



Supplementary Information

Constitutive expression of *Aechmea fasciata* SPL14 (*AfSPL14*) accelerates flowering and changes the plant architecture in *Arabidopsis*

Ming Lei ^{1,2,3,4}, Zhi-ying Li ^{1,2,3,4}, Jia-bin Wang ^{1,2,3,4}, Yun-liu Fu ^{1,2,3,4}, Meng-fei Ao ^{1,2,3,4} and Li Xu ^{1,2,3,4*}

* Correspondence: xllzy@263.net; Tel.: +86-898-2330-0284

Table S1. The sequences of SBP domains and accession numbers of selected plant SPL proteins for phylogenetic analysis.

Protein Name	Sequences of SBP domains	Accession No
AtSPL1	CQVENCEADLSKVVDYHRRHKVCEMHKATSATVGGIL QRFCQQCSRFLHLLQEFDEGKRSCRRRLAGHNKRRRK	AT2G47070
AtSPL2	CQVEGCNLDLSSAKDYHRKHRCENHSKFPKVVVSGVER RQCQQCSRFLHLLSEFDEKKRSCRRRLSDHNARRRK	AT5G43270
AtSPL3	CQVESCTADMSKAKQYHHRHKVCQFHAKAPHVRISG- LHQRFCQQCSRFLHLLSEFDEAKRSCRRRLAGHNERRRK	AT2G33810
AtSPL4	CQVDRCTADMKEAKLYHRRHKVCEVHAKASSVFLSGLN QRFCQQCSRFLHLLQEFDEAKRSCRRRLAGHNERRRK	AT1G53160
AtSPL5	CQVDRCTVNLTEAKQYYRRHRVCEVHAKASAATVAGV RQRFCQQCSRFLHLLPEFDEAKRSCRRRLAGHNERRRK	AT3G15270
AtSPL6	CQVYGCSKDLSSSKDYHHRHVRCEAHSKTSVVIVNGLEQ RQCQQCSRFLHLLSEFDDGKRSCRRRLAGHNERRRK	AT1G69170
AtSPL7	CQVPDCEADISELKGYHHRHVRCLRCATASFVVDGGENK RYCQQCGKFHLLPDFDEGKRSCRRRLERHNNRRRK	AT5G18830
AtSPL8	CQAEGCNADLSHAKHYHRRHKVCEFHASKASTVVAAGL SQRFCCQQCSRFLHLLSEFDNGKRSCRKRLADHNRRRK	AT1G02065
AtSPL9	CQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIE QRFCQQCSRFLHLLPEFDLEKRSCRRRLAGHNERRRK	AT2G42200
AtSPL10	CQIDGCELDLSSSKDYHHRHVRCEHHSKCPKVVVSGLER RQCQQCSRFLHLLSEFDEKKRSCRKRLSHHNARRRK	AT1G27370
AtSPL11	CQIDGCELDLSSAKGYHHRHKVCEHHSKCPKVVVSGLER RQCQQCSRFLHLLSEFDEKKRSCRKRLSHHNARRRK	AT1G27360
AtSPL12	CQVDNCGADLSKVVDYHRRHKVCEIHSKATTALVGGIM QRFCQQCSRFLHLLSEFDEGKRSCRRRLAGHNKRRRK	AT3G60030
AtSPL13	CLVDGCDSDFSNCREYHHRHKVCDVHSKTPVVTINGHK QRFCQQCSRFLHLLSEFDEGKRSCRKRLDGHNNRRRK	AT5G50570
AtSPL14	CQVDNCTEDLSHAKDYHRRHKVCEVHASKATKALVGKQ MQRFCCQQCSRFLHLLSEFDEGKRSCRRRLAGHNRRRK	AT1G20980
AtSPL15	CQVEGCRMDLSNVKAYYSRHKVCCIHSKSSKVVVSG- LHQRFCQQCSRFLHLLSEFDLEKRSCRRRLACHNERRRK	AT3G57920
AtSPL16	CQVDNCKEDLSIAKDYHRRHKVCEVHASKATKALVGKQ MQRFCCQQCSRFLHLLSEFDEGKRSCRRRLDGHNNRRRK	NP_177784.6
OsSPL1	CQVDGCTVNLSSARDYNKRHKVCEVHTKSGVVRIKNVE HRFCQQCSRFLHLLQEFDEGKKSCRSRLAQHNRRRK	XP_015614279.1
OsSPL2	CSVEGCAADLSKCVRDYHRRHKVCEAHSKTAVVTVAGQ QQRFCQQCSRFLHLLGEFDEEKRSCRKRLDGHNNRRRK	XP_015611358.1
OsSPL3	CQVEGCNVDLSSAKPYHHRHVRCEPHSKTLKVVVAGLER RQCQQCSRFLHLLAEFDQKKRSCRRRLHDHNARRRK	XP_015626884.1
OsSPL4	CQVEGCGVELVGKDYHRRHVRCEAHSKFPRVVVAGQ ERRFCQQCSRFLHLLSEFDQKKRSCRRRLYDHNARRRK	XP_015623075.1

OsSPL5	CQAEGCKADLSAAKHYHRRHKVCDHFHAKAAAVLAAG KQQRFCQQCSRFBVLAEFDEAKRSCRKRLTEHNRRRRRK	XP_015624330.1
OsSPL6	CQVEGCTADLTGVRDYHRRHKVCEMHAKATTAVVGNT VQRFCQQCSRFBVLAQEFDEGKRSCRRLAGHNRRRRRK	XP_015631511.1
OsSPL7	CQVEGCDITLQGVKEYHRRHKVCEVHAKAPRVVVHGTE QRFCQQCSRFBVLAEFDDAKKSCRRLAGHNERRRR	XP_015635344.1
OsSPL8	CQAEGCKADLSSAKRYHRRHKVCEHHSKAPVVVTAGGL HQRFCQQCSRFBVLADEFDDAKKSCRKRLADHNRRRRRK	XP_015634037.1
OsSPL9	CQVPGCEADIRELKGYHRRHRVCLCAHAAAVMLDGV QKRYCQQCGKFHILLDFDEDKRSCRRLERHNKRRRR	XP_015640052.1
OsSPL10	CQAEGCKADLSGAKHYHRRHKVCEYHAKASVVAASGK QQRFCQQCSRFBVLADEFDEAKRSCRKRLAEHNRRRRRK	XP_015642406.1
OsSPL11	CQVEGCGLELGGYKEYRKHVRCEPHTKCLR VVAGQD RRFCQQCSRFBVLAPEFDDQEKSCRRLSDHNARRRK	XP_015641499.1
OsSPL12	CQVEGCKVDLSSAREYHRHKVCEAHSKAPKIVVSGLER RFCQQCSRFBVLAQEFDDQKKKSCRRLSDHNARRRK	XP_015643462.1
OsSPL13	CQVERCGVDLSEAGRYNRRHKVCEQTHSKEPVVLVAGLR QRFCQQCSRFBVLAQEFDDAKRSCRRLAGHNERRRK	XP_015645415.1
OsSPL14	CQVEGCGADLSGIKNYYCRHKVCFMHSKAPRVVVAGLE QRFCQQCSRFBVLAPEFDQGKRSCRRLAGHNERRRR	XP_015650813.1
OsSPL15	CQVDDCRADLTNAKDYHRRHKVCEIHGKTTKALVGNQ MQRFCCQCSRFBVLAQEFDEGKRSCRRLAGHNRRRRRK	XP_015649921.1
OsSPL16	CAVDGCKEDLSKCRDYHRRHKVCEAHSKTPLVVVSGRE MRFCQQCSRFBVLAQEFDEAKRSCRKRLDGHNRRRRK	XP_015649377.1
OsSPL17	GGSGGGGGGGGGDDVHGRHKVCEYHAKAPIVVVAG LEQRFCQQCSRFBVLAQEFDDQEKSCRRLAGHNERRRK	XP_015610961.1
OsSPL18	CAVDGCKADLSKRDYHRRHKVCEPHSKTPVVVVSG- REMRFCCQCSRFBVLAQEFDEAKRSCRKRLDGHNRRRRK	XP_015610873.1
OsSPL19	CSVDGCRSDLSRCRDYHRRHKVCEAHAKTPVVVVAGQE QRFCQQCSRFBVLAQEFDDGKKSCRKRLDGHNRRRRK	XP_015617950.1
PpSBP1	CQAEGCKDDLSNAKHYHRRHKVCEHLSKAPTPTVVGGH TQRFCQQCSRFBVLAQEFDEGKRSCRKRLADHNRRRRRK	AJ968320
PpSBP2	CQVDGCTADLSRAKDYHRRHKVCEAHSKAPTTLVSRVR QRFCQQCSRFBVLAQEFDDQKKKSCRRLAGHNKRRRK	CAI91313.1
PpSBP3	CQVQGCADLSCCKDYHRRHKVCEMHSKAATAIAAGI EQRFCQQCSRFBVLAQEFDEGKRSCRRLAGHNQRRRK	CAI91301.1
PpSBP4	CQAEGCKTDLSTSKQYHRRHKVCEHLSKAPNVQVGGQT QRFCQQCSRFBVLAQEFDDGKRSCRKRLADHNRRRRRK	AJ968319
PpSBP5	CQVPACGADLAGLKGYHQRHRVCLQCANSTTVILRDIP HRYCQQCGKFHVLSDFEDEGKRSCRKRLERHNNRRRRRK	ABM67299.1
PpSBP6	CQVEGCKADLSGCKDYHRRHKVCEMHSKAPKICIAAGIE QRFCQQCSRFBVLAQEFDEGKRSCRRLAGHNERRRK	ABM67300.1
PpSBP7	CQAEGCKSDLSTAKQYHRRHKVCEHLSKAPNVVAGGQT QRFCQQCSRFBVLAQEFDDGKRSCRKRLADHNRRRRRK	ABM67301.1
PpSBP8	CQAEGCKFDLSLAKPYHRRHKVCEHLSKAPNVIAGGQT QRFCQQCSRFBVLAQEFDDGKRSCRKRLADHNRRRRRK	XP_001775629.1
PpSBP9	CQAEGCKADLNVTKNYYRRHKVCEFHSTPIVIVGGHT QRFCQQCSRFBVLAQEFDDGKRSCRKRLADHNRRRRRK	ABM67302.1
PpSBP10	CQVDGCTADLSKAKDYHRRHKVCEHLSKASTAQVSRVT QRFCQQCSRFBVLAQEFDEGKRSCRRLAGHNKRRRK	ABM67303.1
PpSBP11	CQVDACKADLSKAKDYHRRHKVCEHLSKATKAPVSRLM QRFCQQCSRFBVLAQEFDEGKRSCRRLAGHNRRRRRK	ABV03806.1
PpSBP12	CQAEGCKADLSQAKQYHRRHKVCEHLSKALNVVANG QTQRFCQQCSRFBVLAQEFDDGKRSCRKRLADHNRRRRRK	ABM67304.1
PpSBP13	CQVEGCKADLSGCKDYHRRHKVCEMHSKAPKICIAAGIE QRFCQQCSRFBVLAQEFDEGKRSCRRLAGHNERRRK	ABM67305.1

Table S2. The consensus sequences of the putative motifs of variable SPLs in group III identified by MEME software online (<http://meme-suite.org/tools/meme>).

Motif name	Sequences
Motif 1	YYCRHKVCYMHSKAPRVVAGLEQRFCQQCSRFBQLPEFDQEKRSRRRL
Motif 2	RCQVEGCGVDLSGVK
Motif 3	GLKFGKKIYFED
Motif 4	ATDSSCALSLSTQPWDHTT
Motif 5	AGHNERRRKPKQ
Motif 6	PLSSRYGRJAPSLHEEPNRFR
Motif 7	FVLDFSYPVPSSVRDAWPAIQPGDRISGGIQWQGGVEPHGHRSAVAGY
Motif 8	FDHSSHMMNWSL
Motif 9	EPPPGQIHNGHFSGELELALQ
Motif 10	QYMEDENT

Table S3. Primers used in this study.

Name	Sequences (from 5' to 3')
<i>AfSPL14</i> 5' RACE GSP1	GCG GCA TTA CTG GAG TTC GGT T
<i>AfSPL14</i> 5' RACE GSP2	GGT GGC GAC TCC TGA GAA GCA TT
<i>AfSPL14</i> 3' RACE GSP1	GTA GGA AAC CAC CTG TCC CTT TGT CA
<i>AfSPL14</i> 3' RACE GSP2	GAT TCG CCT CCG CTG CCC CTA A
<i>AfSPL14</i> cDNA F	CTC TCT CCC TCT CTC TGG GGT GTC T
<i>AfSPL14</i> cDNA R	GCT ATA GTT GGT CAT GAT CAC ATT A
<i>AfSPL14</i> -5outer	GGC ATT TCA TGT GAA CTG GGT C
<i>AfSPL14</i> -5inner	CGG CAT TAC TGG AGT TCG GTT A
<i>AfSPL14</i> -pBD F	CGG AAT TCA TGG AGA AGG GTT CGG GCT CCG TTG
<i>AfSPL14</i> -pBD R	AAC TGC AGC AGA GAC CAG TGC ATG CCG TGA
<i>AfSPL14N</i> -pBD F	GGA ATT CAT GGA GAA GGG TTC GGG CTC
<i>AfSPL14N</i> -pBD R	ACG CGT CGA CTG GTT TCC TAC GAC GCT CG
<i>AfSPL14C</i> -pBD F	GGA ATT CCC TGT CCC TTT GTC ATC TCG
<i>AfSPL14C</i> -pBD R	ACG CGT CGA CCT ACA GAG ACC AGT GCA TGC
<i>AfSPL14</i> -OX F	GGG GTA CCA TGG AGA AGG GTT CGG GCT CCG TTG
<i>AfSPL14</i> -OX R	GCG TCG ACC TAC AGA GAC CAG TGC ATG CCG TGA
<i>AfSPL14</i> qRT-PCR F	CTT CTT CTC ACC CAC GGA ACT
<i>AfSPL14</i> qRT-PCR R	ACA TGG CTA TGC GGC ATT AC
<i>AfACTB</i> qRT-PCR F	TAC AGT GTC TGG ATT GGG GG
<i>AfACTB</i> qRT-PCR R	CGG ATT CAT CAT ACT CAC CCT T
<i>AtLFY</i> qRT-PCR F	CGA GCA CGC TTG TGG GTA T
<i>AtLFY</i> qRT-PCR R	TTG CAA TCG TCT CCG TTC AG
<i>AtAP1</i> qRT-PCR F	TGG GTG GTC TGT ATC AAG AAG ATG
<i>AtAP1</i> qRT-PCR R	CCA AGG TTG CAG TTG TAA ACG
<i>AtAP2</i> qRT-PCR F	GGT GTT GCT TCT GGC TTT CC
<i>AtAP2</i> qRT-PCR R	GGT CCA CGC CGA CTC TTT T
<i>AtAP3</i> qRT-PCR F	GGA GAT TAC GAC TCA GTT CTT GGA T
<i>AtAP3</i> qRT-PCR R	GTG GTG ATG GTT CTG GTG GA
<i>AtFUL</i> qRT-PCR F	CAA CTT GTT GGC CGA GAC G
<i>AtFUL</i> qRT-PCR R	TGG AGC GCA GAT ATG GAT TC
<i>AtSOC1</i> qRT-PCR F	CTA AAC GTA AAC TCT TGG GA
<i>AtSOC1</i> qRT-PCR R	CAG AAC TTG GGC TAC TCT CT
<i>AtFT</i> qRT-PCR F	GGTGGAGAAGACCTCAGGAAC
<i>AtFT</i> qRT-PCR R	TGCCAAGCTGTGCGAAACAATA
<i>AtACTB</i> qRT-PCR F	TGT GCC AAT CTA CGA GGG TTT
<i>AtACTB</i> qRT-PCR R	TTT CCC GCT CTG CTG TTG T

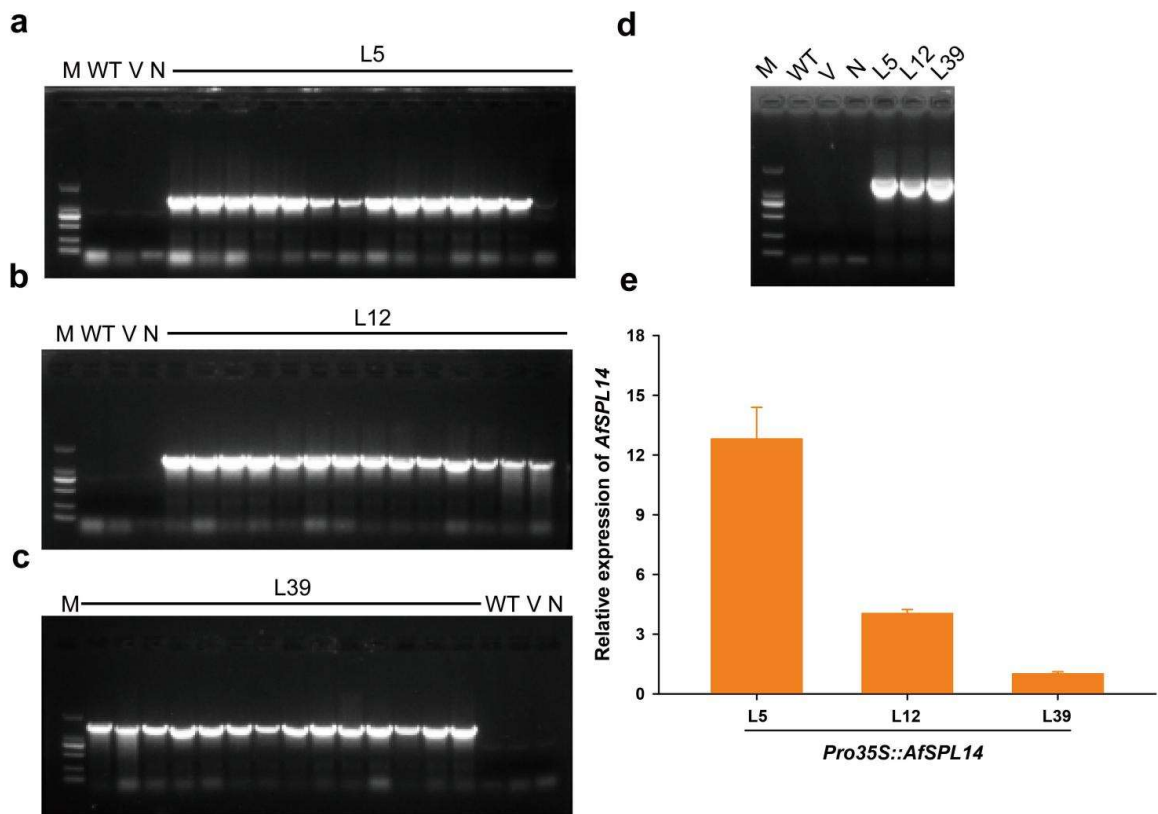


Figure S1 Verification of *Pro35S::AfSPL14* transgenic plants. DNA of randomly selected T3 plants of variable lines (L5, L12, L39) were extracted and used for PCR verification using *AfSPL14*-OX F and *AfSPL14*-OX R primers (a, b, c). Furthermore, RNA of variable transgenic lines were also extracted, and PCR (d) or RT-qPCR (e) were conducted. M: DNA Ladder 2000; WT: the Wild Type; V: Vector; N: negative control which used double distilled H₂O (ddH₂O) as templates in PCR.

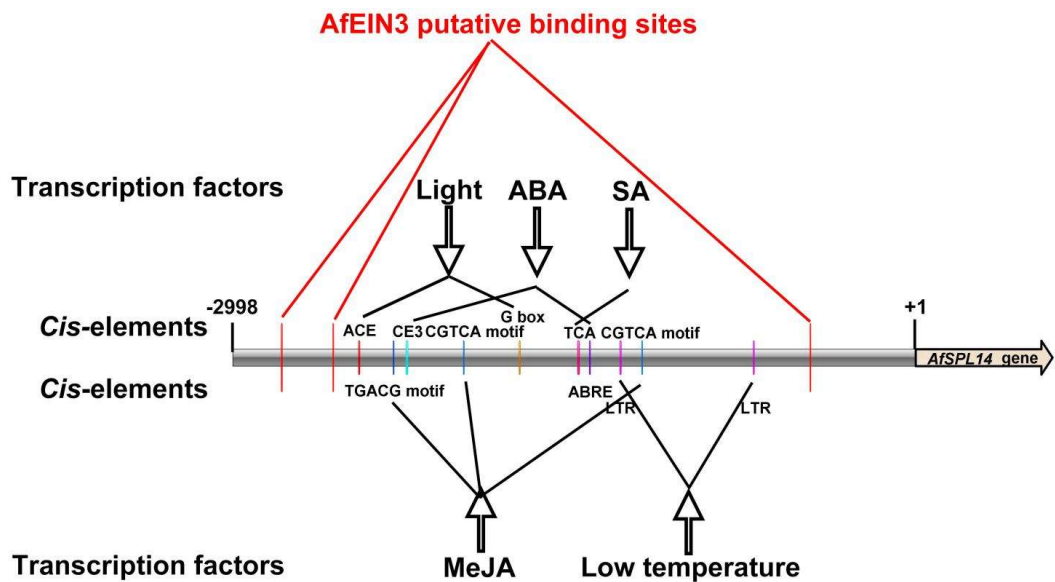


Figure S2 Representative cis-elements enclosed in the nearly 3000-bp-length promoter sequence of *AfSPL14*. Amounts of cis-elements, which might response to light, abscisic acid (ABA), salicylic acid (SA), methyl jasmonate (MeJA), low temperature, etc, were within the promoter. Three 5'-ATGTA-3' core sequences, which might interact with ETHYLENE INSENSITIVE 3 (EIN3), a crucial factor in ethylene signaling pathway that could activate or inhibit the expression of downstream genes in transcriptional level, were also within the promoter.