

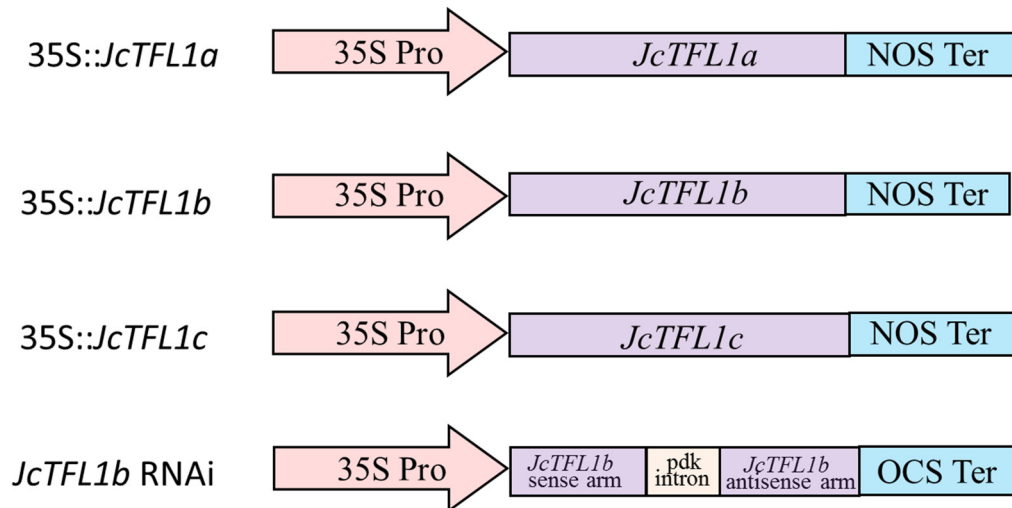
Three *TFL1* homologs regulate floral initiation in the biofuel plant *Jatropha curcas*

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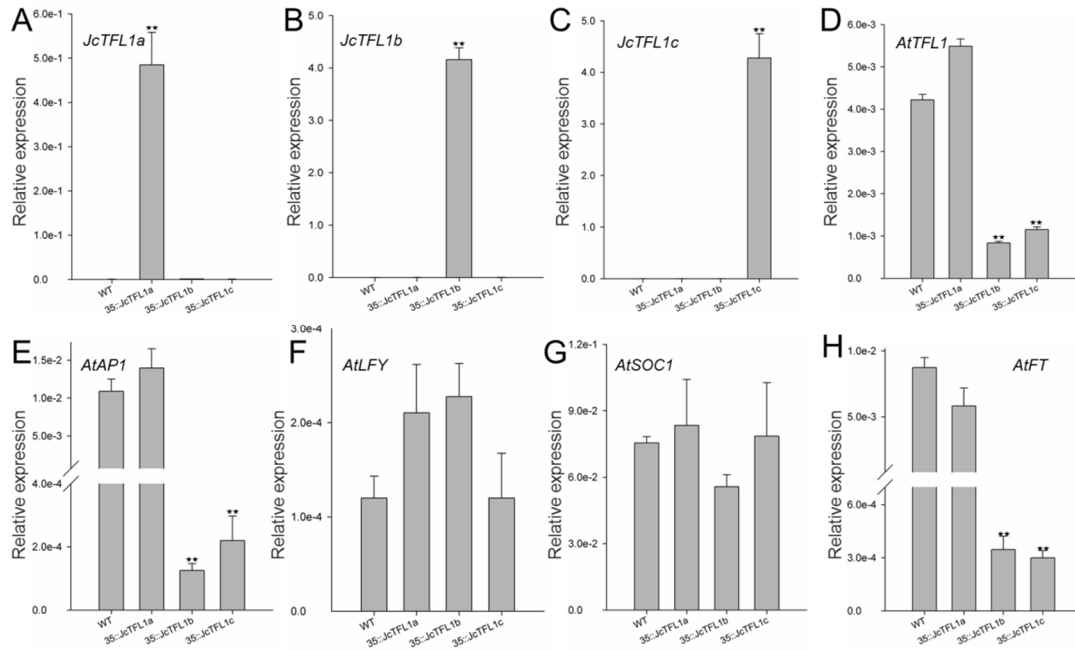
Supplementary Materials

Table S1 Primers used in this study

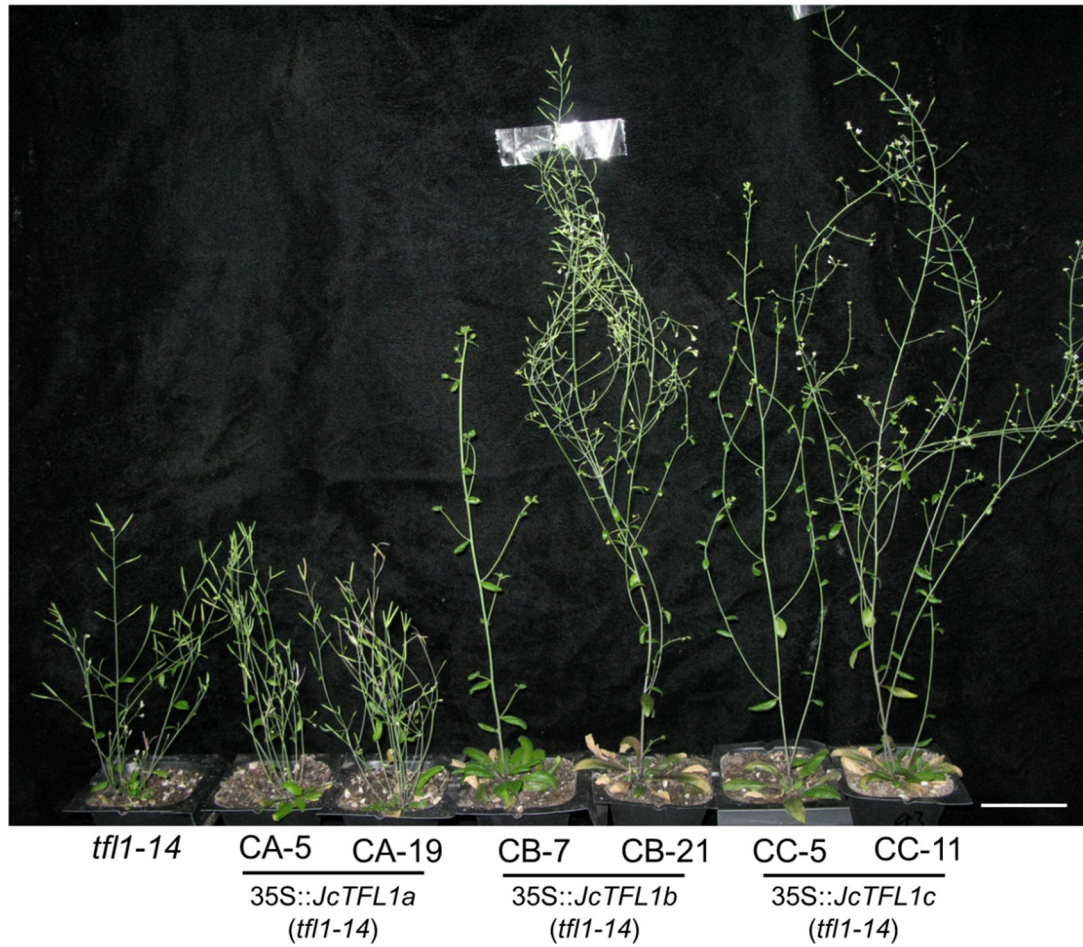
Names	Sequences (from 5' to 3')
<i>AtActin2</i> qRT-PCR F	TGT GCC AAT CTA CGA GGG TTT
<i>AtActin2</i> qRT-PCR R	TTT CCC GCT CTG CTG TTG T
<i>AtAP1</i> qRT-PCR F	GAC GTC AAT ACA AAC TGG TCG A
<i>AtAP1</i> qRT-PCR R	GGA GAT GGC TGA TGA GAG AGC
<i>AtFT</i> qRT-PCR F	GAA CAA CCT TTG GCA ATG AGA
<i>AtFT</i> qRT-PCR R	TCT TCC TCC GCA GCC ACT
<i>AtLFY</i> qRT-PCR F	TCT CTC CCA AGA AGG GTT AT
<i>AtLFY</i> qRT-PCR R	GTA GTG TCG CAT TTT AGG CT
<i>AtSOC1</i> qRT-PCR F	ACT AAA CGT AAA CTC TTG GGA
<i>AtSOC1</i> qRT-PCR R	CAG AAC TTG GGC TAC TCT CT
<i>AtTFL1</i> qRT-PCR F	ATA ATG GGG AGA GTG GTA GGA GA
<i>AtTFL1</i> qRT-PCR R	TCT GGG TCT ATC ATC ACC AAA GT
<i>JcActin</i> qRT-PCR F	CTC CTC TCA ACC CCA AAG CCA A
<i>JcActin</i> qRT-PCR R	CAC CAG AAT CCA GCA CGA TAC CA
<i>JcAP1</i> qRT-PCR F	GGG TTA TTT TGA GGA AAG AAG AGG A
<i>JcAP1</i> qRT-PCR R	AAA CAA TCA AAG CAA CCT CAG CAT C
<i>JcFT</i> qRT-PCR F	AGG CAG ACC GTG TAT CCA CCA G
<i>JcFT</i> qRT-PCR R	ACT GAA TCA CCG TCT CCG TCC TC
<i>JcLFY</i> qRT-PCR F	GGA TAA GAT ACT ACA CAG CAG CGA
<i>JcLFY</i> qRT-PCR R	TAA CCC TTC TTG AGA GAG AGC ATC
<i>JcSOC1</i> qRT-PCR F	TTC TTG GAC GGC AAC GCT TA
<i>JcSOC1</i> qRT-PCR R	CTC TCG GAA AAG TGT GGG ATC
<i>JcTFL1a</i> qRT-PCR F	ACA GAC ATC CCA GGA ACA AC
<i>JcTFL1a</i> qRT-PCR R	AAG AAG ACA GCA GCA ACA GG
<i>JcTFL1b</i> qRT-PCR F	TCA CAA ATA CAG CAC CCA CC
<i>JcTFL1b</i> qRT-PCR R	CTT CTT GCA GCA GTT TCC CT
<i>JcTFL1c</i> qRT-PCR F	ACG GAG CCA CAG CCA CTT ACT GTA G
<i>JcTFL1c</i> qRT-PCR R	ACT CTA GGT TTA GCA GCA ATG ACC G
<i>JcTFL1a</i> F	GCG GAT CCT ATA TGG CAA AAG TGT CA
<i>JcTFL1a</i> R	CGG AGC TCT TAG CGT CTT CTT GC
<i>JcTFL1b</i> F	GCG GAT CCC AAT GGA AAA ACC AGT AG
<i>JcTFL1b</i> R	CGG AGC TCA AAT TAG CGT CTT CTT GC
<i>JcTFL1c</i> F	TAG GAT CCA TGT CAA GGG CGA CGG AG
<i>JcTFL1c</i> R	CGG AGC TCA TCA TCT TCT TCT GGC AGC
<i>JcTFL1b</i> RNAi-1	ACT CGA GAC AGA TGC CAC ATT TGG
<i>JcTFL1b</i> RNAi-2	TGG TAC CAG GTG GGT GCT GTA TTT G
<i>JcTFL1b</i> RNAi-3	CTC TAG AAC AGA TGC CAC ATT TGG
<i>JcTFL1b</i> RNAi-4	CAT CGA TAG GTG GGT GCT GTA TTT G



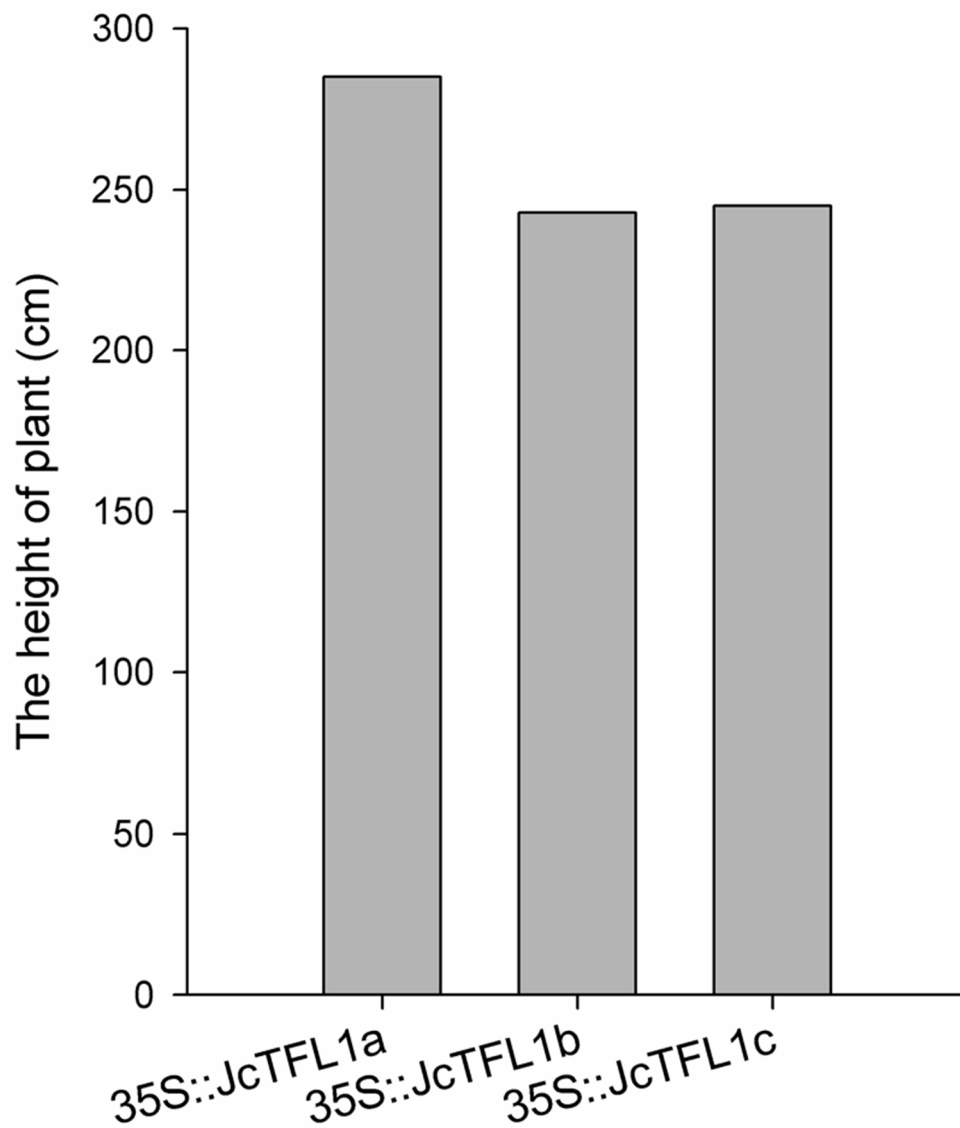
Supplementary Fig. S1 Schematic representation of the transformation vectors, 35S::JcTFL1a, 35S::JcTFL1b, and 35S::JcTFL1c used in this study. 35S Pro, cauliflower mosaic virus 35S promoter; NOS Ter, nopaline synthase gene terminator; OCS Ter, octopine synthase gene terminator.



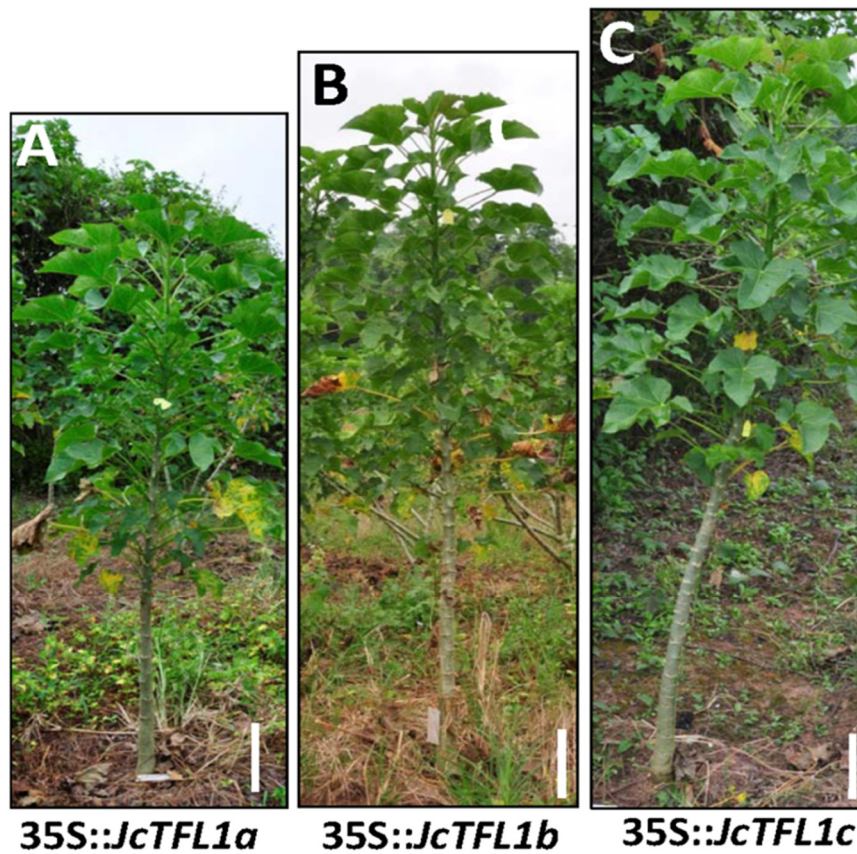
Supplementary Fig. S2 Quantitative RT-PCR analysis of several flowering-related genes in wild-type and transgenic *Arabidopsis*. (A) to (H) are expression levels of *JcTFL1a*, *JcTFL1b*, *JcTFL1c*, *AtTFL1*, *AtAP1*, *AtLFY*, *AtSOC1* and *AtFT*, respectively. *Arabidopsis* seedlings were collected 20 days after germination. The qRT-PCR results were obtained from two independent biological replicates with three technical replicates each. Levels of the detected amplicons were normalized using the amplified products of *AtActin2*.



Supplementary Fig. S3 Overexpression of *JcTFL1*-like genes in transgenic *Arabidopsis* (*tfl1-14* background) under long-day conditions 55 days after germination. Bar represents 5 cm.



Supplementary Fig. S4 The height of transgenic *Jatropha* overexpressing *JcTFL1a*, *JcTFL1b* and *JcTFL1c* two years after transplanting to the field.



Supplementary Fig. S5 Overexpression of *JcTFL1* genes changed plant morphology in *Jatropha*. No branch was found in transgenic *Jatropha* overexpressing *JcTFL1a* (A), *JcTFL1b* (B) and *JcTFL1c* (C) in the first year after transplanting to the field. Bars represent 20 cm.