

Supplementary Materials

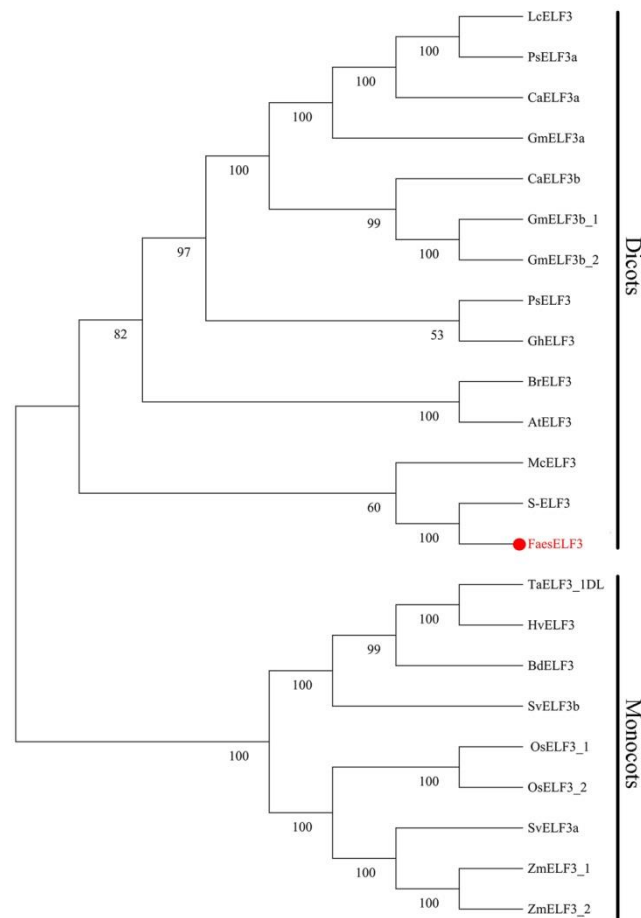
Table S1. Primers used in this study.

Primer name	Primers sequences (5'-3')
3RELF3GSP	GGGATGAGTTTATCCGACAATTC
5RELF3GSP1	TGAATGTGATGCCAGAG
5RELF3GSP2	GCTACTCCCCTGACTTGCTCCACTATGCTGAT
5RELF3GSP3	TGGGTTGTGCCGATTGAAGG
DpELF3SP1	TCCCCTGACTTGCTCCACTATGC
DpELF3SP2	GCCGATTTGAAGGGATAGTAAGTTGC
DpELF3SP3	CCATGGACTTCTCCTCGTATTTAC
DpELF3SP4	GATGGACACAAACCCAATAGACCCA
DpELF3SP5	GGGGTTAGAAAGAAGATTGGGGTTG
DpELF3SP6	AAGGAAAGTGCTATGAGTTGTGGGC
TpFaesELF3F1	ATGATTACGAATTC <u>GAGCT</u> CCGATCAACTAGTTATTTTT
TpFaesELF3F2	ATGATTACGAATTC <u>GAGCT</u> CCAATCAAACCTTAATAATCGAA
TpFaesELF3F3	ATGATTACGAATTC <u>GAGCT</u> CCTATTCCGTATCTTGTAGTTG
TpFaesELF3R	TCTGCAGGTCGACT <u>CTAGACT</u> CTTATTTCAAAATTTTCAACC
Y1HpFaesELF3F	AAGCTTGAATTC <u>GAGCT</u> CTCCATTTAGGGAAACAGGA
Y1HpFaesELF3R	ACATGCCTCGAGGTCGACCTCTTATTTCAAAATTTTC
Y1HFaesAP3_1F	ATGGAGGCCAGTGAATTCCTGCTAAGAACAACAAGTAACA
Y1HFaesAP3_1R	ATTCATCTGCAGCTC <u>GAGCT</u> CGAACACATGAACACAATGAG
Y1HFaesAP3_2F	ATGGAGGCCAGTGAATTCATGTTACAGAGCCAATTACGA
Y1HFaesAP3_2R	ATTCATCTGCAGCTC <u>GAGCT</u> CATATACAATCGGAGACAC
Y1HFaesPIF	ATGGAGGCCAGTGAATTCATGGGGAGAGGGAAGATTG
Y1HFaesPIR	ATTCATCTGCAGCTC <u>GAGCT</u> CTAGGGTTTTTGTCTTGCTAC
Y1HFaesAGF	ATGGAGGCCAGTGAATTCCTTTTTAGTTTCTTCTCCCAG
Y1HFaesAGR	ATTCATCTGCAGCTC <u>GAGCT</u> CTACAACACAGCTTCTCAAC
Dual-pFaesELF3F	GGGCCCCCCTCGAGGTCGACCAATCAAACCTTAATAATCG
Dual-pFaesELF3R	CAGGAATTCGATATC <u>AAGCTT</u> CTCTTATTTCAAAATTTTCAACC
Dual-FaesAP3_1F	CGCGGTGGCGGCCGCTCTAGATGCTAAGAACAACAAGTAACA
Dual-FaesAP3_1R	AAGCTTGATATCGAATTCGAACACATGAACACAATGAG
qFaesELF3F	CGGAAAGAGGAGGGCCAAGAG
qFaesELF3R	GACGCGTATTTCTGGGTGT
qFaesAP3_1F	AACCAACAGACAAGTTACTTATT
qFaesAP3_1R	ACATCCTGCCAGAACTCC
qFaesactinF	ACCTTGCTGGACGTGACCTTAC
qFaesactinR	CCATCAGGAAGCTCATAGTTC

TRV2-FaesELF3F	GTTACCGAATTCTCTAGAGATGAGTTTATCCGACAATTC
TRV2-FaesELF3R	CTCGAGACGCGTGAGCTCTGTCTTTGAAGTCTATCAGCT
TRV2-FaesAP3_1F	GTTACCGAATTCTCTAGACACCTTCCTTACTTCATCTCC
TRV2-FaesAP3_1R	CTCGAGACGCGTGAGCTCCTTCATGCATTATACAGGACA

Table S2. Information of sequences selected for alignments and phylogenetic analyses from NCBI GenBank.

Taxon and species	Protein name	Accession numbers
Poaceae		
<i>Oryza sativa</i>	OsELF3_1	CAA08804.1
	OsELF3_2	CAA08802.1
<i>Zea mays</i>	ZmELF3_1	NP_001169653.1
	ZmELF3_2	PWZ32646.1
<i>Triticum aestivum</i>	TaELF3_1DL	ABL11477.1
<i>Hordeum vulgare</i>	HvELF3	AEZ53982.1
<i>Brachypodium distachyon</i>	BdELF3	XP_003567779.1
<i>Setaria viridis</i>	SvELF3a	TKW15056.1
	SvELF3b	TKW25484.1
Ranunculaceae		
<i>Paeonia suffruticosa</i>	PsELF3	QJP03923.1
Fabaceae		
<i>Cicer arietinum</i>	CaELF3a	XP_004501482.1
	CaELF3b	XP_004498926.1
<i>Lens culinaris</i>	LcELF3	AFZ78447.1
<i>Pisum sativum</i>	PsELF3a	AFR60580.1
<i>Glycine max</i>	GmELF3a	AQX44338.1
	GmELF3b_1	AQX44344.1
	GmELF3b_2	XP_003550290.1
Malvaceae		
<i>Gossypium hirsutum</i>	GhELF3	XP_016744799.2
Brassicaceae		
<i>Arabidopsis thaliana</i>	AtELF3	AAX23847.1
<i>Brassica rapa</i>	BrELF3	AEB33726.1
Polygonaceae		
<i>Fagopyrum esculentum</i>	S-ELF3	BAL45488.1
	FaesELF3	OP572281.1



Supplementary Figure S1. Phylogenetic tree of FaesELF3 and other ELF3 homologous proteins from different species.

> *pFaesELF3*

-1278 CGATCAACTA GTTATTTTTG CTACTCAATA AGCTTAGGTT ATCGATAAAC TTTATATGCG
TATABOX5 CAATBOX1

-1218 ACCAGTAAAC ACAAGGTTTC CAAACGTACC CTCAAACATC AATTTCATAA AACACACTCA
DPBFCOREDCDC3 ACGTATERD1 CAATBOX1

-1158 AATTCCACAG CTTTCAAAAA TTATATTTGG TATATAAACA CTAATTAATA TCACAAACAC
TATABOX4

-1098 AATATAATGT TACACACGAG AGGTGTTTCG TCCCAAATTA GTATAAAAAA TCAGTGTGAA
CArG-box DPBFCOREDCDC3 GTGANTG10

-1038 AATGAATATT TTTTTTATCT TATACCTTTT TTCGTTATAT AAATAAAGGT TGGTGAATA
PYRIMIDINEBOXOSRAMY1A TATABOX4

-978 CATAATAACA TAAGTGCAAG ACCCTCGACA TCTATTTTTT ATACATTAAA TTTATCCTTA

-918 AAAATTGAAA TATTTCAATG CAAATATCAA TCAAACCTTT AATAATCGAA TCAACAAAGA
CAATBOX1 CAATBOX1 AACAAA motif

-858 ACTCGTACTT AAACCGAATC TCTTGTAAC CGATTAGTTT AGGTTGAAAA GTGACACAAG

GTGANTG10

CAATBOX1 MYCCONSUSAT

+523 TGTGCC**TTTG** **TT**GGATTGTT AAGAGAGGTT GAAAATTTTG AAATAAGAG **ATG**
TTTGTT motif

Supplementary Figure S2. *pFaesELF3* promoter sequence. The transcription start site (+1) is in bold and boxed. The start codon ATG is in bold and boxed. Putative cis-acting regulatory elements are in bold and underlined.