

Supplementary Figures and Tables

Supplementary Figure 1. Histochemical localization of GUS activity in cotyledons of transgenic Col-0 expressing the GUS reporter gene under the control of FT promoters as indicated. Leaves were collected at ZT 16 after growth for 12 LDs on GM media.



Supplementary Figure 2. *Block C* enhances a minimal promoter in transient assays

Block C fused to *NOSminp* drives reporter gene *GreenLUC* expression in transient leaf bombardment assays. 35S::RedLUC co-bombarded with *promoter::GreenLUC* was used as the internal control. Values represent mean \pm SE. The asterisk (*) indicates statistically significant differences relative to the control *NOSmin::GreenLUC*. Statistical significance was determined using the Student's t-test (p<0.01).



Supplementary Figure 3. Flowering time of T-DNA insertion lines under MDs conditions.

Flowering time was measured in marginal long day (MD) grown Arabidopsis plants carrying T-DNA insertions either upstream (#1) of *Block C* or between *Block C* and the *Block A* (#2-#5) at positions indicated by triangles in Fig.2a. Line #5 is Ws and all other lines in the Col-0 accession. Number of rosette and cauline leaves are shown as mean \pm SE. The asterisk (*) indicates statistically significant differences relative to the control Col or Ws as indicated. Statistical significance was determined using the Student's t-test (p<0.01).



Supplementary Figure 4. Three types of *FT* **promoters.** DNA was isolated from 13 Arabidopsis accessions and amplified by primer pair 12_forward and 13_reverse. The expected product 1.95 kb, 1.10 kb and 0.85 kb for "long", "medium" and "short" promoters, respectively. PCR products were loaded on 1% agarose gel.



Supplementary Figure 5. Median-joining network of the *FT* **haplotypes**. The blue, green and red colour of the branches and shading corresponds, respectively, to the clades of the short, medium and long *FT* promoter regions. Scale bar, 0.1 nucleotide substitutions per site.



Supplementary Figure 6. SNP-based maximum-likelihood phylogeny of the coding and promoter regions of *FT* from 81 Arabidopsis accessions. Blue, green and red colour of the branches indicates clades of the short, medium and long *FT* promoters, respectively. The *FT* sequence from *A. lyrata* was used as outgroup. Bootstrap values (%) are shown at the nodes. Filled ellipse pictograms denote sub-clades with the footprints of selection defined as the retention of the phylogenetically close *FT* haplotypes within the genetically divergent genotypes. "Ins", "Del" and "Geo" columns describe, respectively, distribution of the insertion and deletion in the *FT* promoter region (see Fig. 4a) and geographical origin of the genotypes. Coloured pie charts illustrate population structure of the genotypes determined by genome-wide analysis¹. n.d. means no data.

а	Chri 24332000 24331700 24256 Protein Coding Gen	2029k e Models	24291 24	ažni 240 Insettor	208k 2420 1. Deteison 6 misted to Ores	9 2435	2011	AT1065450(FT)	Protein Codin	4807x 4807x g Gene Models 1000 11			44E3x related to PT promoter		486 (k)
C Col-0_FTpr Ler_FTpro WS_FTpro ICE226_FT ICE228_FTp ICE212_FTp ICE112_FTp chromosome	5 TGTACTTCTA TGTACTTCTA TGTACTTCTA TGTACTTCTA TGTACTTCTA -GTACTTCTA -ACTTCTA	15 AATCTCGACA AATCTCGACA AATCTCGACA AATCTCGACA AATCTCGACA AATCTCGACA AATCTCGACA	AAATGAAATC AAATGAAATC AAATGAAATC AAATGAAATC AAATGAAATC AAATGAAATC AAATGAAATC	35 AAGCTTTTGT AAGCTTTTGT AAGCTTTTGT AAGCTTTTGT AAGCTTTTGT AAGCTTTTGT AAGCTTTTGT	45 TGGACATT TCAGGACATT TCGGGACATT TCGGGACATT TCGGGACATT TCAGGACATT	55 CAGTTCCGGA CAGTTCCGGA CAGTTCCGGA CAGTTCCGGA CAGTTCCGGA CAGTTCCGGA	65 CAATCGGACT CAATCGGACT CAATCGGACT CAATCGGACT CAATCGGACT CAATCGGACT	75 GCATTCAAAT GTATTCAAAT GTATTCAAAT GTATTCAAAT GTATTCAAAT GTATTCAAAT GTATTCAAAT	85 AACTIGTITT AACTIGTITT AACTIGTITT AACTIGTITT AACTIGTITT AACTIGTITT AACTIGTITT	95 CGGACT-TGG CGGACTGGGA CGGACTTGG CGGAC-TTGG CGGAC-TTGG CGGAC-TTGG	105 ATATGATGTT TATTAAGGTGTT ATATGATGTT ATATGATGTT ATATGATGTT ATATGATGTT	115 AAG TATCA TA AAG AAG AAG AAG AAG	 125 TATTCATATG] 145 AATATCAATT
Col-0_FTpr Ler_FTpro Ws_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE112_FTp chromosome 12.0kb:404	CTACCTATT 155 GACAAAAATT	AATGTCGACA 165 GGATTGACAC	AAACC 175 ATATCTCTTA 	AGGCTTTTGT 185 TATACTAGTG 	TTAAGCCAT- 195 TTTCTTTTA 	205 AAACTTTCAA	215 TGTGGGGATCT	225 TATTAAAAGA	 235 AATCCTCTTC	245 TCAAAACTTT	255 ATAAACTTTC	265 ATTAGACTAR	 275 TTATAAGCTA	285 AACTATCTAA	 295 AATCTCTTAC
Col-0_FTpr Ler_FTpro Ws_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE112_FTp chromosome] 305 ATATTATTTG 	315 AGAAGTCGCA	1 325 ATTTTTTTTTG	335 TCATCTCACT		 355 AAGAATAATA 	 365 TCAAACATAA 	375 AACAAGTTAA	 385 TCTAAGACTT 	395 GCAGATAATA	405 AACCAACATG	415 GGAAGATAAT	 425 TGAAGGATTA	435 TCTTCTAGCT	445 TAGAGAACAT
Col-0_FTpr Ler_FTpro Ws_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE112_FTp chromosome	455 GTGTCGCAAT	465 TAATTTGATG	475 ACAAAGG	 485 GCACTCATGA	495 GGATATGATT	505 TAGAAATGTC	 515 ATCGAATACT	 525 GACGATCGAT	 535 TTTTTTCGAGT	545 CCGATGAATT	555 ACAATTCACP	565 GAGGTAAAGP	 575 AATCTGCTTT	 585 TGAATCACCG	 595 ATTCTTCTAA
Col-0_FTpr Ler_FTpro Ws_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE112_FTp chromosome		615 GATGATAGGT	 625 TAAATGAAGA	 635 AGAAGAAAAA 	645 AAGAGAAGAA		GATCCCTTAT GATCCCTTAT GATCCCTTAT GATCCCTTAT GATCCCTTAT GATCCCTTAT GATCCCTTAT	GCTAGCCCAA GCTAGC-CAA GCTAGC-CAA GCTAGC-CAA GCTAGC-CAA GCTAGC-CAA GCTAGC-CAA	I 685 AATCACATCA AATCACATCA AATCACATCA AATCACATCA AATCACATCA AATCACATCA AATCACATCA		705 ATAATGAGAT ATAATGAGAT ATAAGGAGAT ATAATGAGAT ATAATGAGAT ATAAKGAGAT	TTAGCAAAAA TTAGCAAAAA TTAGCAAAAA TTAGCAAAAA TTAGCAAAAA TTAGCAAAAA TTAGCAAAAA TTAGCAAAAA	TTGTAAACG CTTGTAAACG CTTGTAAACG CTTGTAAACG CTTGTAAACG CTTGTAAACG CTTGTAAACG CTTGTAAACG	735 TAGGTTTGCC TAGGTTTGCC TAGGTTTGCC TAGGTTTGCC TAGGTTTGCC TAGGTTTGCC TAGGTTTGCC	 745 GGATCTCTTG GGATCC-TTA GGATC GGATC GGATC GGATC
Col-0_FTpr Ler_FTpro WS_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE112_FTp chromosome	1	765 ACTTGCCA ACTTGCCAAG	ATCTTCGTAA ATCTTCGTAA	785 TCCAAAAGGT TCCAAAAGGT	795 AAATATCTAT AAATATGTAT	 805 GTT <mark>TAATTAT</mark> GTT	 815 CTTOTAGATT	 825 TTAAGGCACA	 835 ACGGATTGAT 	CGTTCTATAT	B55 TGTATGCACG	865 ATTGAAGAAG	 875 TTGTTTAAGA	885 AGCACAAACA	 895 TTTGACTATC
Col-0_FTpr Ler_FTpro Ws_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE91_FTpr ICE112_FTp		915 CCTTTTTGTC	925 ACTTGGAGAT		945 TTCATGGTGA	955 CGCAGAAGCC	965 TCTACTAGCT	975 CCACCGCAAA			CATGGTCATT	1015 ACACCAATGA	1025 TACTATCAAA	1035 ATCTCTAAAC	 1045 TAATCTCTAT
Col-0_FTpr Ler_FTpro Ws_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE12_FTp			 1075 TTATCAAGTA	 1085 TGTGTCTTTG	 1095 TAATTATCTT TAATTATCTT	1105 CTCTTCTAAG CTCTTCTAAG	 1115 ATTGAATCAT ATTGAATCAT	1125 CACAATGTTT CTCAATGTTT	1135 TTGAATTATT TTGAATTATT	 1145 TGATTTTCAT TGATTTTCAT		1165 AACCAACCAA AACCAACCAA	11175 AATGTTTTCG AATGTTTTCG	1185 TTCTAGAAAT TTCTAGAAAT	 1195 AAAGTCCTAA AAAGTCCTAA
Col-0_FTpr Ler_FTpro Ws_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE112_FTp chromosome	AGTGACGTAC AGTGACGTAC AGTGACGTAC	ATTCGTTTTC	TAATGAAAAT TAATGAAAAAT		AGTTATTCC AAGTTATTCC		 1265 TTTGGTCGT TTTTTGGT 	 1275 CAAAACATAA CAAAACATAA	 1285 GTTAATATTC GTTAATATTC		1305 TGACTAAAAC TGACGAAAAC TGACTAAAAC TGACTAAAAC TGACTAAAAC TGACTAAAAC	1315 TACTITIC-C TACTITIC-C TACTITIC-C TACTITIC-C TACTITIC-C TACTITIC-C	1325 AAAATTTTCA AAAATTTTCA AAAATTTTCA AAAATTTTCA AAAATTTTCA AAAATTTTCA AAAATTTTCA	1335 CCGGG-GAAA CCGGGGGAAA CCGGG-GAAA CCGGG-GAAA CCGGG-GAAA CCGGG-GAAA	
12.0kb:404 Col-0_FTpr Ler_FTpro ICE226_FT ICE228_FTp ICE91_FTpr ICE91_FTpr ICE91_FTpr ICE912_FTp chromosome 12.0kb:404	GA 1355 GCTTTATGAG GCTTTATGAG GCTTTATGAG GCTTTATGAG GCTTTATGAG GCTTTATGAG	ТGTATA-TTC 1365 СТТАЛАСАТА СТТАЛАСАТА СТТАЛАСАТА СТТАЛАСАТА СТТАЛАСАТА СТТАЛАСАТА СТТАЛАСАТА СТТАЛАСАТА	TTTTTAAAAT 1375 TGCAAAGTGT TGCAAAGTGT TGCAAAGTGT TGCAAAGTGT TGCAAAGTGT TGCAAAGTGT TGCAAAGTGT	GCTGTTTCAT 1385 CTCATTAACT CTCATTAACT CTCATTAACT CTCATTAACT CTCATTAACT CTCATTAACT CTCATTAACT CTCATTAACT	ААТТАТТА 1395 ТАААТАААТА ТАААТАААТА ТАААТАААТА ТАААТАААТА ТАААТАААТА ТАААТАААТА ТАААТАААТА	1405 TAGAGTACAA TCGAGTACAA TAGAGTACAA TAGAGTACAA TAGAGTACAA TAGAGTACAA	TTAATTGGT 1415 TTAATTGTT TTAATTGTT TTAATTGTT TTAATTGTT TTAATTGTT TTAATTGTT	GAAATCATAA 1425 CACAACGTTT CACAACGTTT CACAACGTTT CACAACGTTT CACAACGTTT CACAACGTTT CACAACGTTT	GTTAATATTC 1435 TTAATAGGAA TTAATAGGAA TTAATAGGAA TTAATAGGAA TTAATAGGAA TTAATAGGAA	TCTTCT-ATT 1445 ACTTAGAATA ACTTAGAATA ACTTARAAWA ACTTARAAWA ACTTARAAWA ACTTARAAWA	TAAATAAATT 1455 TGTTCTGTGA TGTTCTGTGA TGTTCTGTGA TGTTCTGTGA TGTTCTGTGA TGTTCTGTGA	TACTTTGCC- 1465 TGCACTATGT TGCACTATGT TGCACTATGT TGCACTATGT TGCACTATGT TGCACTATGT	AAAAGTTTCA 1475 GTTGCTTCGT GTTGCTTCGT GTTGCTTCGT GTTGCTTCGT GTTGCTTCGT GTTGCTTCGT	TCGTGG-AAC 1485 AAGGAAATTG AAGGAAATTG AAGGAAATTG AAGGAAATTG AAGGAAATTG AAGGAAATTG AAGGAAATTG	CCTTCTCAAA 1495 CATGCGAAAA CATGCGAAAA CATGCGAAAA CATGCGAAAA CATGCGAAAA CATGCGAAAA
Col-0_FTpr Ler_FTpro Ws_FTpro ICE226_FT ICE218_FTp ICE91_FTpr ICE112_FTp chromosome 12.0kb:404	1505 TCTAGTGG TCTAGTGG TCTAGTGG TCTAGTGG TCTAGTGG TCTAGTGG TCTAGTGG TCTAGTGG TCTAGTGG TCTAGTGG			- Internet						Internal A			STOUTON		

Supplementary Figure 7. Structural variation at the *FT* promoter

a, location and structure of "long", "medium" and "short" FT promoter types. The long *FT* promoter type, corresponding to the reference genome Col, contains two insertions (green

boxes) interrupted by a regions shared with the "medium" type (gray box). The short promoter does not contain any of the additional sequence found in the "long" promoter and carries a further deletion of the sequence shared between "long" and "medium" (red box). The proximal half of the insertion is related to a sequence on chromosome 5 (blue box, 97% sequence identity).

b, location of the duplicated fragment from the FT promoter on chromosome 5.

c, alignment of polymorphic region between "long", "medium" and "short" *FT* promoter types. Yelow boxes indicate the presumed target site insertions in Col-0. The *FT* homologous sequence from chromosome 5 and the Arabidopsis lyrate sequence is included in the alignment.



Supplementary Figure 8. Association of variation in the *FT* promoter with geographic coordinates. Boxplots of the latitudinal and longitudinal distribution of three *FT* promoter types as indicated.¹ Significance codes: p<0.01=**, p<0.05=* p<0.1 =. Long n=12, medium n=55, short n=13. See Supplementary table 2 and Supplementary dataset 1 for statistical tests.



Supplementary Figure 9. Variation in *FT* promoter length explains fitness variation of Arabidopsis accessions grown in Spain but not Halle or Norwich. Common garden experiments performed by Fournier-Level et al. 2011^2 at four different European sites were re-analyzed for 82 accessions for which the *FT* promoter type was confirmed by PCR and for which high density SNP data were available³. The medium version of *FT* promoter slightly outperforms the long version at the Spanish site based on the number of siliques produced by plant but not at two other sites (See Supplementary table 5 and Supplementary dataset 3 for statistical tests). Note that the short *FT* promoter type is intentionally removed from the graphs as only three accessions showing this genotype had been included in the study. Data from an experiment performed in Oulu, Finland were excluded from the analysis because most plants did not survive to seed set.

Analysis of dif	ferences in lat cture k=5 deter	itudinal and lo mined by STRUCI	ongitudinal di TURE	stribution considering
## Associations	with latitude		-	
glm(formula = 1	atitude ~ FTpro	m + IAP1 + IAP2	2 + IAP3 + IAP	4)
Compare to medi	um promoter			
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	43.055	1.046	41.155	< 2e-16 ***
FT long	2.777	1.284	2.163	0.033829 *
FT short	-2.232	1.325	-1.684	0.096389 .
IAP1	4.735	1.785	2.653	0.009782 **
IAP2	5.585	1.461	3.824	0.000274 ***
IAP3	-7.603	2.089	-3.639	0.000508 ***
IAP4	-4.162	4.248	-0.980	0.330414
Compare to long	promoter			
(Intercept)	45.832	1.422	32.229	< 2e-16 ***
FT medium	-2.777	1.284	-2.163	0.033839 *
FT short	-5.010	1.604	-3.123	0.002568 **
IAP1	4.735	1.785	2.653	0.009782 **
IAP2	5.585	1.461	3.824	0.000274 ***
IAP3	-7.603	2.089	-3.639	0.000508 ***
IAP4	-4.162	4.248	-0.980	0.330415
Associations wi	th longitude			
glm(formula = 1	ongitude ~ FTpr	om + IAP1 + IAP	P2 + IAP3 + IA	P4)
compare to medi	um promoter			
(Intercept)	6.4171	2.2604	2.839	0.00586 **
FT long	-3.4560	2.7747	-1.246	0.21692
FT short	2.3017	2.8637	0.804	0.42414
IAP1	0.5146	3.8562	0.133	0.89420
IAP2	61.8686	3.1557	19.605	< 2e-16 ***
IAP3	-14.9889	4.5143	-3.320	0.00141 **
IAP4	86.1141	9.1774	9.383	3.57e-14 ***
Compare to long	promoter			
(Intercept)	2.9612	3.0725	0.964	0.33835
FT medium	3.4560	2.7747	1.246	0.21692
FT short	5.7577	3.4663	1.661	0.10099
IAP1	0.5146	3.8562	0.133	0.89420
IAP2	61.8686	3.1557	19.605	< 2e-16 ***
IAP3	-14.9889	4.5143	-3.320	0.00141 **
IAP4	86.1141	9.1774	9.383	3.57e-14 ***
Signif. codes:	0 `***′ 0.001	`**' 0.01 `*' ().05 `.′ 0.1 `	1

Supplementary Table 1. Differences in longitudinal and latitudinal distribution of FT promoter types were tested by calculating a general linear model that included an estimate of the population structure based on k=5 clusters that was previously determined¹. The data used for the analysis are complied as dataset 1. The model was calculated in R using the function glm (see Supplementary dataset 1).

Crosses	SNPs	Promoter types
An-1XCol	GXC	MXL
LerXTs-1	CXG	MXL
CoIXC24	CXG	LXS
ColXWs	CXG	LXS
LerXC24	CXG	MXS
LerXBr-0	CXG	MXS
LerXWs	CXG	MXS
An-1XCvi	GXC	MXM
An-1XLer	GXC	MXM
CviXKyo	CXG	MXM
LerXKyo	CXG	MXM
ShaXLer	GXC	MXM
LerXRRS7	CXG	MXM
LerXGot-7	CXG	MXM

Supplementary Table 2 F1 hybrids for pyro-sequencing

##for the Fallwinter cohort						
glm(formula = log(Fall\$Seedmass) ~ Fall\$preFTgeno + Fall\$FRIG + Fall\$PC1 + Fall\$PC2 + Fall\$PC3 + Fall\$PC4 + Fall\$PC5 + Fall\$PC6 + Fall\$PC7 + Fall\$PC8 + Fall\$PC9 + Fall\$PC10)						
	Estimate	Std. Error	t value	Pr(> t)		
(Intercept)	5.99579	0.82667	7.253	1.45e-09 ***		
Fall\$preFTgenom	-0.62938	0.24464	-2.573	0.0128 *		
Fall\$preFTgenos	-0.27941	0.51181	-0.546	0.5873		
Fall\$FRIGN	0.45137	0.32342	1.396	0.1684		
Fall\$PC1	-6.26295	7.23199	-0.866	0.3902		
Fall\$PC2	-1.61701	0.97815	-1.653	0.1040		
Fall\$PC3	0.37635	1.08943	0.345	0.7311		
Fall\$PC4	3.01602	1.35699	2.223	0.0304 *		
Fall\$PC5	1.05982	1.19048	0.890	0.3772		
Fall\$PC6	0.70891	0.95464	0.743	0.4609		
Fall\$PC7	0.55376	1.10459	0.501	0.6181		
Fall\$PC8	1.35789	1.08555	1.251	0.2163		
Fall\$PC9	-0.22992	0.89966	-0.256	0.7992		
Fall\$PC10	-0.09429	0.92774	-0.102	0.9194		
##for the Spring c	ohort					
<pre>glm(formula = log(Spring\$PC2 + Sprin Spring\$PC8 + Sprin</pre>	Spring\$Seedma g\$PC3 + Sprin g\$PC9 + Sprin	ss) ~ Spring\$ g\$PC4 + Sprin g\$PC10)	preFTgeno + g\$PC5 + Spri	Spring\$FRIG + Spring\$PC1 + ing\$PC6 + Spring\$PC7 +		
(Intercept)	5.233360	0.428988	12.199	<2e-16 ***		
Spring\$preFTgenom	0.112398	0.116339	0.966	0.3374		
Spring\$preFTgenos	0.335794	0.263601	1.274	0.2070		
Spring\$FRIGN	0.007736	0.154601	0.050	0.9602		
Spring\$PC1	-6.263512	3.748539	-1.671	0.0993 .		
Spring\$PC2	0.275107	0.481551	0.571	0.5697		
Spring\$PC3	0.108806	0.442340	0.246	0.8064		
Spring\$PC4	0.202776	0.517725	0.392	0.6965		
Spring\$PC5	-0.137650	0.487851	-0.282	0.7787		
Spring\$PC6	0.064956	0.430631	0.151	0.8805		
Spring\$PC7	-0.097047	0.440441	-0.220	0.8263		
Spring\$PC8	-0.667620	0.432254	-1.545	0.1271		
Spring\$PC9	-0.538175	0.452742	-1.189	0.2387		
Spring\$PC10	-0.543723	0.448564	-1.212	0.2297		
Signif codes: 0	22***2= 0 001	??**? 0 01	22*2-0.05	$22 2^{-1} 0 1 22 2^{-1}$		

Supplementary Table 3. Statistical test of the association of *FT* **promoter types with seed mass during two growth seasons.** A general linear regression model was applied to the common garden experiments performed by Korves et al. 2007⁴ using the glm function in R. In this model, Seedmass is log transformed data taken from Korves et al. 2007⁴ after fitting a model that considered average weight of seeds per silique, average number of siliques per plant and survival rate, proFTgeno is the FT promoter type (l:long, m:medium and s:small), season was classified as spring and fall, FRIG is the functionality of FRIGIDA (Functional F and non-functional N), PC1 to 10 are the first 10 principal coordinates, which are used for controlling the population structure based on available high density SNP data³ (see Supplementary dataset 2).

##For the Fallwinter season:						
glm(formula = Fall\$DTB ~ Fall\$preFTgeno + Fall\$FRIG + Fall\$PC1 + Fall\$PC2 +						
Fall\$PC3 + Fall\$PC4 + Fall\$PC5 + Fall\$PC6 + Fall\$PC7 + Fall\$PC8 + Fall\$PC9 +						
Fall\$PC10, family	= quasipoisso	on)				
	Estimate	Std. Error	t value	Pr(> t)		
(Intercept)	5.136333	0.140026	36.681	<2e-16 ***		
Fall\$preFTgenom	0.007178	0.043009	0.167	0.8680		
Fall\$preFTgenos	-0.118274	0.091951	-1.286	0.2035		
Fall\$FRIGN	-0.016839	0.055719	-0.302	0.7636		
Fall\$PC1	-0.658018	1.221432	-0.539	0.5922		
Fall\$PC2	0.424880	0.170754	2.488	0.0158 *		
Fall\$PC3	-0.168450	0.166629	-1.011	0.3163		
Fall\$PC4	0.095647	0.190297	0.503	0.6172		
Fall\$PC5	0.307632	0.190908	1.611	0.1126		
Fall\$PC6	0.003413	0.151900	0.022	0.9822		
Fall\$PC7	0.015666	0.166154	0.094	0.9252		
Fall\$PC8	-0.074107	0.161556	-0.459	0.6482		
Fall\$PC9	0.022186	0.156163	0.142	0.8875		
Fall\$PC10	0.104390	0.158945	0.657	0.5140		
##For the Spring season:						
glm(formula = Spring\$DTB ~ Spring\$preFTgeno + Spring\$FRIG + Spring\$PC1 + Spring\$PC2						
+ Spring\$PC3 + Spring\$PC4 + Spring\$PC5 + Spring\$PC6 + Spring\$PC7 + Spring\$PC8 +						
Spring\$PC9 + Sprin	g\$PC10, famil	y = quasipois	son)			
	Estimate	Std. Error	t value	Pr(> t)		
(Intercept)	4.809868	0.032410	148.407	< 2e-16 ***		
Spring\$preFTgenom	0.007481	0.008799	0.850	0.398151		
Spring\$preFTgenos	-0.013654	0.020054	-0.681	0.498280		
Spring\$FRIGN	-0.040353	0.011640	-3.467	0.000918 ***		
Spring\$PC1	-0.156569	0.283547	-0.552	0.582637		
Spring\$PC2	0.184250	0.036533	5.043	3.62e-06 ***		
Spring\$PC3	-0.059973	0.033450	-1.793	0.077436 .		
Spring\$PC4	-0.089806	0.039241	-2.289	0.025216 *		
Spring\$PC5	-0.087145	0.036885	-2.363	0.021013 *		
Spring\$PC6	0.044995	0.033050	1.361	0.177880		
Spring\$PC7	-0.113094	0.033545	-3.371	0.001237 **		
Spring\$PC8	-0.023654	0.032680	-0.724	0.471664		
Spring\$PC9	-0.013980	0.034163	-0.409	0.683655		
Spring\$PC10	0.019985	0.033983	0.588	0.558416		
Signif. codes: 0	`***′ 0.001 `	**' 0.01 `*'	0.05 `.′ 0.2	1 1 1		

Supplementary Table 4. Statistical test of the association of *FT* promoter types with days to bolting (DTB). Bolting time data from the study of Korves et al., 2007^4 was treated as count data. A glm regression model was applied to the data with quasipoisson correction for the overdispersion of the data. Analysis was done following the suggestions of Crawley $(2005)^5$.

quasipoisson).				
	Estimate	Std. Error	t-value	Pr(> t)
(Intercept)	7.34536	0.31716	23.160	<2e-16 ***
proFTgenoM	-0.1159	0.10909	-1.063	0.28890
proFTgenoS	-0.08868	0.22065	-0.402	0.68817
locationNorw	-1.40604	0.19307	-7.282	6.33e-12***
locationValen	-1.17363	0.17091	-6.867	7.14e-11***
FRIGN	0.17493	0.10754	1.627	0.10528
PC1	-2.62194	2.80872	-0.933	0.35162
PC2	-1.29656	0.29857	-4.343	2.18e-05***
PC3	-0.37570	0.40119	-0.936	0.35010
PC4	1.09566	0.37976	2.885	0.00432 **
PC5	-0.4752	0.31718	-1.498	0.13553
PC6	0.47380	0.36127	1.311	0.19111
PC7	0.21856	0.35759	0.611	0.54173
PC8	-1.43248	0.35043	-4.088	6.18e-05***
PC9	-0.13306	0.34375	-0.387	0.69908
PC10	0.24461	0.29238	0.837	0.40373
proFTgenoM:locationNorw	-0.07774	0.21824	-0.356	0.72205
proFTgenoS:locationNorw	0.03069	0.49296	0.062	0.95041
proFTgenoM:locationValen	0.42046	0.18407	2.284	0.02335 *
proFTgenoS:locationValen	-0.26176	0.49313	-0.531	0.59609
locationNorw:FRIGN	-0.30175	0.20633	-1.462	0.14509
locationValen:FRIGN	-0.20970	0.16250	-1.290	0.19829

Supplementary Table 5. Statistical test of the association of FT promoter types with

silique number. Silique number as measure of fitness was taken from a field study performed Fournier-Level et al 2011 at 3 different European sites². Silique number treated as count data in a glm regression model. Quasipoisson correction was applied to account for the overdispersion of the count data. Analysis was done following the suggestion of Crawley (2005)⁵. In this model, SilNb is the silique number, proFTgeno are the *FT* promoter length types (long (L), medium (M), small (S)), location corresponds to three experimental sites, FRIG is the functionality of FRIGIDA⁴, PC1 to 10 are the first 10 principal coordinates according to published high density SNP data³, which are used for controlling the population structure (see Supplementary dataset 3).

Since removing location: FRIG from the model resulted in slightly different results (p=0.09), we kept it as parameter in the final model. Note a significant difference between proFTgeno L and M at the Valencia site. This difference was also mildly supported by a non-parametric Wilcoxon rank sum test (p=0.06).

Purpose	Primer name	Primer name				
Plasmid	5.2kbFTp-GW-FW	GGGGACAAGTTTGTACAAAAAGCAGGCTTCGATTGTTTTACACTACTTCC				
construction	1kbFTp-GW-RE	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTTGATCTTGAACAAACA				
	BlockC-GW-FW	GGGGACAAGTTTGTACAAAAAGCAGGCTCATTTGCTGAACAAAAATCT				
	BlockC-GW-RE	GGGGACCACTTTGTACAAGAAAGCTGGGTAAACGTTTGGAAATAGGAAGTATG				
	BlockC-overlapA-RE	GTACCGCCAAAAACGTTTGGAAATAGGAAGTATG				
	BlockA-overlapC-FW	TTCCAAACGTTTTTGGCGGTACCCTACTTTTT				
Genotyping	ft10_GABI_RP	CAGGTTCAAAACAAGCCAAGA				
	ft10_GABI_LB	CCCATTTGACGTGAATGTAGACAC				
	LBb1.3	ATTTTGCCGATTTCGGAAC				
	12_forward	CAACGAGATTTGGGGTTAAG				
	13_reverse	GATGCATTGTTTAAGAAAATCAGG				
Gene	FT_cDNA_RT_fw	GGTGGAGAAGACCTCAGGAA				
expression analysis	FT_cDNA_RT_re	ACCCTGGTGCATACACTGTT				
	PP2A-RT-fw	АААТАСGCCCААСGААСААА				
	PP2A-RT-re	CAGCAACGAATTGTGTTTGG				
Pyro-	F1	TGTGTGTTACGAAAATCCAAGTCC				
sequencing	R1	(Bio)AGCCACTCTCCCTCTGACAATT				
	S1	GTTTCGACAGCTTGG				
3C	Primer1	ССАТСТТСССАСТСССТТСТ				
	Primer2	TGGAAGTGGAAATGAATGTTAGG				
	Primer3	TGTTGGCCAAGATGTCTCAC				
	Primer4	TGTTCCCATGTGTGTGTGTG				
	Primer5	TTGAATGCAGTCCGATTGTC				
	Primer6	АААААТТGCGACTTCTCAAATAA				
	Primer7	TCTGCGTCACCATGAAGAAA				
	Primer8	GCCACTGTTCTACACGTCCA				
	Primer9	AAAATTCGAAAGCGAAAACG				
	Primer10	GGAACAAAGAAAAATCCCAAGA				

Supplementary Table 6. List of oligonucleotides used in this study.

Supplementary References

- 1. Cao J, *et al.* Whole-genome sequencing of multiple Arabidopsis thaliana populations. *Nat Genet* **43**, 956-963 (2011).
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