Supporting Information

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SI Methods

Plant Material. Representative lines from the *Pisum* germplasm collection at the John Innes Centre (1), and the Chinese national core collection (2) were selected on the basis of published diversity data (1, 2) and obtained through the Australian Temperate Field Crops Collection (Department of Primary Industry, Horsham, VIC, Australia). Details of accessions are included in Table S1. The reference line NGB5839 is an isogenic dwarf derivative of cv. Torsdag that carries a mutation in the gibberellin biosynthesis gene *LE*, and has been extensively used in mutagenesis programs (e.g., refs. 3 and 4). Line JI1794 is a representative accession of the northern race of *Pisum sativum* var. *humile* suggested by Ben Ze'ev and Zohary (5) to be the major wild contributor to the domesticated pea genepool. Dominant alleles at the *HIGH RESPONSE TO PHOTOPERIOD* (*HR*) locus were introgressed into the NGB5839 genetic background from the line Wellensiek's Dominant [Hobart line HL16, John Innes line JI1228, Weibullsholm line WL1771 (6)] through six successive backcrosses, by phenotypic selection for delayed flowering under short day (SD). A small set of diverse lentil lines from the collection at the International Center for Agricultural Research in the Dry Areas was provided by W. Erskine (International Center for Agricultural Research in the Dry Areas, Aleppo, Syria) and genetic control of flowering was examined in crosses between cv. Northfield (ILL5588) and ILL6005, an early-flowering derivative of a cross between cv. Precoz (ILL4605) and cv. Laird (ILL4349).

Plant Growth Conditions and Measurements. Plants were grown in a 1:1 mixture of dolerite chips and vermiculite topped with potting mix, and received nutrient solution weekly. Plants for expression experiments in Fig. 2 were grown in growth cabinets at 20 °C under 150 $\mu mol \cdot m^{-2} \cdot s^{-1}$ light from cool-white fluorescent tubes. Segregating progenies and plants for photoperiod response experiments were grown in the phytotron in the School of Plant Science at the University of Tasmania and received an 8-h photoperiod of natural daylight either with (long day, LD) or without (SD) an 8-h extension of 10 $\mu mol \cdot m^{-2} \cdot s^{-1}$ white light from cool-white compact fluorescent tubes [LDH; red (R):far red (FR) = 4.8], 40 W incandescent globes (LDL; R:FR = 0.6) or a combination of both of these light sources (LD; R:FR = 1.2). Flowering was quantified as the node of flower initiation, and the propensity to branch was expressed as branching index (Figs. 1*C* and 2*A*), calculated as the ratio of the increase in length of newly-released lateral branches to the increase in total plant height over a specified interval.

Mapping and Quantitative Trait Loci Analysis. The genetic control of domestication-related changes in SD flowering was addressed in a population of 92 F_2 individuals from a cross between NGB5839 and JI1794. Morphological and gene-based molecular markers were scored following details given in Table S5. Molecular markers were developed from sequences previously mapped in crosses within domesticated pea (7) or from genes in syntenic regions of the *Medicago truncatula* genome, and targeted to non-coding sequences where possible. Genomic DNA was extracted using a CTAB method as previously described (8) and high-resolution melt (HRM) markers were scored using the Type-it HRM PCR kit (Qiagen) in a Rotor-Gene Q (Qiagen) according to the manufacturer's instructions. Genetic maps were constructed using JoinMap 4, and quantitative trait loci (QTL) were detected using both interval mapping and multiple QTL mapping (MQM) in MapQTL (Kyazma) (9, 10). Interval mapping was first performed, using default parameters of MapQTL6. The LOD threshold for chromosome-wide significance was determined by permutation testing (10,000 replications) and was in the range 2.7–2.9. Map intervals exceeding the significance threshold were individually selected as cofactors for MQM analysis. Individual and joint contributions of *QTL3*, *QTL6*, and other loci to flowering and other traits were variously estimated by the Kruskal–Wallis single marker test in MapQTL6 and by generalized linear model and two-way ANOVA in SAS from genotypes of peak markers. Contributions of known flowering loci were assessed similarly using markers for the genes themselves (*LF*, *GIGAS*) or closely linked markers (*SN*) (Table S3).

Gene Isolation, Expression Analysis, and Complementation. The full-length *ELF3* gene and cDNA were isolated using PCR techniques, genome walking (GenomeWalker universal kit; Clontech), and rapid amplification of cDNA ends (SMART RACE cDNA amplification kit; Clontech) using specific primers designed on an initial DNA fragment obtained with degenerate primers (11). Harvested tissue for expression experiments consisted of both leaflets from the uppermost fully expanded leaf. RNA extraction, reverse transcription, and real-time PCR analysis were performed as described previously (8).

Full-length cDNA fragments for *PsELF3* genes differing only for the putative causal polymorphism were generated by PCR from pea lines NGB5839 and WL1771 using primers listed in Table S6**.** The cDNA fragments were first cloned in pCR8/GW/TOPO (Invitrogen) then recombined into the binary vector pB2GW7 using Gateway cloning (12), and confirmed by sequencing. The *Arabidopsis elf3-1* mutant in the ecotype Colombia background has been previously described and carries a nonsense mutation in exon 3 (13). Transformation of the *Arabidopsis elf3-1* mutant was conducted by floral dipping (14) and the flowering phenotypes of several independent transformants per construct were characterized through several generations under both LD and SD conditions.

Eco-Targeting Induced Local Lesions in Genomes and Sequence Analysis. Details of all primer sequences are given in Table S6. The pea *ELF3* genomic sequence spanning the complete coding region was amplified in two overlapping fragments using primer pairs PsELF3-FF/PsELF3-11R and PsELF3-5F/PsELF3-RR. Genomic and cDNA sequences covering the entire coding region of the lentil *ELF3* gene were similarly isolated using a combination of pea- and lentil-specific primers (Table S6). PCR fragments were sequenced at Macrogen (http://dna.macrogen.com/eng). All sequences were then individually edited and aligned using Sequencher 5.0 (Gene Codes Corporation), with manual refinement. Distance and parsimony-based methods were used for phylogenetic analyses in PAUP*4.0b10 (http://paup.csit.fsu.edu) using the dataset presented in Fig. S2. Eco-Targeting Induced Local Lesions in Genomes (TILLING) was conducted on the *Pisum* germplasm collection maintained at the Centre des Ressources Biologiques (CRB) (15). Because of limitations on amplicon size, analysis was conducted on two amplicons spanning most of the coding sequence but omitting the large intron 2 (Fig. 3).

1. Jing R, et al. (2010) The genetic diversity and evolution of field pea (*Pisum*) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis. *BMC Evol Biol* 10:44.
2. Zong X, et al. (2009) Analysis of a diverse global *Pisum* sp. collection and comparison to a Chinese local *P. sativum* collection with microsatellite markers. *Theor Appl Genet* 118(2):193–204.
3. Hecht V, et al. (2007) Pea *LATE BLOOMER1* is a *GIGANTEA* ortholog with roles in photoperiodic flowering, deetiolation, and transcriptional regulation of circadian clock gene homologs. *Plant Physiol* 144(2):648–661.
4. Hecht V, et al. (2011) The pea *GIGAS* gene is a *FLOWERING LOCUS T* homolog necessary for graft-transmissible specification of flowering but not for responsiveness to photoperiod. *Plant Cell* 23(1):147–161.
5. Ben-Ze'ev N, Zohary D (1973) Species relationships in the genus *Pisum* L. *Isr J Plant Sci* 22:73–91.
6. Murfet IC (1971) Flowering in *Pisum*. Three distinct phenotypic classes determined by the interaction of a dominant early and a dominant late gene. *Heredity* 26:243–257.
7. Bordat A, et al. (2011) Translational genomics in legumes allowed placing in silico 5460 unigenes on the pea functional map and identified candidate genes in *Pisum sativum* L. *G3 (Bethesda)* 1(4):93–103.
8. Liew LC, et al. (2009) *DIE NEUTRALIS* and *LATE BLOOMER 1* contribute to regulation of the pea circadian clock. *Plant Cell* 21(10):3198–3211.
9. Van Ooijen JW (2006) *JoinMap 4* (Kyazma, Wageningen, Netherlands).
10. Van Ooijen JW (2009) *MapQTL 6* (Kyazma, Wageningen, Netherlands).
11. Hecht V, et al. (2005) Conservation of *Arabidopsis* flowering genes in model legumes. *Plant Physiol* 137(4):1420–1434.
12. Karimi M, Inzé D, Depicker A (2002) GATEWAY vectors for *Agrobacterium*-mediated plant transformation. *Trends Plant Sci* 7(5):193–195.
13. Hicks KA, Albertson TM, Wagner DR (2001) *EARLY FLOWERING3* encodes a novel protein that regulates circadian clock function and flowering in *Arabidopsis*. *Plant Cell* 13(6):1281–1292.
14. Bechtold N, Ellis J, Pelletier G (1993) In planta *Agrobacterium* mediated gene transfer by infiltration of adult *Arabidopsis thaliana* plants. *CR Acad Sci Paris.Sciences de la Vie* 316(10):1194–1199.
15. Deulvot C, et al. (2010) Highly-multiplexed SNP genotyping for genetic mapping and germplasm diversity studies in pea. *BMC Genomics* 11:468.

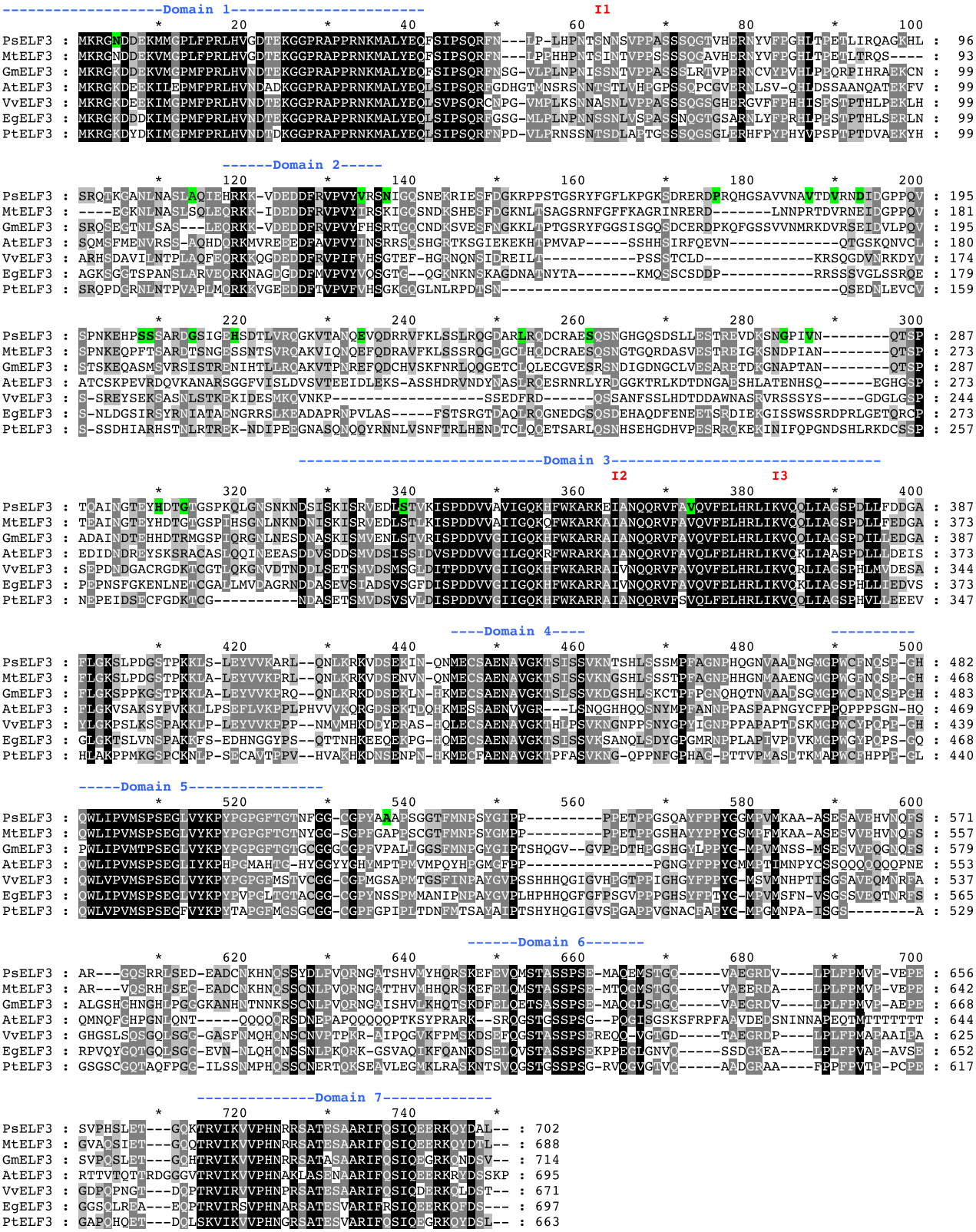

Fig. S1. ELF3 protein alignment. Intron positions are marked in red as I1 (intron 1), I2 (intron 2) and I3 (intron 3). Conserved domains represented in Fig. 3*A* are indicated in blue. Amino acid substitutions identified in the diversity survey (Fig. S2) are highlighted in green. *Pisum sativum*, PsELF3 (JN983406, haplotype B in Fig. S2); *Medicago truncatula*, MtELF3 (Medtr3g140450); *Glycine max*, GmELF3 (Glyma04g05280); *Arabidopsis thaliana,* AtELF3 (At2g25930); *Vitis vinifera*, VvELF3 (CBI20609); *Eucalyptus grandis*, EgELF3 (Egrandis_v1_0.004619m); *Populus trichocarpa*, PtELF3 (EEE93045).

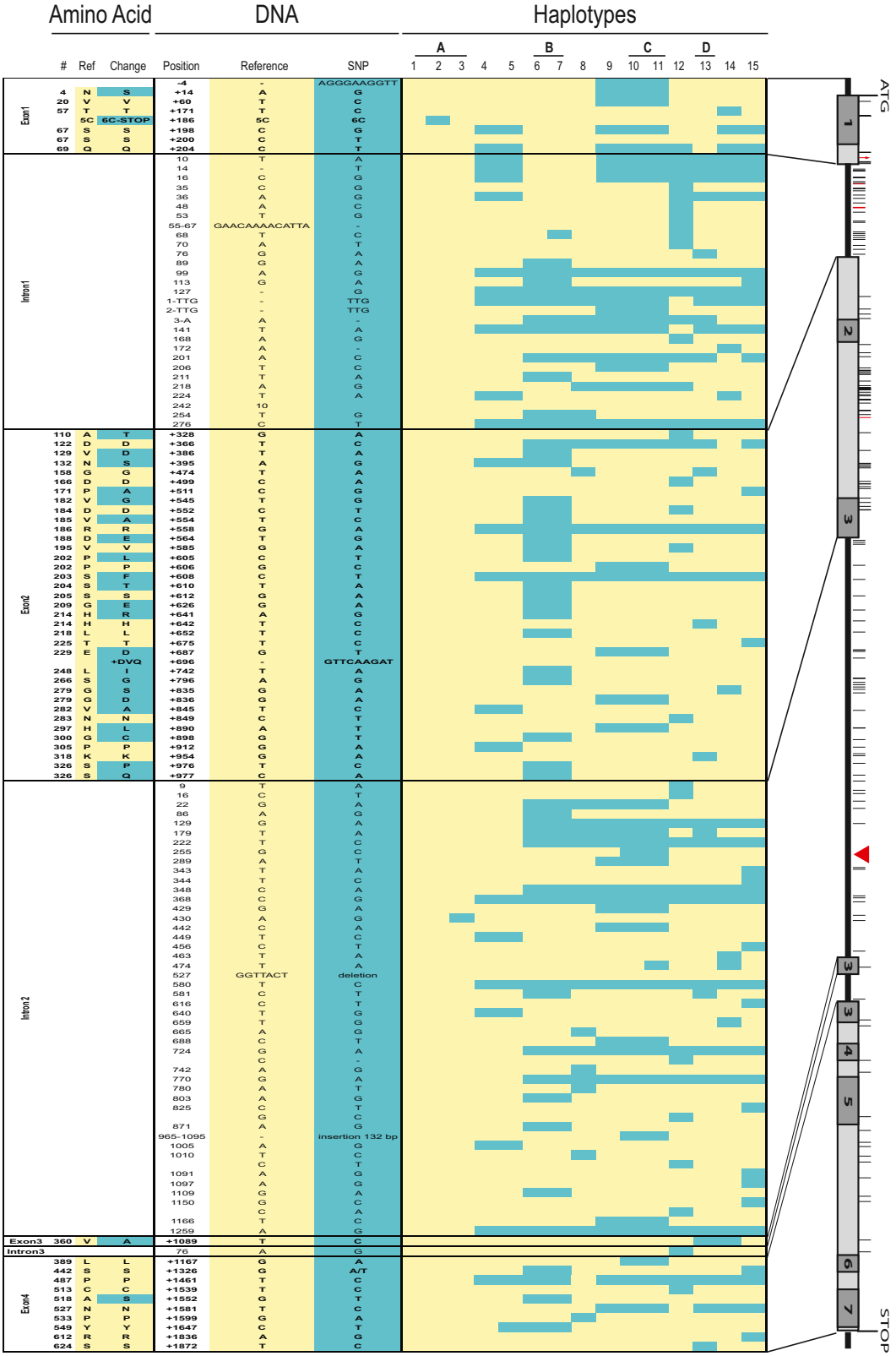

Fig. S2. *ELF3* haplotype details. Details of polymorphism in the entire 3.8-kB *ELF3* gene across a selection of 110 lines. The numbering of the 15 identified haplotypes corresponds to that shown in Fig. 4. Residues identical to those of the reference sequence NGB1771 are shaded yellow, residues differing from the reference sequence are shaded turquoise. The relative positions of each polymorphism within the *ELF3* gene are shown on the diagram to the right. For polymorphisms in coding sequence, the effect on the amino acid sequence is also indicated. The red arrow indicates the location of the 132-bp indel in intron 2.

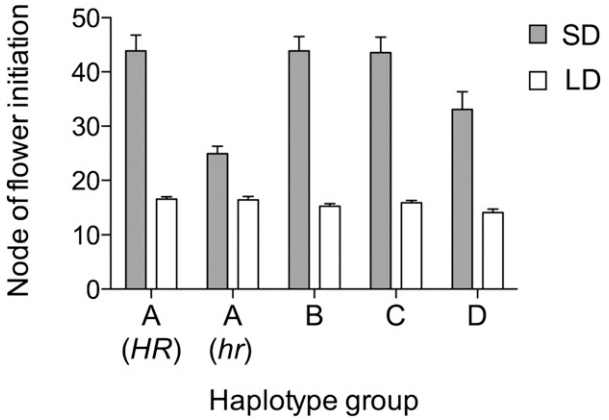

Fig. S3. Effect of *ELF3* haplotype on flowering response to photoperiod. Accessions shown in Fig. 1*A* were grouped according to the major *ELF3* haplotype groups shown in Fig. 4. Data represent means ± SE for n = 7 (A-*HR*), 18 (A-*hr*), 14 (B), 19 (C), and 5 (D) of individual accession data represented in Fig. 1*A*.

Table S1. Details of *Pisum* accessions

Accession ID	Alternative accession ID	Haplo-type group	Haplo-type	Jing et al. (1) group	Species	Variety	Country of origin	*GTY*	*PL*	*M*	*FS*
WL1771	JI 1228	A	1		*P. sativum*	*sativum*	Sweden	*gty*	*PL*	*M*	*FS*
JI 100	ATC 2704	A	1	3.3	*P. sativum*	*sativum*	Afghanistan	*gty*	*PL*	*m*	*FS*
JI 157	ATC 103	A	1	3.5	*P. sativum*	*sativum*	Sudan	*GTY*	*pl*	*M*	*fs*
JI 189	ATC 1192	A	1	3.5	*P. sativum*	*sativum*	Sudan	*gty*	*PL*	*m*	*fs*
JI 281		A	1		*P. sativum*	*sativum*	Ethiopia	*GTY*	*pl*	*m*	*fs*
JI 290	ATC 1474	A	1	3.5	*P. sativum*	*sativum*	Ethiopia	*gty*	*PL*	*m*	*FS*
JI 1497	ATC 3459	A	1	3.4	*P. sativum*	*sativum*	Mongolia	*gty*	*PL*	*m*	*FS*
JI 2077	ATC 1662	A	1	3.1	*P. sativum*	*sativum*	Sudan	*gty*	*pl*	*M*	*FS*
JI 2289	Champagne	A	1		*P. sativum*	*sativum*	—	*gty*	*PL*	*M*	*FS*
CRB 056	Assas	A	1		*P. sativum*	*sativum*	France				
CRB 062	Blixt 484	A	1		*P. sativum*	*sativum*	Sweden				
CRB 096	Holly 7	A	1		*P. sativum*	*sativum*	—				
CRB 122	PI269763	A	1		*P. sativum*	*sativum*	England				
CRB 128	PI180693	A	1		*P. sativum*	*sativum*	Germany				
CRB 186	Rosakrone	A	1		*P. sativum*	*sativum*	Germany				
CRB 390	DP	A	1		*P. sativum*	*sativum*	—				
CRB 395	JI 1184	A	1		*P. sativum*	*sativum*	Latvia				
CRB 435	Glacier	A	1		*P. sativum*	*sativum*	USA				
TOR le.3	NGB 5839	A	2		*P. sativum*	*sativum*	Sweden	*gty*	*pl*	*m*	*fs*
JI 182	ATC 1405	A	2	3.5	*P. sativum*	*sativum*	Nepal	*gty*	*pl*	*m*	-
JI 399	Cennia	A	2		*P. sativum*	*sativum*	Germany	*gty*	*pl*	*m*	-
JI 1214	ATC 2925	A	2	3.1	*P. sativum*	*sativum*	—	*gty*	*pl*	*m*	-
JI 1268	ATC 1534	A	2	3.U	*P. sativum*	*sativum*	India	*gty*	*pl*	*M*	*FS*
JI 1547	ATC 1564	A	2	3.5	*P. sativum*	*sativum*	Afghanistan	*gty*	*pl*	*m*	*FS*
JI 1756	ATC 1624	A	2	3.5	*P. sativum*	*sativum*	Nepal	*gty*	*pl*	*m*	-
JI 1792	ATC 1629	A	2	3.5	*P. sativum*	*sativum*	Nepal	*gty*	*pl*	*m*	-
JI 1877	ATC 1652	A	2	3.1	*P. sativum*	*sativum*	Ethiopia	*gty*	*pl*	*m*	*FS*
JI 3108	Térèse	A	2		*P. sativum*	*sativum*	France	*gty*	*pl*	*m*	*fs*
JI 1577	ATC 3807	A	2	2.1	*P. sativum*	*sativum*	China	*gty*	*pl*	*m*	*fs*
ATC 7009	GD2	A	2		*P. sativum*	*sativum*	China	*gty*	*pl*	*m*	*FS*
ATC 7030	SC2	A	2		*P. sativum*	*sativum*	China	*gty*	*PL*	*m*	*FS*
ATC 7032	YN1	A	2		*P. sativum*	*sativum*	China	*gty*	*pl*	*m*	*FS*
ATC 7044	SX1	A	2		*P. sativum*	*sativum*	China	*gty*	*PL*	*m*	*FS*
ATC 7056	SX2	A	2		*P. sativum*	*sativum*	China	*gty*	*Pl*	*m*	*FS*
ATC 7094	TB2	A	2		*P. sativum*	*sativum*	China	*gty*	*pl*	*m*	*FS*
ATC 7097	XJ2	A	2		*P. sativum*	*sativum*	China	*gty*	*PL*	*m*	*FS*
ATC 7139	AH1	A	2		*P. sativum*	*sativum*	China	*gty*	*pl*	*m*	*FS*
ATC 7156	GZ1	A	2		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
ATC 7157	GZ2	A	2		*P. sativum*	*sativum*	China	*gty*	*PL*	*m*	*FS*
ATC 7168	IM4	A	2		*P. sativum*	*sativum*	China	*gty*	*PL*	*m*	*FS*
ATC 7177	GX2	A	2		*P. sativum*	*sativum*	China	*gty*	*pl*	*m*	*FS*

Table S1. Cont.

Accession ID	Alternative accession ID	Haplo-type group	Haplo-type	Jing et al. (1) group	Species	Variety	Country of origin	*GTY*	*PL*	*M*	*FS*
CRB 006	Dove	A	2		*P. sativum*	*sativum*	France				
CRB 119	90–2079	A	2		*P. sativum*	*sativum*	USA				
CRB 123	PI271936	A	2		*P. sativum*	*sativum*	Sweden				
CRB 130	552	A	2		*P. sativum*	*sativum*	USA				
CRB 193	Cuzco 1	A	2		*P. sativum*	*sativum*	Peru				
CRB 200	Haiti Colore	A	2		*P. sativum*	*sativum*	Haiti				
CRB 253	Timo	A	2		*P. sativum*	*sativum*	Sweden				
CRB 258	Rodogune	A	2		*P. sativum*	*sativum*	France				
CRB 360	K30	A	2		*P. sativum*	*sativum*	Russia				
CRB 370	Chinois 2	A	2		*P. sativum*	*sativum*	China				
CRB 383	CE101 = FP	A	2		*P. sativum*	*sativum*	France				
CRB 432	Finale	A	2		*P. sativum*	*sativum*	Holland				
CRB 439	MIR12	A	2		*P. sativum*	*sativum*	Germany				
CRB 448	JI 296	A	2		*P. sativum*	*sativum*	France				
CRB 324	ZP130	A	3		*P. sativum*	*sativum*	Spain				
JI 2055		—	4	3.2	*P. sativum*	*elatius*	Italy	*GTY*	*PL*	*M*	*FS*
JI 1096		—	5	3.2	*P. sativum*	*elatius*	Greece	*GTY*	*PL*	*M*	*FS*
JI 95	ATC 2702	B	6	3.3	*P. sativum*	*sativum*	Afghanistan	*gty*	*PL*	*M*	*FS*
JI 181	ATC 1054	B	6	3.4	*P. sativum*	*sativum*	Nepal	*gty*	*pl*	*M*	*FS*
JI 252	ATC 2333	B	6	3.4	*P. sativum*	*sativum*	Ethiopia	*gty*	*PL*	*M*	*FS*
JI 1040	ATC 1500	B	6	3.3	*P. sativum*	*sativum*	Afghanistan	*gty*	*pl*	*M*	*FS*
JI 1261	ATC 1531	B	6	3.4	*P. sativum*	*sativum*	India	*gty*	*pl*	*M*	*FS*
JI 2069	ATC 1658	B	6	3.4	*P. sativum*	*sativum*	Nepal	*gty*	*pl*	*M*	*FS*
CRB310	China	B	6		*P. sativum*	*sativum*	China	*gty*			
ATC 6961	XJ1	B	6		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
ATC 6972	QH2	B	6		*P. sativum*	*sativum*	China	*gty*	*pl*	*m*	*FS*
ATC 7061	SX3	B	6		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
ATC 7102	IM2	B	6		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
ATC 7108	IM3	B	6		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
ATC 7125	SX4	B	6		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
ATC 7142	AH2	B	6		*P. sativum*	*sativum*	China	*gty*	*pl*	*M*	*FS*
JI 252	ATC 864	B	6	3.4	*P. sativum*	*sativum*	Ethiopia	*gty*	*PL*	*M*	*FS*
ATC 6939	IM1	B	6		*P. sativum*	*sativum*	China	*gty*	*PL*	*m*	*FS*
ATC 6931	HN1	B	7		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
JI.261		—	8	3.1	*P. sativum*	*elatius*	Turkey	*GTY*	*PL*	*M*	*FS*
JI 64	ATC 858	C	9	3.2	*P. sativum*	*elatius*	Israel	*GTY*	*pl*	*m*	*FS*
JI 85	ATC 3470	C	10	3.5	*P. sativum*	*sativum*	Afghanistan	*gty*	*pl*	*M*	*FS*
JI 94	ATC 1389	C	10	3.3	*P. sativum*	*sativum*	Afghanistan	*gty*	*pl*	*M*	*FS*
JI 96	ATC 859	C	10	3.3	*P. sativum*	*sativum*	Afghanistan	*gty*	*pl*	*M*	*FS*
JI 103	ATC 2711	C	10	3.5	*P. sativum*	*sativum*	Afghanistan	*gty*	*PL*	*M*	*FS*
JI 108	ATC 1390	C	10	3.U	*P. sativum*	*sativum*	Afghanistan	*gty*	*PL*	*M*	*FS*
JI 715	ATC 1484	C	10	3.5	*P. sativum*	*sativum*	Russia	*gty*	*PL*	*M*	*FS*
JI 1249	ATC 1526	C	10	3.3	*P. sativum*	*sativum*	India	*gty*	*PL*	*M*	*FS*
JI 1543	ATC 2706	C	10	3.5	*P. sativum*	*sativum*	Mongolia	*gty*	*pl*	*M*	*FS*
JI 2019	ATC 1654	C	10	3.U	*P. sativum*	*sativum*	India	*gty*	*PL*	*M*	*FS*
CRB014	JI 15	C	10		*P. sativum*	*sativum*	Sweden	*gty*			
CRB151	PI212112	C	10		*P. sativum*	*sativum*	Afghanistan	*gty*			
CRB152	Moshong	C	10		*P. sativum*	*sativum*	Afghanistan	*gty*			
ATC 6964	QH1	C	10		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
ATC 7017	GX1	C	10		*P. sativum*	*sativum*	China	*gty*	*pl*	*M*	*FS*
ATC 7033	YN2	C	10		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
ATC 7087	HN2	C	10		*P. sativum*	*sativum*	China	*gty*	*pl*	*m*	*FS*
ATC 7178	GX3	C	10		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*fs*
ATC 7203	SC3	C	10		*P. sativum*	*sativum*	China	*gty*	*pl*	*M*	*FS*
ATC 7218	HB1	C	10		*P. sativum*	*sativum*	China	*gty*	*PL*	*m*	*FS*
ATC 6958	GD1	C	10		*P. sativum*	*sativum*	China	*gty*	*pl*	*M*	*FS*
ATC 6974	QH3	C	10		*P. sativum*	*sativum*	China	*gty*	*pl*	*M*	*FS*
ATC 7025	SC1	C	10		*P. sativum*	*sativum*	China	*gty*	*PL*	*m*	*FS*
ATC 7008	TB1	C	11		*P. sativum*	*sativum*	China	*gty*	*PL*	*M*	*FS*
CRB191	POL 6806	—	12		*P. sativum*		Poland				
JI 2	ATC 1067	D	13	3.1	*P. sativum*	*abyssinicum*	Ethiopia	*gty*	*PL*	*m*	*fs*

Table S1. Cont.

Accession ID	Alternative accession ID	Haplo-type group	Haplo-type	Jing et al. (1) group	Species	Variety	Country of origin	*GTY*	*PL*	*M*	*FS*
JI 224	ATC 105	D	13		*P. sativum*	*abyssinicum*	Israel	*gty*	*PL*	*m*	*fs*
JI 225	ATC 1429	D	13	3.1	*P. sativum*	*abyssinicum*	Ethiopia	*gty*	*PL*	*m*	*fs*
JI 691	ATC 109	D	13	3.1	*P. sativum*	*abyssinicum*	Ethiopia	*gty*	*PL*	*m*	*fs*
JI 2385	ATC 1735	D	13	3.1	*P. sativum*	*abyssinicum*	Yemen	*gty*	*PL*	*m*	*fs*
CRB203	Braun-Yemen	D	13		*P. sativum*	*abyssinicum*	Yemen				
JI 1794		—	14		*P. sativum*	*humile*	Israel	*GTY*	*PL*	*M*	*FS*
JI 1796	ATC 1633	—	15	3.6	*P. fulvum*		Israel	*GTY*			

Accessions were obtained from the John Innes Centre (JI) collection (United Kingdom), The CRB collection (France), and the Chinese National Core Collection. Accessions obtained via the Australian Temperate Field Crops Collection (ATFCC) are indicated by an ATC accession ID. Haplotype and haplotype group designations correspond to those given in Fig. 4. Also indicated are the grouping in the Structure analysis of Jing et al. (1), and the genotype at four classic seed markers *FS* (purple testa patterning), *GTY* (rough thick testa), *M* (brown testa marbling), and *PL* (hilum color).

Table S2. Details of QTL for node of flower initiation in NGB5839 × JI1794 F_2

Name	LG	Analysis	Position (cM)	Peak marker	LOD	% explained	Genotype means		
							JI1794	het	NGB5839
QTL3	III	1	28.1	*MAX1*	9.3	17.6	40.9	36.2	21.8
		2 (with *ELF3*)	28.4	*ELF3*	10.4	18.3	41.1	36.5	21.1
QTL6	VI	1	67.2	*RNAhel*	21.4	54.6	47.1	22.7	15.6
		2 (with *ELF3*)	67.2	*RNAhel*	22.4	55.6	46.9	22.0	15.3

QTL on linkage groups III and VI were detected by MQM analysis in MapQTL 6 (Kyazma).

Table S3. Single marker effects on node of flower initiation in NGB5839 × JI1794 F_2

Marker	Linkage group	r^2	Probability	Probability (Bonferroni)	Genotype means ± SE		
					JI1794	het	NGB5839
LF/TFL1c	II	2.7	0.30	1	25.6 ± 3.9	30.3 ± 2.3	34.0 ± 3.5
GIGAS/FTa1	V	1.0	0.64	1	30.1 ± 3.2	29.3 ± 2.4	33.4 ± 4.0
PRR37	VII	3.7	0.19	1	30.8 ± 3.9	27.7 ± 2.0	35.0 ± 3.8
LE	III	0.9	0.68	1	33.1 ± 2.9	29.4 ± 2.7	30.7 ± 3.5

Contributions of individual loci were assessed using generalized linear model in SAS. *PRR37* is a marker closely linked to the *SN* locus.

Table S4. Medicago orthologs of functional candidates for pea *HR* locus

Gene	Medicago BAC	MtGenome 3.5	Inferred location in pea (7)
FRIGIDA-LIKE b (FRLb)	AC137079	Medtr5g094400	LGI, ~11cM
EARLY FLOWERING 3 (ELF3)	CU468275	Medtr3g103970	LGIII, ~40cM
FRIGIDA (FRI)	CT010504	Medtr3g098560	LGIII, ~65cM
FRIGIDA-LIKE a (FRLa)	AC121232	Medtr3g056070	LGIII, ~185cM
FAR-RED ELONGATED HYPOCOTYL 3 (FHY3)	CT030192	Medtr3g010690	LGIII, ~205cM
LUX ARRHYTHMO (LUX)	AC202498	Medtr4g064730	LGVI, ~125cM

Table S5. Marker details

Name	LG	Accession number	Source	Type	Population	Primers	Tm (°C)	Enzyme/ Product Tm (°C)
LF	II	AY343326	{Foucher, 2003 #562} (1)	CAPS	NGB5839 × JI1794	F:CTGGCCCAAGTGATCCTTAC R:AAGCATCAAATGATCAATCAAA	58	BsrI
SBE2	III	X80010	{Aubert, 2006 #6277} (2)	CAPS	NGB5839 × JI1794	F:CCCCGATGCTGATGGAAATCC R:CTTTGGCCCACATCAAAGCCG	60	HpaI
RMS1	III	AY557341	{Sorefan, 2003 #6512} (3)	CAPS	NGB5839 × JI1794	F:AGGGCTGAACCAACTCCTTT R:GCCCTAGCAACCTCTTCAAA	60	TaqI
CRY-DASH	III	JI960646	Present study	CAPS	NGB5839 × JI1794	F:CTGGGTTTTGTTCGAGTTGA R:CCACGATTTGACATGAAACCT	60	MseI
COLc	III	JN982281	Present study	HRM	NGB5839 × JI1794	F:CACATACGGAGATAGAGACACC R:TTCTCCATCGGGAACAACTC	55	~79.5
MAX1	III	A de Saint-Germain pers comm.	Present study	CAPS	NGB5839 × JI1794	F:GCAGATGCAGAACTGTGTAAAG R:CGCAGCAACCAAATAGACTA	57	AccI
ELF3	III	JN983407	Present study	CAPS	NGB5839 × JI1794	F:GCAGTAATAGGCCAAAAACATTTCGG R:AACTCAAACACTTGGACTGC	62	TaqI
ELF3	III	JN983406	Present study	CAPS	NGB5839 × WL1771	F:AAATTGTTATCATTCCGAACACA R:GGAATACTAAATTGCTCATACAAAGCC	60	HaeIII/SpeI
LcELF3	—	JX946295	Present study	CAPS	ILL6005 × ILL5588	F:GCAGTAATAGGCCAAAAACATTTCTGG R:CGATCCGGCAATCAGTTGTT	55	DraI
M	III	—	{Bordat, 2011 #6441} (4)	Morph.	NGB5839 × JI1794			
COQ1	III	JI914833	Present study	Size	NGB5839 × JI1794	F:ATTTAGTCCTGGCCCGGTTC R:TCCATATATCAAGCGGCAAC	55	—
TIC22	III	AF095284	Present study	HRM	NGB5839 × JI1794	F:TCTGGCAGCTTACAAATCATC R:TGTTGAAGGTTGAAGGTATTGC	55	~76
HYL	III	JX946299	Present study	CAPS	NGB5839 × JI1794	F:AAAGCAGCAGAGCAGTCAGC R:TCTTGCACAATCCAGTTTCA	55	HaeIII
NIP	III	U15036	{Aubert, 2006 #6277} (2)	HRM	NGB5839 × JI1794	F:GGATTCTACTAACCACATGGACC R:CAATACTTTTTAAACTAACAACCAAAAA	53	~74
FRI	III	JX946297	Present study	Size	NGB5839 × JI1794	F:TGCAACCATTTGTTTTAAGGTC R:AGGGAAATTTTGGGTGGAAT	60	—
UNI	III	AF010190	{Hofer, 1997 #4175} (5)	CAPS	NGB5839 × JI1794	F:CATCAGAGCTGAAAGAAGG R:GCTTCCTTTTCACGTTGC	55	RsaI, MboII
AAP2	III	G Aubert pers comm.	{Aubert, 2006 #6277} (2)	HRM	NGB5839 × JI1794	F:TTTACAATTTTTCTTTAGCTGCAT R:TGGATGTAGTCATTTTATTAAACACAGA	53	~69
RKP	III	JN982282	Present study	HRM	NGB5839 × JI1794	F:CTTTGTCGGAGTCAATCAGC R:CCCATCAATCATGACAATGC	55	~74
PRR59	III	FJ609179	Present study	CAPS	NGB5839 × JI1794	F:ATGCATGTTGAGAGGTGCAG R:AGCTTCCATGTTTGGCTTTG	58	RsaI
OMT1	III	JI897876	Present study	Size	NGB5839 × JI1794	F:CCTCATGTCATTGAAGACGC R:TTCCCACCTGGATTATGAGC	50	—
SEP3	III	AJ223318	Present study	CAPS	NGB5839 × JI1794	F:GGAGAAGATCTTGGCCCTCT R:CATCATCATGGTAACCATCC	58	PciI
COLe	III	JX946296	Present study	CAPS	NGB5839 × JI1794	F:AGAGCAAAAGCCATGTCTAC R:CCAAGGACGGAGAATCAGC	55	HpyCH4IV
LONG1	III	FJ374121	{Weller, 2009 #6333} (6)	HRM	NGB5839 × JI1794	F:GCTGACAAAGAAAGCAAACG R:AGCTGAAACTCGGTTCCTCA	52	~77
ELF4	III	AY830926	{Liew, 2009 #6376} (7)	HRM	NGB5839 × JI1794	F:GCATGGCAAAATAATCAGAGG R:TCTTCCATGATTTACAAACTCC	55	~76
LE	III	AF001219	{Martin, 1997 #4223} (8)	CAPS	NGB5839 × JI1794	F:TCTGGCCTCAAGATTATACC R:GGTTCACTAAAACTCGATGG	60	BanI
FTa1	V	HQ538822	{Hecht, 2011 #6456} (9)	CAPS	NGB5839 × JI1794	F:GCAACATCCAAATAAAATGAAGG R:TACACGACCAACAGCGAGAG	60	BglI
FTc	V	HQ538826	{Hecht, 2011 #6456} (9)	CAPS	NGB5839 × JI1794	F:CCTTCGGCAGGGATTCATCG R:GCAGGTGCTGGTCTCTTTCC	62	HpyCH4IV
SEP1-2	V	AY884290	{Hecht, 2005 #327} (10)	CAPS	NGB5839 × JI1794	F:CATCTCTGAAGCATGTTAGG R:TTGTTGAGCTTGACTTGTGG	60	BbvI
FTb1	V	HQ538824	{Hecht, 2011 #6456} (9)		NGB5839 × JI1794	F:CTCTATTTCAACTGTCAGCGAC R:TGCACAATTGTTAGCTTGTTCG	62	BccI
SLN	VI	AF101383	{Deulvot, 2010 #6437} (11)	CAPS	NGB5839 × JI1794	F:CACAACCAATCAAGAACACAATTTC R:CCCTTCTGCCATCAAATCAAG	60	DdeI, TaqI

Table S5. Cont.

Name	LG	Accession number	Source	Type	Population	Primers	Tm (°C)	Enzyme/ Product Tm (°C)
PIN1	VI	AY222857	{Deulvot, 2010 #6437} (11)	CAPS	NGB5839 × JI1794	F:GACGTCGACTCTATCTGACACG R:AACATAAAGTGGCACCATTGC	60	RsaI
UNK4	VI	JN982285	Present study	CAPS	NGB5839 × JI1794	F:GCCCTCTTCTTGGGAAAGC R:TAAACCCGCAAGATGCTCA	55	EcoRV
AGO1	VI	EF108450	{Deulvot, 2010 #6437} (11)	HRM	NGB5839 × JI1794	F:TTACTCCCATGTCATCCTTGG R:CAAGCATTAAAGAACCAGCAAG	55	~72 °C
WRI-33	VI	JN982283	Present study	CAPS	NGB5839 × JI1794	F:TGACCAAAGAGGAGTACTTGG R:AGCACGTGCAGCTTCTTCTT	55	BbvI
PCFS4	VI	JN982284	Present study	CAPS	NGB5839 × JI1794	F:GTACGGTCCACCAGTTTTGC R:GGATCAACTCAATGCCAAC	52	BtgI
RUG5/ Gbsts2	VI	X88790	{Aubert, 2006 #6277} (2)	CAPS	NGB5839 v JI1794	F:GCCGGTGTATCTGAAAGCAT R:ACACCGTTCACAATTCCCCG	60	AccI
MLO1	VI	FJ463618	{Humphry, 2011 #6457} (12)	HRM	NGB5839 × JI1794	F:TGGCTCTTAGGCATGGATTT R:TTGTGCATCATGTCCTGGAG	55	~74 °C
RNAhel	VI	PSCC24A19u (IPK Crop EST database)	{Aubert, 2006 #6277} (2)	CAPS	NGB5839 × JI1794	F:GGGTTTGGTAGGTTTGGTAGAGG R:GCTATCAAAATTGTAGTGGGTGGG	60	MseI
CABB	VI	CD859031	{Deulvot, 2010 #6437} (11)	HRM	NGB5839 × JI1794	F:AGGATCTTCTTGCCTGATGG R:CTTGCTTAGACCAAAAGGATCA	55	~81 °C
GA20ox1	VI	AF138704/ U70471	{Aubert, 2006 #6277} (2)	CAPS	NGB5839 × JI1794	F:CATTCCATTAGGCCAAATTTCAAT R:CTGCCCTATGTAAACAACTCTTGTATCT	60	SspI
GRITTY	VI	—	{Bordat, 2011 #6441} (4)	Morph	NGB5839 × JI1794	—	—	—
FVE	VI	AY830931	{Hecht, 2005 #327} (10)	CAPS	NGB5839 × JI1794	F:GCAAAATTCTAAGATAGTGG R:GTTGGGCACATCGCAAGAGC	58	BsaI
LKP1	VI	JX946298	Present study	CAPS	NGB5839 × JI1794	F:AGAATGGGCGACGAAGGTAT R:AAACCGCACCGTCCTCTAC	62	RsaI
PHYB	VI	AF069305	{Weller, 2001 #5727} (13)	CAPS	NGB5839 × JI1794	F:AATCCCTTGAGTGGCATACG R:CAGCATGCAGAAGAGTGAGC	60	RsaI, BslI
NA	VI	AF537321	{Davidson, 2003 #6458} (14)	Size	NGB5839 × JI1794	F:ATTGGTGGTTTTTCGAGAGG R:CCATGTAAGCACTTTCCAAC	60	—
PRR37	VII	FJ609177	Present study	CAPS	NGB5839 × JI1794	F:TGGCAACATGTTTGGAGAAG R:ACACTCAAGCCTCTGCTTCC	60	XmnI

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Table S6. *ELF3* Primer sequences

Name	Sequence	Use
PsELF3-FF	5′-GTTTAGAGTTTAGGATAGAAAAGGGGTAGG-3′	PCR and sequencing
PsELF3-11R	5′-GCAATTTCTTTTCTGGCTTTCC-3′	PCR and sequencing
PsELF3-4R	5′-GTTTCCCAGCCTGACGAAT-3′	Sequencing
PsELF3-5F	5′-ACCAGTCCAACCCAGGCTAT-3′	PCR and sequencing
PsELF3-RR	5′-GATCCTCCATGTCAATATACACCACTAC-3′	PCR and sequencing
PsELF3-7F	5′-TGTTTGCAGTCCAAGTGTTTG-3′	Sequencing
PsELF3-7R	5′-CGATCCGGCAATTAGTTGTT-3′	Sequencing
LcELF3-F1	5′-TGGACATGGACAAAGTGACG-3′	PCR and sequencing
LcELF3-R1	5′-CCGTTACATGATGGCACACC-3′	PCR and sequencing