Table 1 Suppl. Fluorescence quantitative sequence of activity of bcl complex (ABC1) protein family PCR primers.

Serial number	Primer name	Sequence (5′-3′)	Tm [°C]	GC [%] (l00 μM)
c6383_g1	*Abc1*-l-F	GCTTGTACATCCCGCTGTTT	50.00	52.14
	Abc1-l-R	CACGATGTGTGGATTCTTCG	50.00	48.26
c15065_g1	*Abc1*-2-F	CAGCTCCCAAAAAGAAACCA	45.00	42.14
	Abc1-2-R	CGAGCAGAAGATCACACCAG	55.00	42.68
c13379_g1	*Abc1*-3-F	TTTTGGTTCCAAGGGTTCTG	45.00	49.48
	Abc1-3-R	ATCCGCATGAAAGAAACCAC	45.00	42.54
c9338_g1	*Abc1*-4-F	TCACCACACATTGCCCTTTA	45.00	50.03
	Abc1-4-R	TAAATGCTTGCGCAATTTGA	35.00	44.90
c22062_g1	*Abc1*-5-F	ATGGCAGTCTTCGGATTCAG	50.00	46.77
	Abc1-5-R	AGGAAGCAGTTCTCGAACCA	50.00	43.63
c21890_g1	*Abc1*-6-F	TTTTGCGAAGTTCAGCCTTT	40.00	49.65
	Abc1-6-R	CCGTTTGATTCCAGCACTTT	45.00	51.15
c12914_g1	*Abc1*-7-F	TTAACGGAATCCCGATCTTG	45.00	46.93
	Abc1-7-R	AGTCCAGCAGTGCAACCTCT	55.00	47.60
c22903_g2	*Abc1*-8-F	CGTGCTGTTGATGCTTCTGT	50.00	51.55
	Abc1-8-R	GGTCCGAGACGTGTGAAAAT	50.00	43.22
c22279_g1	*Abc1*-9-F	ACATTTGAGGCTGCATACCC	50.00	47.26
	Abc1-9-R	CAGCATCTCTGTCCGTTTGA	50.00	50.40
c22062_g2	*Abc1*-l0-F	CACGTCAAGGAAGGTTCTTACA	45.45	40.52
	Abc1-l0-R	CATTGCCTTGTGGTGTGATT	45.00	49.48
c8932_g2	*Abc1*-11-F	GGAACCACAGTCCTTCAACC	55.00	47.00
	Abc1-11-R	ACGCCTCTGCTTTCTACCTG	55.00	53.79
c10431_g1	*Abc1*-l2-F	CGTGGACTCAGGTTGAGACA	55.00	44.78
	Abc1-l2-R	ATTCTCGGCTTTGGACAGAA	45.00	45.98
c22596_g1	*Abc1*-l3-F	AGGCCAGAATTACGTGATGG	50.00	43.22
	Abc1-l3-R	CCTAAGTCGCCAAGCAAGTC	55.00	46.15
c22316_g1	*Abc1*-l4-F	ACTGAGCACGAGACCAGACA	55.00	42.68
	Abc1-l4-R	TGTCCAGAATGCAGATGAGC	50.00	44.05
c19216_g1	*Abc1*-l5-F	CCGGATATTCCCATCATTTG	45.00	49.48
	Abc1-l5-R	TCCATGAACTCCATCGTCAA	45.00	47.42
c20945_g2	*Abc1*-l6-F	GCGGCTTAGTAGTGCCTGAC	60.00	47.94
	Abc1-l6-R	ACCTGGACCCATAGCACTTG	55.00	47.60
c23357_g1	*Abc1*-l7-F	AGCCGGCGGGTACTTACTAT	55.00	47.10
	Abc1-l7-R	GGGATATCCGACCAACAATG	50.00	43.63
c21106_g1	*Abc1*-l8-F	GCGAGATCTAAGTCGCCAAT	50.00	44.92
	Abc1-18-R	ACTCATCGGATTCCACAGGT	50.00	47.26
c8932_g1	*Abc1*-19-F	GTTGAGGCATTTCCAGAGGA	50.00	44.48
	Abc1-19-R	TCCTGGCCATGGGTATAGTC	55.00	48.61
c18258_g1	*Abc1*-20-F	GCAGAAAGATTGGCTCTTGG	50.00	44.48
	Abc1-20-R	AGTCAGCTTCGATTGCCAGT	50.00	47.76
c21578_g1	*Abc1*-2l-F	GGTCCATCGAACTCTGGAAA	50.00	44.92
	Abc1-2l-R	CCACTGGCTCCTCTTCAAAC	55.00	51.36
	β-actin-F	CCAAAGGCCAACAGAGAGAAGAT	47.83	35.10
	β-actin-F	TGAGACACACCATCACCAGAAT	45.45	39.81

Table 2 Suppl. Karyotic ortholog group classification of activity of bcl complex (ABC1) protein family genes of *Lepidium apetalum.*

Transcript sequence	KOG ID	Acronym for the KOG class	KOG description
c6383_g1	KOG1236	R	General function prediction only
c13379_g1	KOG1236	R	
c22062_g1	KOG1235	R	
c21890_g1	KOG1235	R	
c12914_g1	KOG1235	R	
c22903_g2	KOG1235	R	
c22279_g1	KOG1235	R	
c21578_g1	KOG1236	R	
c22596_g1	KOG1235	R	
c22316_g1	KOG1235	R	
c19216_g1	KOG1235	R	
c20945_g2	KOG1235	R	
c23357_g1	KOG1235	R	
c21106_g1	KOG1235	R	

Table 3 Suppl. Wilting seedlings treated with different concentrations of NaCl and different stress duration. Slightly yellow and curly leaves were thought to be wilted. Rew - seedling recovery at 0 mM NaCl for 12, 24, and 48 h after 48-h salt stress.

NaCl [mM]	0	1	6	12	24	36	48	Rew 12	Rew 24	Rew 48
0	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %
50	0 %	8 %	16 %	7 %	6 %	0 %	0 %	0 %	0 %	0 %
100	0 %	28 %	34 %	20 %	20 %	0 %	0 %	0 %	0 %	0 %
150	0 %	32 %	39 %	26 %	25 %	0 %	0 %	0 %	0 %	0 %
200	0 %	40 %	40 %	37 %	36 %	0 %	0 %	0 %	0 %	0 %
250	0 %	60 %	63 %	48 %	37 %	12 %	0 %	0 %	0 %	0 %
300	0 %	72 %	86 %	53 %	48 %	19 %	0 %	0 %	0 %	0 %

Table 4 Suppl. Wilting seedlings treated with different concentrations of polyethylene glycol (PEG) 6000 for different stress duration. Slightly yellow and curly leaves were thought to have wilted. Rew - seedling recovery at no PEG 6000 for 12, 24, and 48 h after 48-h osmotic stress.

PEG [%]	0	1	6	12	24	36	48	Rew 12	Rew 24	Rew 48
0	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %
10	0 %	10 %	13 %	38 %	21 %	0 %	0 %	0 %	0 %	0 %
15	0 %	12 %	48 %	72 %	78 %	14 %	0 %	0 %	0 %	0 %
20	0 %	13 %	57 %	82 %	85 %	20 %	13 %	0 %	0 %	0 %
25	0 %	25 %	60 %	78 %	88 %	70 %	53 %	26 %	12 %	12 %
30	0 %	27 %	78 %	88 %	91 %	75 %	53 %	47 %	18 %	18 %

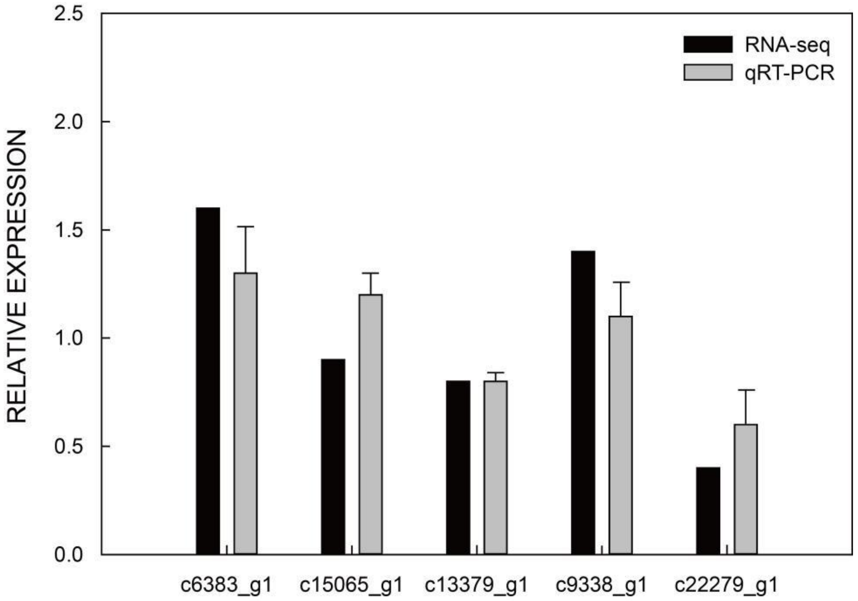

Fig. 1 Suppl. Verification of the transcriptome by quantitative reverse transcription PCR; RNA-seq - transcriptome sequencing, RT-qPCR - real-time quantitative PCR.

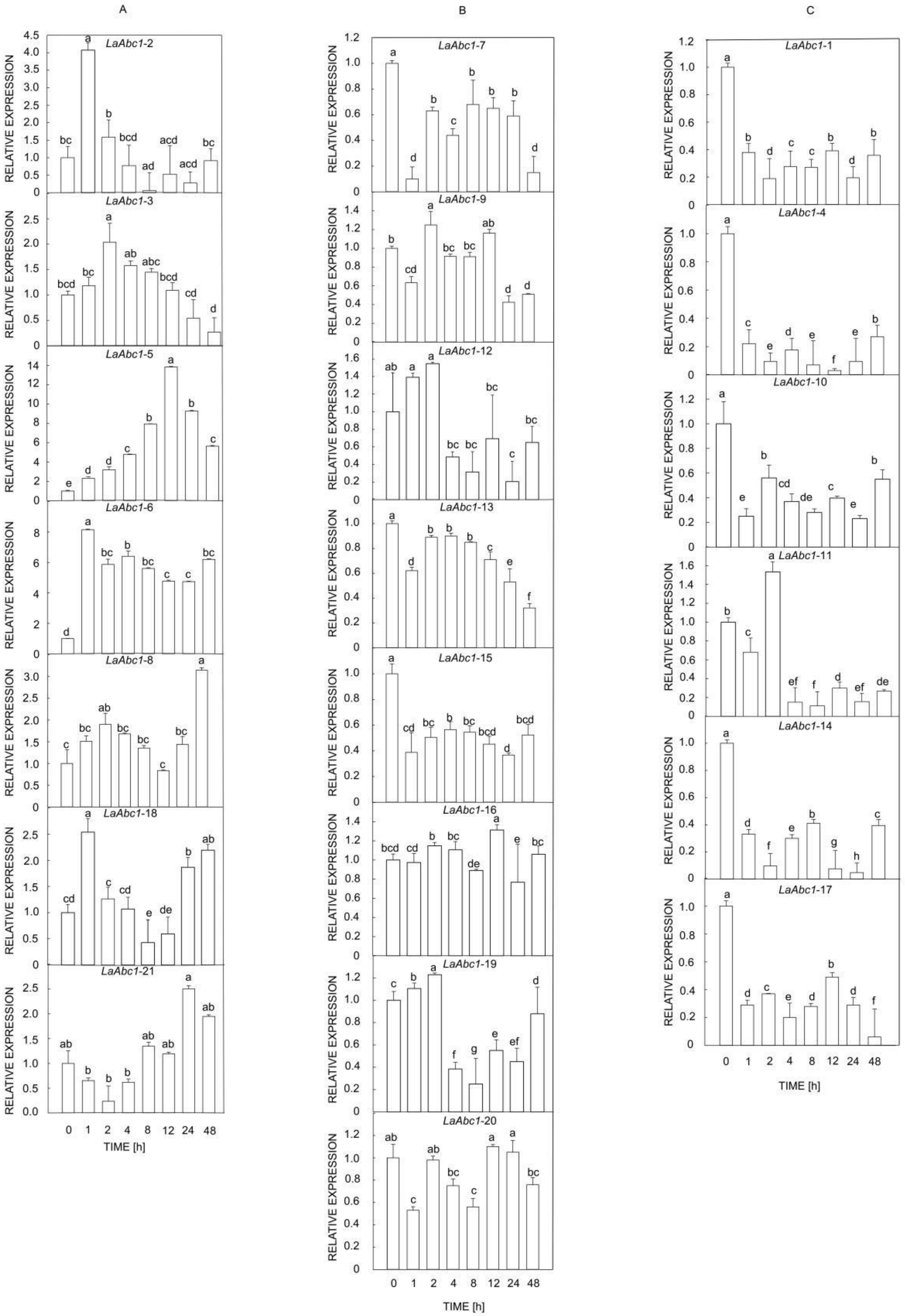

Fig. 2 Suppl. Regulated expression characteristics of *Lepidium apetalum activity of bcl complex* (*LaAbc1*) at 0 °C treatment. *A* - up-regulated expression, *B* -no significantly different expression, *C* - down-regulated expression. Means ± SEs, $n = 3$; different letters indicate significant differences among treatments based on the least significant difference at $P \leq 0.05$.

atgcatgggttcgatttcaaagcgattcgtgagaagatctccgagagctttcttccatggtaacgatcctttcggttctgggttcgagctaccgatatttacactggctacaaggtgttt

M H G F D F K A I R E K I S E S F L P W * R S F R F W V R A T D I Y T G Y K V F

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Q L R V S L V K D A K K Q E E M W E R Q H E Q A A D K I Y F M C S D L G G F F L

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L R D M V T K G V L V M E Y I N G I P I L S L G D E M A K R G I N P H G K I T E

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A A K L N I L N A I S R A Y G Q M I L K S G F F H A D P H P G N I L I C E G P E

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V A L L D Y G Q V K E L P D N L R L G Y A N L V I A M A D N N S S R V S Q S F G

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Fig. 3 Suppl. The sequence of cDNA and the putative amino acid sequence of *Lepidium apetalum activity of bcl complex LaAbc1-3*.

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K L S E I F E E F E E E P V A S G S I A Q V H R A S L R F Q Y P G Q K S K S S L

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V A V K V R H P G V G E S I R R D F V I I N L V A K I S T L V P A L K W L R L D

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K P H I V F L D V G M T A E L S K N D R E N L L E F F K A V A C R D G R T A A K

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C M H E L L E K V R R H K V N I D G N V R T V M V T T L V L E G W Q R K L D P G

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Y D V M H T L Q T M V M K T D W A K S L S Y T V D G L M A P *

Fig. 4 Suppl. The sequence of cDNA and the putative amino acid sequence of *Lepidium apetalum activity of bcl complex LaAbc1-21*.

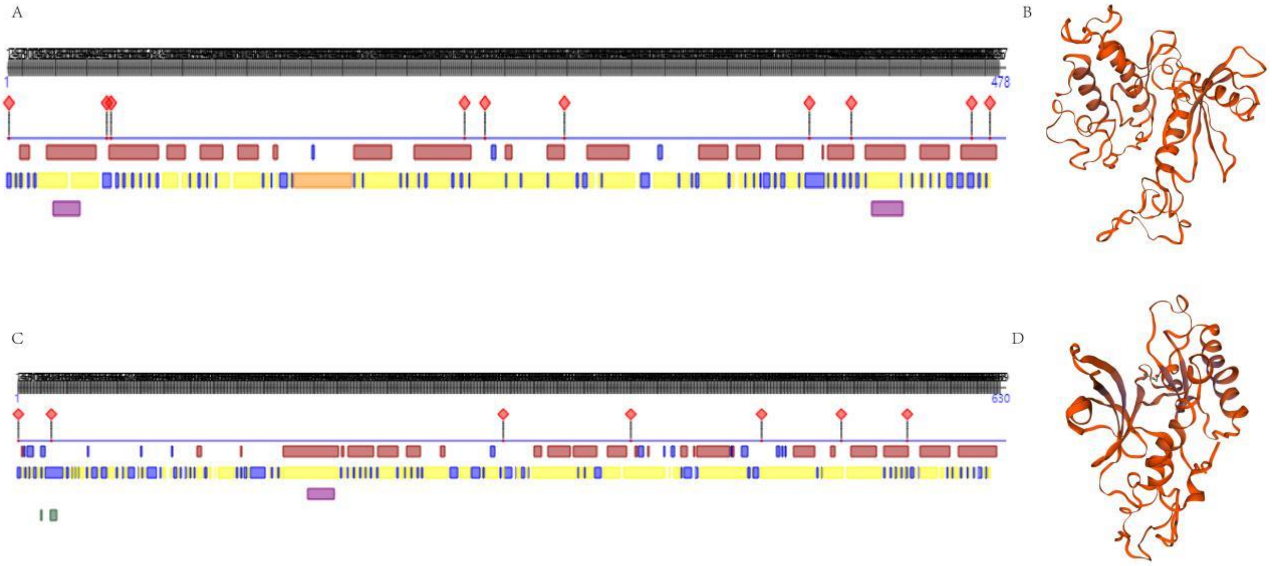

Fig. 5 Suppl. The predicted structure of *Lepidium apetalum* activity of bcl complex LaABC1 encoded protein. *A* - secondary structure prediction of *Lepidium apetalum* LaAbc1-3 encoded protein. *B* - tertiary structure prediction of *Lepidium apetalum* LaAbc1-3 encoded protein. *C* - secondary structure prediction of *Lepidium apetalum* LaAbc1-21 encoded protein. *D* - tertiary structure prediction of *Lepidium apetalum* LaAbc1-21 encoded protein.

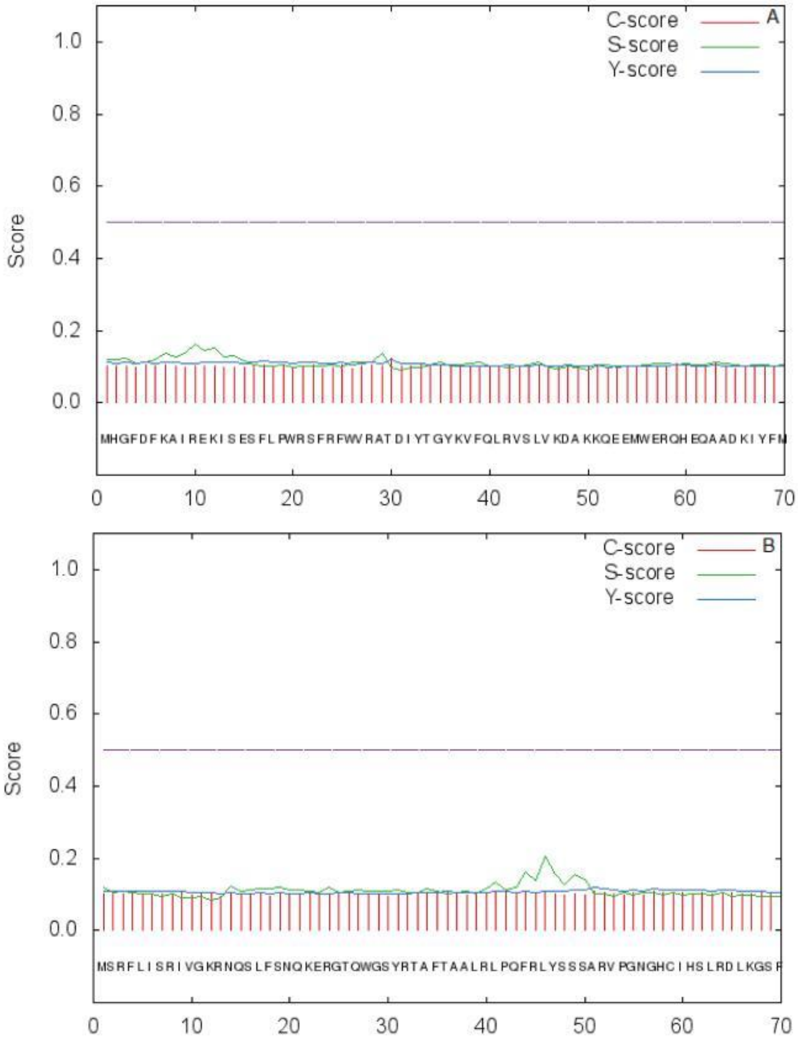

Fig. 6 Suppl. *A* - prediction analysis of a signal peptide in *Lepidium apetalum* activity of bcl complex LaAbc1-3. *B* - prediction analysis of a signal peptide in *Lepidium apetalum* activity of bcl complex LaAbc1-21.

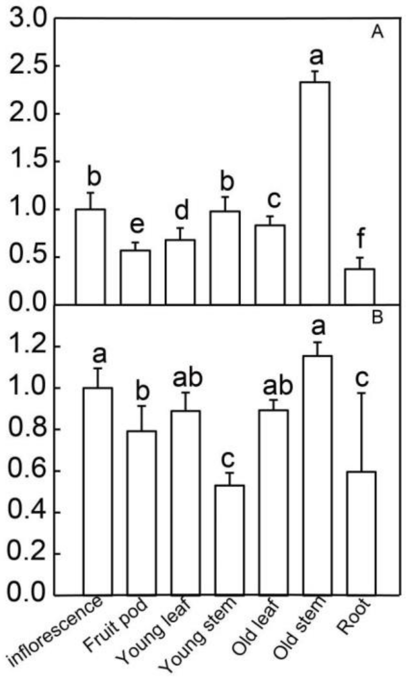

Fig. 7 Suppl. Analysis of specific expression of genes in different tissues of *Lepidium apetalum. A* - *L. apetalum activity of bcl complex* (*LaAbc1*)-3, *B* - *L. apetalum. LaAbc1*-21.