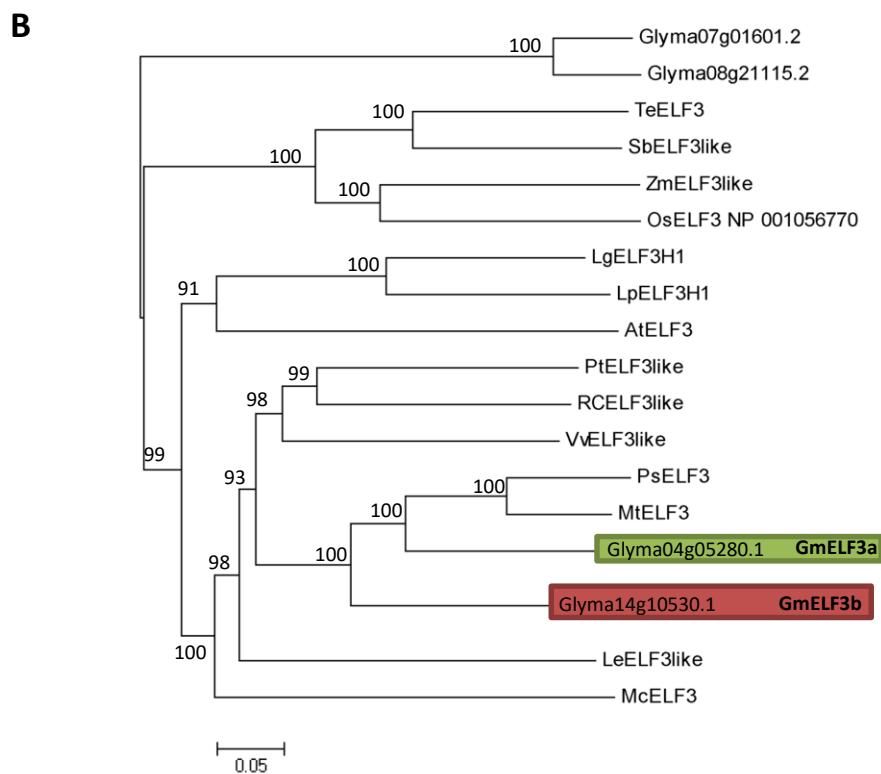
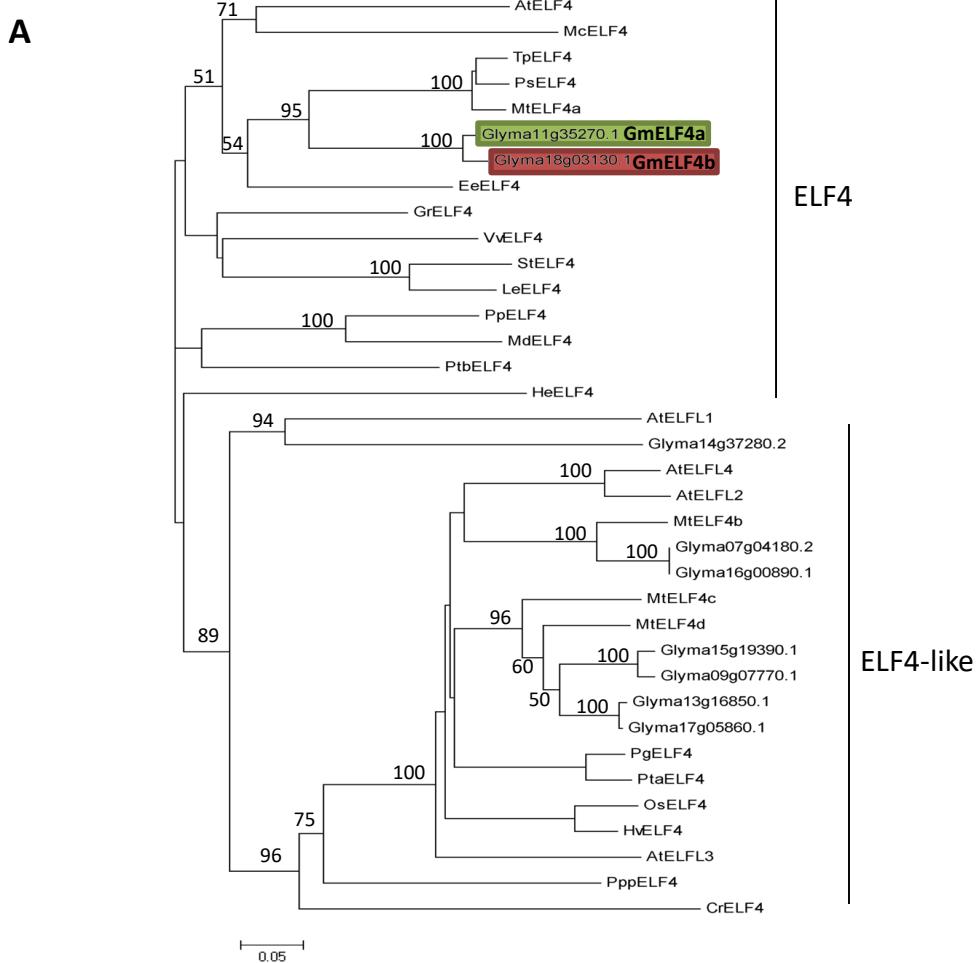
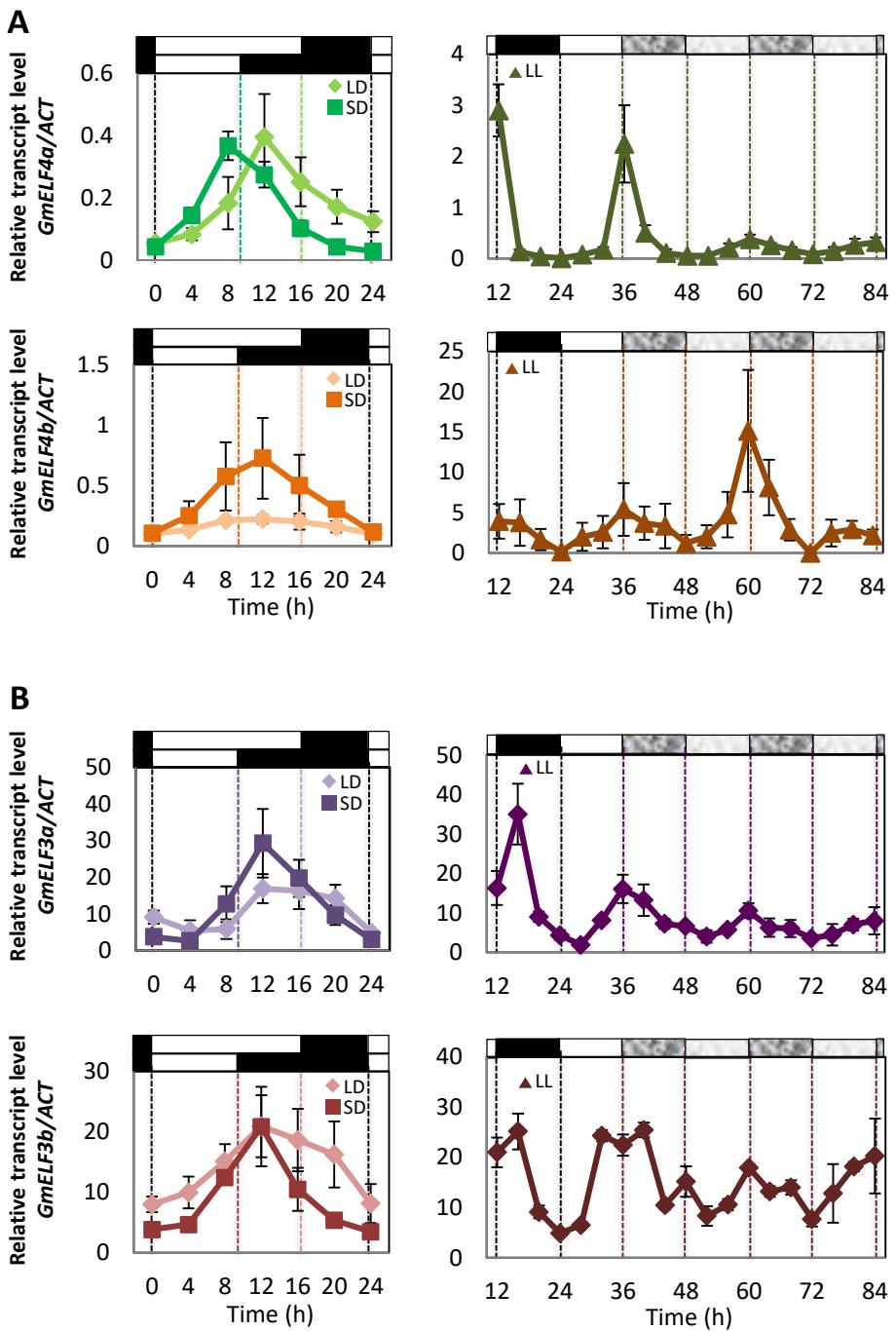


GmLUXc	: MGEEVKTSEYDEE-----RVMEWEAGLPTANDLTPLSQPLIPPE	: 39
GmLUXb	: MGEEVKTSEYDEE-----RVMEWEAGLPTANDLTPLSQPLIPPE	: 39
GmLUXa	: -----	: -
PsLUX	: MGEEIR---TDEE-----RVTTEWEKGLPNLHDLTPLSMTLIPPE	: 36
MtLUXlike	: MGEEVR---TDEE-----RVTTEWEKGLPNLHDLTPLSMALIPPE	: 36
LjLUXlike	: MGEEVCRM---MDEE-----RLMEWEKGLPSVHDLTPLSQPLIPPE	: 37
AtLUX	: MGEEVQMSDY----DVSGDGD--RVSEWEMGLPSDEI A SLSYSLIPPN	: 43
AtBOA	: MGKEVMVSDYGDDGEDAGGGDEYR I PWEIGLPNGDLTPLSQYLVPSI	: 50
GmLUXc	: LASAFSILPEPHRTLLDVNRASRNTLSTLRGGGGSVHQAFSSNNN-HNY	: 88
GmLUXb	: LASAFSISPEPHRTLLEVNRASRNTLSTIRGGG-SVHQAFSSNNNNHHY	: 88
GmLUXa	: -----MSLEPHRIVLNVKRGSCNTLSTIRSDR-TMQHAFFSNNNNNQHY	: 43
PsLUX	: LASAFSISPEPHRTLIDVNRSRNTLSILRGGG-TNHQTFSNNNEE-IIIE	: 84
MtLUXlike	: LASAFSISPEPHRTLFDVNRASRNTLSSLRSN--SGTITNQINQTM-SCE	: 83
LjLUXlike	: LATAFSISPEPRTLLDVNRSRNTLISLRSGG-APLQLASSSDEEGEGG	: 86
AtLUX	: LAMAFSITPERSRTIQDVNRASETTLSSLRGSSGPNTSSSNNNVEEDR	: 93
AtBOA	: LALAFSMIPERSRTIHDVNRASQITLSSLR----SSTNASSVMEEVDR	: 95
GmLUXc	: DGDGDGGVEEEDDDDRDGSG-PDSRKQRKIDCGAAEADSAVQTETSA	: 137
GmLUXb	: DGDGDGG-DEEYDDADRDGSG-SDSRKQRKIDCGVAEEADSAVRTETSA	: 136
GmLUXa	: NGDGDVN-DKEDNDDTDKCKDSR-SDSR-----TETSA	: 73
PsLUX	: EED-----EEMEEETDRDGSG-SDSRKLRKIDSATEE-----ADSAVRT	: 122
MtLUXlike	: IED-----IEEDEEPDRDGSG-SDSRKHRKIDS V IEEAEADSAVRT	: 125
LjLUXlike	: GGG-----GEEDDTTDRDGSGGSGSRKQRKVDCAAEE-----ADSAVRT	: 126
AtLUX	: VGS-----SSPGSDSKKQKTSNGDGDGGGVPDPSAMAEEGDSGTEDL	: 137
AtBOA	: VES-----SVPGSDPKKKQKS--DGGEAAAEDS---TAEEGDSPEDA	: 134
MYB domain		
GmLUXc	: ERTAVKRPRLVWTPQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGLTREN	: 187
GmLUXb	: ERTAVKRPRLVWTPQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGLTREN	: 186
GmLUXa	: KRTTVKRLQLVWTLQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGLS	: 121
PsLUX	: -ETTLKRPRLVWTPQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGLTREN	: 171
MtLUXlike	: -TETIKRPRLVWTPQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGLTREN	: 174
LjLUXlike	: DTATLKRPRLVWTPQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGLTREN	: 176
AtLUX	: SGKTLKRPRLVWTPQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGLTREN	: 187
AtBOA	: SGKTSKRPRLVWTPQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGLTREN	: 184
MYB domain		
GmLUXc	: VASHLQKYRLYLKRMQGLSNEGP--SASDQLFASTPVF-QSLHDSAPPN	: 234
GmLUXb	: VASHLQKYRLYLKRMQGLSNEGP--SSSDQLFASTAVP-QSLHDSAPPSA	: 233
GmLUXa	: -----	: -
PsLUX	: VASHLQKYRLYLKRMQGLSNDAP--SSSDHFLFASTPVF-QSLHESASAVN	: 218
MtLUXlike	: VASHLQKYRLYLKRMQGLSNDAP--SSSDHFLFASTPVF-QSLHETASAN-	: 220
LjLUXlike	: VASHLQKYRLYLKRMQGLSNEGP--SSSDHFLFASTPVF-QSLHDSAAA	: 223
AtLUX	: VASHLQKYRLYLKRMQGLTNEGP--SASDKLFSSTPVEPQSFDI-----	: 230
AtBOA	: VASHLQKYRLYLKRIQGLTEEDPYSSSDQLFSSTPVEPOSFQD-----	: 228
GmLUXc	: HSNHGHHGHGSNGRHHGHGHGHGHS-----VPMM S MPYPPPLMSMPY	: 278
GmLUXb	: HSN-----GHGHL P -----VPMM S MPYPPPMSMPY	: 259
GmLUXa	: -----	: -
PsLUX	: S-----HSQSNHGHN S HHS-----V T T IM S MPYPPPPPMS	: 250
MtLUXlike	: -----HSNSHSHSHSHSHHS-----V T T IM P YPPPPPSSMMS	: 251
LjLUXlike	: AAT-----AHSNSHSQTHSHSHHGHNFFHLPVPI P MPYPPP-----MMS	: 262
AtLUX	: -----GGGGGSSGNVG-----V P IFGAYGTQOMMQ	: 255
AtBOA	: -----GGGSNGKLG-----V P V P --VPSMVP	: 247
GmLUXc	: PP--PMMSGMP--HGHMGIPMPN SSA -----TSAYHPYNM I HQRD	: 314
GmLUXb	: PP--PMMSGMPAHGHMGIPMPN SSA -----TSAYHPYNM I HQRD	: 297
GmLUXa	: -----	: -
PsLUX	: MP--LLGMP--PHPHGHMG M ALHPPSG-----SSSYRSHPFNM M HHRD	: 289
MtLUXlike	: MPPMIGMG--HHPHGHMGMSLPPPSGG-----SSSYRSHPFNM M HHRD	: 292
LjLUXlike	: MP--FHGM G PHLHHGHGHGM G -----	: 281
AtLUX	: MPVYAHHMGMQGYHHQNHNNHD P YHQ N RHHHGAGGNGAFESNPY M QQNK	: 305
AtBOA	: IPGYGNQMG M QGYQQYSNH-----GN--ESNQY M QQNK	: 280
GmLUXc	: WP-----HLAPNDK-- : 323	
GmLUXb	: WP-----HLAPNDK-- : 306	
GmLUXa	: -----	: -
PsLUX	: WPPPHSHSHPHMSPNDSNK : 309	
MtLUXlike	: WPPNPHSHSHPHMSSNDSNK : 312	
LjLUXlike	: -----KKKKKK : 288	
AtLUX	: FGSMASYP S VGGGSANEN-- : 323	
AtBOA	: FGTMV T YPSVGGGDVNDK-- : 298	

Supplementary Figure 1
Amino acids alignment for LUX-Like protein

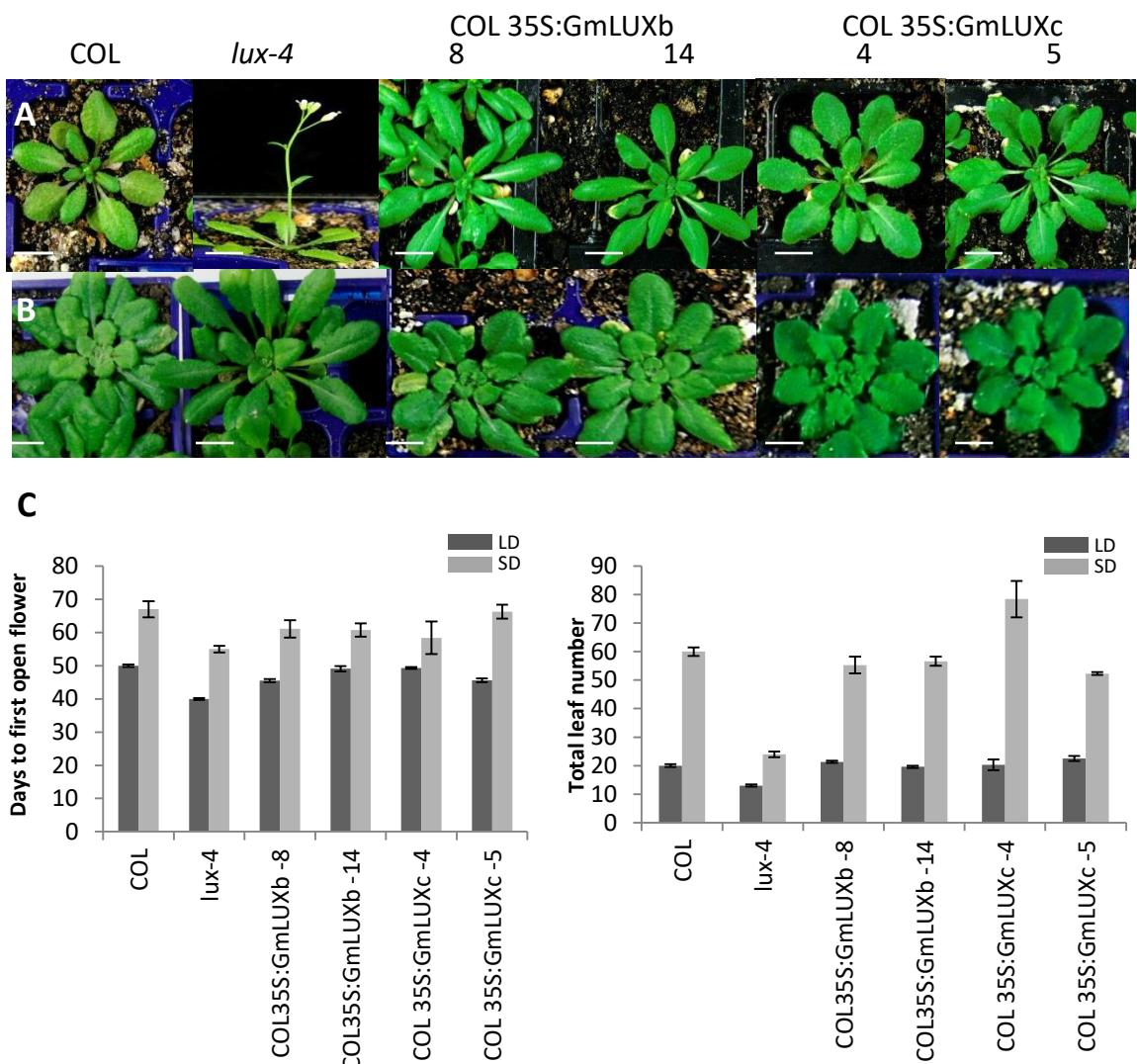


Supplementary Figure 2. Phylogenetic analyses of ELF4-like and ELF3-like proteins.



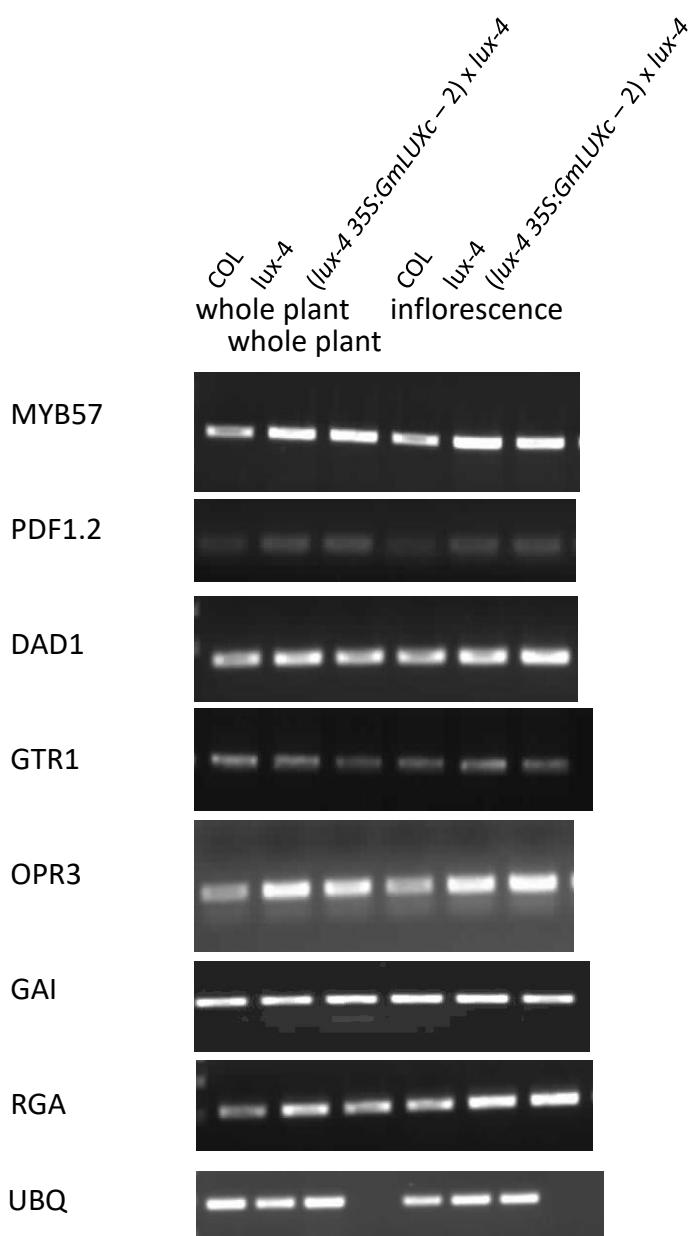
Supplementary Figure 3. Homologues of soybean *ELF4* and *ELF3* transcripts show diurnal and circadian rhythms.

(A) *GmELF4a* and *GmELF4b* expression level under long-day long-day (LD; 16h light, 8h dark) or short-day (SD; 10h light, 14h dark), or constant light (LL; 12h light:12h dark then continuous light). **(B)** *GmELF3a* and *GmELF3b* expression level under LD (16L: 8D), SD (10L:14D), or LL (12L: 12D then continuous light). All plants were three weeks old at the time of sampling. Data are mean \pm SE for $n =$ three biological replicates, each consisting of pooled material from two plants. Day and night periods are indicated by open and closed bars, respectively, above the graph.



Supplementary Figure 4. Ectopic expression of *GmLUXb* and *GmLUXc* in *Arabidopsis Columbia* (*Col*) show similar phenotype as in *lux-4* mutant.

(A) Representative plants are grown in LD (16L: 8D). **(B)** Representative plants are grown in SD (10L:14D). **(C)** Flowering time of plants grown in LD and SD, data are mean ± SE for n = 15-20.



Supplementary Figure 5. Expression of *MYB57*, *GTR1*, *PDF1*, *DAD1*, *OPR3*, *RGA*, *GAI* genes in *35S::GmLUXc* transgenic plants.

Supplementary Table 1. *Cis*-element analysis of 5' regions of *GmLUXb* and *GmLUXc* in comparison to *AtLUX*.

Response	Site Name	Sequence	AtLUX	GmLUXb	GmLUXc
Circadian	Clock	CAANNNNATC	3	2	4
	CCA1	AAMAATCT	0	0	1
	Evening element	AAAATATCT	1	1	1
	LBS (LUX binding sites)	GATWCG	2	0	1
Gibberellin	TAACA(A/G)A element	TAACA(A/G)A	1	1	1
	TATCCA(C/T) element	TATCCA(C/T)	1	1	0
	pyrimidine box	(C/T)CTTTT(C/T)	7	4	10
Ethylene	GCC element	GCCGCC	1	0	0
	A(A/T)TTCAAA element	A(A/T)TTCAAA	1	0	1
Cytokinin	cytokinin response motif (CRM)	(A/G)GAT(T/C)	30	16	17
Auxin	ABRE	(C/T)ACGTG	3	3	1
	TGTCTC element	TGTCTC	1	1	1
Light	I-box	GATAAGR	1	0	1
	G-box	CACGTG	2	2	0
	H-box	ACCTA(A/C)C(A/C)	1	0	0
	Sp1	CC(G/A)CCC	0	1	1
Sugars	TATCCA element	TATCCA	1	2	0
	SURE	(AA)TACTA(A/T)T	1	0	2
	W-box	(T)TGAC(C/T)	0	1	1
Cold	C-repeat	CCGAC	3	1	0
	LTR	CCGAAA	0	2	1

Supplementary Table 2. Primers sequences used in gene isolation, Real-Time PCR, and construct cloning.

Primer name	Sequence (5'-3')	Uses
ACT-F	ATCATGTTGAGACCTCAATGTG	RT-PCR
ACT-R	CTCGAGTTCTGCTCATAACTAGG	
LUXb-3F	AATGGCCATGGTCATCTCCC	RT-PCR
LUXb-3R	GCACCTTCTATAACATTGTA	
LUXc-4F	AATGGTCATGGTCATGGGCA	RT-PCR
LUXc-1R	ATGATGGTGATGGCTGACCT	
BamHI-GFP-F	GGATCCATGGTGAGCAAGGGCGAGGAG	pUC18/2x35S::GFP::GmLUXb, 2x35S::GFP::GmLUXc
GFP-NS-XbaI-R	GCTCTAGACTTGTACAGCTCGTCCATG	
LUX-XbaI-F	GCTCTAGAATGGGGGAAGAGC	pUC18/2x35S::GFP::GmLUXb, 2x35S::GFP::GmLUXc
LUX-KpnI-R	CCGGGTACCTCATTATCATTAG	
LUX-EcoRI-F	CCGGGAATTCATGGGGAAAG	vector pMLBART/35S::GmLUXb or 35S::GmLUXc
LUX-BamHI-R	CGCGGGATCCTCATTATCA	
CaMV35S-NotI-F	ATTTGCGGCCGCATGGTGGAGCACGAC	pMLBART/35S::GmLUXb or 35S::GmLUXc
polyA-NotI-R	AGGAGCGGCCGCACTGGATTTGGTTT	
T7 promoter 2	TAATACGACTCACTATAGGGCGA	
3' BD sequencing 2	AGCAACCTGACCTACAGGAA	Yeast-two hybrid cloning
3' AD sequencing	AGATGGTGCACGATGCACAG	
Gal4_N_term_primer	GAGTAGTAACAAAGGTCAA	
pHybLex_rev_primer	GAGTCACTTAAAATTGTATACAC	Yeast-three hybrid cloning
AtUBQ10-F	GGCCTTGTATAATCCCTGATGAATAAG	RT-PCR
AtUBQ10-R	AAAGAGATAACAGGAACGGAAACATAGT	
AtGTR1-F	GTCCATTGGCTGGTATTGCT	RT-PCR
AtGTR1-R	ACTTGCTGCAACGTGCATAG	
AtPDF1.2-F	TTTGCTGCTTCGACGCAC	RT-PCR
AtPDF1.2-R	CGCAAACCCCTGACCATG	
AtDAD1-F	GTGAAGACGAAGAAGAAGAGCAATC	RT-PCR
AtDAD1-R	GTGAAGACAGCGAAAACGACATAC	
AtOPR3-F	TTGGACGCAACTGATTCTGAC	RT-PCR
AtOPR3-R	GTAGGCGTGGTAGCGAGGTT	
AtMYB21-F	AAAATGCCAACATCTTCC	RT-PCR
AtMYB21-R	AATTATAACCCCAAACCTCTACAA	
AtMYB24-F	ATGCAAAATGGGGAAATAGGTG	RT-PCR
AtMYB24-R	AAGATCATCGACGCTCCAATAGTT	
AtMYB57-F	GTGCGCGAGGGAACATAA	RT-PCR
AtMYB57-R	TCAGCAATAGAAAAACCAAATAAC	
AtGA2ox1-F	CGGTTGGGTCCACTATTC	RT-PCR
AtGA2ox1-R	ACCTCCCATTGTCATCACCTG	
AtGA2ox2-F	CCGGCAGAGAAAGAACACGAA	RT-PCR
AtGA2ox2-R	TACGCCTAAACTTAAGCCCAGAA	
AtRGA-F	AGAAGCAATCCAGCAGA	RT-PCR
AtRGA-R	GTGTACTCTCTTACCTTC	
AtGAI-F	CACACGACCGCTCATAG	RT-PCR
AtGAI-R	TGCCTATCCAATTACCCCTC	