SUPPLEMENTARY DATA

TABLE S1. Linkage group location and additive effect (*a*) of QTL governing between-population differentiation in flowering traits and leaf morphology in *Arabidopsis lyrata* from Plech (Germany) and Spiterstulen (Norway) grown in LD14 : 10 (light : dark) with (V+) and without (V–) vernalization. Four QTL with significant QTL × vernalization interactions were detected. Eight QTL with significant additive effects were detected when the plants from the two treatments were analysed jointly (effect of vernalization taken into account as an additive covariate). Positive values: Spiterstulen alleles promote flowering (earlier flowering and greater inflorescence or flower number) and leaf size (greater leaf dimensions). LG, linkage group; LOD, logarithm of the odds; *a*, additive effect; s.e., standard error.

				V–			V+		
Trait	LG	Position	LOD	а	s.e.	P-value	а	s.e.	<i>P</i> -value
$QTL \times vernalization interactions$									
leaf width (cm)	LG2	48	4.45	1.0385	0.4742	0.0324	-1.3919	0.2535	1.55E-07
leaf length (cm)	LG2	50.7	2.61	4.0388	2.2828	0.0818	-3.6636	1.2559	0.0040
	LG4	56	2.37	7.796	2.469	0.0024	1.0745	1.4697	0.4658
number of flowers after 3 weeks	LG6	8	2.64	1.8235	0.9922	0.0739	-6.2877	1.3883	1.17E-05
QTL with main effects									
leaf length (cm)	LG1	0	3.83	2.7666	1.8381	0.1374	3.1902	1.2401	0.0110
rosette height (cm)	LG1	6	4.66	1.93	1.0024	0.0589	3.1285	0.9009	0.0006
	LG2	48	3.63	0.0560	1.0529	0.958	3.3476	0.897	0.0002
days from inflorescence shoot elongation to flowering start	LG4	64	3.79	3.0383	1.9482	0.127	1.2759	0.4122	0.0023
leaf width (cm)	LG5	2	4.8	0.9189	0.3682	0.0153	0.7453	0.2644	0.0054
number of flowers after 3 weeks	LG5*	⁶	4.32	0.9481	1.1576	0.418	2.8576	1.307	0.0303
	LG7	0	4.47	-0.6979	1.3131	0.598	-5.891	1.554	0.0002
inflorescence shoot length (cm)	LG7	32	5.47	-6.21	5.473	0.2609	-11.283	3.228	0.0006

* QTL detected with non-parametric analysis

FIG. S1. Between-population differentiation of vernalization response in flowering phenology for the two parental *Arabidopsis lyrata* populations Plech (Germany) and Spiterstulen (Norway) in the growth chamber in LD14 : 10 (light : dark). Mean (\pm s.e.; 95% confidence interval for flowering propensity) is shown for Spiterstulen (triangles) and Plech (squares) parental populations for non-vernalized (V–) and vernalized plants (V+). Vernalization response differed significantly between populations in (A) and (F) (see Table 2 in text).



FIG. S2. Between-population differentiation of vernalization response in morphology for the two parental *Arabidopsis lyrata* populations Plech (Germany) and Spiterstulen (Norway) in the growth chamber in LD14 : 10 (light : dark). Mean (\pm s.e.) is shown for Spiterstulen (triangles) and Plech (squares) parental populations for non-vernalized (V–) and vernalized plants (V+). Vernalization response differed significantly between populations in (A), (B), (D), (F), (H) and (I) (see Table 4 in text).



FIG. S3. Putative QTL for days from bud emergence to inflorescence shoot elongation in case of no vernalization at the top of linkage group 6 near candiate genes *FLC* and *CO* in *Arabidopsis lyrata*. Phenotype means and standard errors (vertical dashed lines) for each group defined by the genotypes at the ng106 marker. Grey line: vernalized, black line : non-vernalized. 'Sp': Spiterstulen (Norway), 'Pl': Plech (Germany). Spiterstulen alleles delay inflorescence elongation when not vernalized.



Fig. S4. LOD profiles along the genome for the traits for which QTL with significant QTL \times vernalization interactions (grey line) and with significant additive effects (detected when the plants from the two treatments were analyzed jointly; black line) were detected. Horizontal line indicates a genome-wide LOD significance threshold based on 1000 permutations (alpha = 0.05), estimated separately for each trait for the two corresponding analyses.

Effect plots are also shown for the two types of QTL: the ones with significant $QTL \times vernalization$ interactions and the ones with significant additive effects detected (effect of vernalization taken into account as an additive covariate). Genotypic means and standard errors (vertical dashed lines) are indicated in black in the nonvernalized treatment and in grey in the vernalized treatment.



Leaf width

Chromosome

QTL on LG2 with significant QTL \times vernalization interactions in both cold treatments. QTL on LG5 with significant additive effects in both cold treatments. Non-significant additive effects for QTL on LG4.



c2.loc48 genotype (LG2)



c5.loc2 genotype (LG5)

Leaf length



QTL on LG2 and LG4 with significant QTL \times vernalization interactions. QTL on LG1 with significant additive effects in case of V+ treatment only.







Number of flowers after 3 weeks



QTL on LG6 with significant QTL \times vernalization interactions in case of V+ only. QTL on LG7 with significant additive effects in case of V+ treatment only.





With non-parametric analysis, an additional QTL on LG5 is detected with significant additive effect in case of V+ treatment.



Chromosome



Rosette height







c2.loc48 genotype (LG2)

Days from inflorescence shoot elongation to flowering start







QTL on LG7 with significant additive effects in case of V+ treatment only.

