

Table 1 Suppl. Primers used in real time quantitative PCR. F - forward, R - reverse, E - amplification efficiency.

Primer name	Primer sequence (5'-3')	E [%]	R^2	Slope
<i>BrEXL6</i>	F: AGAGTTGTACCCGCTTAT R: GTCGCATTCTTTAGTTTC	95.9 %	0.999	-3.424
<i>Brlact7</i>	F: CGAAACAACCTTACAACCTCA R: CTCTTTGCTCATAACGGTCA	100.9 %	0.999	-3.301

Table 2 Suppl. *BLASTX* analysis of full-length cDNA sequence of candidate gene.

Accession No.	Description	Query coverage [%]	E-value	Max ident. [%]
NP_177721.1	GDSL esterase/lipase EXL6 [<i>A. thaliana</i>] AT1G75930	97	1.00E-178	74
NP_001077830.1	GDSL esterase/lipase EXL5 [<i>A. thaliana</i>] AT1G75920	97	3.00E-145	61
XP_002887620.1	family II extracellular lipase 5 [<i>A. lyrata subsp. lyrata</i>]	96	2.00E-136	58
NP_177719.1	GDSL esterase/lipase EXL4 [<i>A. thaliana</i>] AT1G75910	95	5.00E-124	56
XP_002887493.1	GDSL-motif lipase. [<i>A. lyrata subsp. lyrata</i>]	97	3.00E-95	46
NP_173764.1	GDSL esterase/lipase [<i>A. thaliana</i>] AT1G23500	89	2.00E-93	50
NP_001117318.4	GDSL-like lipase. [<i>A. thaliana</i>] AT1G20135	92	2.00E-90	48
NP_201122.1	GDSL esterase/lipase [<i>A. thaliana</i>] AT5G63170	96	1.00E-88	44
AAF79900.1	anther-specific proline-rich protein APG [<i>A. thaliana</i>]	89	7.00E-82	48
XP_003629270.1	GDSL esterase/lipase [<i>M. truncatula</i>]	92	6.00E-69	40
AAM64323.1	APG precursor [<i>A. thaliana</i>]	88	9.00E-68	39
XP_002279353.2	EXL3-like [<i>V. vinifera</i>]	92	2.00E-67	38
XP_003544387.1	EXL3-like [<i>G. max</i>]	91	2.00E-66	40
XP_003566161.1	GDSL esterase/lipase At2g31550-like [<i>B. distachyon</i>]	89	2.00E-65	37
NP_001150904.1	APG precursor [<i>Z. mays</i>]	91	4.00E-65	37
XP_003603778.1	GDSL esterase/lipase [<i>M. truncatula</i>]	88	6.00E-63	39
XP_003603782.1	EXL3 [<i>M. truncatula</i>]	86	2.00E-62	38
NP_001055799.1	lipase/hydrolase [<i>O. sativa Japonica Group</i>]	87	3.00E-62	38
XP_003527440.1	GDSL esterase/lipase EXL3-like [<i>G. max</i>]	91	3.00E-62	37
XP_002510573.1	zinc finger protein [<i>R. communis</i>]	87	9.00E-62	39
XP_003567248.1	GDSL esterase/lipase At2g40250-like [<i>B. distachyon</i>]	86	3.00E-61	36
ACG32957.1	APG precursor [<i>Z. mays</i>]	92	3.00E-61	37
CAA42925.1	APG [<i>A. thaliana</i>]	89	1.00E-58	37
XP_003564518.1	GDSL esterase/lipase At1g58430-like [<i>B. distachyon</i>]	93	2.00E-58	36

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1   AATTGTCGATATGTTAAGGGAAAAGATATTGGTGTTAACATTATTTTCGATTATTGCCTTTCATCAGCGGCTGG
1   M L R E K I L V L T L F S I Y C L S S A A G
76  ACAAACAAATCCTTTCTGCACTTTTCGCTTTTGGAGATTCAATACTAGATACTGGTAACAATAATCGCTTTCT
26  Q N K S F S A L F A F G D S I L D T G N N N R L L
151 TACTTACTCAAGGGAAATTTTGGCCATATGGTTGGAACATGACTATAAGATACCGACGGGCAGATTGGAAA
51  T L L K G N F W P Y G W N Y D Y K I P T G R F G N
226 TGAAGAGTTTTCACCGATATGGTTGCTCAAGAGTTGGGGTGAAAAGAGTTGTACCCGCTTATCGCAGGTTGCG
76  G R V F T D M V A Q E L G V K R V V P A Y R R L R
301 TCGCATCAAGCCCGACGACCTTAAACTGGCGTTTGTTCGCATCAGGTGGTTCAGGAATTGACCATCTTACATC
101 R I K P D D L K T G V C F A S G G S G I D H L T S
376 CAGAACACTGGGAGTTTGTCCACAGGCGACCAATAGGAGATTTCAAAAATATTTGAAGAACTAAAGAATGC
126 R T L G V L S T G D Q I G D F K K Y L K K L K N A
451 GACGAAAAATAAGAAAGAAATGAAAAAATAATTTCAAACGCAGTGTTTCTTATTCTGAAGGAAATAACGATAT
151 T K N K K E M K K I I S N A V F L I S E G N N D I
526 TGGATATTCGTGACTCCCGCTCGTCTACGATTACGATCCATAGATACATACACAAGTGACATGGTTTTTTGGAC
176 G Y F V T P A R L R L R S I D T Y T S D M V F W T
601 AAAAGCATTCCACAAGATTATATGATCTTGGAGCGAGAAAATTCGCGGTGATGGGAGTGATTCCGGTAGGATG
201 K A F L Q D L Y D L G A R K F A V M G V I P V G C
676 CTTGCCTTTCCATCGCTTCCTATTGGTGGAGTATTCGCATGGTGTAACTTCATGATGAATAGAATTCGGAAGA
226 L P F H R F L F G G V F A W C N F M M N R I S E D
751 CTTCAACACAAAATTACAGAAAAGCTCTTATTGGTTACGAAGTAGAAAAAGTTTTAAAGGTGCAAAGTTTGTTTA
251 F N T K L Q K A L I G Y E V E K S F K G A K F V Y
826 CGTCGACATGTACGGCTCTATTATGGATCTTATCAACCATCCTAAGGCCCTATGGGTTTACAGAAGCGAAAAGATC
276 V D M Y G S I M D L I N H P K A Y G F T E A K R S
901 GTGTTGTGTATGGTGACATCGATAATACCATGCCGAAACCCGGATGAGTACGTATTCTATGACTTCGCTCACCC
301 C C C M V T S I I P C R N P D E Y V F Y D F A H P
976 CACCATGAAAACCTATGAAGTAATATCTAAACCTCTTGTCTATCAGATGAGGAAAGGCCTTGATGATTTAGTTC
326 T M K T Y E V I S K P L V Y Q M R K G L A *
1051 CTTG

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Fig. 1 Suppl. Nucleic acid and amino acid sequences of the candidate gene. The signal peptide sequence is *underlined*. The GDSL-motif domain region is *boxed*. The differentially expressed fragment from the subtractive cDNA library is *shadowed*. The primers for full-length cDNA are *double underlined*. The primers for RT-qPCR are indicated with *arrowed lines*.

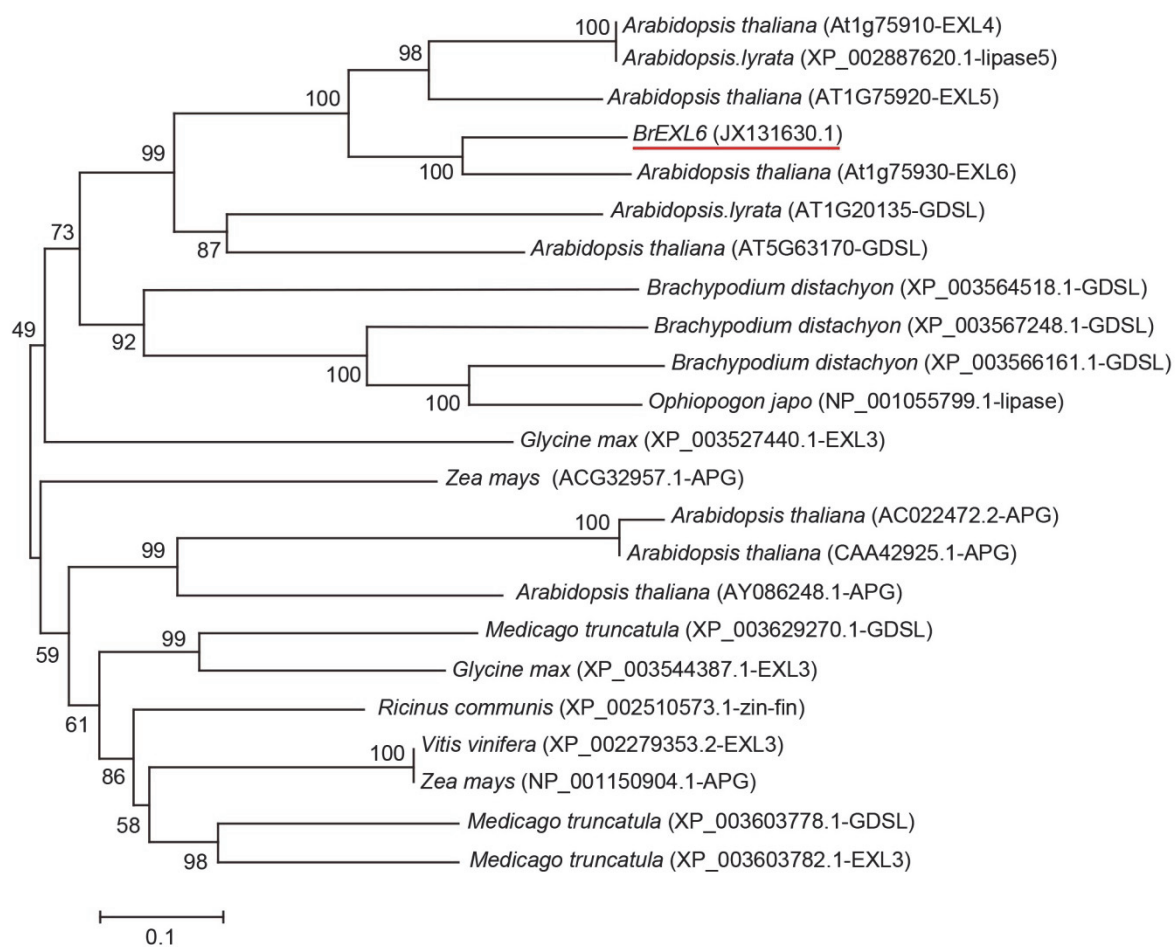


Fig. 2 Suppl. Phylogenetic analysis of *BrEXL6* based on amino acid sequences in various plants. Numbers on the tree represent confidence values from the bootstrap test (1 000 replicates).