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

Primer name	Sequence (5`-3`)
LAS2	CCAGGCAAGATTAGCCCAGATGCCCTGTAG
LF6	GTGCTCCAATTTCCTTAGGGTTGCTG
LAS10	TAGCCGTTCCAAATCCAGTTCTTA
LF3	CTTGATGAGAGTGGT
LR1	GCCGTTCCAAATCCAGTTC
LF1	GAATGCTTTGGGTGACCTC
Actin F	GTGCTAACGAATACAGTTCACG
Actin R	CCAGCAGATGTGGATTTCAAAG
LAS11	CCGGCCACCGAGCTGCTGCTCTCGACAAA
LAS14	GGATAAAAAGGAAGAAGGGTTTTGACAGAG
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 / (+)	*cis*-acting element conferring high transcription levels
2	AAGAA-motif	GAAAGAA / (-)	
3	ACE	GCGACGTACC / (-)	*cis*-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 / (-)	*cis*-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 (-/+)	*cis*-acting element involved in low-temperature responsiveness
10	Skn-1_motif	GTCAT / (-)	*cis*-acting element required for endosperm expression
11	TCA-element	CCATCTTTTT / (-)	*cis*-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

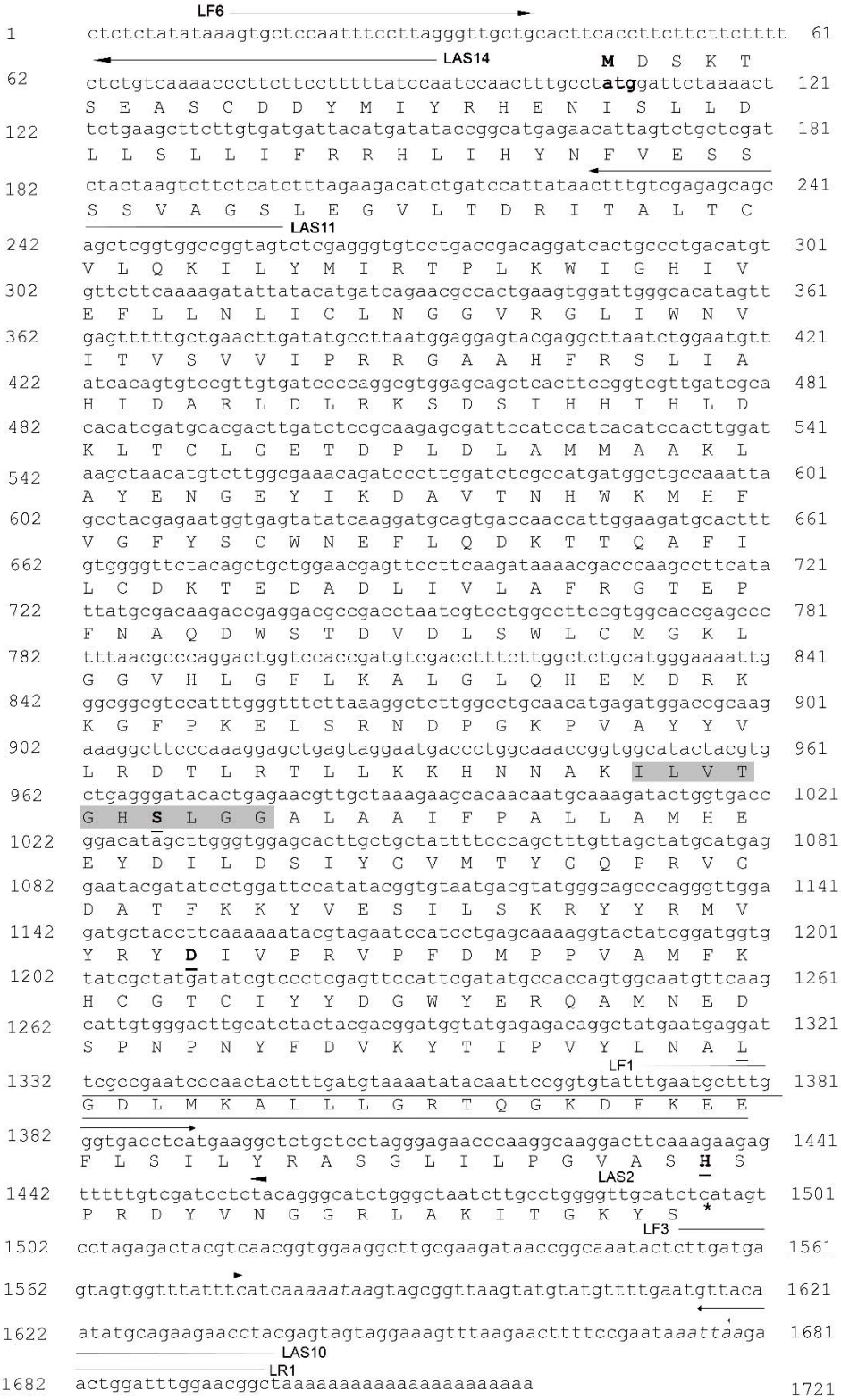

Fig. 1 Suppl. Nucleotide and inferred amino acid sequences of *FLL1*. The nucleotide sequence is shown in lower case letters, whereas the amino acid sequence is in capital letters. Numerals at both ends of the nucleotide row indicate a nucleotide number. The first start codon (atg) is *bold* and the 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*.

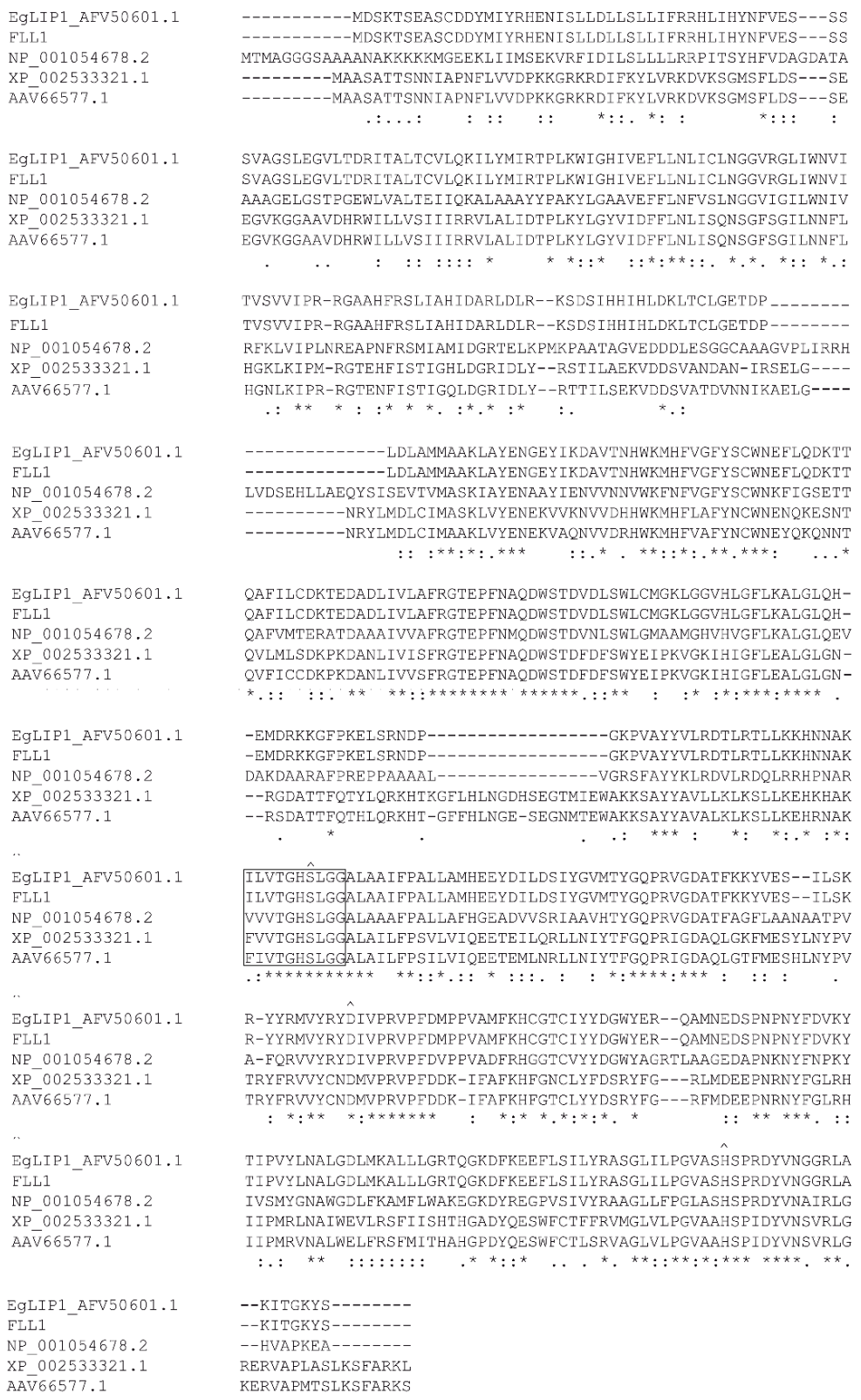

Fig. 2 Suppl. Multiple sequence alignment of FLL1 against the top four *BLASTX* hits in the *NCBI* sequence database. The ':' denotes conservation of strong groups. The '.' denotes conservation of weak groups, whereas those without any symbol denote no consensus (*CLUSTWALW*, Biology Workbench Version 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 '^'.

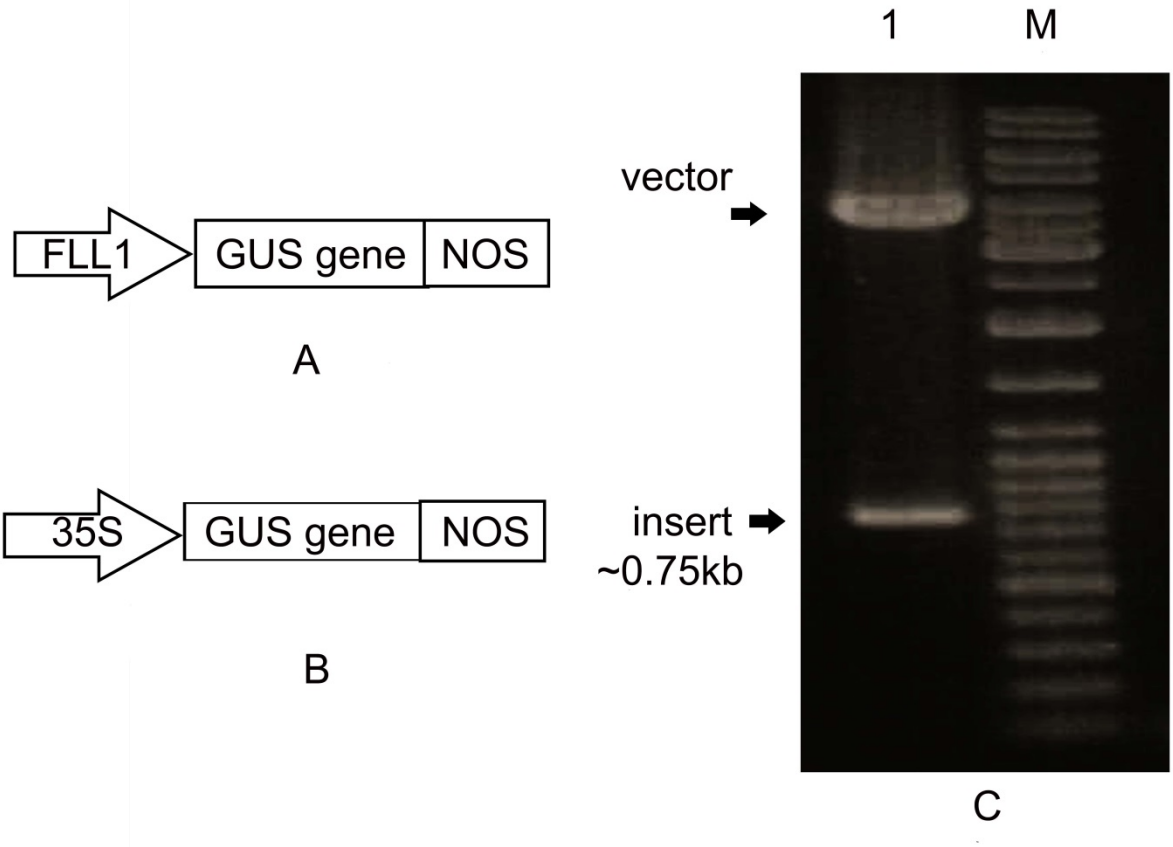

Fig. 3 Suppl. A schematic diagram of the FLL1GUS plasmid (*A*), pBI221 plasmid (*B*), and HindIII-Xba1 digestion of a transformation vector pBI221 carrying the FLL1 promoter on 1 % (m/v) agarose gel electrophoresis (*C*).