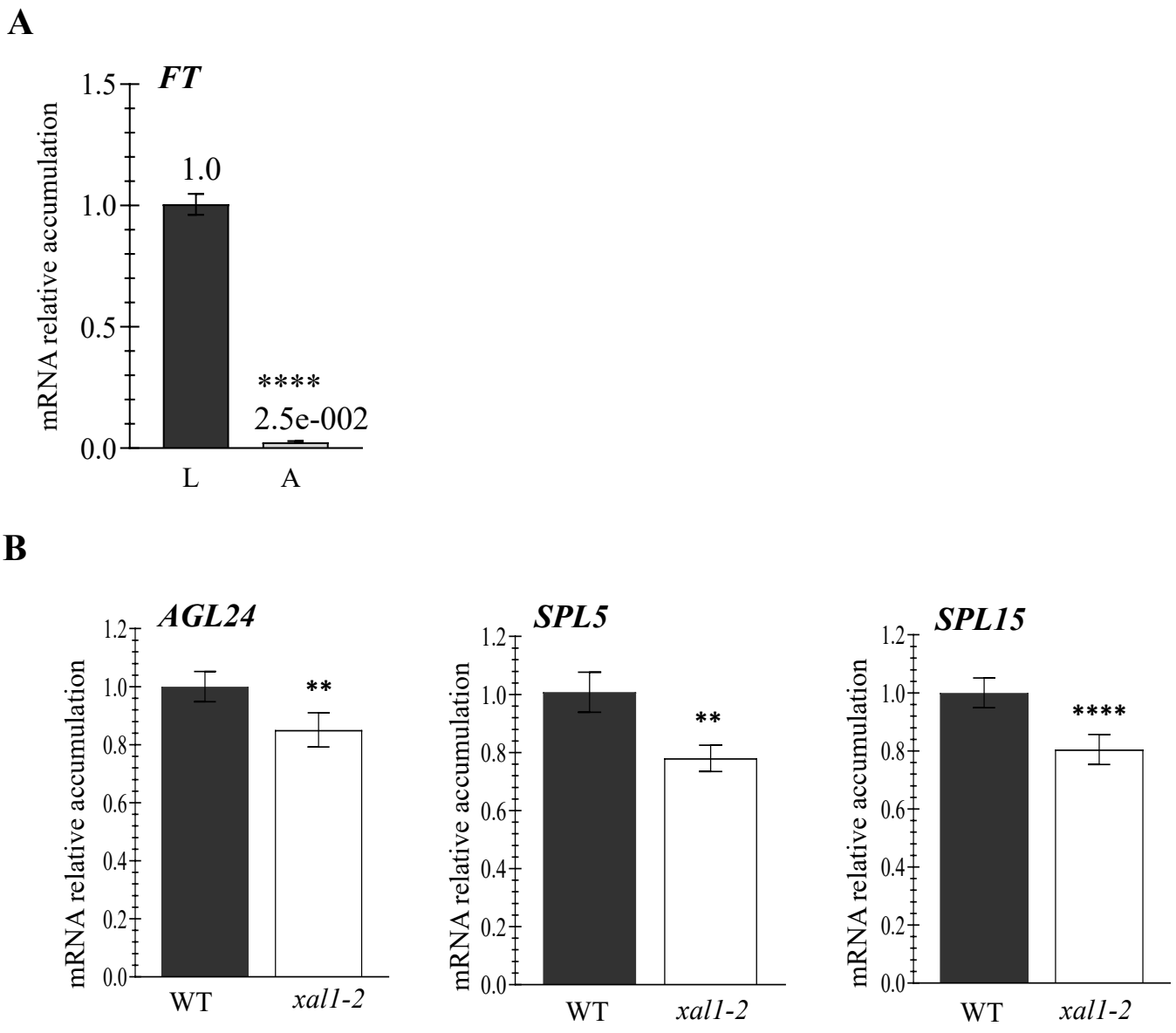


**Figure S1.** Expression analysis of additional flowering genes. (**A)** *FT* is highly accumulated in leaves (L) compared to apices (A) collected from WT control plants. (**B)** XAL1 positively regulates *AGL24, SPL5,* and *SPL15.* RT-qPCRs were performed with RNA extracted from shoot apices of WT and *xal1* plants. *PDF2* and *RNAH* were used as qPCR internal controls. Data represent the mean value ± standard error of three biological replicates. Statistical analysis was performed by a T-Student Test (** $p<0.01$; ****$p<0.0001$). 14-day-old plants were used in all cases.

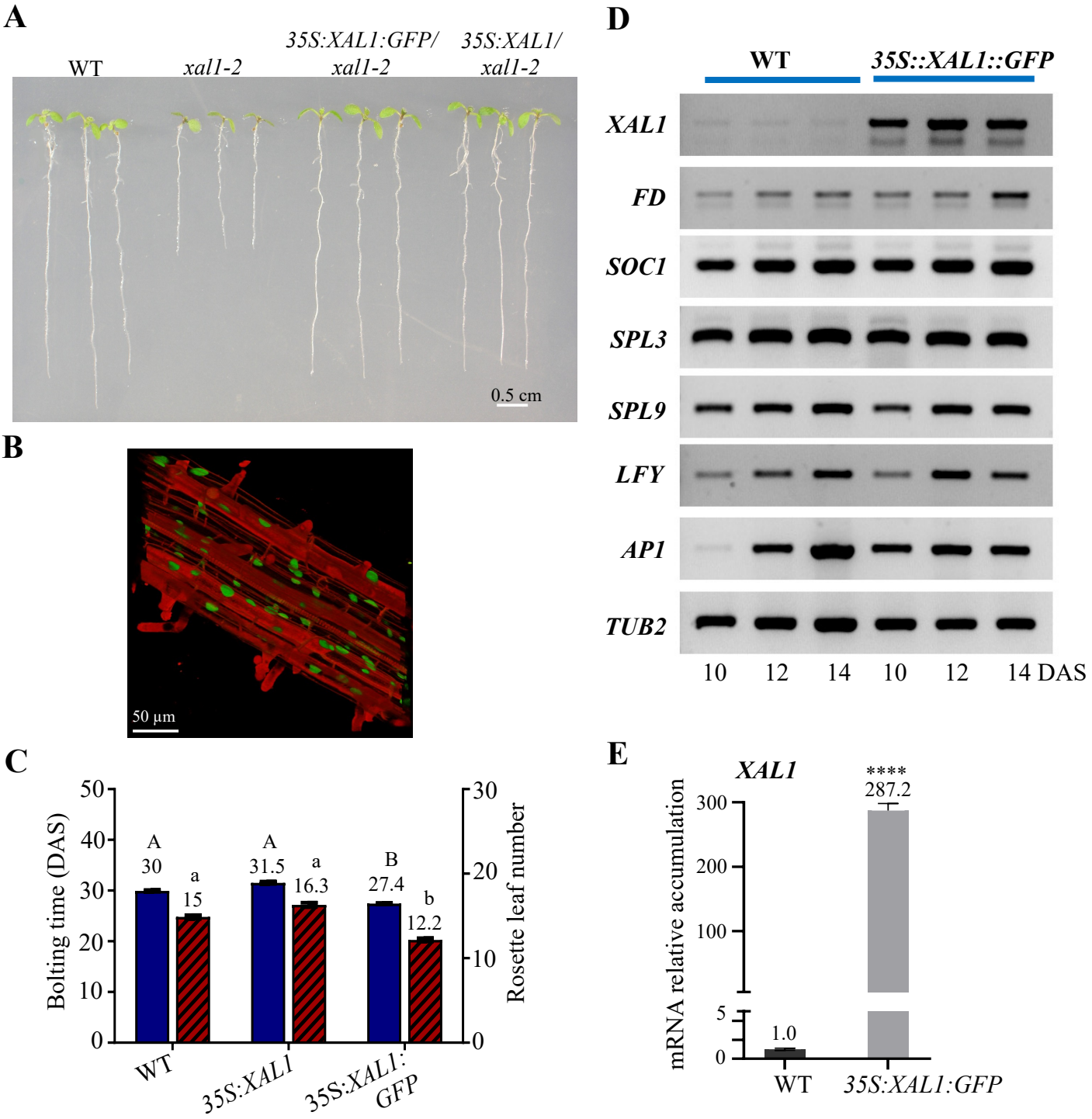


**Figure S2.** Expression analysis and effect of the *XAL1* overexpression lines. (**A)** Complementation of the *xal1-2* root phenotype with *35S::XAL1::GFP* and *35S::XAL1,* respectively. (**B)** *XAL1* expression in the nuclei of *35S::XAL1::GFP/xal1-2* roots observed by confocal microscopy. Z-stack image of 165 optical sections, step-size of 0.8 µm. (**C)** Flowering time of both overexpression lines in the *xal1-2* background compared to WT, under LD photoperiod. Statistical analysis was performed by a Kruskal-Wallis test followed by a Dunn's analysis $P < 0.001$ (n = 39-46). (**D)** Expression analysis of some flowering time genes in the complete aerial section of the *35S::XAL1::GFP/xal1-2* seedlings compared to the WT. Plants were grown on MS plates for 10, 12, and 14 days after sowing (DAS). *TUB2* was used as an internal RT-PCR control. (**E)** Relative *XAL1* accumulation levels in the aerial section of the *35S::XAL1::GFP /xal1-2* line compared to WT seedlings of 14 DAS. *RNAH* and *UPL7* genes were used as internal controls. Statistical difference was obtained by a T-student test ****$P < 0.0001$ (n = 3 biological replicates).

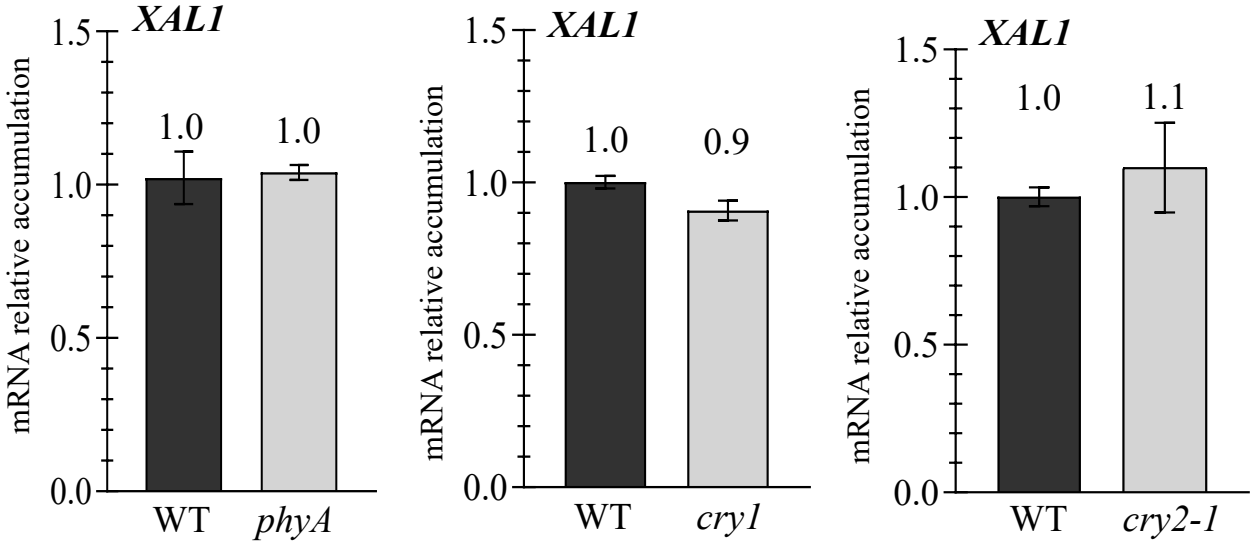


**Figure S3**. PHYA, CRY1 and CRY2 do not regulate *XAL1* in apices from 18 DAS plants grown under LD photoperiod. RT-qPCR were performed using three replicates in each case. *PDF2* and *UPL7* were used as internal constitutive controls. Data represent the mean value ± standard error. Statistical analysis performed with a T-student test.

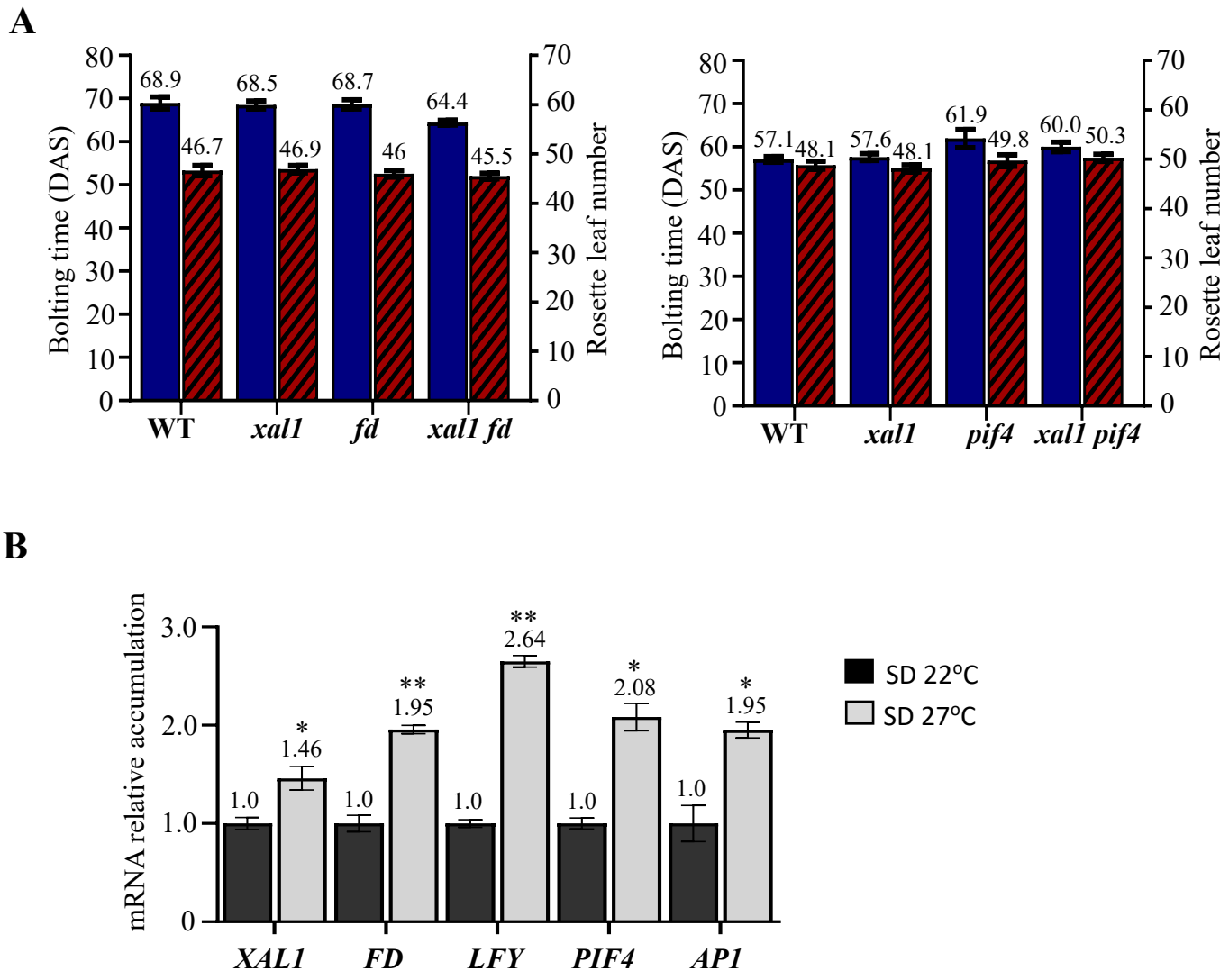


**Figure S4.** Control experiments of flowering time under SD at 22 ºC and induction of key flowering genes at 27 ºC. **(A)** Single and double mutants show no significant difference between them and the WT when grown under SD photoperiod at 22 ºC. Blue bars correspond to the bolting time, and stripped red columns show the rosette leaf number (left graphic n = 30-35, right graphic n = 16-34). **(B)** RT-qPCR of some flowering genes in WT shoot apices from plants grown under SD at 22 or 27 ºC, respectively. Statistical differences were obtained by a T-student test **P* < 0.05; ***P* < 0.01. *RNAH* and *UPL7* genes were used as internal qPCR controls. Data represent the mean value ± s. e.

**Table S1**. Primers used for genotyping, semiquantitative RT-PCR and RT-qPCR

| **Genotyping** | **Sequence (5'-3')** | **Reference** |
|---|---|---|
| ***co-1*** | | |
| *CO-F* | CCATTGTCGTTGTAGTGAGT | (Han et al., 2008) |
| *CO-GT1* | CTGCAAACCCACTTGCTAGA | |
| ***fd-3*** | | |
| *Salk_LBb1* | GCGTGGACCGCTTGCTGCAACT | |
| *FD-F* | AGCCAGCGCCGGAATTCAAG | |
| *FD-R* | CTCTCTGCGTGTAGGATACTAC | |
| ***phyB*** | | |
| *Salk_LBb1* | GCGTGGACCGCTTGCTGCAACT | |
| *PHYB-F* | GCAATGGGAAGTTTGTTCAGG | |
| *PHYB-R* | TGACTTACAATCGCGTTTATGAC | |
| ***pif4*** | | |
| *Sail_LB3* | TAGCATCTGAATTTCATAACCAATCTCGATA | |
| *PIF4-F* | CAC | (Leivar et al., |
| *PIF4-R* (EMO207) | ACCAACGATCAGGATCAAACC | 2008) |
| | TCCAAACGAGAACCGTCGGT | |
| ***soc1*** | | |
| *Salk_LBb1* | GCGTGGACCGCTTGCTGCAACT | |
| S-138131-F | TACACAAACCCTTTATCCTCG | |
| S-138131-R | AGCACTGAGAGGTCAAAGGC | |
| ***xal1-2*** | | Tapia-López et al., |
| GK T-DNA | CCCATTTGGACGTGAATGTAGACAC | 2008 |
| NASC12-LP | ACCCAAACGTCAAATCATCAG | |
| NASC12-RP | CTTCATTCCGAAACACAATGC | |
| | | |
| **RT-PCR** | | |
| ***XAL1*** | | |
| XAL1-F | ATGGCTCGTGGAAAGATTCAGC | |
| XAL1-R | GAACTGAAATATTTCACTTGGCA | |
| ***FD*** | | |
| FD-F | CTCTCTGCGTGTAGGATACTAC | |
| FD-R | AGCCAGCGCCGGAATTCAAGC | |
| ***SOC1*** | | |
| SOC-F | TGAGGCATACTAAGGATCGAGTCAG | |
| SOC-R | GCGTCTCTACTTCAGAACTTGGGC | |
| ***LFY*** | | |
| LFY-F | AGCATCCGTTTATCGTAACGG | |
| LFY-R | ACGATCCGGTACAGCTAATAC | |
| ***AP1*** | | |
| AP1-F | GCACCTGAGTCCGACGTC | |
| AP1-R | CGGCGAAGCAGCCAAGG | |
| ***SPL3*** | | |

| | | |
|---|---|---|
| SPL3-F<br>SPL3-R | TCATGTTCGGATCTCTGGTC<br>ACCATGTCGTAGGTTTAGCAG | |
| ***SPL9***<br>SPL9-F<br>SPL9-R | <br>GATCTACTTCGAGGACGGTG<br>CACCATTTTCGTAAAGCGAAG | |
| ***TUB2***<br>Tub-F<br>Tub-R | <br>AGGACTCTCAAACTCACTACC<br>TCACCTTCTTCATCCGCAGTT | |
| | | |
| **qPCR** | | |
| *AGL24-F*<br>*AGL24-R* | GAGGCTTTGGAGACAGAGTCGGTGA<br>AGATGGAAGCCCAAGCTTCAGGGAA | (Liu et al., 2008) |
| *AP1-F*<br>*AP1-R* | CATGGGTGGTCTGTATCAAGAAGAT<br>CATGCGGCGAAGCAGCCAAGGTT | (Liu et al., 2008) |
| *FD-F*<br>*FD-R* | CTCAAGAGACAACAAGATCAG<br>CACTTCTTCATGAGACAATCTC | |
| *FT-F*<br>*FT-R* | GGTGGAGAAGACCTCAGGAA<br>ATATTCTCGGAGGTGAGGGT | |
| *FUL-F*<br>*FUL-R* | GTTCTTCTGCCTCAATACTG<br>GAGATAGTTCTACTCGTTCGT | |
| *LFY-F*<br>*LFY-R* | ATCGCTTGTCGTCATGGCTG<br>GCAACCGCATTGTTCCGCTC | (Han et al., 2008) |
| *PDF2-F*<br>*PDF2-R* | TAACGTGGCCAAAATGATGC<br>GTTCTCCACAACCGCTTGGT | (Czechowski et al., 2005) |
| *PHYB-F*<br>*PHYB-R* | ATGCACCATCTCAAGAGTGG<br>GCCATTCTGAATTCTGTGCG | |
| *RNAH-F*<br>*RNAH-R* | CCATTCTACTTTTTGGGCGGCT<br>TCAATGGTAACTGATCCACTCTGATG | (Czechowski et al., 2005) |
| *SOC1-F*<br>*SOC1-R* | AGCTGCAGAAAACGAGAAGCTCTCG<br>GGGCTACTCTCTTCATCACCTCTTCC | (Liu et al., 2008) |
| *SPL3-F*<br>*SPL3-R* | TCATGTTCGGATCTCTGGTC<br>TTCCGCCTTCTCTCGTTGTG | |
| *SPL4-F*<br>*SPL4-R* | CAGTAGGTTTCATGACCTCC<br>CCATAAGTACTCTCACCAGAG | |
| *SPL5-F*<br>*SPL5-R* | GCCAAGCAGTATTACCGCAG<br>TCTGGTAGCTCATGAAACCTG | |
| *SPL9-F*<br>*SPL9-R* | GGAATTTGACCTAGAGAAAAG<br>CACCATTTTCGTAAAGCGAAG | |
| *SPL15-F*<br>*SPL15-R* | CAGCCACCGCCCATTTCAAC<br>GGAAATCTGCTGGCTCCGAGA | (Wei et al., 2012) |
| *TSF-F*<br>*TSF-R* | ATGCCTTTGGCAATGAGGTG<br>ACCGTTTGTCTTCCGAGTTG | |
| *UPL7-F*<br>*UPL7-R* | TTCAAATACTTGCAGCCAACCTT<br>CCCAAAGAGAGGTATCACAAGAGACT | (Czechowski et al., 2005) |
| *XAL1-F*<br>*XAL1-R* | CGAAAAGATAGAGGAAAACAAC<br>GGCATTGTTAGCGGATAGGA | |

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**Table S2.** Primers used in ChIP assays

| Gene | Sequence |
|---|---|
| ***FD*** | |
| Fragment 1 | F CCAAGGCCCTCTCTACTTGA |
| | R GATTGTGACATTGAACCTATTCT |
| Fragment 2 | F CCATCTTGACTATCCAACGGT |
| | R TCCGTAGGTTGTCTCTAGAC |
| Fragment 3 | F ACCCAATGTTTGGAAACATGTAA |
| | R TTATCGAAAATGCAAGCTCCTC |
| Fragment 4 | F CATATAATAGTTTATGGAATTTCTC |
| | R ATGATGGGGTTGGGTCCAAG |
| | |
| ***SOC1*** | |
| Fragment 1 | F CTCCCGATATAGATAAAAGATC |
| | R AGTAGCGACGTGTCTAAAGAG |
| Fragment 2 | F TGAATTTTATCTGTTGGGATGG |
| | R ACACTCTCTCGTACCTATATG |
| Fragment 3 | F GTGTTTGTGTCCACATTAAAAAC |
| | R GCTTGAAACCTCATCCTTTAC |
| Fragment 4 | F CATTACCATAACTACAACGAGA |
| | R TTGATTCTCTGCGAAAGGAAG |
| | |
| ***LFY*** | |
| Fragment 1 | F ATCCATTTTTCGCAAAGGAAAG |
| | R GGTTCACAAGAACGGAATCAC |
| Fragment 2 | F TCTTCCCCTAACAATACTTCC |
| | R TTAACTGTATTGGCATGGACG |
| Fragment 3 | F CCCAGCAAGACACATATCTTC |
| | R CTTTCTTTACTCTTTTGAGCAG |
| | |
| ***AP1*** | |
| Fragment 1 | F TTGTTTTCTCTAAGGCTTATGC |
| | R GCTCAATTTGCTTAATCACTTC |
| Fragment 2 | F CAACATAGCACATATTCAACTG |
| | R ACTGTGTAATGTATTGCGTCG |
| Fragment 3 | F TAAAGATCCCGAGACTCAAAC |
| | R TACCCCTTCCCATTTTTGATC |
| Fragment 4 | F GCCCTAATTATTCACTACTGC |
| | R TTCTAGGGTTCACTTCACTAC |