

Supplementary Text 1. Expression of the StSP6A gene fully correlates with tuberisation induction. Expression analyses of the StSP6A FT-homologue showed that this gene is strongly up-regulated in leaves and stolons of short day induced plants (Fig. 1f). Accumulation of this transcript is observed as early as 2-4 days after transfer to short day inductive conditions (Fig. 1f) and thus precedes tuber formation. Interruption of the long nights with a 30 min night break inhibits tuberisation and prevents StSP6A accumulation both in the leaves and stolons. Moreover, high levels of the StSP6A mRNA are detected in leaf or stolon tissues of long day grown antisense *phyB* plants, with a defect in photoperiodic tuberisation control¹. This transcript is not detected in lines over-expressing the *Arabidopsis* CO protein (AtCOox) after 8 days cultivation in short days. These plants are strongly delayed in tuberisation² and need longer than 30 inductive days to tuberize.

Supplementary Text 2. Roles of the StSP6A and StSP3D genes in short day tuberization induction and in day length-independent floral promotion. To assess a role of StSP6A in tuberization control, we generated transgenic *Andigena* lines that over-expressed or were silenced for expression of this gene. Transgenic StSP6Aox lines tuberized under non-inductive long days (Fig 2a, b) and were induced to flower, although their flowering phenotype was less severe than that of *Hd3a* lines (Supplementary Fig. 3). A good correlation was observed between the tuberisation response of these plants and StSP6A transcript levels (Fig. 2a, b), consistent with a principal role of this gene in tuberization control. RNA profiling analyses of the stolons revealed up-regulated levels of expression of tuber-specific transcripts in long days (Supplementary Fig. 4), thus confirming induction of these plants. StSP6Aox scions grafted to wild-type stocks induced the stocks to tuberize (Fig. 3c, d), supporting movement of the StSP6A inductive signal through the graft junction, as seen for *Hd3a* plants. Transgenic StSP6A-RNAi (SP6Ai) lines, in opposite, exhibited strongly delayed tuberization in short days (Fig. 2c, d). RNA profiling studies of the RNAi stolons showed that tuber-specific genes are not yet up-regulated after 6 inductive days (Supplementary Fig. 4). While non-transgenic plants tuberize after 6-8 days under short days, SP6Ai plants required on average more than 3 weeks prior to tuberize. However, when cultivated under high irradiance conditions, they flowered at the same time as the untransformed controls, evidencing that StSP6A repression does not affect floral transition. By RT-PCR studies we confirmed that expression of the StSP3D and StSP5G genes was not affected in these plants (Supplementary Fig. 5a, b), silencing therefore being specific to the StSP6A gene.

To test whether *StSP3D* is essential for floral induction, we down-regulated expression of this gene by using an RNAi construct. Silenced lines showed a late flowering response, with 20% of the less severely repressed lines succeeding to flower (line 32, Fig. 2e, f). Flowering was suppressed in the strongest silenced lines. Scanning micrographs confirmed that the silenced plants were in a vegetative stage or had just started floral transition (Fig. 2g, h), whereas fully open flowers were observed in the controls. These plants, however, tuberized in short days at the same time as the untransformed controls and produced an equivalent number of tubers (Supplementary Fig. 7), which demonstrates that expression of this gene is not required for normal tuber development. RT-PCR studies confirmed that *StSP6A* gene expression is not affected in these plants (Supplementary Fig. 5c), *StSP3D* playing a major role in flowering but not in day length tuberization control.

Supplementary Text 3. Possible *StSP6A*-antagonistic function of the *StSP5G*

and *StSP5G*-like *FT*-paralogs. Expression analyses of the two additional *FT*-like members, *StSP5G* and *StSP5G*-like (*PGSC0003DMG400016180*) showed that transcripts for these genes are elevated in leaves of long day grown plants (Figure 1e). The *StSP5G* transcript, in addition, accumulates to high levels in the stolons of short day induced plants, although expression in these organs is delayed with respect to the *StSP6A* gene. These expression profiles are suggestive of a negative role of these *FT*-like paralogs in day length control of tuberization. In line with such function, recent studies in sugar beet showed that in this long day vernalization-requiring species, flowering time is controlled by the interplay of an antagonistic pair of mutually exclusive *FT*-homologs that respectively promote or suppress flowering³. *BvFT2* is essential for flowering, while *BvFT1* prevents bolting in non-vernalized plants. This gene is down-regulated in long days, in annual and vernalized-biennial plants, decreased levels of expression being required for *BvFT2* expression and floral transition. Interestingly, *BvFT1* carries three amino acid substitutions in an external loop formed by the fourth exon of the protein and both *StSP5G* and *StSP5G*-like homologs differ from the *StSP6A* and *StSP3D* proteins in this region (Supplementary Fig. 9).

Supplementary Text 4. Potato *StCO* represses *StSP6A* gene expression in

long days. In potato, *CO* is encoded by three tandem duplicated genes but only one of these gene copies is expressed to relatively high levels. This transcript oscillates with a diurnal rhythm of expression that peaks at dawn⁴. Several lines of evidence suggest that potato *StCO* represses *StSP6A* gene expression in long days and that

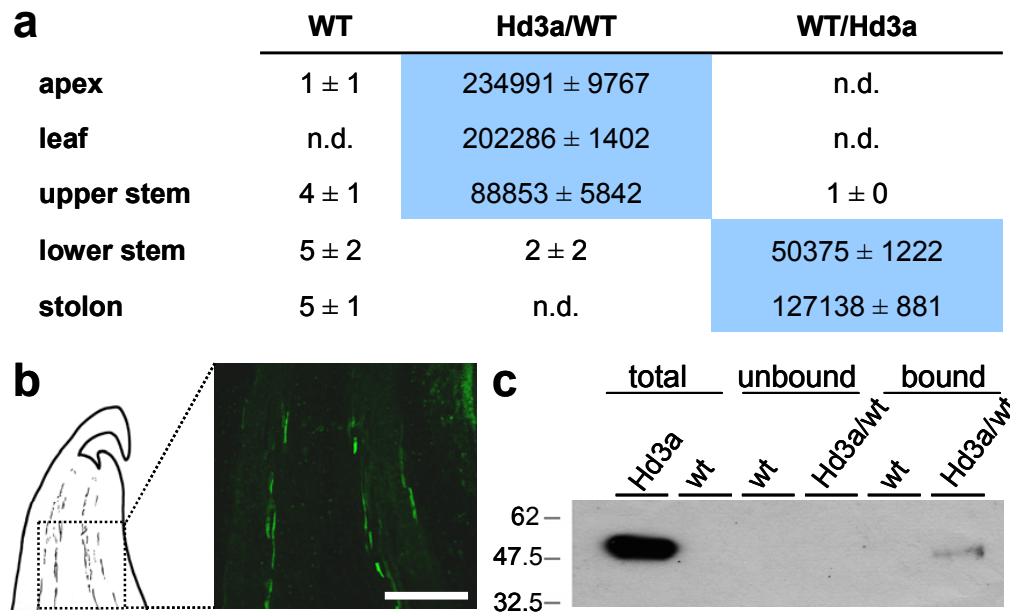
transfer to short day conditions relieves this repression. In line with this activity, leaves of StCO-RNAi (COi) lines were found to express high levels of the StSP6A transcript in long days, and to tuberize in these non-inductive conditions (Supplementary Fig. 11d-f). StSP6A gene expression, by contrary, is repressed in StCO over-expressing (COox) plants, although expression is fully restored after 6 days of transfer to short day conditions (Supplementary Fig. 11a-c), hence pointing to a day length dependent switch in StCO repressor activity as reported for the rice Hd1 protein^{5,6}.

Supplementary Text 5. Local induction of the StSP6A protein in stolons activates tuber-specific gene expression. To assay if StSP6A promotes tuberisation transition when locally expressed in stolons, we generated transgenic lines in which expression of this protein is driven by the AlcA/AlcR ethanol inducible system. StSP6A expression was locally activated by submerging the belowground part of the plant in a 0.5% ethanol solution and gene expression analyzed after 4 hours of induction. As seen in Figure 4d, a strong up-regulation of the tuber-specific StGA2ox1 transcript⁷ is observed in the stolons of these plants but not in transgenic controls expressing a fragment of the GUS gene under control of the same AlcA/AlcR inducible system (Alc-uid). Likewise, many other genes reported to be induced during early stages of tuber-development⁸ are found to be up-regulated in Alc-StSP6A stolons, although to lower levels than the StGA2ox1 gene (Figure 4e). Relative StGA2ox1 transcript levels in ethanol induced stolons actually were similar to those observed in swelling stolons, after 6 days of transfer to short day conditions (Supplementary Fig. 13), consistent with a function of this GA catabolic enzyme as a direct target of the StSP6A protein. Rapid induction (4 hours) of this transcript, on the other hand, excludes transport of the protein from the leaves or the transport of any further downstream mobile signal, which demonstrates that StSP6A is active in stolon cells and likely corresponds to a mobile protein.

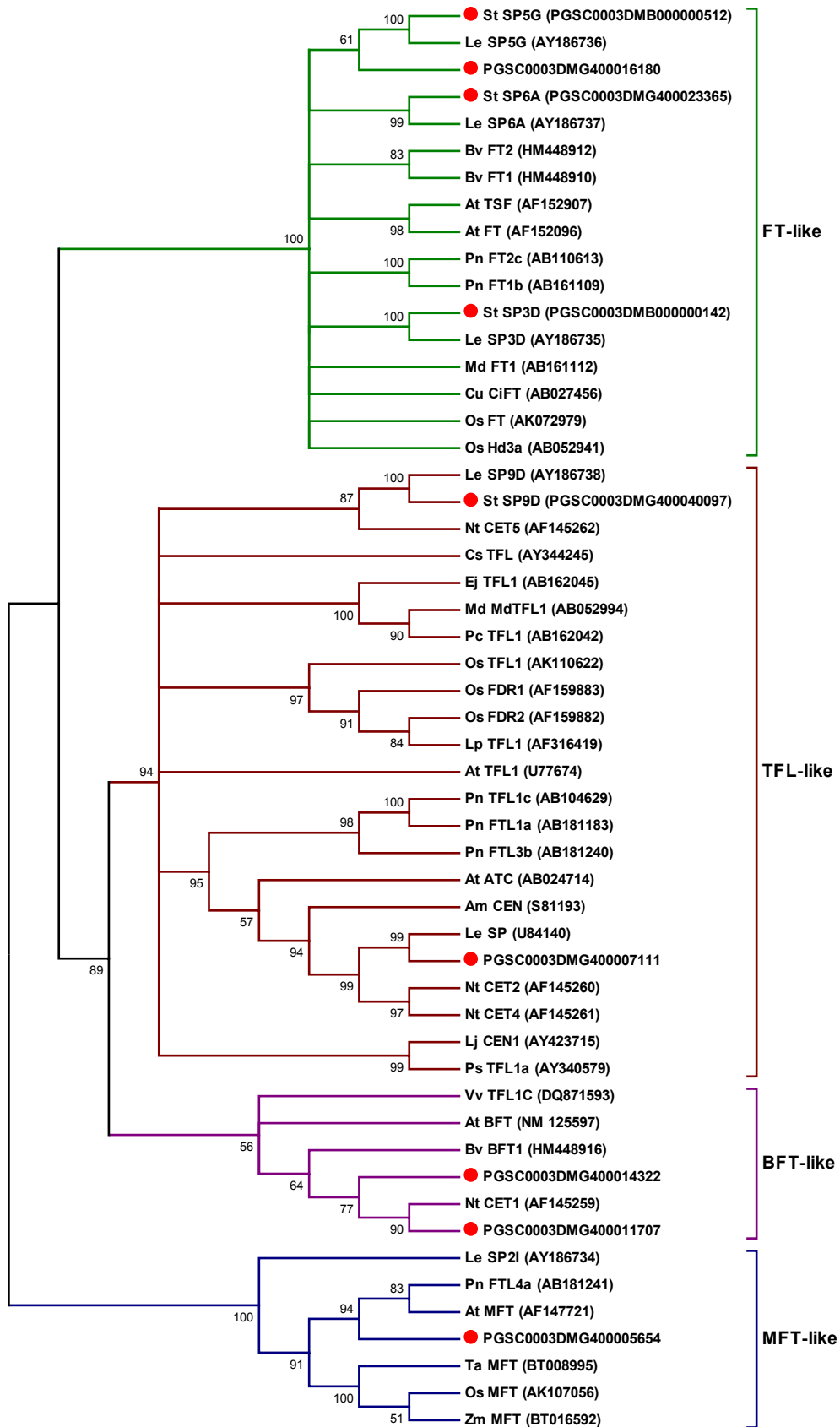
Supplementary Text 6. Model for StSP6A and StSP3D regulation of tuberisation and floral transition. StSP6A is repressed by StCO in long days, the light receptor phyB being somehow involved in the modulation of this repressor activity. Transfer to short days induces a switch in StCO repressor function and activates StSP6A gene expression in the leaves. During transport this signal is amplified by an auto-relay mechanism partially mediated by StCO. StSP6A activation in leaves and stolons promotes tuber formation. Although StCO weakly induces StSP3D gene expression in short days, this gene mainly responds to cues such as high light irradiance. The StSP3D protein promotes flowering in the shoot apex.

Supplementary Information References

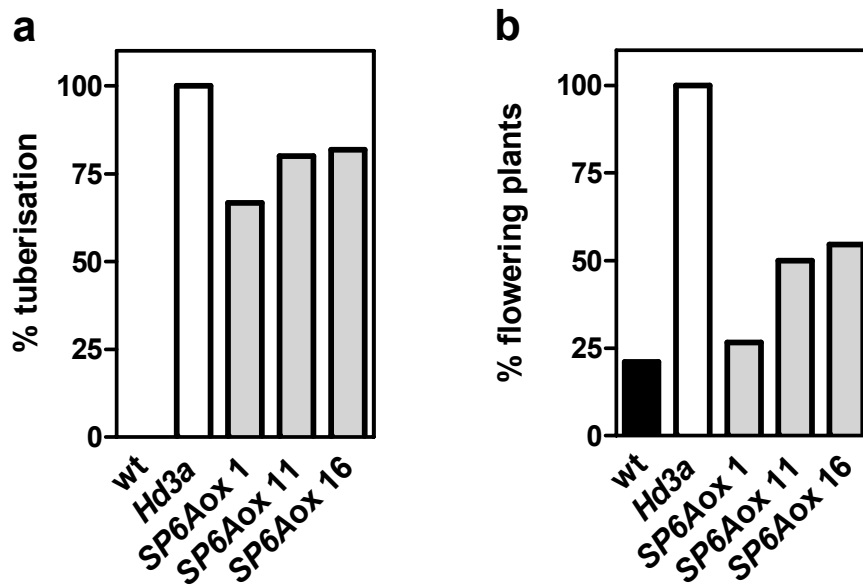
- 1 Jackson, S. D., Heyer, A., Dietze, J. & Prat, S. Phytochrome B mediates the photoperiodic control of tuber formation in potato. *Plant J.* **9**, 159–166 (1996).
- 2 Martinez-Garcia, J. F., Virgos-Soler, A. & Prat, S. Control of photoperiod-regulated tuberization in potato by the *Arabidopsis* flowering-time gene CONSTANS. *Proc. Natl Acad. Sci. USA* **99**, 15211–15216 (2002).
- 3 Pin, P. A. *et al.* An antagonistic pair of *FT* homologs mediates the control of flowering time in sugar beet. *Science* **330**, 1397–1400 (2010).
- 4 Rodríguez-Falcón, M., Bou, J. & Prat, S. Seasonal control of tuberization in potato: conserved elements with the flowering response. *Annu. Rev. Plant Biol.* **57**, 151–180 (2006).
- 5 Kojima, S. *et al.* Hd3a, a rice ortholog of the *Arabidopsis* FT gene, promotes transition to flowering downstream of Hd1 under short-day conditions. *Plant Cell Physiol.* **43**, 1096–1105 (2002).
- 6 Hayama, R., Yokoi, S., Tamaki, S., Yano, M. & Shimamoto, K. Adaptation of photoperiodic control pathways produces short-day flowering in rice. *Nature* **422**, 719–722 (2003).
- 7 Kloosterman, B. *et al.* *StGA2ox1* is induced prior to stolon swelling and controls GA levels during potato tuber development. *Plant J.* **52**, 362–373 (2007).
- 8 Kloosterman, B. *et al.* Genes driving potato tuber initiation and growth: identification based on transcriptional changes using the POCl array. *Functional & Integrative Genomics* **8**, 329–340 (2008).
- 9 Chincinska, IA *et al.* Sucrose transporter StSUT4 from potato affects flowering, tuberization, and shade avoidance response. *Plant Physiol.* **146**, 515–28 (2008).



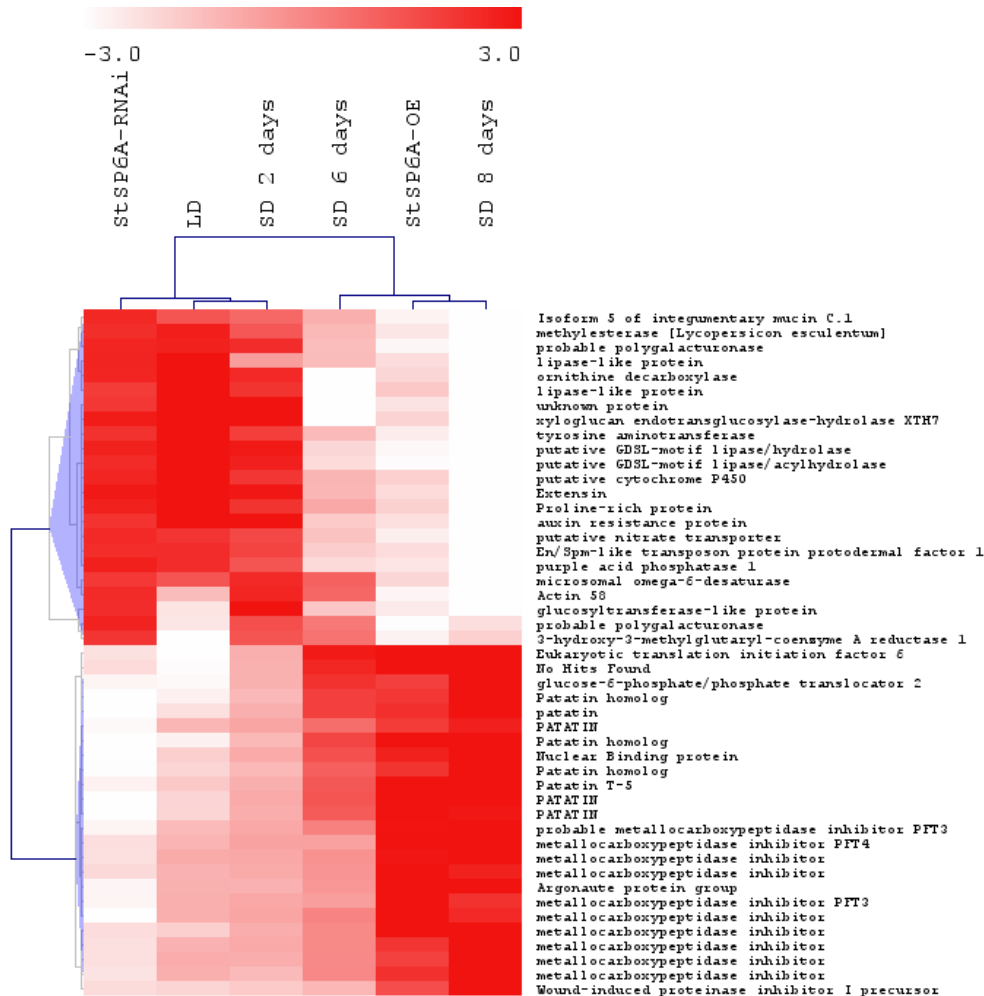
Supplementary Figure 1. RNA and protein analyses of *Andigena rol/C::Hd3a-GFP* lines. **a**, RT-qPCR amplification of the *Hd3a* transcript in grafted plants. Highlighted in blue are the transgenic *Hd3a* tissues. Data are means \pm standard deviation ($n=3$). **b**, Confocal microscopy of transgenic *Hd3a* stolons. *Hd3a-GFP* fluorescence is detected in phloem companion cells. Scale bar: 250 μ m. **c**, Western blot detection of the *Hd3a-GFP* protein in the stolon tips of grafted wild-type stocks (*Hd3a/wt*). Protein extracts of transgenic stolons (*Hd3a*) were loaded for comparison and wild-type stolons (wt) were used as negative controls. Extracts were concentrated by affinity binding to an anti-GFP agarose matrix (bound). The unbound fraction (unbound) was loaded to test for binding efficiency.



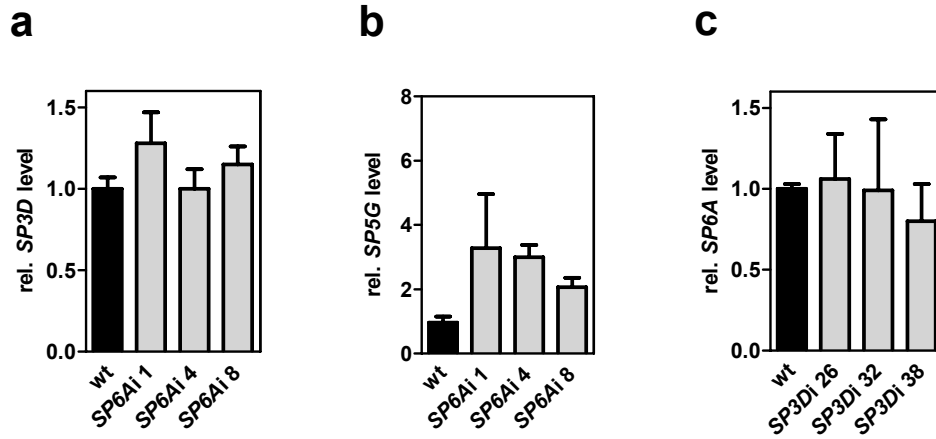
Supplementary Figure 2. The potato FT/TFL1-like gene family. Neighbor-Joining phylogenetic tree of FT/TFL1-like genes from different species. FT, TFL1, BFT and MFT clades are highlighted in green, brown, purple and blue, respectively. Genes from potato are marked with a red dot. Am: *Antirrhinum majus*, At: *Arabidopsis thaliana*, Bv: *Beta vulgaris*, Cs: *Citrus sinensis*, Cu: *Citrus unshiu*, Ej: *Eriobotrya japonica*, Le: *Solanum lycopersicum*, Lj: *Lotus japonicus*, Lp: *Lolium perenne*, Pn: *Populus nigra*, Md: *Malus x domestica*, Nt: *Nicotiana tabacum*, Os: *Oryza sativa*, Pc: *Pyrus communis*, Ps: *Pisum sativum*, St: *Solanum tuberosum*, Ta: *Triticum aestivum*, Vv: *Vitis vinifera*, Zm, *Zea mays*.



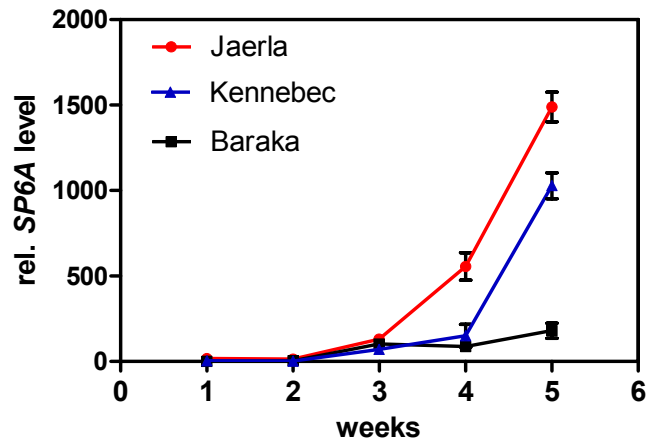
Supplementary Figure 3. Long day tuberization and flowering phenotypes of *Hd3a* and *StSP6A* over-expressing plants (*SP6Aox*). **a**, Tuberization of *Hd3a* and *StSP6A* over-expressing plants (*SP6Aox*) in long days scored when 100% of the *Hd3a* plants had initiated tuberization. **b**, Percentage of flowering plants, scored when all the *Hd3a* plants were flowering. n=27 in wt and n=15 in *Hd3a* and *StSP6Aox* lines.



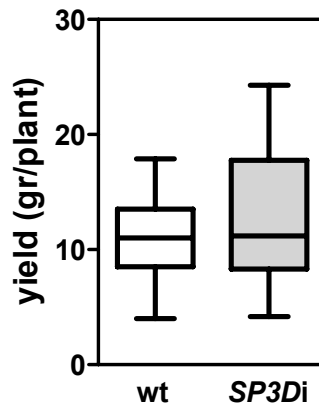
Supplementary Figure 4. Hierarchical clustering of genes differentially expressed in stolons of *StSP6A* over-expression and RNAi plants. Heat map representation of relative expression profiles of *StSP6A*ox and *StSP6A*-RNAi stolons, analyzed under non inductive long days (LD) and inductive short days (SD 6 days), respectively. Gene expression in non-induced wild-type stolons and time course regulation of these genes after 2 days, 6 days and 8 days of transfer to short days is also shown for comparison. Note that the expression profiles of short days *StSP6A*-RNAi stolons group with non-induced/2 days induced wild-type stolons, while those of long day *StSP6A*ox stolons group with 6 days and 8 days induced wild-type stolons. Gene description and numeric values are provided in Supplementary Table 1.



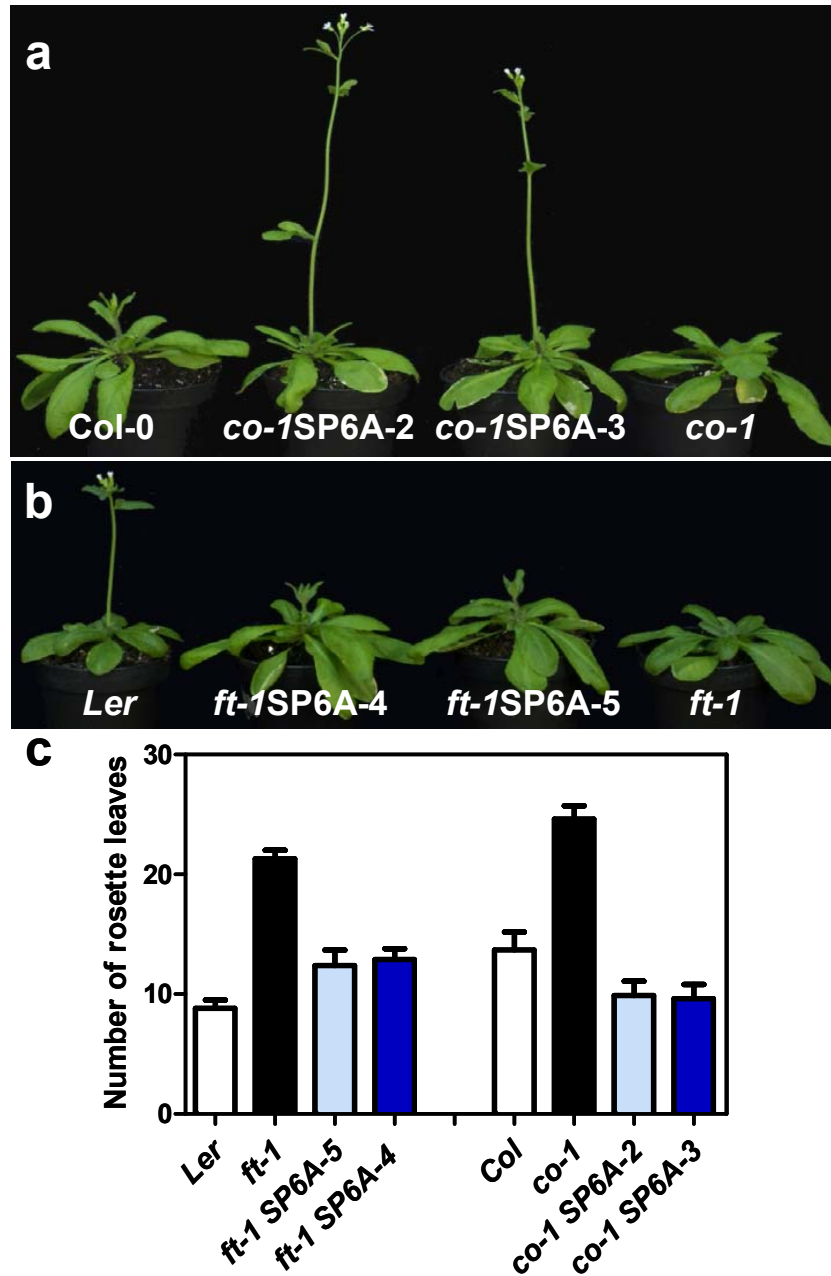
Supplementary Figure 5. Expression of the *StSP3D* and *StSP5G* transcripts in *StSP6A*-RNAi (*SP6Ai*) lines (a-b) and *StSP6A* transcript levels in *StSP3D*-RNAi (*SP3Di*) lines (c). Transcript levels were quantified by RT-qPCR analyses of the transgenic leaves sampled after 6 days of transfer to short day inductive conditions. Error bars indicate standard deviation (n=3).



Supplementary Figure 6. StSP6A expression in commercial varieties. Time course of StSP6A relative expression in three commercial potato varieties: *Jaerla* (early-maturing), *Kennebec* (intermediate) and *Baraka* (late-maturing). Error bars represent standard deviation (n=3).



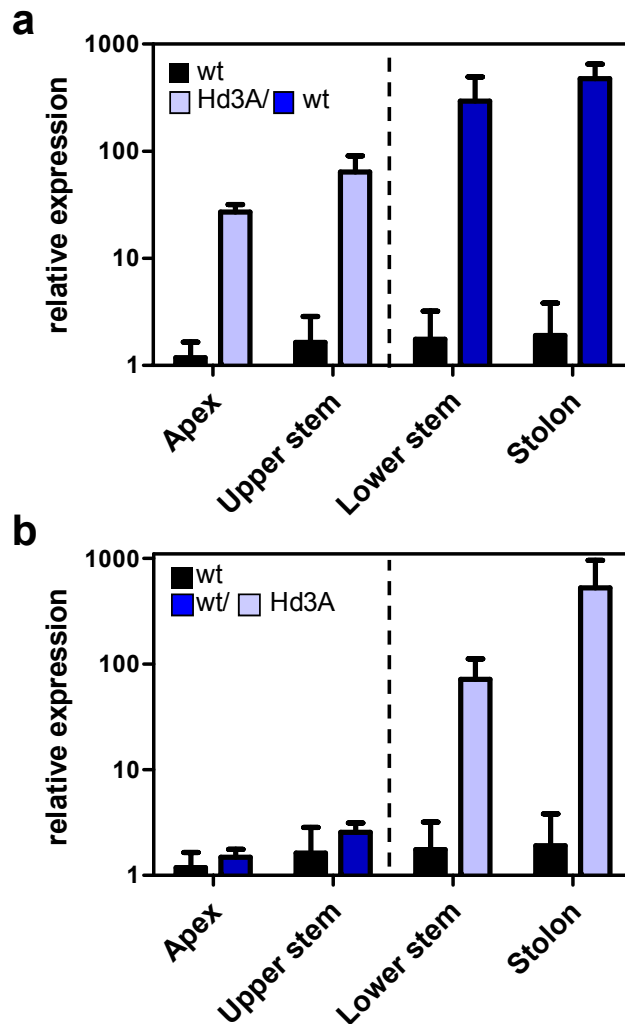
Supplementary Figure 7. Tuber yield per plant in StSP3D-RNAi lines. Box-whisker plots of tuber yield (gr/plant) distributions of wild-type and StSP3D-RNAi (*SP3Di*) plants under short day conditions (n=30, wt and n=24, *SP3Di*). A t-test analysis (two tailed p-value 0.1484) showed no significant difference between these populations.



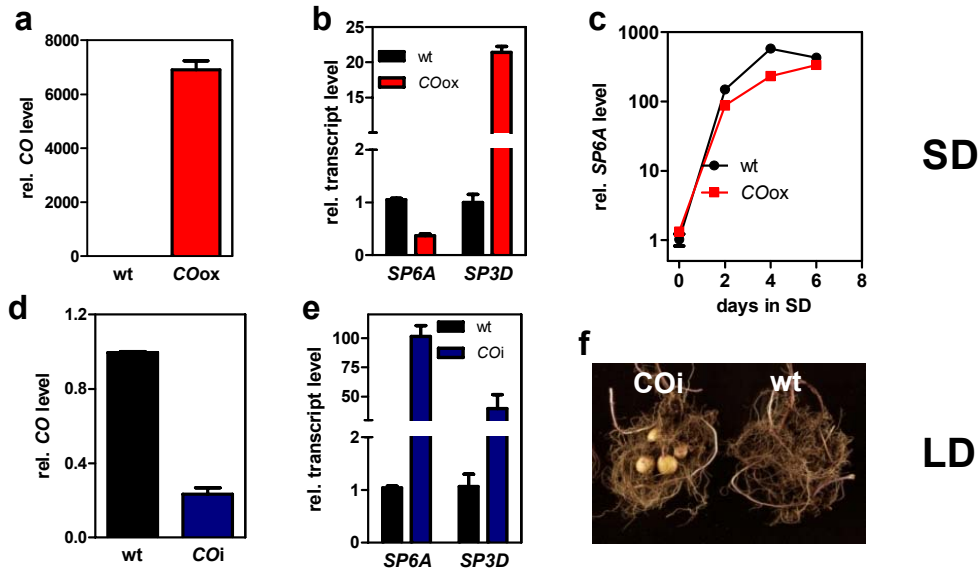
Supplementary Figure 8. Complementation of the late flowering phenotype of the *co-1* and *ft-1* *Arabidopsis* mutants by the *StSP6A* gene. a, b, Lines harboring the potato *StSP6A* transgene bolted earlier than the corresponding *co-1* (a) and *ft-1* (b) mutants. c, Flowering time of the transgenic lines estimated as the number of rosette leaves at flowering. Error bars indicate standard deviation (n=10).

				*		**	
Arabidopsis FT	..Y.	QLGROT	VYAP	---	GW	-	RQNFNT
Rice Hd3a	..Y.	QLGROT	VYAP	---	GW	-	RQNFNT
Potato SP6A	..Y.	QSRRE	VYAP	---	GW	-	RQNFNT
Potato SP3D	..Y.	QLGROT	VYAP	---	GW	-	RQNFNT
Sugar Beet BvFT2	..Y.	QLGROT	VYAP	---	GW	-	RQNFNT
Potato SP5G	..Y.	QLGREAIN	APDI	IDS	-	RQNFNT	
Potato SP5G like	..Y.	QLRREI	VHAP	---	EN	-	RQNFDT
Sugar beet BvFT1	..Y.	QLGROT	VNAP	---	QQ	-	RQNFNT

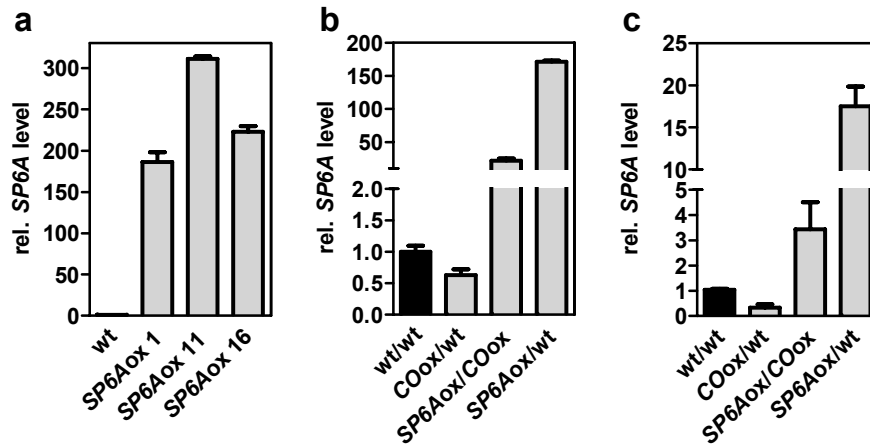
Supplementary Figure 9. StSP6A, StSP5G and PGSC0003DMG200016180 (SP5G-like) amino acid sequence alignment with other FT-like proteins. Partial alignment showing amino acid exchanges in the segment region B of the fourth exon. Black stars in the upper part and red letters in the sugar beet BvFT1 sequence indicate the amino acid residues found to be implicated in flowering repression in sugar beet³.



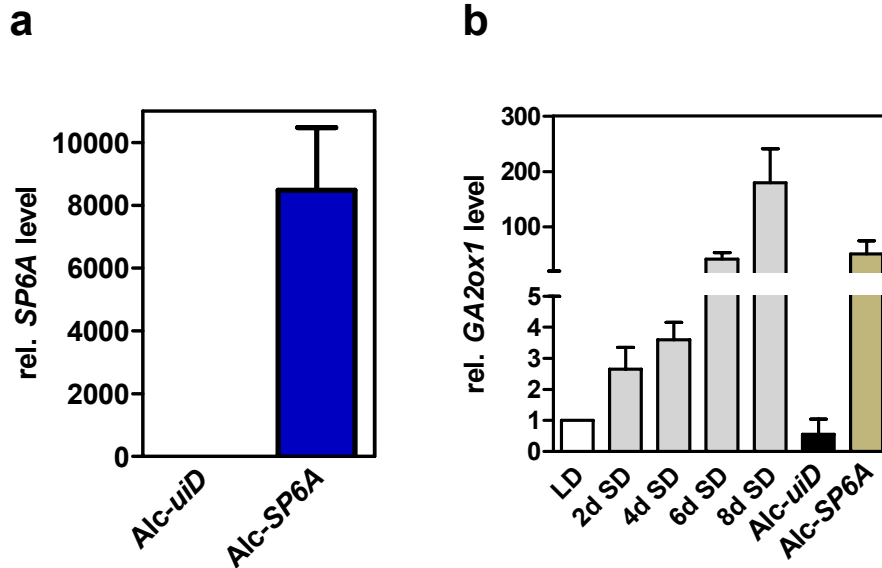
Supplementary Figure 10. *StSP6A* expression in *Hd3A* grafted plants. RT-qPCR was used to analyze relative *StSP6A* expression in different organs of grafted plants grown under long days. **a**, *Hd3a* scions grafted onto wild-type stocks. **b**, Wild-type scions grafted onto *Hd3a* stocks. *StSP6A* transcript levels in wild-type (dark blue bars) and *Hd3a* tissues (light blue bars) were estimated as the $2^{-\Delta\Delta C_T}$ value relative to the mean values obtained in wild-type control tissues. Values are represented in a logarithmic scale. The dashed line indicates the graft junction. Error bars indicate standard deviation of three independent experiments.



Supplementary Figure 11. StCO acts as a repressor of tuberization under long days. **a**, StCO transcript levels in leaves of StCO over-expressing lines (COox). **b**, Relative StSP6A and StSP3D expression in leaves of wild-type and transgenic StCOox, after 4 inductive days. **c**, Short days (SD) kinetics of StSP6A regulation in StCOox leaves. Values are represented in a logarithmic scale. **d**, StCO transcript reduction in leaves of RNAi plants (COi). **e**, StSP6A and StSP3D regulation in leaves of StCO-RNAi plants under long days (LD). Error bars indicate standard deviation of three biological replicates. **f**, Tuberization of StCO-RNAi plants (left) under non-inductive long days. Wild-type controls (right) do not tuberize.



Supplementary Figure 12. StCO repression of the relay mechanism is conserved in two different StSP6Aox lines. StSP6A expression in leaves of different StSP6Aox lines (a). Relative StSP6A expression in grafting experiments with two different StSP6Aox lines, line 11 (b) and line 16 (c). Error bars indicate standard deviation (n=3).



Supplementary Figure 13. StGA2ox1 response to local StSP6A induction. a, StSP6A expression in Alc-SP6A stolons relative to Alc-uid controls, after four hours of ethanol induction. **b,** StGA2ox1 expression in wild-type Andigena stolons after transfer to short day inductive conditions, compared to StGA2ox1 in long days (LD) grown Alc-SP6A lines after four hours of StSP6A induction with ethanol. Error bars indicate standard deviation of two independently treated samples. This experiment was repeated in different transgenic lines with similar results.

Supplementary Table 1. Description and numeric values of the set of genes represented in Supplementary Figure 4. Gene expression is represented as the relative log ratio.

Photoperiod	SD	LD	LD	SD 2 days	SD 6 days	SD 8 days	Accessions	GeneName	Description
Genotype	StSP6AI	StSP6Aox	WT	WT	WT	WT			
	-2.68	3.82	-1.62	-1.00	1.25	3.44	NA 00000	ACDA01685E05.T3m.scf	Patatin T-5
	-2.19	3.06	-1.11	-0.66	-0.61	3.07	NA 00000	bf_arrayxxx_0049e03.17m.scf	probable metalloproteinase inhibitor PFT4 - potato dbj_BAA21500.1_metalloproteinase inhibitor [Solanum tuberosum]
	-2.75	2.99	-1.26	-0.79	0.22	3.21	NA 00000	bf_arrayxxx_0053a08.17m.scf	probable metalloproteinase inhibitor PFT3 - potato dbj_BAA21495.1_metalloproteinase inhibitor [Solanum tuberosum]
	-2.11	1.52	-1.94	-1.68	-1.18	4.30	gb P08454	bf_cswwxxx_0007b05.13m.scf	Wound-induced proteinase inhibitor 1 precursor (Chymotrypsin inhibitor 1 D subunit) gb_AAA69781.1, proteinase inhibitor I
	2.48	-2.59	2.16	1.68	-1.46	-8.93	gb BAD86972	bf_mxfxxx_0014b09.13m.scf	putative nitrate transporter [Oryza sativa (japonica cultivar-group)] dbj_BAB56042.1_putative nitrate transporter [Oryza sativa (japonica cultivar-group)]
	-2.75	1.87	-2.87	-1.03	2.23	3.24	gb AAO19451	MICRO.1076.C1	glucose-6-phosphate/phosphate translocator 2 [Solanum tuberosum]
	2.57	-1.81	3.00	2.11	-1.14	-7.98	gb AAM61354	MICRO.13031.C1	putative cytochrome P450 [Arabidopsis thaliana] gb_AAD30263.1
	2.21	-2.21	3.72	3.84	-1.66	-11.46	gb CAH59413	MICRO.13184.C1	auxin resistance protein [Plantago major]
	2.68	-2.35	2.38	1.36	-2.07	-7.35	gb AAT37529	MICRO.15077.C1	purple acid phosphatase 1 [Solanum tuberosum]
	-3.43	2.30	-2.22	-0.97	1.88	4.47	gb AAZ75960	MICRO.1520.C14	patatin [Solanum tuberosum] pir_S51596 patatin precursor non-sucrose-inducible - Solanum brevifolium gb_AAA66198.1_patatin precursor
	-2.88	2.01	-1.16	-0.74	0.69	2.71	gb AAZ75962	MICRO.1520.C23	patatin [Solanum tuberosum] pir_A26017 patatin T5 precursor
	-3.66	4.15	-1.95	-0.85	1.35	3.15	pir A29810	MICRO.1520.C3	patatin [Solanum tuberosum] sp_P07745_PATO_SOLTU PATATIN PRECURSOR (POTATO TUBER PROTEIN)
	-4.24	4.42	-1.93	-0.93	1.17	2.91	gb AAZ75958	MICRO.1520.C9	patatin [Solanum tuberosum] pir_S51596 patatin precursor non-sucrose-inducible - Solanum brevifolium gb_AAA66198.1_patatin precursor
	2.49	-2.72	1.34	0.84	-0.98	-3.80	NA 00000	MICRO.15952.C1	isoform 5 of integumentary mucin C.1
	2.87	-2.09	3.98	2.91	-1.16	-12.00	gb BAC43682	MICRO.15956.C1	At1g26948 [Arabidopsis thaliana] ref_NP_849712.1_expressed Polien protein. Allergen and extensin family
	2.67	-1.84	3.65	2.18	-0.80	-10.36	gb AAD24597	MICRO.17678.C1	ref_NP_179254.2_proline-rich family protein [Arabidopsis thaliana]
	2.09	-2.30	8.72	10.31	-5.83	-20.66	gb AAV59327	MICRO.18299.C1	unknown protein [Oryza sativa (japonica cultivar-group)] ref_XP_476200.1_unknown protein [Oryza sativa (japonica cultivar-group)]
	-2.75	3.38	-1.00	-0.80	-0.53	2.24	gb BAA21495	MICRO.2033.C1	probable metalloproteinase inhibitor PFT3 - potato dbj_BAA21495.1_metalloproteinase inhibitor [Solanum tuberosum]
	-2.21	2.13	-1.05	-0.83	-0.01	3.04	NA 00000	MICRO.2033.C11	metalloproteinase inhibitor
	-3.07	3.69	-1.00	-0.73	0.13	2.46	gb BAA21493	MICRO.2033.C2	metalloproteinase inhibitor [Solanum tuberosum]
	2.31	2.29	-0.96	-1.26	0.03	4.02	gb AAZ94194	MICRO.2033.C6	metalloproteinase inhibitor [Solanum tuberosum]
	-2.35	-2.14	2.38	1.76	-1.77	-8.56	gb AAD21725	MICRO.2406.C1	[Arabidopsis thaliana] gb_AAD33868.1_protodermal factor 1 [Arabidopsis thaliana]
	-2.10	3.60	-2.91	-1.03	2.51	3.86	NA 00000	MICRO.3274.C2	No Hits Found
	-2.27	4.23	-3.22	-0.98	2.84	4.30	NA 00000	MICRO.3274.C4	Eukaryotic translation initiation factor 6 (EIF-6)-like protein; n=1; Arabidopsis thaliana
	2.66	-2.82	4.88	2.87	-1.97	-10.71	gb AAM65485	MICRO.4133.C1	putative GDSL-motif lipase/hydrolase [Arabidopsis thaliana]
	2.58	-2.14	3.37	-0.54	-1.30	-3.76	gb CAB78857	MICRO.4160.C1	lipase-like protein [Arabidopsis thaliana] emb_CAA16735.1
	2.01	-1.60	5.74	2.20	-3.19	-6.18	gb CAB78857	MICRO.4160.C6	lipase-like protein [Arabidopsis thaliana] emb_CAA16735.1_lipase-like protein
	2.39	-2.92	5.05	2.71	-2.10	-10.42	gb AAM64916	MICRO.4199.C1	putative GDSL-motif lipase/hydrolase [Arabidopsis thaliana] gb_AAC05014.1
	2.83	-1.90	4.89	5.14	-3.28	-9.85	gb AAS46243	MICRO.4590.C1	xyloglucan endotransglucosylase/hydrolase XTH7 [Lycopersicon esculentum]
	2.56	-1.98	5.33	2.46	-3.20	-5.43	gb AAB82301	MICRO.561.C1	ornithine decarboxylase [Lycopersicon esculentum] gb_AAB82301.2_ornithine decarboxylase [Lycopersicon esculentum]
	2.32	-2.37	2.73	1.26	-1.19	-5.34	gb AAV87156	MICRO.6179.C1	methyltransferase [Lycopersicon esculentum]
	2.15	-2.71	-3.36	1.37	0.56	-1.81	pir S59944	MICRO.6420.C1	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (HMG-CoA reductase 1) (HMG1)
	2.37	-2.48	-2.34	3.16	-1.57	-4.00	gb AAM13292	MICRO.6450.C1	glucosyltransferase-like protein [Arabidopsis thaliana] gb_AAM13292.1
	2.39	-2.78	-1.32	2.56	0.87	-12.15	gb CAA39278	MICRO.6793.C1	actin [Solanum tuberosum] pir_S20094 actin 58 - potato sp_P30167_ACT3_SOLTU Actin 58
	2.06	-1.98	1.36	2.46	1.02	-12.57	gb CAH48076	MICRO.8531.C1	microsomal omega-6-desaturase [Nicotiana tabacum]
	2.57	-2.81	2.65	2.38	-1.33	-5.86	gb AAB39556	MICRO.8715.C1	probable polygalacturonase (EC 3.2.1.15) 1 - tomato gb_AAB39556.1_AROGP2
	2.63	-2.97	-2.38	1.49	0.41	-2.18	gb AAB39557	POABU26TP	POABU26TP_501-probable polygalacturonase (EC 3.2.1.15) 1 - tomato gb_AAB39557.1_AROGP3
	2.02	-2.55	4.89	1.92	-1.26	-10.59	gb CAD30341	SDBN002A15u.scf	SDBN002A15u.scf_448-tyrosine aminotransferase [Solenostemon scutellarioides]
	-2.15	3.29	-1.78	-0.91	-0.01	4.16	NA 00000	TBSK00763FH07.13m.scf	metalloproteinase inhibitor
	-2.22	1.84	-0.89	-0.92	-0.02	3.11	NA 00000	TBSK01466FC02.13m.scf	metalloproteinase inhibitor [Solanum tuberosum]
	-3.38	2.67	-1.79	-0.85	1.47	3.63	NA 00000	TBSK02196FG12.13m.scf	Nuclear Binding protein DMG3200020488
	-2.05	3.06	-1.07	-0.86	-0.30	2.67	gb AAZ94194	TBSK03109FD01.13m.scf	metalloproteinase inhibitor [Solanum tuberosum]
	-2.22	2.95	-0.87	-0.81	-0.23	3.07	NA 00000	TBSK03444FG12.13m.scf	metalloproteinase inhibitor [Solanum tuberosum]
	-3.49	2.10	-2.63	-1.22	1.86	4.45	NA 00000	TBSK03752FA08.13m.scf	Patatin homolog
	-2.77	3.60	-1.03	-1.07	-0.36	3.04	NA 00000	TBSK04121FH05.13m.scf	Argonaute protein group
	-2.96	2.18	-1.94	-1.19	1.08	3.20	NA 00000	TBSK04176FD12.13m.scf	Patatin homolog
	-3.88	3.61	-2.63	-1.21	1.75	3.98	NA 00000	TBSK04996FA04.13m.scf	Patatin homolog

Supplementary Table 2. FT/TFL1 family members identified in the Potato Genome (<http://potatogenomics.plantbiology.msu.edu/>).

Locus	Protein	Transcript	Chr.	Start poss.	End poss.	Superscaffold	Scaffold	comments
PGSC0003DMG400016180	DMP200028269	DMT400041726	11	4756770	5999682	PGSC0003DMB000000152	PGSC0003DMS000002042	SP5G like
PGSC0003DMG400014322	DMP200025227	DMT400037143	3	22117937	22761173	PGSC0003DMB000000154	PGSC0003DMS000001644	CEN 1
PGSC0003DMG400007111	DMP200012606	DMT400018307	6	61340731	61409304	PGSC0003DMB000000091	PGSC0003DMS000002691	SELF-PRUNING
PGSC0003DMG400023365	DMP200040404	DMT400060057	5	53183226	53934257	PGSC0003DMB000000072	PGSC0003DMS000000201	SP6A
PGSC0003DMG400011707	DMP200020755	DMT400030575	1	37852084	37877323	PGSC0003DMB000000560	PGSC0003DMS000002631	CEN 1
PGSC0003DMG400015751	DMP200027622	DMT400040735	5	66063	69181	PGSC0003DMB000000512	PGSC0003DMS000002164	SP5G
PGSC0003DMG400040097	DMP200062201	DMT400090526	9	7462255	7564753	PGSC0003DMB000000021	PGSC0003DMS000000876	SP9D
PGSC0003DMG400005654	DMP200009953	DMT400014409	3	51272594	52284276	PGSC0003DMB000000026	PGSC0003DMS000001550	MOTHER of FT
No ID	No ID	No ID	3	1063000	1068600	PGSC0003DMB000000142	PGSC0003DMS000000135	SP3D

Supplementary Table 3. Primer sets used in this study. *StGA2 oxidase 1* and *StSUT1* primers have been described elsewhere^{7,9}.

PRIMER NAME	SEQUENCE (5' to 3')	TARGET GENE	AMPLICON LENGTH	USAGE
Hd3a:GFP for	GGAAAAGCTTGCCTATGTGG and	<i>Hd3a</i>	72 bp	qPCR
Hd3a:GFP rev	CTGCTCCTGGCAGTTTCAA	<i>Hd3a</i>	72 bp	qPCR
actin for	GGAAAAGCTTGCCTATGTGG	<i>Stactin8</i>	59 bp	qPCR
actin rev	CTGCTCCTGGCAGTTTCAA	<i>Stactin8</i>	59 bp	qPCR
SP6A for	GACGATCTTCGCAACTTTTACA	<i>StSP6A</i>	74 bp	qPCR
SP6A rev	CCTCAAGTTAGGGTCGCTTG	<i>StSP6A</i>	74 bp	qPCR
SP3D for	GGACCCAGATGCTCCAAGTC	<i>StSP3D</i>	96 bp	qPCR
SP3D rev	CTTGCCAAAACCTTGAACCTG	<i>StSP3D</i>	96bp	qPCR
q5G_Afor	GGTGTGTAGACTTTGGTGTGGTTT	<i>StSP5G</i>	64 bp	qPCR
q5G_Arev	GGCCTCAAGGCACATCCAT	<i>StSP5G</i>	64 bp	qPCR
CO_q_For	GTAGCAACAATTGGGCAAGGG	<i>StCO</i>	64 bp	qPCR
CO_q_Rev	AGTAAACGGTACATGTTGCGGA	<i>StCO</i>	64 bp	qPCR
PGSC0003DMT200041726 for	CCAACCTCCGAGCAATCCTTA	<i>PGSC0003DMG400016180</i>	63 bp	qPCR
PGSC0003DMT200041726 rev	TGCTGGGATATCAGTGACCA	<i>PGSC0003DMG400016180</i>	63 bp	qPCR
PGSC0003DMP200020755 for	TGCCTCTTGTCATTGCTTCTAA	<i>PGSC0003DMG400011707</i>	110 bp	qPCR
PGSC0003DMP200020755 rev	AGGATCACTAGGACCTGGAACA	<i>PGSC0003DMG400011707</i>	110 bp	qPCR
PGSC0003DMP200025226 for	ACCATCAACAAGGGATCAATTC	<i>PGSC0003DMG400014322</i>	100 bp	qPCR
PGSC0003DMP200025226 rev	AGTTTCTCTCTGGGCATTGAAA	<i>PGSC0003DMG400014322</i>	100 bp	qPCR
PGSC0003DMP200012606 for	TCCAGATGTTCTGTGCTCCTAGT	<i>PGSC0003DMG400007111</i>	86 bp	qPCR
PGSC0003DMP200012606 rev	AGCAATCTGTAGTGCCTGGAAT	<i>PGSC0003DMG400007111</i>	86 bp	qPCR
PGSC0003DMP200062201 for	AGGATCTGTATGACCAGTGTG	<i>PGSC0003DMG400040097</i>	89 bp	qPCR
PGSC0003DMP200062201 rev	TTTTCCCTTCTGCTGTTTCTTC	<i>PGSC0003DMG400040097</i>	89 bp	qPCR
qMFT_for	GGAAATTTTGCAGCCACCAGTAG	<i>PGSC0003DMG400005654</i>	125 bp	qPCR
qMFT_rev	TTTCGATTTGCTGGTTCTTGT	<i>PGSC0003DMG400005654</i>	125 bp	qPCR
SP3D_RNAi for	CACCGTTCAGACAATTAGGTCGACA	<i>StSP3D</i>	310 bp	RNAi construct
SP3D_RNAi rev	AAGTAGTAGAGATTGGTGGTT	<i>StSP3D</i>	310 bp	RNAi construct
SP6A_RNAi for	CACCTAGAATAAAGTCTATATTGAC	<i>StSP6A</i>	257 bp	RNAi construct
SP6A_RNAi rev	ATCATATGCTAACCAATATACTC	<i>StSP6A</i>	257 bp	RNAi construct
Co_RNAi for	CACCGTTAGCGGTGGTTCTATGAT	<i>StCO</i>	1052 bp	RNAi construct
Co_RNAi rev	AGAACTCTTTTTACATATAACA	<i>StCO</i>	1052 bp	RNAi construct
Col1_for	CACCATGTTGAAAAAGAGAAGTG	<i>StCO</i>	1239 bp	OE construct
Col1_rev	GAATGAAGGGACAATCCATAAC	<i>StCO</i>	1239 bp	OE construct
SP6A-ATG	ATCATGCCTAGAGTTGATCCATTG	<i>StSP6A</i>	522 bp	OE construct
SP6A-TAA	TTTTTATGCGCGCAGCTCCTCCAGTAC	<i>StSP6A</i>	522 bp	OE construct
SP6A-SQ for	CCATTGATAGTTGGTCGTGTG	<i>StSP6A</i>	458 bp	semi-quantitative PCR
SP6A-SQ rev	ACAGCTGCAACAGGCAATCC	<i>StSP6A</i>	458 bp	semi-quantitative PCR
ActinF-SQ	CCTTGATGCTAGTGGTCG	<i>Stactin8</i>	251 bp	semi-quantitative PCR
ActinR-SQ	GCTCATAGTCAAGAGCCAC	<i>Stactin8</i>	251 bp	semi-quantitative PCR
<i>StGA2ox1</i> forward ⁷	AGGCACAGAGTGATCGCAGAT	<i>StGA2 oxidase 1</i>	65 bp	qPCR
<i>StGA2ox1</i> reverse ⁷	TGGTGGCCCTCCAAAGTAAA	<i>StGA2 oxidase 1</i>	65 bp	qPCR
AGL8_q_for	AGCAAAACAACCAGCTTTCCAA	<i>StAGL8</i>	73 bp	qPCR
AGL8_q_rev	TGATCCCACTGATTTTCTGTG	<i>StAGL8</i>	73 bp	qPCR
PIN1For	CGTGTTCGGTGGAATGAT	<i>StPIN1</i> like protein	56 bp	qPCR
PIN1Rev	CTCCATCGGATCGACCTGAT	<i>StPIN1</i> like protein	56 bp	qPCR
PIN4For	GTTTCATTGCGCGCGATTTC	<i>StPIN4</i> like protein	60 bp	qPCR
PIN4Rev	CCCATAGCGAAAGAACAACCA	<i>StPIN4</i> like protein	60 bp	qPCR
AuxTF_For	CAGCCTAAGCGGCATCTTCT	<i>StARF8</i>	59 bp	qPCR
AuxTF_Rev	AGCCTTTTGGCGCTAACAAA	<i>StARF8</i>	59 bp	qPCR
LC-SUT1_for ⁹	TTCCATAGCTGCTGGTGTTC	<i>StSUT1</i>	127 bp	qPCR
LC-SUT1_rev ⁹	TACCAGAAATGGGTCCACAA	<i>StSUT1</i>	127 bp	qPCR
FD forward	GGAGACGGAAGTGGCACATT	<i>StFD</i>	55 bp	qPCR

FD reverse	TAACTGCAGCTAAGCGTAACTGTTG	St <i>FD</i>	55 bp	qPCR
FPF_q_rev	CTAGTTGAGAACGCCGGTGACT	St <i>FPF1</i>	127 bp	qPCR
FPF_q_for	CCCATCCAAGAGAGTACAAAATTCC	St <i>FPF1</i>	127 bp	qPCR
CDC2_q_for	ATGTCGCCAGTGTAGGGAATGT	St <i>CDC2</i>	142 bp	qPCR
CDC2_q_rev	TTTCCCTTCTTGATGCTCTCA	St <i>CDC2</i>	142 bp	qPCR
SP6A-Topo-For	CACCATGCCTAGAGTTGATCCATTG	St <i>SP6A</i>	522 bp	AlcA-SP6A Cloning
SP6A-Topo-Rev	GTA CTGGAGGACGTCGCGCATAA	St <i>SP6A</i>	522 bp	AlcA-SP6A Cloning