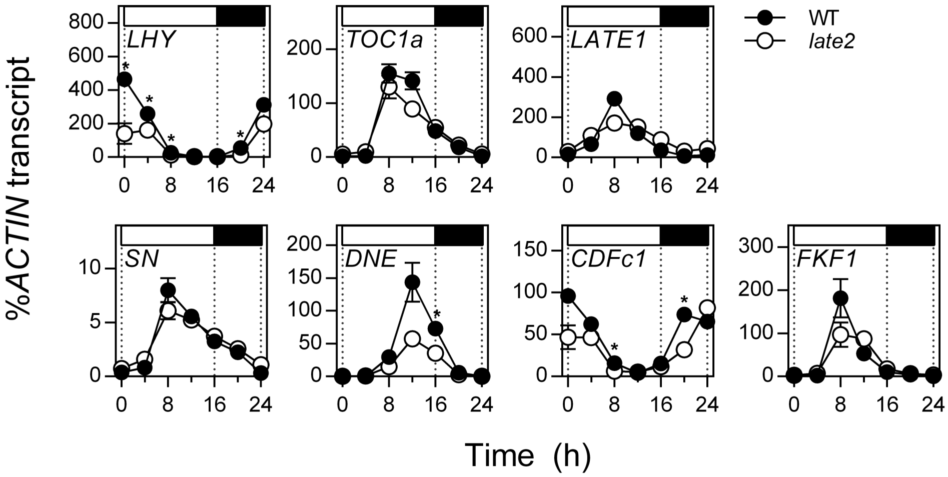
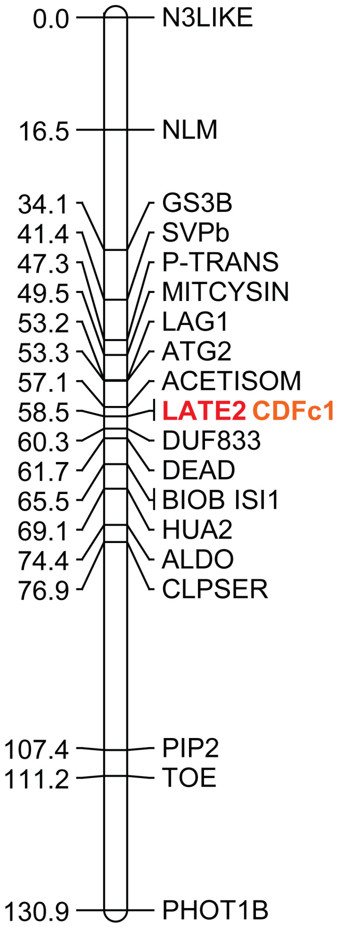
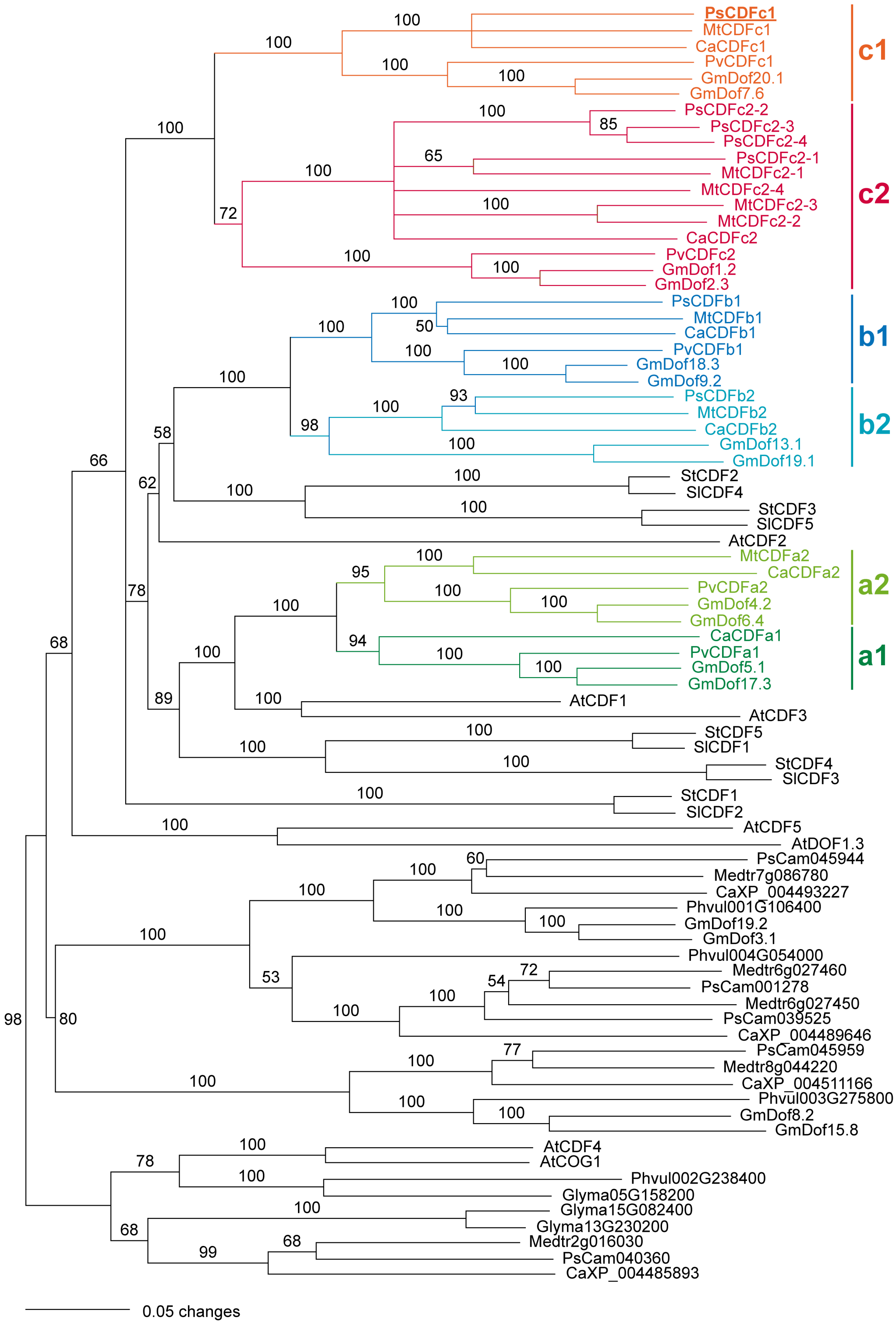


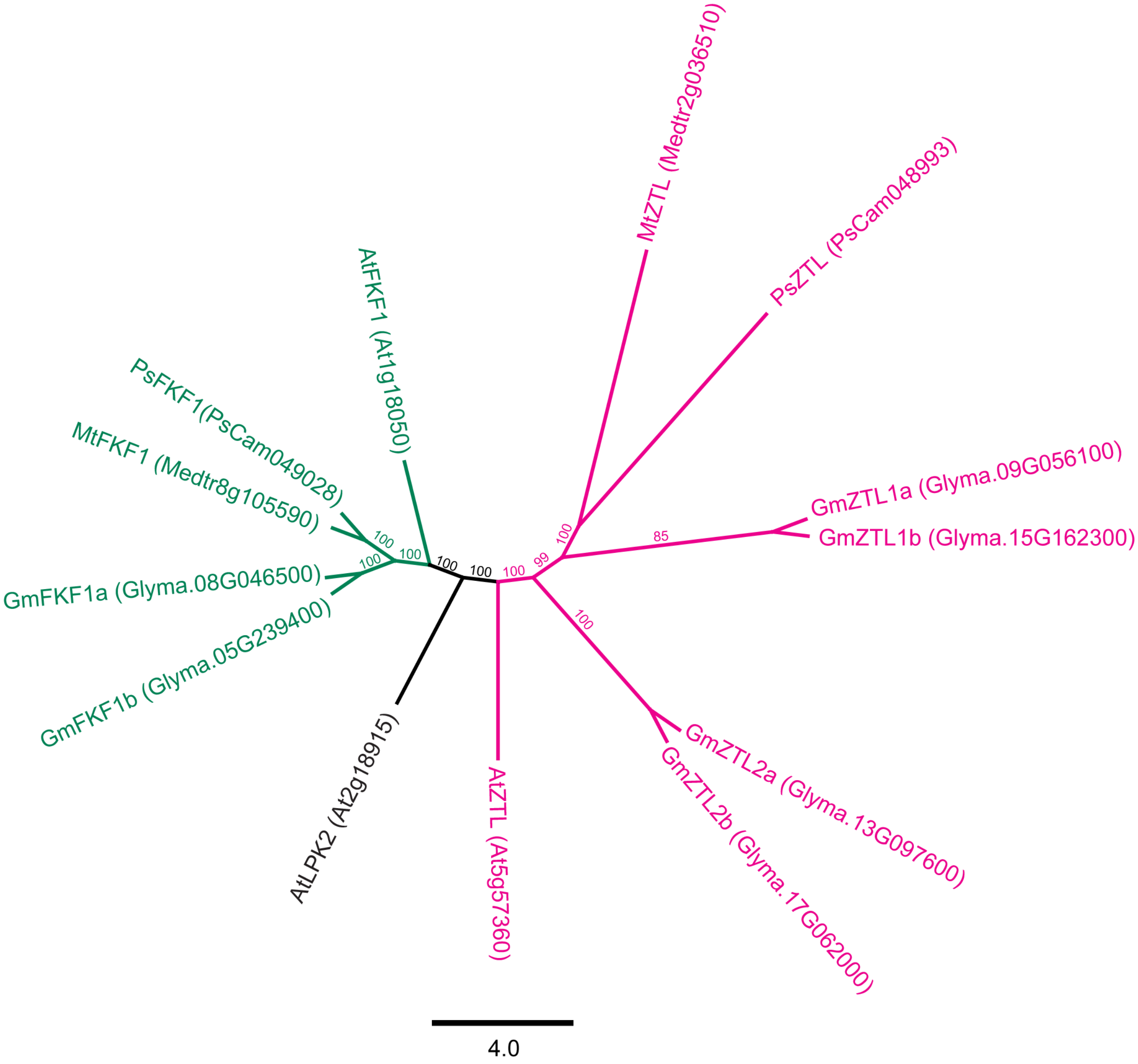
Supplemental Figure 1: Rhythmic expression patterns of circadian clock genes under LD cycles.
Transcript levels were determined in the second uppermost fully expanded leaf of 3-week-old wild-type (NGB5839) and *late2-1D* mutant plants grown under a 16 h LD photoperiod at 20°C. Mean values ± SE are shown for *n* = 2 biological replicates, each consisting of pooled material from two plants. Asterisks indicate significantly different values ($P \leq 0.05$). Day and night periods are respectively indicated by white and black bars above the graph. Note that both genotypes carry the *hr* mutation (Weller et al., 2012).



Supplemental Figure 2: Position of *LATE2* in pea linkage group VII.
Partial map of linkage group VII derived from analysis of segregation data in the F_2 generation of a cross between *late2-1D* and cv. Térèse (219 F_2 plants), using JoinMap software (v4; Kyazma B.V., Wageningen, Netherlands). A marker for *CDFc1* based on the C1348T transition (**Figure 5**), co-segregated perfectly with the *late2-1D* genotype. Full details for markers are given in **Supplemental Table 2**.

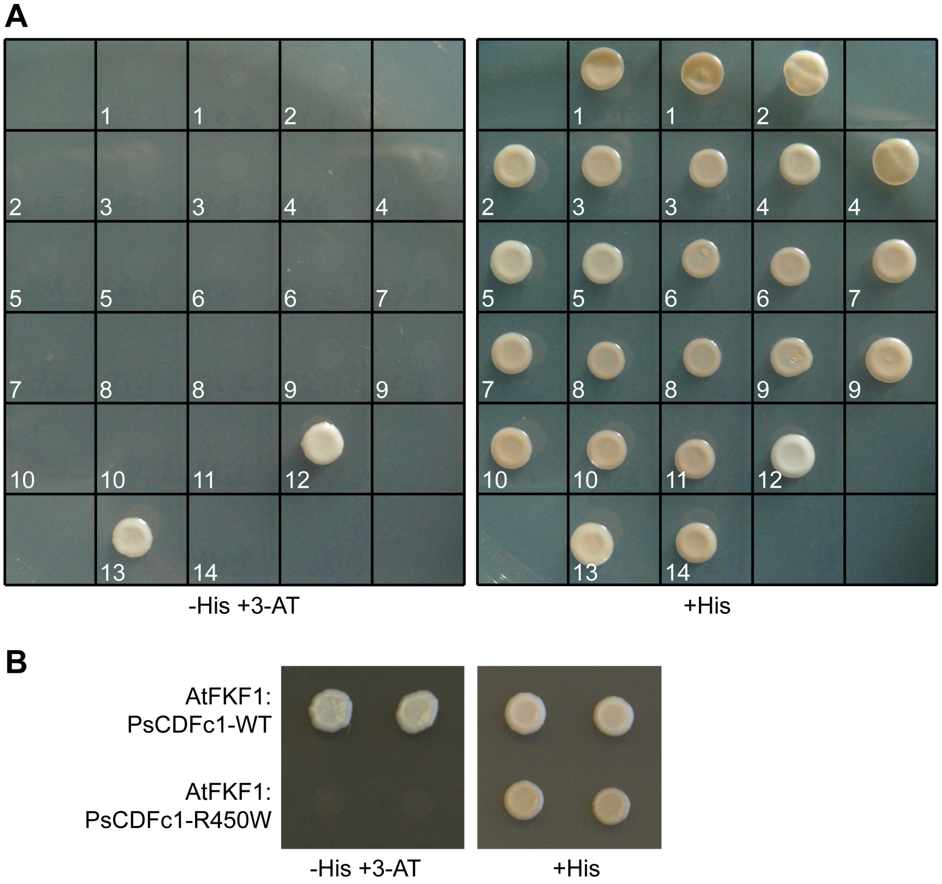


Supplemental Figure 3: Phylogram of the legume CDF family and related DOF transcription factors. Legume clades are indicated. Bootstrap values obtained from 1,000 trees are indicated as a percentage above each branch. Branches with bootstrap values <50% have been collapsed. The analysis is based on the sequence alignment shown in **Supplemental File 2**. Sequence details and species abbreviations are given in **Supplemental Table 1**.



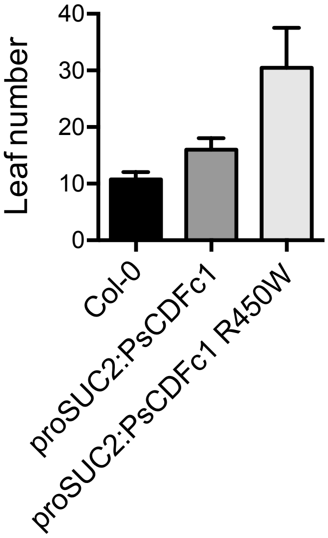
Supplemental Figure 4: Phylogram of the legume FKF1 protein family.
Previously characterised family members from Arabidopsis are included (Nelson et al., 2000; Somers et al., 2000; Schultz et al., 2001). Additional pea, Medicago and soybean genes were identified by BLASTp or tBLASTn searches conducted using Arabidopsis protein sequences to query the pea expressed sequences at the pea RNA-seq gene atlas (http://bios.dijon.inra.fr/FATAL/cgi/pscam.cgi) or GenBank EST, TSA or nucleotide databases, and Medicago (v4.0) and soybean (Wm82.a2.v1) protein databases at Phytozome (phytozome.jgi.doe.gov). The analysis is based on the sequence alignment shown in **Supplemental File 3**. Branches with bootstrap values <50% obtained from 1,000 trees have been collapsed.

At, *Arabidopsis thaliana*; Gm, *Glycine max*; Mt, *Medicago truncatula*; Ps, *Pisum sativum*.

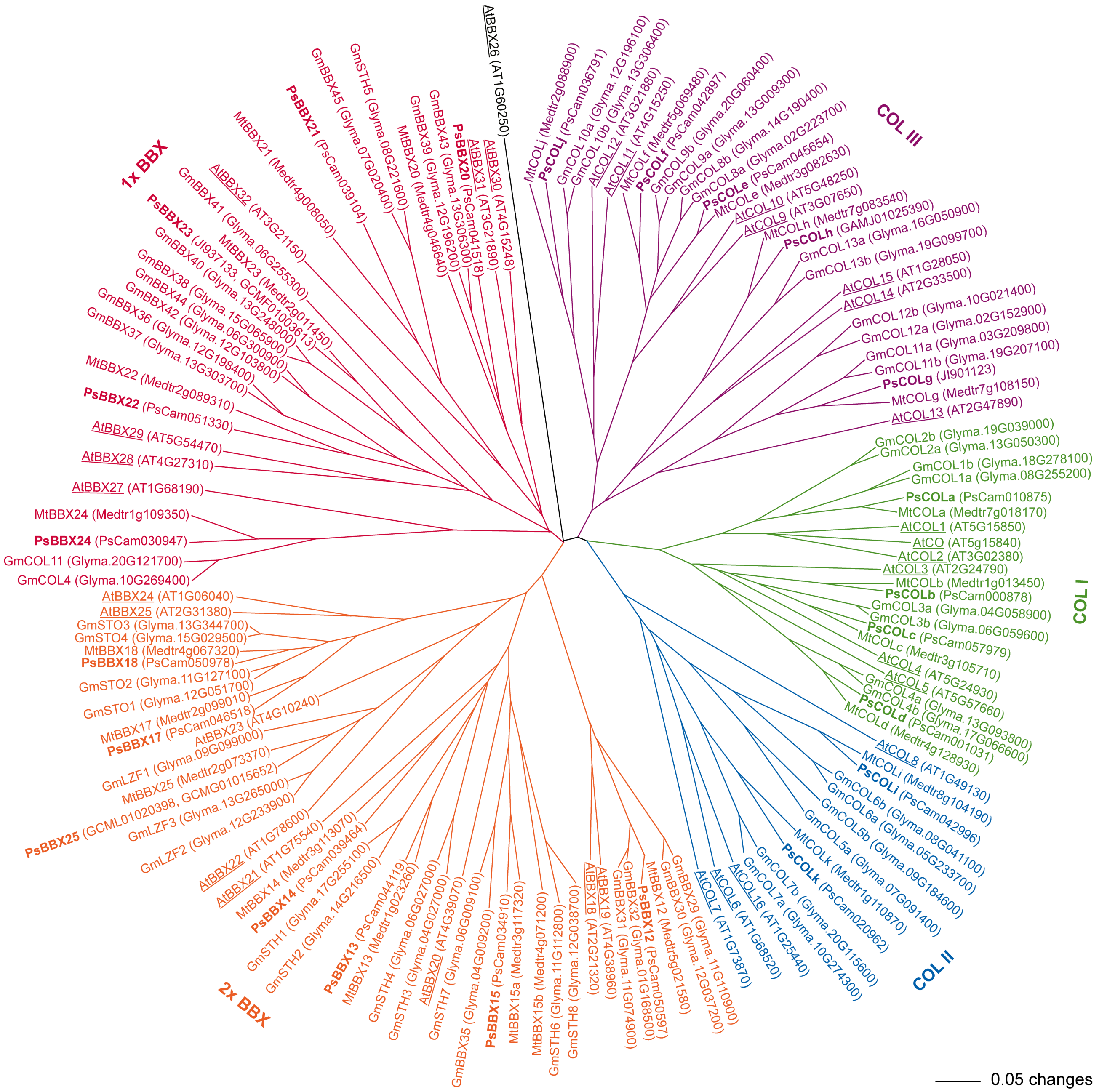


	Bait	Prey
1.	pDEST32	AtFKF1
2.	AtCDF1	pDEST22
3.	pDEST32	PsFKF1
4.	PsCDFc1-WT	pDEST22
5.	PsCDFc1-R450W	pDEST22
6.	pDEST32	AtCDF1
7.	AtFKF1	pDEST22
8.	pDEST32	PsCDFc1-WT
9.	PsFKF1	pDEST22
10.	pDEST32	PsCDFc1-R450W
11.	pDEST32	pDEST22
12.	Krev1	RalGDS-WT
13.	Krev1	RalGDS-m1
14.	Krev1	RalGDS-m2

Supplemental Figure 5: Yeast two-hybrid controls.
(A) Negative controls. Each bait and prey construct was tested separately for autoactivation with an empty prey (pDEST22) or bait (pDEST32) vector, respectively to confirm the lack of autoactivation. Two clones are shown for each. Strong (12), weak (13) and no interaction (14) controls from the Invitrogen™ ProQuest™ Two-Hybrid System, are also shown.
(B) Two independent clones of controls confirming interaction between AtFKF1 (bait) and PsCDFc1-WT (prey), but not PsCDFc1-R450W (prey), for Arabidopsis complementation studies. These controls confirm that interaction with FKF1 would be conserved in a transgenic Arabidopsis system.
Clones are shown after 4 d of growth at 30˚C on selective medium (with 3-amino-1,2,4-triazole added; -His+3-AT) and non-selective medium (+His).



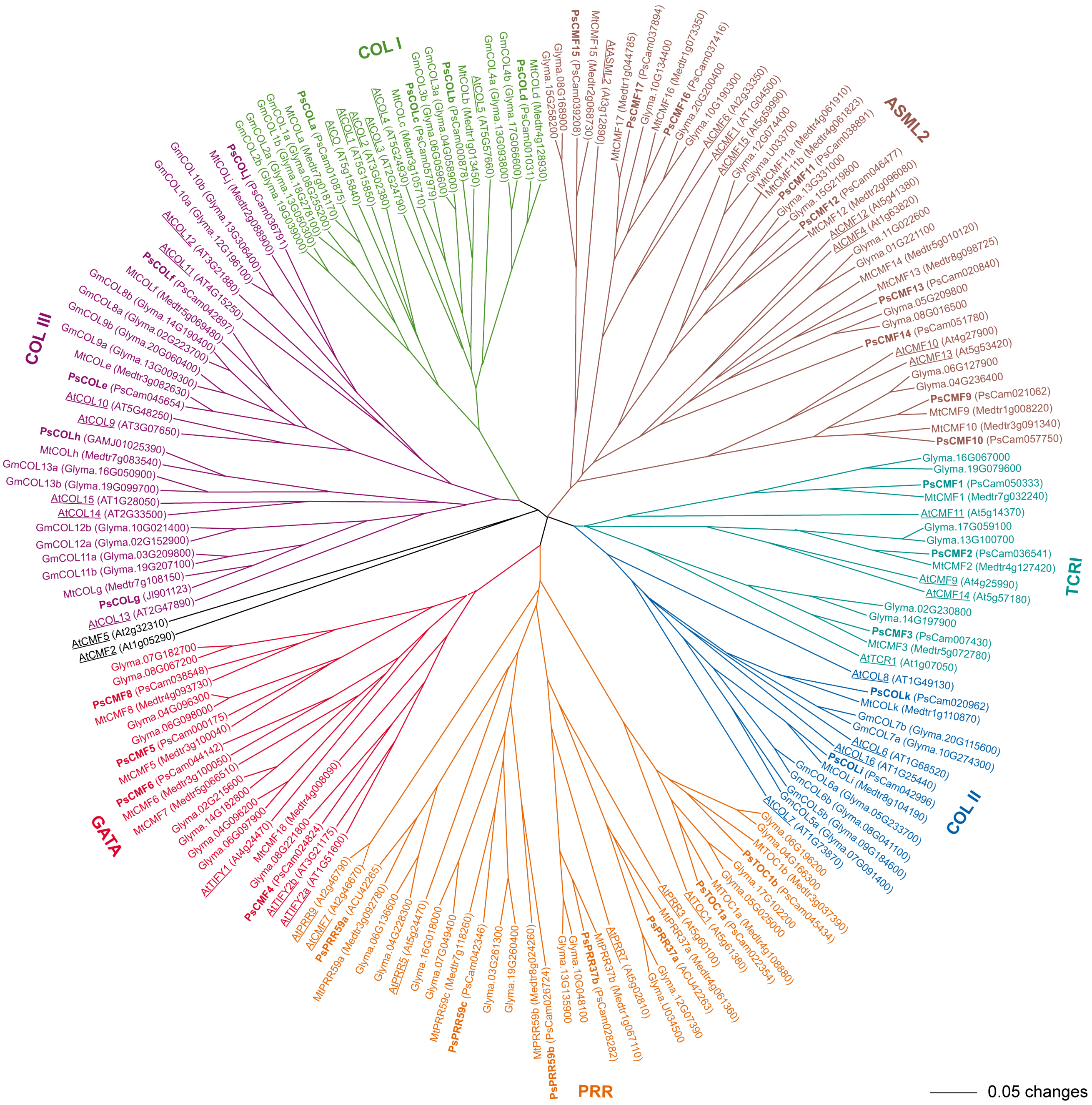
Supplemental Figure 6: Leaf number at flowering in both wild-type and transgenic Arabidopsis lines expressing WT and R450W forms of *PsCDFc1* from the *SUC2* promoter.Plants were grown under LD. Values represent mean ± SE for n=8 to 9.



Supplemental Figure 7: Phylogram of the legume BBX protein family.

Previously characterised family members from Arabidopsis, soybean (excluding those not present in the current Wm82.a2.v1 genome annotation) and Medicago are included (Robson et al., 2001; Khanna et al., 2009; Fan et al., 2014; Wong et al., 2014; Wu et al., 2014). Additional pea and Medicago proteins were identified by BLASTp or tBLASTn searches conducted using Arabidopsis protein sequences to query the pea expressed sequences at the pea RNA-seq gene atlas (http://bios.dijon.inra.fr/FATAL/cgi/pscam.cgi) or GenBank EST, TSA or nucleotide databases, and the Medicago (v4.0) protein database at Phytozome (phytozome.jgi.doe.gov). The analysis is based on the sequence alignment shown in **Supplemental File 4**. Branches with bootstrap values <50% obtained from 1,000 trees have been collapsed.

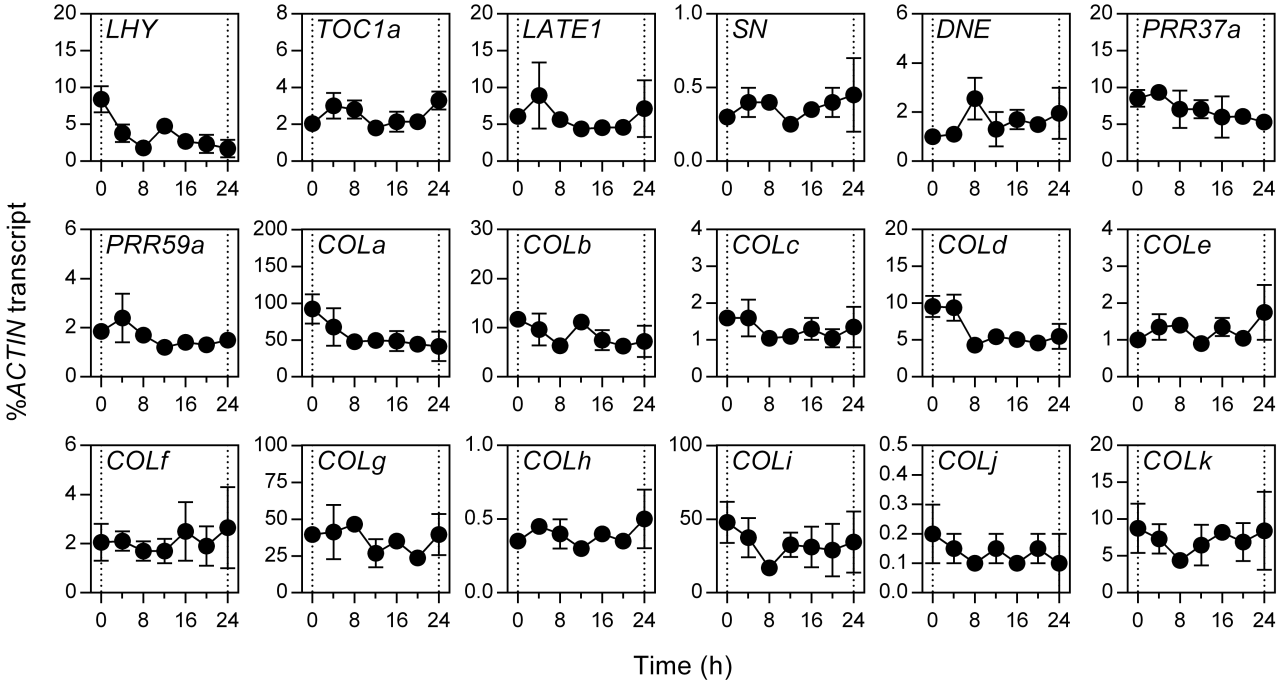
At, *Arabidopsis thaliana*; Gm, *Glycine max*; Mt, *Medicago truncatula*; Ps, *Pisum sativum*.



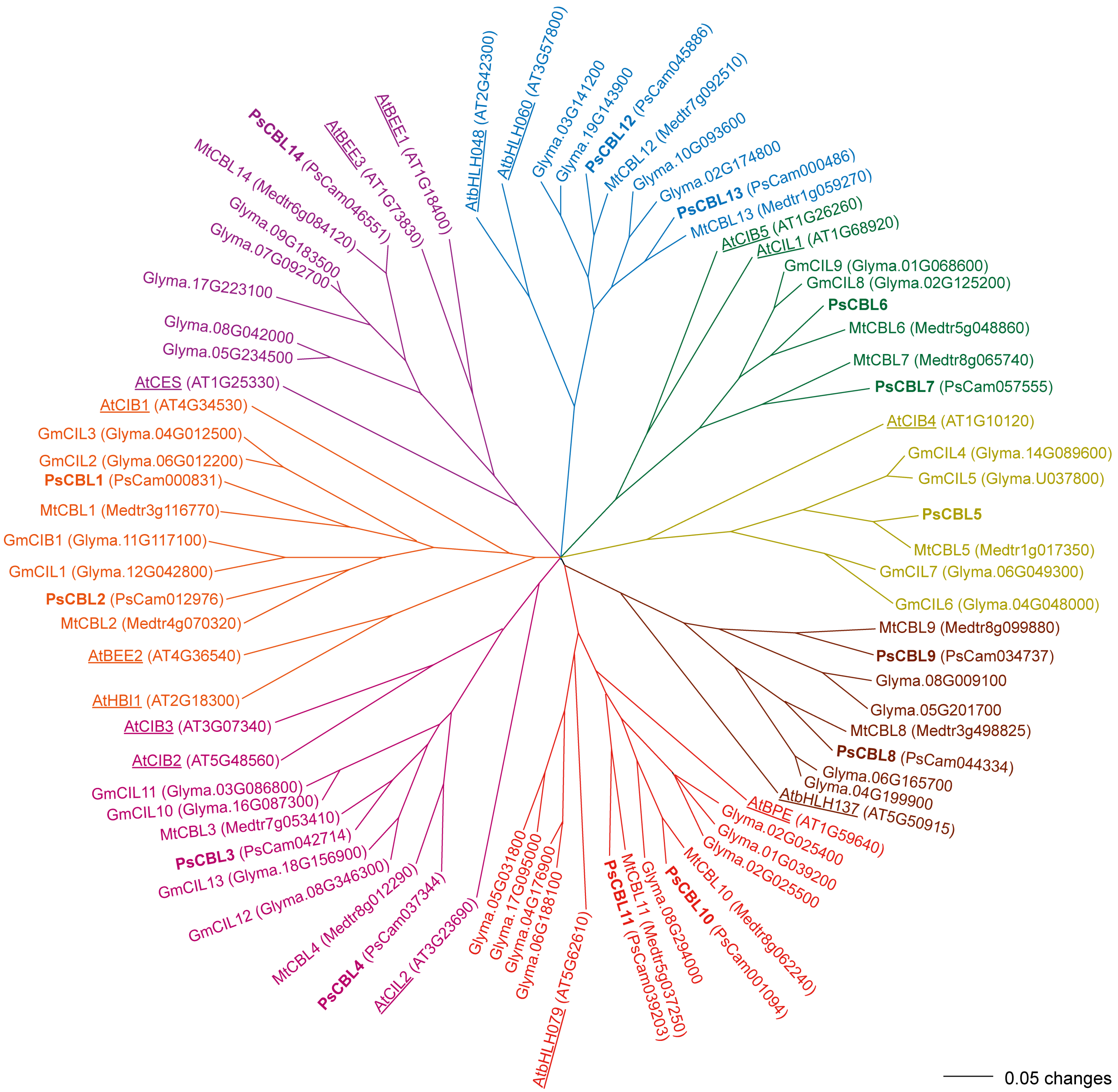
Supplemental Figure 8: Phylogram of the legume CCT protein family.

Previously characterised family members from Arabidopsis, soybean and Medicago are included (Iwata et al., 2008; Fan et al., 2014; Wong et al., 2014; Wu et al., 2014). Additional pea, Medicago and soybean genes were identified by BLASTp or tBLASTn searches conducted using Arabidopsis protein sequences to query the pea expressed sequences at the pea RNA-seq gene atlas (http://bios.dijon.inra.fr/FATAL/cgi/pscam.cgi) or GenBank EST, TSA or nucleotide databases, and Medicago (v4.0) and soybean (Wm82.a2.v1) protein databases at Phytozome (phytozome.jgi.doe.gov). The analysis is based on the sequence alignment shown in **Supplemental File 5**. Branches with bootstrap values <50% obtained from 1,000 trees have been collapsed.

At, *Arabidopsis thaliana*; Gm, *Glycine max*; Mt, *Medicago truncatula*; Ps, *Pisum sativum*.

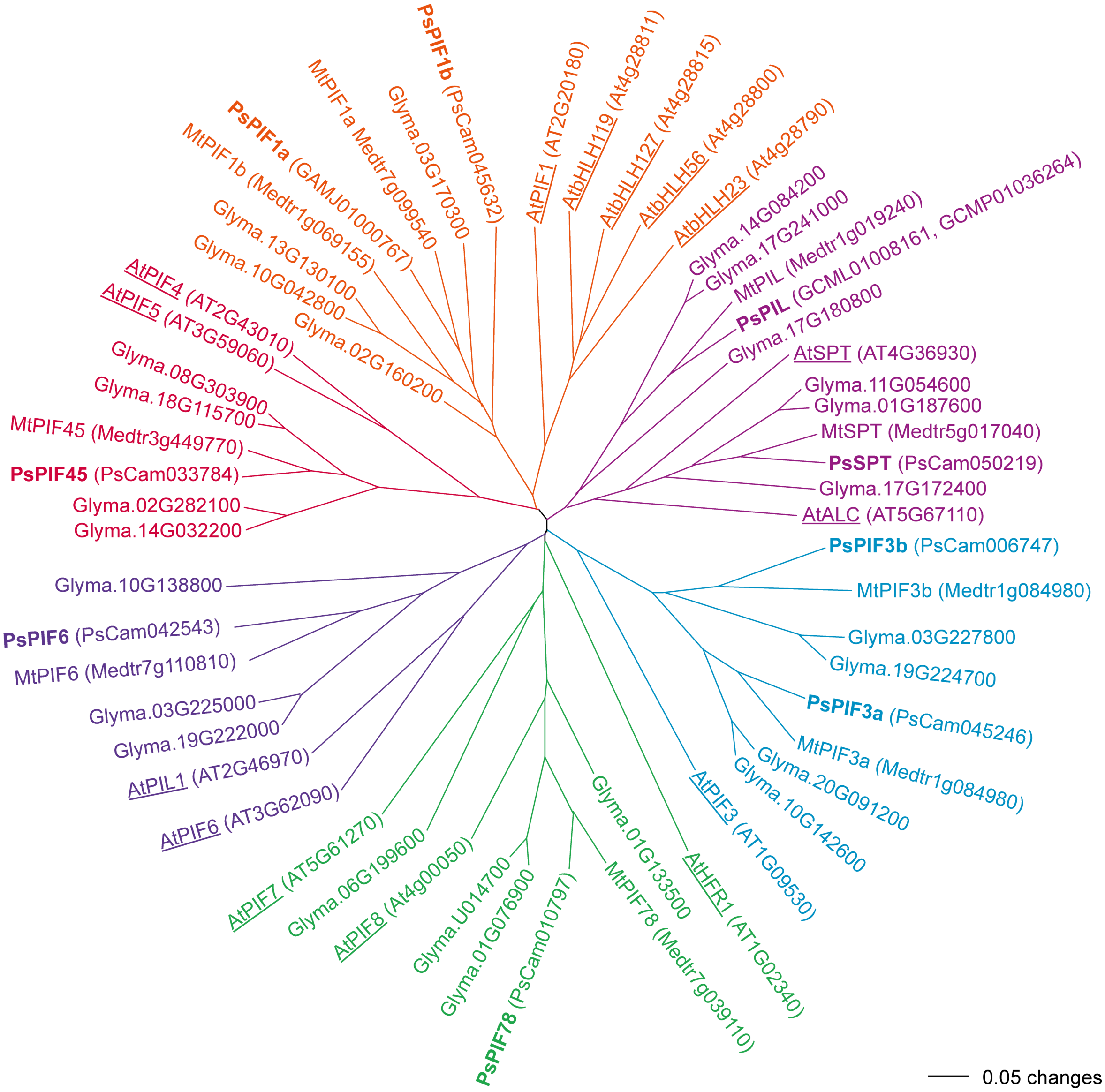


Supplemental Figure 9: Expression patterns of clock-related and *COL* family genes under constant light. Transcript levels were determined in the second uppermost fully expanded leaf of 3-week-old wild-type (NGB5839) plants grown under constant light conditions at 20°C. Seeds were sown in soil and allowed to germinate for several days in complete darkness by covering the pot top with aluminium foil and maintaining plants in a dark growth cabinet. First exposure of emerging seedlings to light was then synchronized by turning lights on and removing the foil. Mean values ± SE are shown for *n* = 2 biological replicates, each consisting of pooled material from two plants.



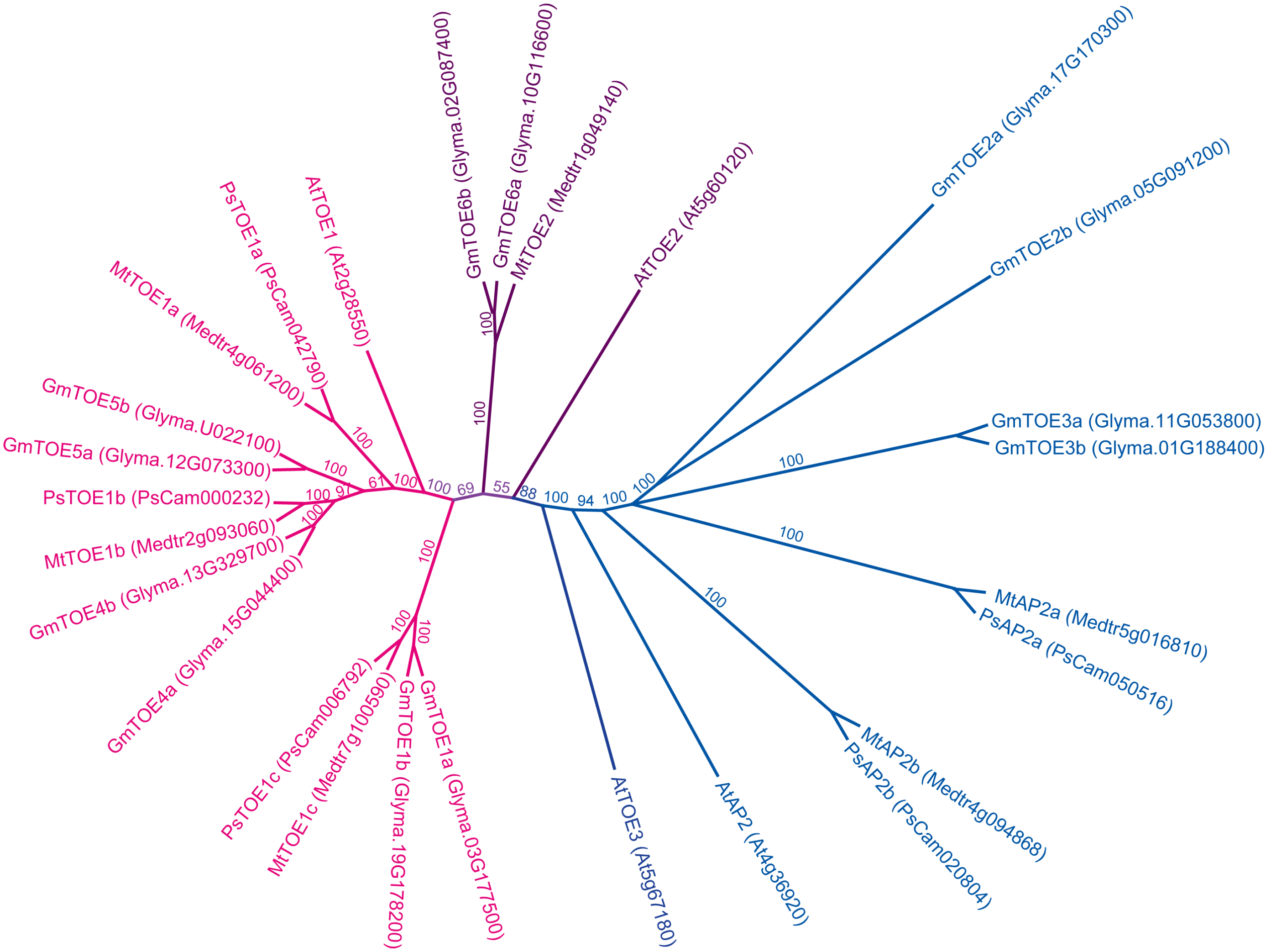
Supplemental Figure 10: Phylogram of legume CIB/BEE-like (CBL) proteins within the bHLH subfamily XII. Previously characterised subfamily members from *Arabidopsis* (Heim et al., 2003; Pires and Dolan, 2010) and soybean (Yang et al., 2015) are included. Pea, Medicago and additional soybean proteins were identified by BLASTp or tBLASTn searches conducted using Arabidopsis protein sequences to query the pea RNA-seq gene atlas (http://bios.dijon.inra.fr/FATAL/cgi/pscam.cgi), and Medicago (v4.0) and soybean (Wm82.a2.v1) protein databases at Phytozome (phytozome.jgi.doe.gov). The analysis is based on the sequence alignment shown in **Supplemental File 6**. Branches with bootstrap values <55% obtained from 10,000 trees have been collapsed.

At, *Arabidopsis thaliana*; Gm, *Glycine max*; Mt, *Medicago truncatula*; Ps, *Pisum sativum*.



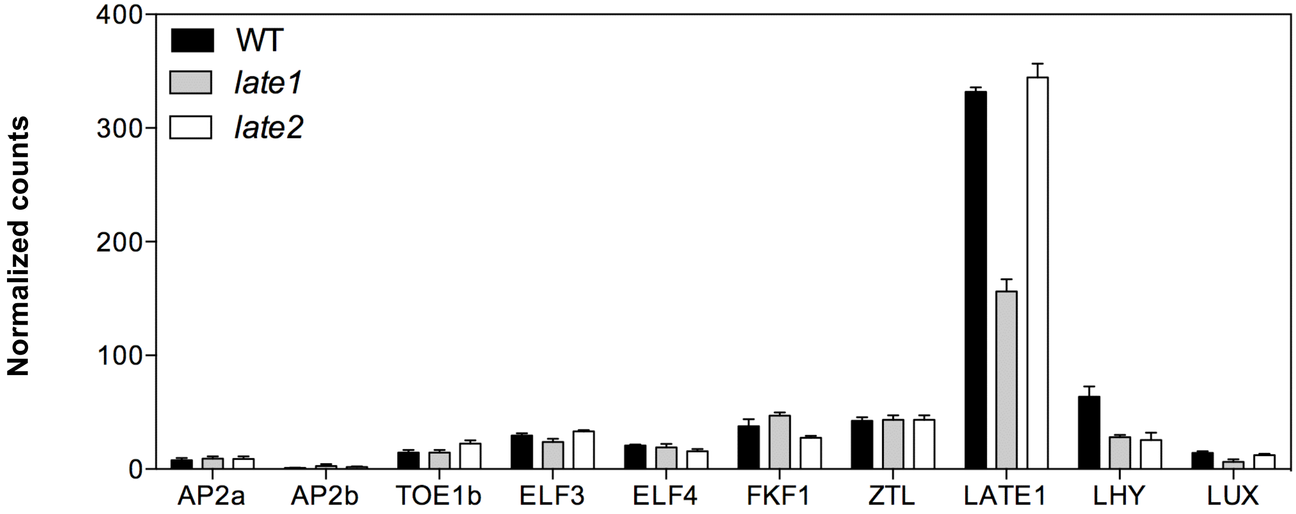
Supplemental Figure 11: Phylogram of legume PIF-like proteins within the bHLH subfamily VII(a+b). Previously characterised members of this subfamily from *Arabidopsis* (Heim et al., 2003; Pires and Dolan, 2010) are included. Pea, Medicago and soybean proteins were identified by BLASTp or tBLASTn searches conducted using Arabidopsis protein sequences to query the pea expressed sequences at the pea RNA-seq gene atlas (http://bios.dijon.inra.fr/FATAL/cgi/pscam.cgi) or GenBank EST or TSA databases, and Medicago (v4.0) and soybean (Wm82.a2.v1) protein databases at Phytozome (phytozome.jgi.doe.gov). The analysis is based on the sequence alignment shown in **Supplemental File 7**. Branches with bootstrap values <50% obtained from 1,000 trees have been collapsed.

At, *Arabidopsis thaliana*; Gm, *Glycine max*; Mt, *Medicago truncatula*; Ps, *Pisum sativum*.



Supplemental Figure 12: Phylogram of the legume AP2 protein family.
Previously characterised family members from Arabidopsis and soybean (Aukerman and Sakai, 2003; Wang et al., 2014) are included. Additional pea, Medicago and soybean genes were identified by BLASTp or tBLASTn searches conducted using Arabidopsis protein sequences to query the pea expressed sequences at the pea RNA-seq gene atlas (http://bios.dijon.inra.fr/FATAL/cgi/pscam.cgi) or GenBank EST, TSA or nucleotide databases, and Medicago (v4.0) and soybean (Wm82.a2.v1) protein databases at Phytozome (phytozome.jgi.doe.gov). The analysis is based on the sequence alignment shown in **Supplemental File 8**. Branches with bootstrap values <50% obtained from 1,000 trees have been collapsed.

At, *Arabidopsis thaliana*; Gm, *Glycine max*; Mt, *Medicago truncatula*; Ps, *Pisum sativum*.



Supplemental Figure 13: Transcript levels in expanded leaf tissue from WT, *late1-2* and *late2-1D* mutants grown from sowing under continuous white light. Values represent mean ± SE for *n*=3 biological replicates, each consisting of pooled material from two plants.

Supplemental Table 1: Details of sequences for DOF transcription factors used in phylogenetic analyses and alignments.
Sequences were obtained from GenBank (www.ncbi.nlm.nih.gov), Phytozome (phytozome.jgi.doe.gov; Goodstein et al., 2012), The Arabidopsis Information Resource (TAIR; www.arabidopsis.org; Lamesch et al., 2012), or the pea RNA-seq gene atlas (http://bios.dijon.inra.fr/FATAL/cgi/pscam.cgi; Alves-Carvalho et al., 2015), as indicated. *Sequence alignments and comparison with Genbank accession suggests PsCam048092 sequence is partially incorrect.

Species	Gene name	Accession number	Source	Reference(s)
Arabidopsis thaliana	AtCDF1	AT5G62430	TAIR	(Yanagisawa, 2002; Fornara et al., 2009)
	AtCDF2	AT5G39660		
	AtCDF3	AT3G47500		
	AtCDF4	AT2G34140		
	AtCDF5	AT1G69570		
	AtCOG1	AT1G29160		
	AtDOF1.3	AT1G26790		
	AtDOF1.6	AT1G47655		
	AtDOF5.8	AT5G66940		
	AtOBP1	AT3G50410		
Cicer arietinum	CaCDFa1	XP_004508727	GenBank	This study
	CaCDFa2	XP_004514828		
	CaCDFb1	XP_004491816		
	CaCDFb2	XP_004489399		
	CaCDFc1	XP_004505416		
	CaCDFc2	XP_004490083		
Glycine max	GmDof1.2	Glyma.01G049400	*Glycine max* genome Wm82.a2.v1 (Schmutz et al., 2010) at Phytozome	(Guo and Qiu, 2013)
	GmDof2.3	Glyma.02G108600		
	GmDof3.1	Glyma.03G007900		
	GmDof4.2	Glyma.04G168300		
	GmDof5.1	Glyma.05G025900		
	GmDof5.4	Glyma.05G158200		
	GmDof6.4	Glyma.06G194800		
	GmDof7.6	Glyma.07G229600		
	GmDof8.2	Glyma.08G228900		
	GmDof9.2	Glyma.09G237000		
	GmDof13.1	Glyma.13G062500		
	GmDof13.5	Glyma.13G230200		
	GmDof15.7	Glyma.15G082400		
	GmDof15.8	Glyma.15G215500		
	GmDof17.3	Glyma.17G101000		
	GmDof18.3	Glyma.18G260500		
	GmDof19.1	Glyma.19G023200		
	GmDof19.2	Glyma.19G118000		
	GmDof20.1	Glyma.20G035200		
Medicago truncatula	MtCDFa2	Medtr3g435480	*Medicago truncatula* genome project v4.0 (Young et al., 2011) at Phytozome	This study
	MtCDFb1	Medtr7g010950		
	MtCDFb2	Medtr6g012450		
	MtCDFc1	Medtr4g082060		
	MtCDFc2-1	Medtr5g041420		
	MtCDFc2-2	Medtr5g041400		
	MtCDFc2-3	Medtr5g041380		
	MtCDFc2-4	Medtr5g041530		
Phaseolus vulgaris	PvCDFa1	Phvul.003G189300	*Phaseolus vulgaris* genome v1.0	This study
	PvCDFa2	Phvul.009G186600		
	PvCDFb1	Phvul.008G037000		

	PvCDFc1	Phvul.002G170600	(Schmutz et al., 2014) at Phytozome	
	PvCDFc2	Phvul.002G084000		
Pisum sativum	PsCDFb1	PsCam037510	The pea RNA-seq gene atlas (Alves-Carvalho et al., 2015)	This study
	PsCDFc1	PsCam036807		
	PsCDFc2-1	PsCam038247		
	PsCDFc2-2	PsCam038945		
	PsCDFc2-3	PsCam014419		
	PsCDFc2-4	PsCam014395		
	PsCDFb2	GCMG01002096; PsCam048092*	GenBank	
Solanum lycopersicum	SlCDF1	Solyc03g115940	Tomato genome ITAG2.3 (Tomato Genome Consortium, 2012) at Phytozome	(Corrales et al., 2014)
	SlCDF2	Solyc05g007880		
	SlCDF3	Solyc06g069760		
	SlCDF4	Solyc02g067230		
	SlCDF5	Solyc02g088070		
Solanum tuberosum	StCDF1	PGSC0003DMG400018408	*Solanum tuberosum* genome annotation v3.4 at Phytozome (Potato Genome Sequencing Consortium, 2011)	(Kloosterman et al., 2013)
	StCDF2	PGSC0003DMG400025129		
	StCDF3	PGSC0003DMG400001330		
	StCDF4	PGSC0003DMG400033046		
	StCDF5	PGSC0003DMG400019528		

Supplemental Table 2: Mapping marker details.

Gene	**Marker type**	**Primer names**	**Primer sequence (5' to 3')**	**Tm (ºC)**	**Accession number(s) / Reference**	**Corresponding Medicago locus (Mt4.0)**
ACETISOM	CAPS (MseII)	PsAP2-F5 PsAP2-R8	`GTAGTGGAAGTGATCACAATTTGG` `GAAGAGAGTGAATCAAGAGG`	56	(Aubert et al., 2006)	Medtr4g079780
ALDO	Size	ALDO-F ALDO-R	`GAGAATTCCCCCTGCTGTCC` `CAGCATAATACTCAGTAGCACC`	65	Ps-M97476/ Ps-M97477 (Aubert et al., 2006)	Medtr4g071880
ATG2	HRM	ATG2-F3 ATG2-R3	`TTTGGAGGGTATTAAAAGTTCTGC` `TCGTAAAGGACGCCTACCAC`	53	JI925672	Medtr4g086370
BIOB	CAPS (BccI)	BIOB-F2 BIOB-R2	`ATGAGCGCCTTCAAACACTT` `AGGAACGCTCTCTGGATGTG`	60	JI898613	Medtr4g076870
CLPSER	Size	CLP-F CLP-R	`GTATTGGAGGAGGATTTTAGGG` `GCTTATGAGTTTGGAGGGGAGGGG`	58	Ps-AJ276507 (Aubert et al., 2006)	Medtr4g069800
DEAD	Size	DEAD-F4 DEAD-R4	`TGTGCAAGTCAACATTTTCCA` `AGTTGGAGCAGGCAGCAAT`	60	JI937351; JI931111; JI902906	Medtr4g079320
DUF833	HRM	DUF-F1 DUF-R1	`GTGGCAAGCTCATCCAAAAT` `CTACCGCCCAAGATTGTTTC`	55	JI918734; JI925517; JI920006	Medtr4g083440
GS3B	Size	GS3B-F GS3B-R	`GGGTCTTTCTTTTAAAGACCAAAGC` `GTATACTCTTGTTCAATACCATACC`	57	Ps-U28925 (Aubert et al., 2006)	Medtr6g071070
HUA2	CAPS (SspI)	HUA2-3F HUA2-3R	`TCTTGTTGATTCTATCACCC` `TTTTCCTCTCAAGCCACAAC`	54	PsCam000043	Medtr4g075060
ISI1	CAPS (HpaII)	ISI1-F1 ISI1-R1	`GTGCTCTCCGTTCCATTCTC` `AACTTCATGGGTTCCACACC`	60	JR954799	Medtr4g078140
LAG1	Size	LAG1-F4 LAG1-R4	`CCGTGGTAAGACCAGAGTTATTG` `AAATGGGATAGCGGGATAGC`	60	JI945859; JI958010; JI938125	Medtr4g086150
MITCYSIN	Size	MITCYSIN-F2 MITCYSIN-R2	`CAGGTCGGTTTCGGTTTCACACTG` `GAGCTGTGCAAAGGAGATACGTC`	58	(Aubert et al., 2006)	Medtr4g087520
N3LIKE	CAPS (Hinf)	N3L-F MtN3L-R	`GAGCCCATGCTTCTATCAACTC` `TATATCACCATCTGAATTATGCC`	55	(Aubert et al., 2006)	Medtr8g096320
NLM	CAPS (HpyCH4IV)	NLM-F NLM-R	`GCTTTTCTCTGTTCTTCACAAGCC` `GAGAGAAGCAGTGGCATGTGCGG`	60	Ps-AJ243308 (Aubert et al., 2006)	Medtr8g087720
PHOT1B	CAPS (NspI)	PHOT1b-F1 PHOT1b-R1	`GAGGGCGGTAGGGGAATACC` `CAATCCGTTGGGACGCAGCA`	58	AY295348	Medtr4g061610
PIP2	CAPS (HpaII)	PIP2-F PIP2-R	`GCCGGTATCTCTGGTATGATACC` `CAGGAACATGAGAGTCCCTAGCG`	65	PS-AJ243307 (Aubert et al., 2006)	Medtr4g059390
PTRANS	Size	PTRANS-F PTRANS-R	`TCGTCGTGTTCCTTGATTTATGG` `CACCAAACAATACACCACTCCC`	55	Ps-X68077 (Aubert et al., 2006)	Medtr4g088350
SVPb	HRM	PsSVPb-5F PsSVPb-6R	`GGTAAAAATGCTAAACCAAAAACC` `GGGAGTAGCAGAAAGATGTGC`	53	JI898361; JI909838; JI910349	Medtr4g093970
TOE	CAPS (MlyI)	TOE-3F TOE-3R	`GAAGAGCGTCATTCTTTACGG` `TGACCTGGCCATTACTTTGC`	58	PsCam042790	Medtr4g061200

Supplemental Table 3: Primer details.
(Ps, *Pisum sativum*; *At*, *Arabidopsis thaliana*.)

Gene	Purpose/details	Primer names	Primer sequence (5' to 3')	Tm
PsACT	qRT-PCR	ACT-F ACT-R	GTGTCTGGATTGGAGGATCAATC GGCCACGCTCATCATATTCA	59
AtCDF1	Yeast two-hybrid analysis	AtCDF1-Y2H-1F AtCDF1-Y2H-1R	ATGCTGGAAACTAAAGATCCTG TCACATCTGCTCATGGAAAT	58
PsCOLa	qRT-PCR	COP-2F COP-2R	GCTGGATTCAGTTACAATGG CTGGTACAACACCAACATCC	60
PsCOLb	qRT-PCR	CO1P-1F CO1P-2R	AGACGGAGTTGTGCCGGTGC ACGAATTGTCTTCTCGAACC	60
PsCOLc	qRT-PCR	COLc-1F COLc-1R	CGCTTATGCGTTCAAAAACA TTCTCCATCGGGAACAACTC	58
PsCOLd	qRT-PCR	COLd-qF1 COLd-qR1	GCTTCGACATCGATTTTTGC AACTCCGACACCACGTTCC	58
PsCOLe	qRT-PCR	COLe-qF1 COLe-qR1	CTTCAATTCCCGAATCAAGC ATTTCAGGGCATTTCGTAGC	58
PsCOLf	qRT-PCR	COLf-F2 COLf-R3	AAGTCGCCGATCTTCCTAGC AAGTGCAGATGCCGTACTACC	58
PsCOLg	qRT-PCR	COLg-qF1 COLg-qR1	GAAGAAAGTTTTGGGGATGG TCTTTCTGTCTCCCACATGC	58
PsCOLh	qRT-PCR	COLh-qF1 COLh-qR1	TGGTGTTCTTCTCTGGAATCG CACATCCTGCAATGATTTTGG	58
PsCOLi	qRT-PCR	COLi-qF3 COLi-qR3	GACTACCGCAAACCCACCTA CTCTTGCTTCTCTTCCTCCA	58
PsCOLj	qRT-PCR	COLj-2F COLj-2R	GAGGGTACGTGTGCAGAAGC CTTGCTTTGCGAGAGGCATA	60
PsCOLk	qRT-PCR	COLk-2F COLk-2R	ATGGGATGGCCAAAAATGTC CCATATCCACCAAATTCACCA	64
PsDET (TFL1a)	qRT-PCR	TFL1a-1F TFL1a-2R	CGTTGGTAGAGTCATAGG AGGATCACTAGGGCCAGG	58
PsDNE	qRT-PCR	ELF4-1F ELF4-1R	GTGCTTGACAGGAACAGAGC CAGAATAAAGAGAAGCAACC	56
AtFKF1	Yeast two-hybrid analysis	AtFKF1-Y2H-1F AtFKF1-Y2H-1R	CTCACCACTCTTGAAGCTGTGT TCTTTACAGATCCGAGTCTTGC	62
PsFKF1	qRT-PCR	FKF-F227 FKF-5RACE	GGTCGTAACTGCCGGTTCTTA GGAACTCAATACCGTCCTCAAGACA	59
	Yeast two-hybrid analysis	PsFKF1-Y2H-2F PsFKF1-Y2H-1R	CTTACTACTCTCGAGGCAGTTTGTTG TTACATGTCGGAGTCCTGTCG	62
PsFTa1	qRT-PCR	FTLa-6F FTLa-2R	GCCCAAGCAACCCTACTTTT CCATCCTGGAGCGTAAACCC	60
PsFTa2	qRT-PCR	FTLb-3F FTLb-5R	GGAAATGACCCCGTGATCTA TGAATCCCTAAGTTGGGTCG	60
PsFTb2	qRT-PCR	FTLe2-F7 FTLe2-R7	CGACTACCGGGACAGCATTT CAGGTGAACCAAGGTTATAAAC	62
PsFTc	qRT-PCR	FTLc-8F FTLc-7R	GATATTCCAGCCACAACAAGC TTATGACGCCACTCTGGAGCAA	62
PsLF (TFL1c)	qRT-PCR	LF-CR2 LF-CR3	AAATAAGCAGCAGCAACAGGG CAGACATTCCAGGGACAACAG	60
PsLATE1	qRT-PCR	GI-GSP1 GI-12R	GGTATATACAAATTCCACGACAGTATGG CCTTGGCTATCCAGGGTTGC	60
PsLATE2 (CDFc1)	Isolation of CDS	CDF3a-1F CDF3a-1R	TCTCTTTGATCCATCCATCACT CCTGTTCAGTTACACAGGCTCA	62
	Sequencing	CDF3a-2F CDF3a-2R	TCGTCGAGGAAAGAACTCG GACAAAATGTCGGAGGAGGA	-
	qRT-PCR	CDF3a-Q1F CDF3a-Q1R	CTTCTTCTCCGCCACAATTC CGATGCTGCGAGTGATTTTA	60
	HRM functional marker	CDF3a-HRM-1F CDF3a-HRM-1R	AAGCGTCACCGCTGATGTA TGTGATTCGCAATTAGGTTCC	53
	Yeast two-hybrid analysis	CDF3a-Y2H-1F CDF3a-HRM-1R	ATGTCAGAGGTTAAAGACCCTGC TGTGATTCGCAATTAGGTTCC	62
PsLHY	qRT-PCR	MYB1-Q1 MYB1-Q2	GACGGATGCGCTAGAGAAGAATGG AGAATAGAGCCCGAAACGCAAGTC	60
PsPIM	qRT-PCR	PIM-4F PIM-6R	GCTTCAGAGTTTGGAACAGC GACTCCATGGTGGTTTGG	58
PsPRR37a	qRT-PCR	PRR37-5F PRR37-5R	TGGCAACATGTTTGGAGAAG ACACTCAAGCCTCTGCTTCC	60
PsPRR59a	qRT-PCR	PRR59-2F PRR59-4R	GGTATCTGGCTATGCACTTCTCTCG CAAACATGCTGCCACAGATT	60

PsSN	qRT-PCR	LUX-Q1F LUX-Q1R	TTCTCACCCTCACATGTCTCC TGGACGAAGTCACAATCAACA	56
PsTOC1a	qRT-PCR	TOC1-92-1F TOC1-92-1R	GCCTGGAATTTCAATCCAAC GGATGCTGTCCTGATGAACC	58
PsUNI	qRT-PCR	UNI-1F UNI-2R	CATCAGAGCTGAAAGAAGG GCTTCCTTTTCACGTTGC	55
PsVEG1	qRT-PCR	FULc-2F FULc-2R	CGATGCCTTGAAACCATAGG AATTCCAATGACCCTCTTGC	58
PsVEG2	qRT-PCR	FD-6F FD-3R	ATTTGATCCAAACGTCGGTGT ATCAACTTTTTGCTCCAGTTCG	60

Supplemental Table 4: RNAseq Mapping results.
RNAseq reads were mapped to pea transcriptome reference (PsUniLowCopyClusters, including organelles; Alves-Carvalho et al., 2015) using STAR (Spliced Transcript Alignment to a Reference; Dobin et al., 2013).

	NGB5839 (WT)			***late1-2***			***late2-1D***		
	rep1	**rep2**	**rep3**	**rep1**	**rep2**	**rep3**	**rep1**	**rep2**	**rep3**
# input reads	6951737	2306874	3880898	6270944	2144604	3457203	6120831	1583277	3689226
average input read length	150	149	150	150	149	150	150	149	150
uniquely mapped reads	4475805	1484633	2496971	4005219	1416949	2139211	3948023	986113	2228214
uniquely mapped reads (%)	**64.38**	**64.36**	**64.34**	**63.87**	**66.07**	**61.88**	**64.5**	**62.28**	**60.4**
Average mapped length	149.69	148.7	149.27	149.71	148.51	149.12	149.66	148.68	148.9
non canonical	6678	2731	4449	5482	2376	3123	5846	1874	4070
Mismatch rate per base (%)	0.52	0.27	0.27	0.54	0.26	0.3	0.52	0.28	0.31
Deletion rate per base (%)	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.02	0.01
Deletion average length	2.05	2.17	2.21	1.99	2.1	2.03	2.08	2.22	2.18
Insertion rate per base (%)	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
Insertion average length	1.75	1.77	1.68	1.54	1.61	1.56	1.62	1.63	1.68
Multi mapping reads	486855	187955	292785	415921	163087	264363	448588	127774	291553
Multi mapping reads (%)	7.01	8.17	7.54	6.63	7.62	7.65	7.33	8.09	7.92
Unmapped reads (%)	**28.61**	**27.47**	**28.12**	**29.5**	**26.31**	**30.47**	**28.17**	**29.63**	**31.68**

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