Table 1 Suppl. Sequences of oligonucleotide primers used in this study. The 5' end of the primers was extended with 8 bp to generate a *Sph*I digest site in the forward primers and a *Bgl*II digest site in the reverse primers (*in bold italics*). *GUS* - *β-glucuronidase*, TAIL - thermal asymmetric interlaced.

Primer	Sequence	Usage
SP1	AGAGCAACTTCAGCATCGCAGAGGAC	TAIL PCR
SP2	CCTTCGCTTAGCAAACGTGACCTGAC	
SP3	GTTCAACTCGTCCTCTCCCCATTCT	
pPlacSEP1.1FL	G*GCATGC*CACTAATATAAGCACAGAA	*GUS* fusion vectors construction
pPlacSEP1.1D1	A*GCATGC*CGTTCATTTTGCTTCCTTTG	
pPlacSEP1.1D2	G*GCATGC*ATGGGTTTAGCAATGAGTGT	
pPlacSEP1.1D3	T*GCATGC*ACATCAACCATTTCCCCAT	
pPlacSEP1.1D4	G*GCATGC*GGACCTGTGGTTGTGGGGCT	
pPlacSEP1.1D5	C*GCATGC*ACCAGGGCGTTAAATG	
pPlacSEP1VR	TC*AGATCT*ACTCGTCCTCTCCCCAT	
BarnaseVF	CC*AGATCT*CAGGTTATCAACACGTT	*pPlacSEP1::Barnase-Barstar* and
BarstarVR	C*GGTGACC*ATATTGTTCATCTCCCATT	*pPlacSEP1::Barnase-mic35S-Barstar* construction
35SVF	C*TCTAGA*CGTAAGGGATGACGCACAAT	*Barnase-mi35S-Barstar* construction
35SVR	TCACCAGTCCCCCGTGTTCTCTCC	
1303R	CTGAATGCCCACAGGCCGTCGAGTT	plasmid verification
pPlacSEP1VF	GGCAGTGACATTGGCTCCATCTAAG	transgenic plants verification
GUSVR	TGTAGAGCATTACGCTGCGATGGATT	

Table 2 Suppl. Putative *cis*-elements identified in the *Platanus acirifolia SEPALLATA1* promoter sequence.

Motif	Sequence	Distance from ATG	Function
CAAT-box	CCAAT/CAAT/CAATT	-561,-569,-585,-868,-988, -1,149,-1,210,1,220,-1,390, -1,424,-1,813,-1,924,-1,998, -2,035, -2,085	common cis-acting element in promoter and enhancer regions
TATA-box	TATAAT/TATA	-4,-7,-320,-457,-548,-558,-592, -874,-1,130,-1,144,-1,331, -1,921,-1,981,	core promoter element for transcription start
A-box	CCGTCC	-435	*cis*-acting regulatory element
ACE	GACACGTTTG	-378	light responsive element
Box I	TTTCAAA	-251	
GT1-motif	GGTTAA	-738,-772	
I-box	AAGATAAGA/GATAAGG	-277, -480	
GAG-motif	GGAGATG	-652,-1,684	
G-Box	CACGTT	-380	
IBOXCORE	GATAA	-30,-279,-482,-1,535	conserved sequence upstream of light-regulated genes
ARE	TGGTTT	-356	*cis*-acting regulatory element essential for the anaerobic induction
CGTCA-motif	CGTCA	-665	MeJA-responsiveness element
TCA-element	GAGAAGGATA/GAAGAAGAAG	-31, -40, -55, -58	salicylic acid responsiveness element
GAREAT	TAACAAR	-26,-1,108,-1,613	gibberellin-responsive element
GARE-motif	AAACAGA	-450, -826	
ARFAT	TGTCTC	-781	auxin responsive element
MBS	TAACTG	-313,-512	MYB binding site involved in drought response
HSE	AAAAAATATC	-263	heat stress responsiveness element
TC-rich repeats	AATTTCTTCA	-1,284	*cis*-acting element involved in defense and stress responsiveness
GATABOX	GATA	-31,-280,-483,-1,040, -1,049,-1,536	tissue specific expression element
CCGTCC-box	CCGTCC	-435	meristem specific activation element
CARGCW8GAT	CTAATATAAG	-546	*cis*-acting element in promoter of MADS-box genes
POLLEN1LELAT52	AGAAA	-96,-208,-275,-411,-525, -538,-616,-622,-762,-795, -816,-971,-1,381,-1,526, -1,899	motif required for pollen specific expression in tomato
GTGANTG10	GTGA	-116,-925,-1,572	
Skn-1_motif	GTCAT	-664, -1694, -1847	*cis*-acting regulatory element required for endosperm expression
PROLAMINBOXOSGLUB1	TGCAAAG	-420	
DOFCOREZM	AAAG	-24,-94,-173,-207,-225,-283,-367,-420,-427,-524,-619, -625,-680,-765,-792,-798, -1,082,-1,297,-1,378,-1,384,-1,510,-1,539, -1,843,-2,113	core site required for binding of endosperm specific proteins
SEF1MOTIF	ATATTTAWW	-1,124	soybean embryo factor
ACGTCBOX	GACGTC	-1,989	seed development relate element
UP1ATMSD	CCCATT	-2,010	regulate gene expression during initiation of axillary bud outgrowth
XYLAT	ACAAAGAA	-1,382	xylem development regulatory elements
L1BOXATPDF1	TAAATGYA	-1,852	trichome specific regulatory elements
WBOXATNPR1	TTGAC	-341,-2,063	negative regulatory elements
WBOXNTERF3	TGACY	-923,-1,458,-2,062	
WRKY71OS	TGAC	-115,-341,-924,-1,036, -1,459,-1,796,-2,063	