

Table 1 Suppl. The list of primers for PCR amplifications.

Primer name	Sequence (5'-3')
LAS2	CCAGGCAAGATTAGCCCAGATGCCCTGTAG
LF6	GTGCTCCAATTTCTTAGGGTTGCTG
LAS10	TAGCCGTTCCAAATCCAGTTCTTA
LF3	CTTGATGAGAGTGGT
LR1	GCCGTTCCAAATCCAGTTC
LF1	GAATGCTTTGGGTGACCTC
Actin F	GTGCTAACGAATACAGTTCACG
Actin R	CCAGCAGATGTGGATTTCAAAG
LAS11	CCGGCCACCGAGCTGCTGCTCTCGACAAA
LAS14	GGATAAAAAGGAAGAAGGGTTTGACAGAG
PLF2	CGGAAGCTTCTACATATGTGTGTTAGC
PLR1	GGGTCTAGAATAAAAAAGGAAGAAGGG

Table 2 Suppl. Putative *cis* regulatory motifs in the *FLL1* promoter sequence.

No.	Name	Sequence 5' to 3' /Strand	Function description
1	5'UTR Py-rich stretch	TTTCTTCTCT / (+)	<i>cis</i> -acting element conferring high transcription levels
2	AAGAA-motif	GAAAGAA / (-)	
3	ACE	GCGACGTACC / (-)	<i>cis</i> -acting element involved in light responsiveness
4	AT1-motif	AATTATTTTTTATT/(+)	part of a light responsive module
5	Box4	ATTAAT / (+)	part of a conserved DNA module involved in light responsiveness
6	G-box	CACATGG / (-)	<i>cis</i> -acting regulatory element involved in light responsiveness
7	GATA-motif	AAGGATAAGG / (+)	part of a light responsive element
8	I-box	CCTTATCCT and gGATAAGGTG/(+/-)	part of a light responsive element
9	LTR	CCGAAA and CCGAC (-/+)	<i>cis</i> -acting element involved in low-temperature responsiveness
10	Skn-1_motif	GTCAT / (-)	<i>cis</i> -acting element required for endosperm expression
11	TCA-element	CCATCTTTTT / (-)	<i>cis</i> -acting element involved in salicylic acid responsiveness
12	Unnamed_4	CTCC / (+/-)	
13	As-2-box	GATAatGATG / (-)	involved in shoot-specific expression and light responsiveness
14	chs-CMA2a	TCACTTGA / (-)	part of a light responsive element

1	ctctctatataaagtgtctccaatttccttaggggtgtgctgcaacttcaccttcttcttctttt	61
62	ctctgtcaaaaccccttcttctttttatccaatccaactttgcctatggtgattctaaaact	121
122	S E A S C D D Y M I Y R H E N I S L L D	181
182	tctgaagcttctgtgatgattacatgatataccggcatgagaacattagtctgctcgat	241
242	L L S L L I F R R H L I H Y N F V E S S	301
302	ctactaagtcttctcatctttagaagacatctgatccattataactttgtcgagagcagc	361
362	S S V A G S L E G V L T D R I T A L T C	421
422	agctcggtggccggtagtctcgaggggtgtcctgaccgacaggatcactgccctgacatgt	481
482	V L Q K I L Y M I R T P L K W I G H I V	541
542	gttcttcaaaagatattatacatgatcagaacgccactgaagtggattgggcacatagtt	601
602	E F L L N L I C L N G G V R G L I W N V	661
662	gagtttttctgaacttgatagtccttaatggaggagtacgaggcttaacttggaatgtt	721
722	I T V S V V I P R R G A A H F R S L I A	781
782	atcacagtgtccgttgatccccaggcgtggagcagctcacttccggctcgttgatcgca	841
842	H I D A R L D L R K S D S I H H I H L D	901
902	cacatcgatgcacgacttgatctccgcaagagcgattccatccatcacatccacttgat	961
962	K L T C L G E T D P L D L A M M A A K L	1021
1022	aagctaacatgtcttggcgaacagatcccttggatctcgccatgatggctgccaaatta	1081
1082	A Y E N G E Y I K D A V T N H W K M H F	1141
1142	gcctacgagaatggtagtatatcaaggatgcagtgaccaaccatttgaagatgcacttt	1201
1202	V G F Y S C W N E F L Q D K T T Q A F I	1261
1262	gtgggggtttacagctgctggaacgagttccttcaagataaaacgacccaagccttcata	1321
1332	L C D K T E D A D L I V L A F R G T E P	1381
1382	ttatgcgacaagaccgaggacgccacctaactcgtcctggccttccgtggcaccgagccc	1441
1442	F N A Q D W S T D V D L S W L C M G K L	1501
1502	tttaacgccaggaactgggtccaccgatgtcgaccttcttggctctgcatgggaaattg	1561
1562	G G V H L G F L K A L G L Q H E M D R K	1621
1622	ggcggcgtccatttgggtttcttaaaggctcttggcctgcaacatgagatggaccgaag	1681
1682	K G F P K E L S R N D P G K P V A Y Y V	1721
	aaaggttcccaaaggagctgagttagaatgacctggcaaacgggtggcatactactgtg	
	L R D T L R T L L K K H N N A K I L V T	
	ctgagggatacactgagaacgttgctaaagaagcacaacaatgcaagatactggtagacc	
	G H S L G G A L A A I F P A L L A M H E	
	ggacatagcttgggtggagcacttctgctatcttccagcttggtagctatgcatgag	
	E Y D I L D S I Y G V M T Y G Q P R V G	
	gaatcgatatacctggattccatatacgggtgtaatgacgtatgggcagccaggggttgg	
	D A T F K K Y V E S I L S K R Y Y R M V	
	gatgtaccttcaaaaaatacgtagaatccatcctgagcaaaaggtagctatcgatgggtg	
	Y R Y D I V P R V P F D M P P V A M F K	
	tatcgtatgatatcgctccctcgagttccattcgatagccaccagtggaatgttcaag	
	H C G T C I Y Y D G W Y E R Q A M N E D	
	cattgtgggacttgcattactacgacggatggtatgagagacaggctatgaatgaggat	
	S P N P N Y F D V K Y T I P V Y L N A L	
	tccgccgaatcccaactactcttggatgtaaaatatacaattccgggtgtatttgaatgctttg	
	G D L M K A L L L G R T Q G K D F K E E	
	ggtagacctatgaaggctctgctcctaggagaacccaaggcaaggacttcaaagaagag	
	F L S I L Y R A S G L I L P G V A S H S	
	tttttgcgatcctctacagggcatctgggctaactcttgcctggggttgcatctcatagt	
	P R D Y V N G G R L A K I T G K Y S	
	cctagagactacgtcaacgggtggaaggcttgcaagataaccggcaataactcttgatga	
	gtagtggttttatttcatcaaaaaataagtagcgggttaagtatgtatgttttgaatgttaca	
	atatgcagaagaacctacagtagtagtagaaagttaaagaacttttccgaataaatttgaaga	
	actggatttgaacggctaaaaaataaataaataaataaataaataaataaataaataaataa	

Fig. 1 Suppl. Nucleotide and inferred amino acid sequences of *FLL1*. The nucleotide sequence is shown in lower case letters, whereas the amino acid sequence is in capital letters. Numerals at both ends of the nucleotide row indicate a nucleotide number. The first start codon (atg) is **bold** and the stop codon (tga) is marked with an *asterisk*, respectively. The putative polyadenylation signals are in *italics*. The serine, aspartic acid, and histidine residues that form the catalytic triad are in **bold** and *underlined*. The lipase consensus motif surrounding the active serine residue is *shaded*. Arrows represent sense (LF6, LF1, and LF3) and antisense (LAS10, LAS2, LR1, LAS11, and LAS14) primer sequences designed for 5' RACE, LD-PCR, RT-PCR, and promoter isolation. The overlapping region between 5' RACE and O65EST cDNA is *underlined*.

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EgLIP1_AFV50601.1 -----MDSKTSEASDDYMIYRHENISLLDLLSLLIFRRHLIHYNFVES---SS
FLL1 -----MDSKTSEASDDYMIYRHENISLLDLLSLLIFRRHLIHYNFVES---SS
NP_001054678.2 MTMAGGSAANAANKKKMGEEKLIIMSEKVRFDILSLLLRPITSYHFVDAGDATA
XP_002533321.1 -----MAASATTSNNIAPNFLVVDPKKGRKRDIKFYLVRKDVKSGMSFLDS---SE
AAV66577.1 -----MAASATTSNNIAPNFLVVDPKKGRKRDIKFYLVRKDVKSGMSFLDS---SE
               .:..: : : : * :. * : : * :. :

EgLIP1_AFV50601.1 SVAGSLEGVLTDRITALTCVLQKILYMIRTPLKWIGHIVEFLNLIICLNGGVRGLIWNVI
FLL1 SVAGSLEGVLTDRITALTCVLQKILYMIRTPLKWIGHIVEFLNLIICLNGGVRGLIWNVI
NP_001054678.2 AAAGELGSTPGEWLVALTEIIQKALAAAYYPAYLGAAVEFFLNFVSLNGGVIGLWNIV
XP_002533321.1 EGVKGGAAVDHRWILLVSIIRRVLALIDTPLKYLGYVIDFFLNLISQNSGFSGLNNFL
AAV66577.1 EGVKGGAAVDHRWILLVSIIRRVLALIDTPLKYLGYVIDFFLNLISQNSGFSGLNNFL
               . . : : : : * * * : * : : : * . * : : .

EgLIP1_AFV50601.1 TVSVVIPR-RGAAHFRSLIAHIDARLDLR--KSDSIHHIHLDKLTCLGETDP-----
FLL1 TVSVVIPR-RGAAHFRSLIAHIDARLDLR--KSDSIHHIHLDKLTCLGETDP-----
NP_001054678.2 RFKLVIPLNREAPNFRSMIAMIDGRTELKPMKPAATAGVEDDDLESGGCAAGVPLIRRH
XP_002533321.1 HGKLIKIP-RGTEHFISTIGHLDGRIDLY--RSTILAEKVDDSVANDAN-IRSELG----
AAV66577.1 HGNLKIPR-RGTENFISTIGQLDGRIDLY--RTTILSEKVDDSVATDVNNIKAEKG---
               . : * * * : : * * . : * * : * . * :

EgLIP1_AFV50601.1 -----LDLAMMAAKLAYENGEYIKDAVTNHWKMHFVGFYSCWNEFLQDKTT
FLL1 -----LDLAMMAAKLAYENGEYIKDAVTNHWKMHFVGFYSCWNEFLQDKTT
NP_001054678.2 LVDSEHLLAEQYSISEVTVMASKIAYENAAIENNVNNVWKFNFVGFYSCWNEFGSETT
XP_002533321.1 -----NRYLMDLCIMASKLVYENEKVNVVDDHWMKMFALFYNCWNEQKESNT
AAV66577.1 -----NRYLMDLCIMAAKLVEYENKVAQNVDVDRHWMKMFVAFYNCWNEYQKQNNNT
               : : : * : . * : : * : . * : : * : . * : .

EgLIP1_AFV50601.1 QAFILCDKTEDADLIVLAFRGTEPFNAQDWSTVDLSWLCMGKLGGVHLGFLKALGLQH-
FLL1 QAFILCDKTEDADLIVLAFRGTEPFNAQDWSTVDLSWLCMGKLGGVHLGFLKALGLQH-
NP_001054678.2 QAFVMTERRATDAAIVVAFRGTEPFNMQDWSTDVNLWLGMAAMGHVHVGFLKALGLQEV
XP_002533321.1 QVLMLSDKPKDANLIVISFRGTEPFNAQDWSTDFDFSWEIIPKVGKIHIGFLEALGLGN-
AAV66577.1 QVFICCDKPKDANLIVVSRGTEPFNAQDWSTDFDFSWEIIPKVGKIHIGFLEALGLGN-
               * : : : : * : * : : * : : * : : * : : * : : * : .

EgLIP1_AFV50601.1 -EMDRKKGFPPKELSRNDP-----GKPVAYYVLRDTRLTLKKHNNNAK
FLL1 -EMDRKKGFPPKELSRNDP-----GKPVAYYVLRDTRLTLKKHNNNAK
NP_001054678.2 DAKDAARAFPREPPAAAAL-----VGRSFAYYKLRDVLRLDQLRRHPNAR
XP_002533321.1 --RGDATTFQTYLQRKHTKGFHLNGDHSSEGTMIWEAKKSAYYAVLLKLKSLLEKHKHAK
AAV66577.1 --RSDATTFQTHLQRKHT-GFFHLNGE-SEGNMTEWAKKSAYYAVALLKLKSLLEKHRNAK
               . * . . : : * : : * : * : * :

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EgLIP1_AFV50601.1 ILVTGHS^LGALAAIFPALLAMHEEYDILDSIYGVMTYGGQPRVGDA^TFKKYVES--ILSK
FLL1 ILVTGHS^LGALAAIFPALLAMHEEYDILDSIYGVMTYGGQPRVGDA^TFKKYVES--ILSK
NP_001054678.2 VVVTGHS^LGALAAIFPALLAFHGEADVVSRIAAVHTYGGQPRVGDA^FAGFLAANAATPV
XP_002533321.1 FVVTGHS^LGALAILFPSVLVIQEE^TEILQRLLNIYTFGQPRIGDAQLGKFMESYLNYPV
AAV66577.1 FIVTGHSLG^ALAILFPSILVIQEE^TEMLNRLNIYTFGQPRIGDAQLGTFMESHLNYPV
               . : * : * : * : * : * : * : * : * : * : * : * : .

..
EgLIP1_AFV50601.1 R-YYRMVYRYDIVPRVPFDMPPVAMFKHCGTCIYYDGWYER--QAMNEDSPNPYFDVKY
FLL1 R-YYRMVYRYDIVPRVPFDMPPVAMFKHCGTCIYYDGWYER--QAMNEDSPNPYFDVKY
NP_001054678.2 A-FQRVVYRYDIVPRVPFDPVADFRHGGTCVYYDGWYAGRTLAAGEDAPNKNYFNPKY
XP_002533321.1 TRYFRVVCNDMVPVPFDDK-IFAFKHFGNCLYFDSRYFG---RLMDEEPNRYFGLRH
AAV66577.1 TRYFRVVCNDMVPVPFDDK-IFAFKHFGTCLYYDSRYFG---RFMDEEPNRYFGLRH
               : * : * * : * : * : * : * : * : * : * : * : * :

..
EgLIP1_AFV50601.1 TIPVYLNALGDLMKALLGRTQGKDFKEEFLSILYRASGLILPGVASHSPRDYVNGGRLA
FLL1 TIPVYLNALGDLMKALLGRTQGKDFKEEFLSILYRASGLILPGVASHSPRDYVNGGRLA
NP_001054678.2 IVSMYGNAGWDLFKAMFLWAKEGKDYREGPVSIVYRAAGLLEFGLASHSPRDYVNAIRLG
XP_002533321.1 IIPMRNLAIWEVLRSEIISHTHGADYQESWFCTFFRVMGVLVPGVAAHSPIDYVNSVRLG
AAV66577.1 IIPMRVNALWELFRSFMITHAGPDYQESWFCTLSRVAGLVLPVAAHSPIDYVNSVRLG
               : : * * : : : : : . * * : * . . . * . * : : * : * : * : * :

EgLIP1_AFV50601.1 --KITGKYS-----
FLL1 --KITGKYS-----
NP_001054678.2 --HVAPKEA-----
XP_002533321.1 RERVAPLASLSKFARKL
AAV66577.1 KERVAPMTSLKSFARKS
               : : : :

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Fig. 2 Suppl. Multiple sequence alignment of FLL1 against the top four *BLASTX* hits in the *NCBI* sequence database. The ‘.’ denotes conservation of strong groups. The ‘.’ denotes conservation of weak groups, whereas those without any symbol denote no consensus (*CLUSTWALW*, Biology Workbench Version 3.2, the University of California). The lipase consensus motif is boxed, whereas the serine, aspartic acid, and histidine residues that forms the putative catalytic triad is marked with the ‘^’.

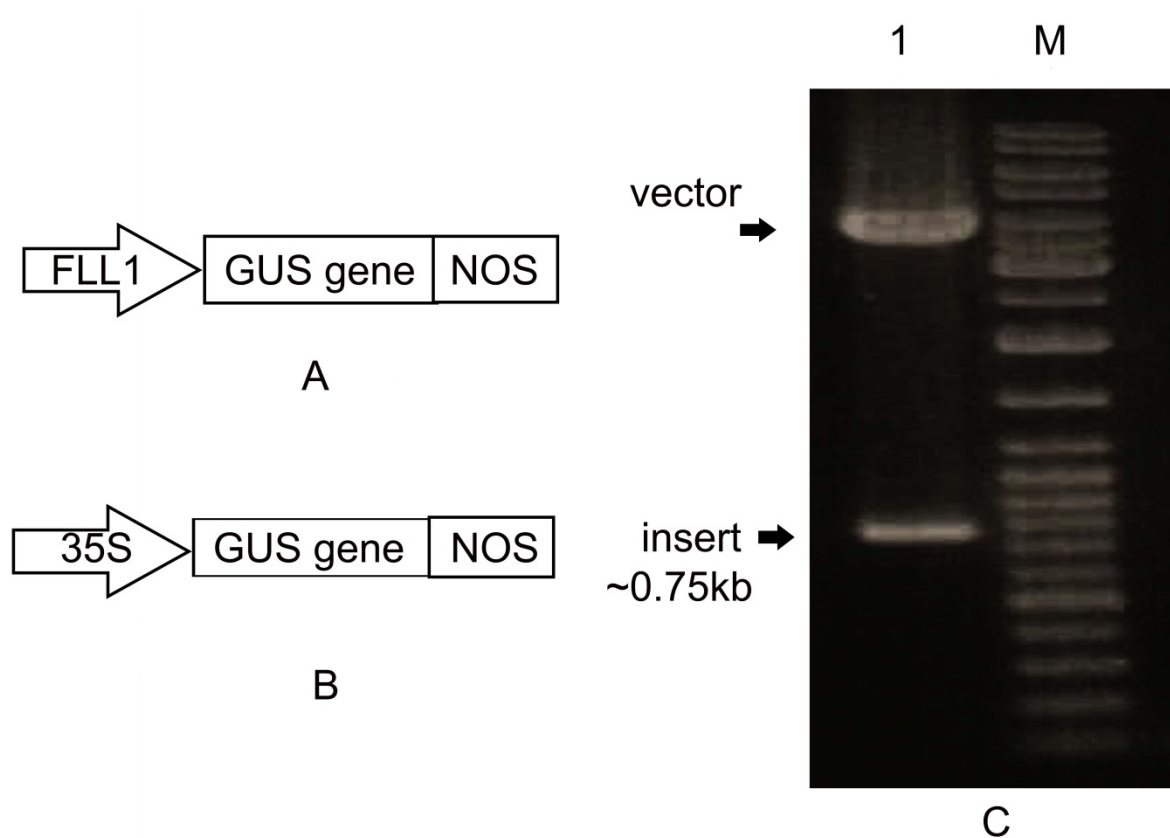


Fig. 3 Suppl. A schematic diagram of the FLL1GUS plasmid (A), pBI221 plasmid (B), and HindIII-XbaI digestion of a transformation vector pBI221 carrying the FLL1 promoter on 1 % (m/v) agarose gel electrophoresis (C).