTAG-GAAATTGAAAATCCCTCAAAA------CTTGTCTTCATATAAGAAA----
AtVRE            TCACACA--GCC-TTGTTTCTTTGGTGCCTCTAG-GAAATTGAAAATCCCACAACA------CTTGTCTTCATGTAAGAAATA--
ThVRE-Like       TAACATG--CCCCTTGTATCTTTGGCGCCTCTAG-GAAATCGAGAACCCTACAGAAAAACTTTTTGTCTTCATGGAAGAAATACC
CrVRE-Like       TAACTCA--ACC-TTGTTTCTCTGTTGCCTCTAATGAAATTGAAAACTTCACAAAA------CTTGTCTTCATGTAAGAAATAC-
AaVRE-Like1      TAACACT--AAC----TTTCTTTGGTGCCTCTTG-GAAATCGACAATCCCAC------------------CAAAAAA--------
AaVRE-Like2      TAACACTGTACC----TTTCTTTGGTGCCTCTTG-GAAATCAATAATCCCAC------------------CA-------------
                 * **       *    * *** **  ******   *****    **     *                 **
```

Supplementary Figure 2: First intron conservation among *FLC* orthologues and alignment of VRE-Like sequences

GATA alignment of *A. thaliana FLC* first intron to first intron of *A. lyrata FLC1* orthologue **(a)**, *A. lyrata FLC2* orthologue **(b)**, of *C. rubella FLC* orthologue **(c)** and of *T. halophila FLC* orthologue **(d)**. GATA alignment of *A. thaliana* first intron to the region spanning exon 1a to exon 2 of *A. alpina PEP1* **(e)**. Multiple alignment of the AtVRE, AlVRE-Like from *AlFLC1,* AlVRE-Like from *AlFLC2*, CrVRE-Like, ThVRE-Like, AaVRE-Like 1 and AaVRE-Like 2 nucleotide sequences **(f)**.

```
AlFLC1          GACAAAAAGGTTGATGA-----------AACTTTGTACCTTATTCGTGAGAGAA-TTGCA 48
AlFLC2          GACAAAAAGGTTGATGA-----------AACTTTGTACCTTATTCGTGAGAGAA-TTGCA 48
AtFLC           GACAAAAGG-TTGATG------------AACTTTGTACCTTATTCGTGTGAGAA-TTGCA 46
PEP1            GACATAACTATTTATGG-----------ATCTTCGTACCCTTGTTTCGAGAGAAGTTGCA 49
CrFLC           GACAAAACTAAACTACTGTACGATGAAACGTATTGTACCTTATCCGAGGGAGAG-TTTTT 59
ThFLC           GACAAGAGTATGTAACT---------------TTGTACCTTTTTCGAGAGAGAA-TTCTT 44
                ****  *                        * ***** *      * ****  **

AlFLC1          TCGAGATCTTGCGTGTATGTGTTCT-TCTCTTCTCT--CTAAAACTTGTGTTTGCTTCAC 105
AlFLC2          TCGAGATCTTGCGTGTACGTGTTCT-TCTCTTCTCT--CTAAAACTTGTGTTTGCTTCAC 105
AtFLC           TCGAGATCTTGAGTGTATGTGTTCT-TCACTTCTGT--CAAAAACTTGTGTTTGCTTCAC 103
PEP1            GCGAG--CTT--GTTCATGTGTTCT-TGTGTTCTAT--CAAAAACTTGAGTTTGCTTCAC 102
CrFLC           GCA----------TCGACATGTTGTGTGTGTTCTTCTTCTCTTCTTTGTGTTTCCTTCAC 109
ThFLC           -CAGT--------TCTTTGTGTTCT-TCCGTTCCGC--CAAAAACTTGTGTTTGCTTCAG 92
                 *           *     **** * *   ***     *      *** **** *****

AlFLC1          TGTGAAGAAG--CCTACGGCCTATTTTGCAAAGAAAACGTGGC------GCTCTCT-CAG 156
AlFLC2          TGTGAAGAAG--CCTACGGCCTATTTTGCAAAGAAAACGTG--------GCTCTCT-CAG 154
AtFLC           AGTGAAGAAG--CCTACGGCTTATTTTGCAACAGGGACGTGGCTCTCTCTCTCT-CTG 160
PEP1            GGTGAAGAAGCCCCTACGGCTTATTTTGCAAAACCGACGTG--------GCACACTTCTC 154
CrFLC           AGTGAAGAAG-CCTTTCTGCTTATTTTGCAATGGAGGCGTG--------GCACAATTCTG 160
ThFLC           GGTGAAGAAG-CCT-ACGGCTTATTTTGCAATCGAAACGTG--------GC-CGTCTCTG 141
                 *********  *   * ** **********      ****         * *    *

AlFLC1          TGCGTTTTTTTTCTCGTCGTAATTAAT-------------AAACGCG-AATGGTTGGAAT 202
AlFLC2          TGCGTTTTTTTTCTCGTCGTAATTAATTTGTTTTTATCCTAAAAGCG-TATGGTTGGAAT 213
AtFLC           CGCGTTTTTTCTCTCGTCGTAATTAATTTGTTTTTATCCTAAACGCG-TATGGTTGGCAT 219
PEP1            TGCTGGCTTCTCTTCGTAATTAATAATTGGGTTTTGTTTTTATTTAG-AACG--CGTTTT 211
CrFLC           CTATTT-ATGTCTTCGTG-AGTTAGTTTGTTTTTATCTTAAAACGCGTTGTGGTCGTCAT 218
ThFLC           CTTTTTTCTGATATTTTG-TCTCAG-----TTTTAATTTAAAACGCG-TATGGCTGTCAT 194
                       *    *  *                       *    *    *   *   *

AlFLC1          GG--GTTTATTGGGCCCATGTCGGTCACCTT-- 231
AlFLC2          GG--GTTTCTTGGGCCC---------------- 228
AtFLC           GG--GTTTTTTGGGCCTATGTCGGTCACATT-- 248
PEP1            GGTTGTGTCATGGGTTCATGTCGGTCAGCTT-- 242
CrFLC           GGGTTTCTCTTGGGCCCATGTCGGTCATTTTTT 251
ThFLC           GGGTTTCTAT-GGGCCCTCGTCGGTCACCTG-- 224
                **   * *   ***
```

Supplementary Figure 3: Conserved block at the 3' end of *FLC* homologues
Multiple alignments of the nucleotide sequences present in the conserved regions at the 3' ends of *FLC* orthologues and shown in Fig. 1c. Stars indicate 100% conserved bases.

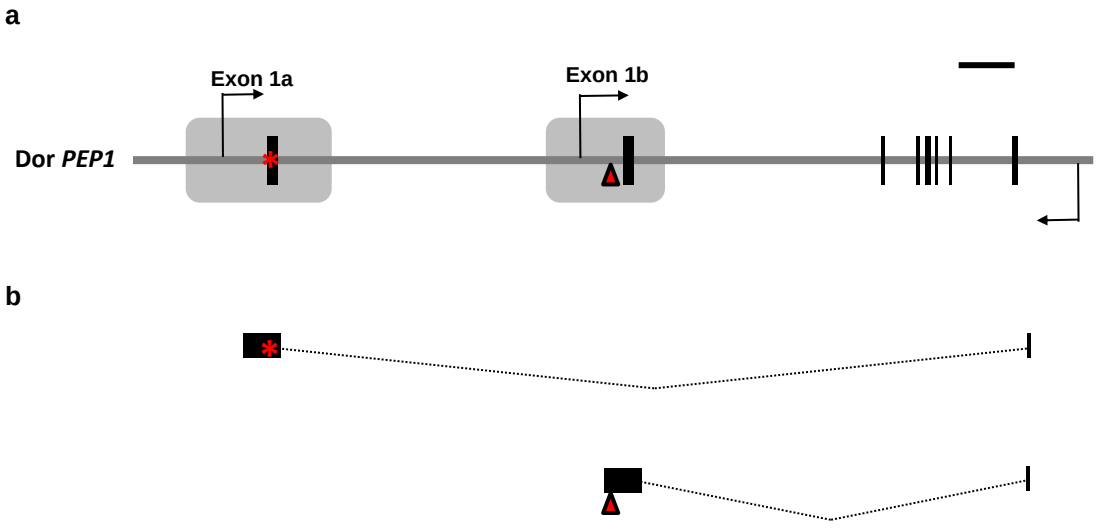


Supplementary Figure 4

Supplementary Figure 4: Alignment of 3' intergenic region of 10 randomly chosen MADS box genes

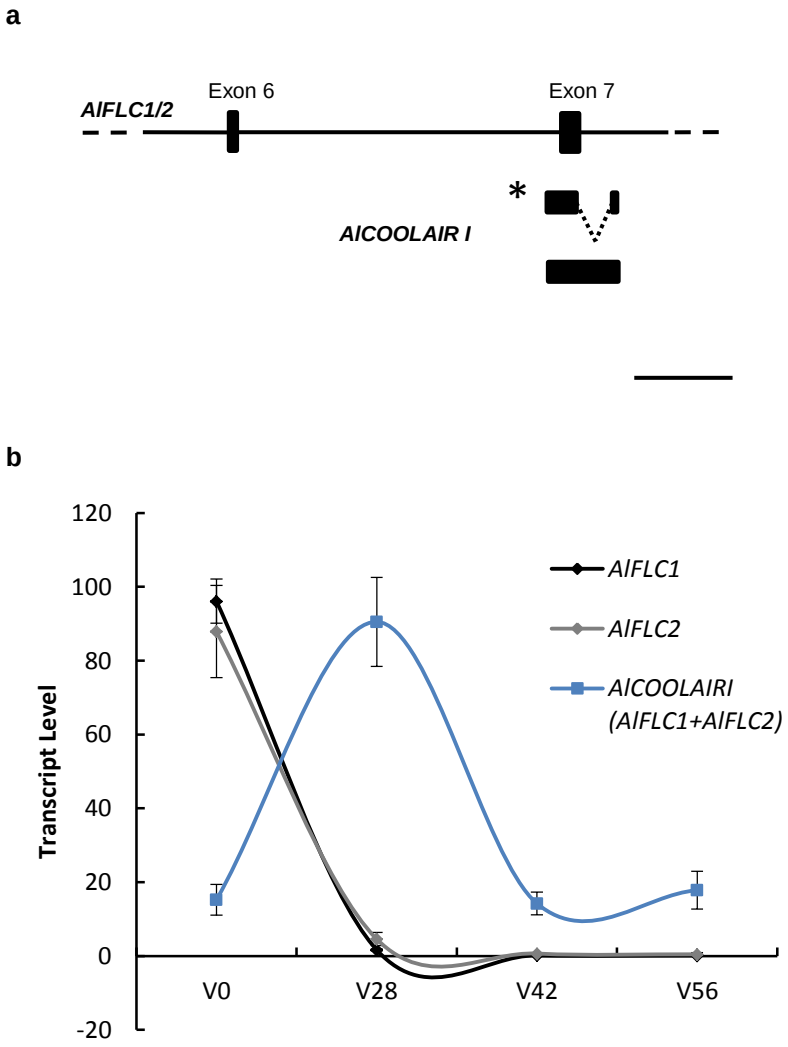
3' Intergenic region (spanning the last exon of the MADS box gene on the left to the first exon of the dowstream gene on the right) from from *A. lyrata* (1), *C. rubella* (2), *T. halophila* (3) and *A. alpina* (4) MADS box genes have been aligned to their *A. thaliana* homologue (based line) using mVista pairwise alignment tool. (**a**) Genes with conserved synteny with *A. thaliana*. For *SHP2,* the antisense non coding gene exons are represented by grey boxes, (**b**) Genes with conserved synteny with *A. thaliana* and overlapping untranslated regions, (**c**) Genes for which the synteny with *A. thaliana* is not conserved in one, two or all species aligned.

Gene names and transcript models are presented on top of the alignments. The arrow points towards the 3'end of the gene. Colored areas illustrate stretches of homology greater than 75% identity at the nucleotide level. Pink, regions of homology; dark blue, exonic sequences; light blue, untranslated region.



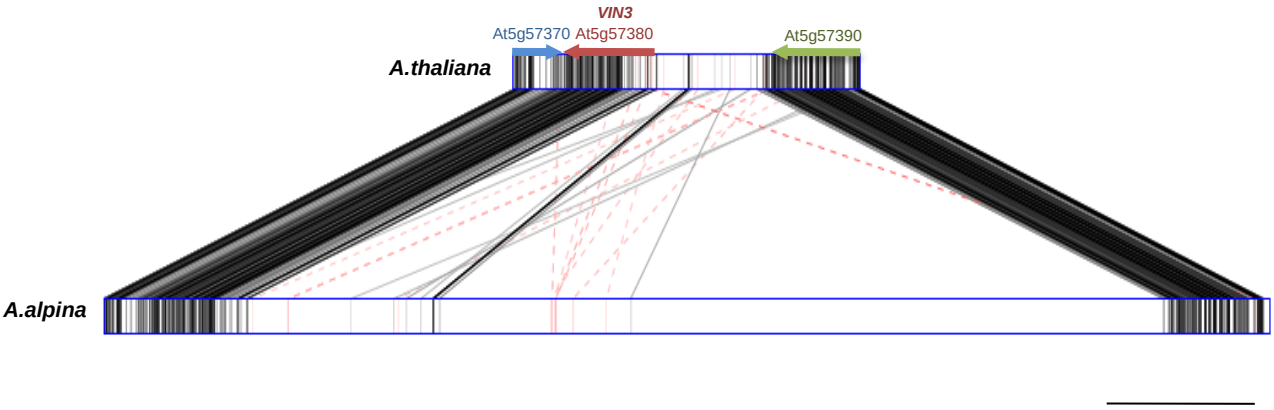
Supplementary Figure 5: Class II antisense transcripts at the Dor*PEP1*

(a) Schematic representation of *PEP1* locus in the Dor accession. Black boxes are exons, lines introns and non-coding regions. Grey boxes indicate the region tandemly duplicated. The red star marks a G to A substitution and the red triangle a 248 bp insertion as compared to the Pajares sequence in exon 1a and the 5´UTR of exon 1b respectively. Arrows indicate transcriptional start sites at *PEP1*. **(b)** Class II antisense transcripts obtained by cloning and sequencing of qRT-PCR products in non-vernalized 21 days old Dor leaf samples. Scale bar, 1kb.



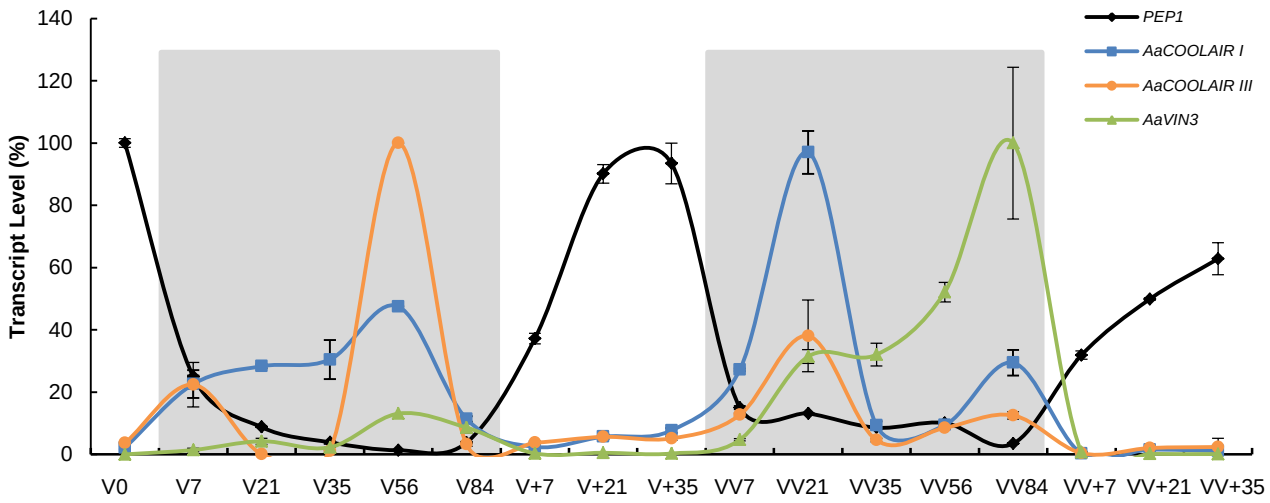
Supplementary Figure 6: Class I antisense transcript at *A. lyrata FLC* genes

(a) Black boxes are exons; lines are introns and other non-coding regions. A star indicates the most abundant form among splicing variants obtained by qRT-PCR product sequencing. Scale bar, 0.5 kb. **(b)** AlCOOLAIR I (*AlFLC1+AlFLC2*), *AlFLC1* and *AlFLC2* qRT-PCR (see Supplementary Table 1 for primers) on leaf RNA of *A. lyrata* plants exposed to 0, 28, 42 and 56 days of vernalization (V0, V28, V42, and V56) . Transcript levels were expressed relative to those of the reference gene *AlRAN3* ± SD (n=3 to 5 individuals) and plotted as a % of their maximal expression.

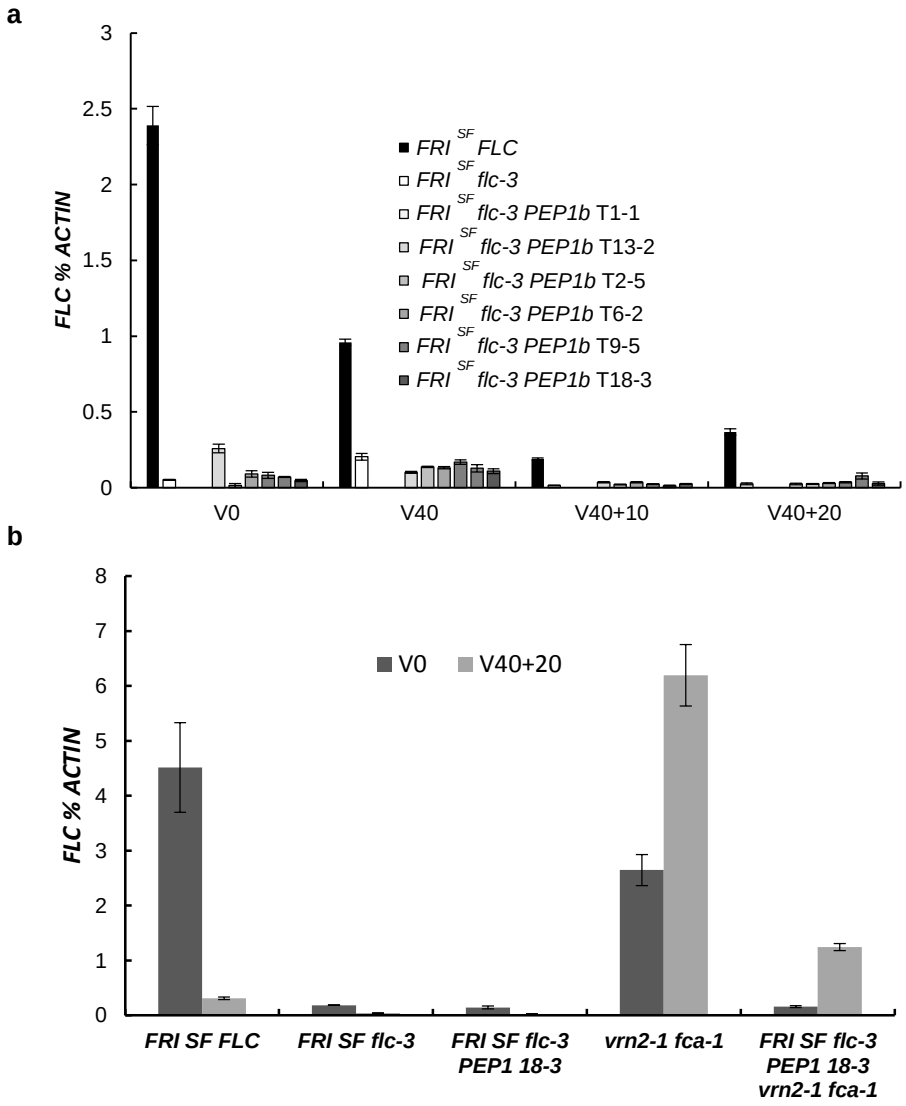


Supplementary Figure 7: Conservation of synteny between *A. thaliana* and *A. alpina* genomic regions carrying *VIN3* orthologues

GATA plot showing the conservation of synteny between the *A. thaliana* chromosome V region containing *VIN3* (At5g57380) and its two neighboring genes (At5g57370 and At5g57390) and the corresponding region in *A. alpina*. Scale bar, 5kb.



Supplementary Figure 8: Seasonal expression patterns of *PEP1*, AaCOOLAIR I, AaCOOLAIR III and *AaVIN3* expression over two successive vernalization treatments
A. alpina plants were vernalized for 0, 7, 21, 35, 56 and 84 days (V0, V7, V21, V35, V56, V84) followed by 7, 21 and 35 days of growth in normal temperature (V+7, V+21, V+35) then vernalized again for 7, 21, 35, 56 and 84 days (VV7, VV21, VV35, VV56, VV84) and grown for 7, 21 and 35 more days in normal growth temperatures (VV+7, VV+21, VV+35). Grey areas indicate the cold treatments. Transcript levels were measured by qRT-PCR relative to those of the reference gene *RAN3* ± SD (n=3 technical replicates). The maximum level of expression of each gene is set at 100%.



Supplementary Figure 9: *FLC* expression in *FRI*^{SF} *flc3 PEP1* transformants and *FRI*^{SF} *flc3 PEP1 18-3 vrn2-1 fca-1* line

(a) *FLC* mRNA levels in *A. thaliana FRI*^{SF} *flc-3 PEP1b* independent transformants as compared to those of the parental line *FRI*^{SF} *flc-3* and the control line *FRI*^{SF} *FLC* before vernalization (V0), after 40 days of vernalization (V40), and after 40 days of vernalization followed by 10 or 20 days of growth at normal growth temperatures (V40+10, V40+20).

(b) *FLC* mRNA levels in *vrn2-1 fca-1* and *FRI*^{SF} *flc-3 PEP1b vrn2-1 fca-1* as compared to those in *FRI*^{SF} *flc-3 PEP1b 18-3* parental line, *FRI*^{SF} *flc-3* and *FRI*^{SF} *FLC* the control lines before vernalization (V0) and after 40 days of vernalization followed by 20 days of growth at normal growth temperatures (V40+20).

Transcript levels were measured by qRT-PCR relative to those of the reference gene *ACTIN* ± SD (n=3 technical replicates).

	PEP1 cloning	
	forward	reverse
EcoRI-Flank1-SalI	GGGGTGTTGGAATTCTGGATTCTTGTAATAATTTGTTTTTCAC	GGAAGAGGGTCGACCGTAGTATAAGAACACCAAGAAATCAAG
SalI-Flank2-BamHI	GGGGTGTTGGTCGACGCGGCCGCAATAATTGAGTTCAAGTGATTTCCAAC	GGGAAGAGGGGATCCAAGCATTTTAACACTTAACTACGATACG
	PEP1 genotyping	
	forward	reverse
EcoRI-Flank1-SalI	GGGGTGTTGGAATTCTGGATTCTTGTAATAATTTGTTTTTCAC	GGAAGAGGGTCGACCGTAGTATAAGAACACCAAGAAATCAAG
Set1	CTGTCTTGCCGGAGTATATTG	GAAGAGATGATGAAACAAATAGC
Set2	GGGCCTTACAGTCAAAACAAAG	AAGGACATTCTTCCCCAAGG
Set3	TGAGTACATGCATGGTTTG	CTTTTGACTGAAGATCCTGTCC
SalI-Flank2-BamHI	GGGGTGTTGGTCGACGCGGCCGCAATAATTGAGTTCAAGTGATTTCCAAC	GGGAAGAGGGGATCCAAGCATTTTAACACTTAACTACGATACG
	3´RACE PCR	
	forward	reverse
AaCOOLAIR	ACCGTGAAGCAAACTCAAGT	UAP
AaCOOLAIR nested	GATAGAACACAAGAACACAT	AUAP
	AaCOOLAIR II 3´"tiling" PCR	
	forward	reverse
Set1	ACCGTGAAGCAAACTCAAGT	TCCTCCGGTGATAAGTATGA
Set2	ACCGTGAAGCAAACTCAAGT	AACGCTTAGTATCTCAGGCGAC
Set3	ACCGTGAAGCAAACTCAAGT	AAGAGGGTAATTATGGAATCTT
	Q-PCR	
	forward	reverse
VIN3	AGAAGCTGTGTTCTCAGGCAATGG	TCTTCGTCCTTCGACTTTCGACAAA
FLC	TGATAAGGGCGAGCGTTT	CACGAATAAGGTACAAAGTTC
ACTIN	GGTAACATTGTGCTCAGTGGTGG	AACGACCTTAATCTTCATGCTGC
AtCOOLAIR I	CTCGATGCAATTCTCACACG	TCCTTGGATAGAAGACAAAAAGAGA
AtCOOLAIR II	CTCGATGCAATTCTCACACG	TTCTCCTCCGGCGATAAGTA
AaVIN3	AGGACTTGAACCCGAGACC	GGGCAAAGATGGATTACTGC
PEP1	CTTGTCGTCTCCTCCTCTGG	ACTACGGCGAGAGCAGTTTC
AaRAN3	CACAGGAAAAACCACATTCGT	CCATCCCTAAGACCACCAAAT
AaCOOLAIR I	ACCGTGAAGCAAACTCAAGT	CAGAAGCCAAAACAAAGAAAGTG
AaCOOLAIR II	ACCGTGAAGCAAACTCAAGT	TCCTCCGGTGATAAGTATGA
AaCOOLAIRIII	ACCGTGAAGCAAACTCAAGT	GAAGAATGTCCTTTTCAAGCTG
AlFLC1	GAGTGCCGAAACTCTTCTTCAACTA	GCCAAAACCTGGTTCTCTTCT
AlFLC2	GGGAAACAACATGCTGATGA	CAATTGAACAAGAGTATCGACACTC
AlRAN3	CACAGGGAAAACACATTTGT	CCATCCCTCAGACCACCAAA
AlCOOLAIR I	CTCGATGCAATTCTCTCACG	TGATGGTATGAAAAAGATATTCC

Supplementary Table 1: Primer list

VRE-Like1 5'RACE PCRs		
	forward	reverse
PCR1	AAP	TGTCATTTCCAACGACCAAA
PCR2	AAP	GATTTCCAAGAGGCACCAAA
PCR3	AAP	GACCAGCATGGCCAAACTAC
PCR4	AAP	TCCAAGGTTGGACCTAGCAT
PCR5	AAP	GAGTATATAGAAGGAAACGACA
PCR6	AAP	TGGAAACGCAACTGAAAACA
VRE-Like1 5'RACE nested PCRs		
	forward	reverse
nested PCR1	AUAP	TACAATTCTCCCGGATTTGC
nested PCR2	AUAP	TGTCATTTCCAACGACCAAA
nested PCR3	AUAP	GATTTCCAAGAGGCACCAAA
VRE-Like1 5'RACE PCRs combinations		
	PCR	nested PCRs
PCR followed by nested PCR	1	1, 2
PCR followed by nested PCR	2	2,3
PCR followed by nested PCR	3	1,2,3
PCR followed by nested PCR	4	2
PCR followed by nested PCR	5	2
PCR followed by nested PCR	6	2
VRE-Like2 5'RACE PCRs		
	forward	reverse
PCR1	AAP	TTTTAGTGACCAAAGC
PCR2	AAP	GATTTCCAAGAGGCACCAAA
PCR3	AAP	ACTACTTGGTTAATGTT
PCR4	AAP	TTGCACCAAAATCAAGGATG
VRE-Like2 5'RACE nested PCRs		
	forward	reverse
nested PCR1	AUAP	AAGGACATTCTTCCCCAAGG
nested PCR2	AUAP	GATTTCCAAGAGGCACCAAA
VRE-Like2 5'RACE PCRs combinations		
	PCR	nested PCRs
PCR followed by nested PCR	1	1
PCR followed by nested PCR	2	1, 2
PCR followed by nested PCR	3	1, 2
PCR followed by nested PCR	4	1, 2

Supplementary Table 2: ***Arabis alpina*** **5'RACE PCR primers and PCR combinations**

Genotype	*AtFRI^{SF} flc3*	*AtFRI^{SF} FLC*	*AtFRI^{SF} flc3 PEP1b 1-1*	*AtFRI^{SF} flc3 PEP1b 2-5*	*AtFRI^{SF} flc3 PEP1b 9-5*	*AtFRI^{SF} flc3 PEP1b 6-2*	*AtFRI^{SF} flc3 PEP1b 13-2*	*AtFRI^{SF} flc3 PEP1b 18-3*
Rosette Leaf Number of individuals	8	51	9	9	8	8	9	9
	8	50	9	9	9	7	9	10
	9	55	9	9	9	9	9	9
	8	57	9	9	9	9	9	9
	9	43	9	10	9	9	9	9
	8	56	8	9	10	9	9	9
	8	50	9	9	9	8	9	8
	9	50	9	9	9	9	8	9
	8	45	8	9	8	9	10	9
	7	40	9	9	9	9		9
	7	44	8	9	9	9		9
	8	40		10	9	9		9
	8	55			9	9		9
	7	50			9	9		
	7	40			9	9		
	8	43			9	9		
	7	47			8	9		
	8	40				9		
	8							
	9							
	8							
	8							
	8							
Mean	7.96	47.56	8.73	9.17	8.88	8.78	9.00	9.00
SD	0.64	5.92	0.47	0.39	0.49	0.55	0.50	0.41
p value (Student T-test vs *AtFRI^{SF} flc3*)		1.418E-29	1.172E-03	9.951E-07	1.316E-05	9.627E-05	1.289E-04	7.058E-06

Supplementary Table 3: **Rosette leaves number of *AtFRI^{SF} flc3 PEP1* transformants at bolting and statistical analysis**

Mean value and standard deviation per genotype are represented in Fig. 3b. A star indicate genotypes with a p value <0,005.

Supplementary Methods

Arabidopsis lyrata growth conditions, RNA extraction and qRT-PCR

A. lyrata plants from the North American Mayodan population [1] were grown (after three days of stratification at 4°C) for 35 days at 20°C in daylenght of 14 hours (14h light/10h dark) and vernalized at 4°C up to 56 days in short days (8h light/16h dark). Total RNA from leaf samples was isolated with a phenol-based 96-well extraction method [2] from three to five individuals and subsequently digested with DNAse I Amplification grade (Invitrogen) according to the manufacturer's protocol. Reverse transcription was performed with oligo (dT) primers on 1µg of total RNA using SuperScript II Reverse Transcriptase (Invitrogen) according to the manufacturer's protocols. qPCRs for *AlFLC1* and AlCOOLAIR I were performed on the Roche Light Cycler 480II instrument using the primer sets listed in Supplementary Table 1 and the IQ SYBR Green Supermix (BIO-RAD). Transcripts levels were measured relatively to the references genes *AlRAN3.*

VIN3 synteny analysis

A. thaliana chromosome 5 region spanning At5g57370 and At5g57390 was aligned to part of *A. alpina* genome containing *AaVIN3* (GenBank KC162887) using GATAligner and plotter in order to check synteny conservation.

Analysis of sequences of *FLC* orthologues

Multiple sequence alignments were performed with T-coffee using the default settings [3].

5´RACE PCRs and 5` RACE "tiling"PCRs

5´RACE PCRs were carried out with the 5′ RACE System for Rapid Amplification of cDNA Ends Version 2 (Invitrogen, catalog # 18374-058) on *A. alpina* and *A. thaliana FRI* ^{SF} *FLC* samples collected during the vernalization time courses described in Fig. 2b and Fig. 4b

respectively. cDNA were obtained by reverse transcription of 5µg of total RNAs with random primers and were subsequently tailed according to the manufacturer protocols. Real time PCRs were performed with the IQ SYBR Green Supermix (BIO-RAD) in the Roche Light Cycler 480II instrument. To amplify COLDAIR from Arabidopsis *FRI* ^{SF} *FLC* 5´RACE samples, the Abridge Anchor Primer (AAP) provided with the 5´RACE kit was used together with AtCOLDAIR specific reverse primer as described by Heo *et al.* [4]. *PEP1* "tiling" PCRs were performed on 5´RACE samples with a series of successive reverse primers located downstream of the VRE-like 1 and VRE-like 2 sequences and coupled to the AAP (see Supplementary Table 2). Each PCR was used as a template for nested PCRs to improve detection (see Supplementary Table 2). PCR amplification products, when detected, were cloned and sequenced to test their validity.

Supplementary References

1 Leinonen, P H, Remington, D L, Leppälä J & Savolainen O. Genetic basis of local adaptation and flowering time variation in Arabidopsis lyrata. *Mol Ecol.* **22**, 709-723, doi: DOI 10.1111/j.1365-294X.2012.05678.x (2013).

2 Box M S, Coustham V, Dean C & Mylne J S. Protocol: A simple phenol-based method for 96-well extraction of high quality RNA from Arabidopsis. *Plant Methods*. **13**; 7:7. doi: DOI 10.1186/1746-4811-7-7 (2011).

3 Notredame, C., Higgins, D. G. & Heringa, J. T-Coffee: A novel method for fast and accurate multiple sequence alignment. *J Mol Biol* **302**, 205-217, doi:DOI 10.1006/jmbi.2000.4042 (2000).

4 Heo, J. B. & Sung, S. Vernalization-Mediated Epigenetic Silencing by a Long Intronic Noncoding RNA. *Science* **331**, 76-79, doi:DOI 10.1126/science.1197349 (2011).