Supplementary Material

Molecular characterisation and expression profiling of *calcineurin B-like* (*CBL*) genes in Chinese cabbage under abiotic stresses

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Table S1. List of primers used in RT-PCR and Realtime PCR

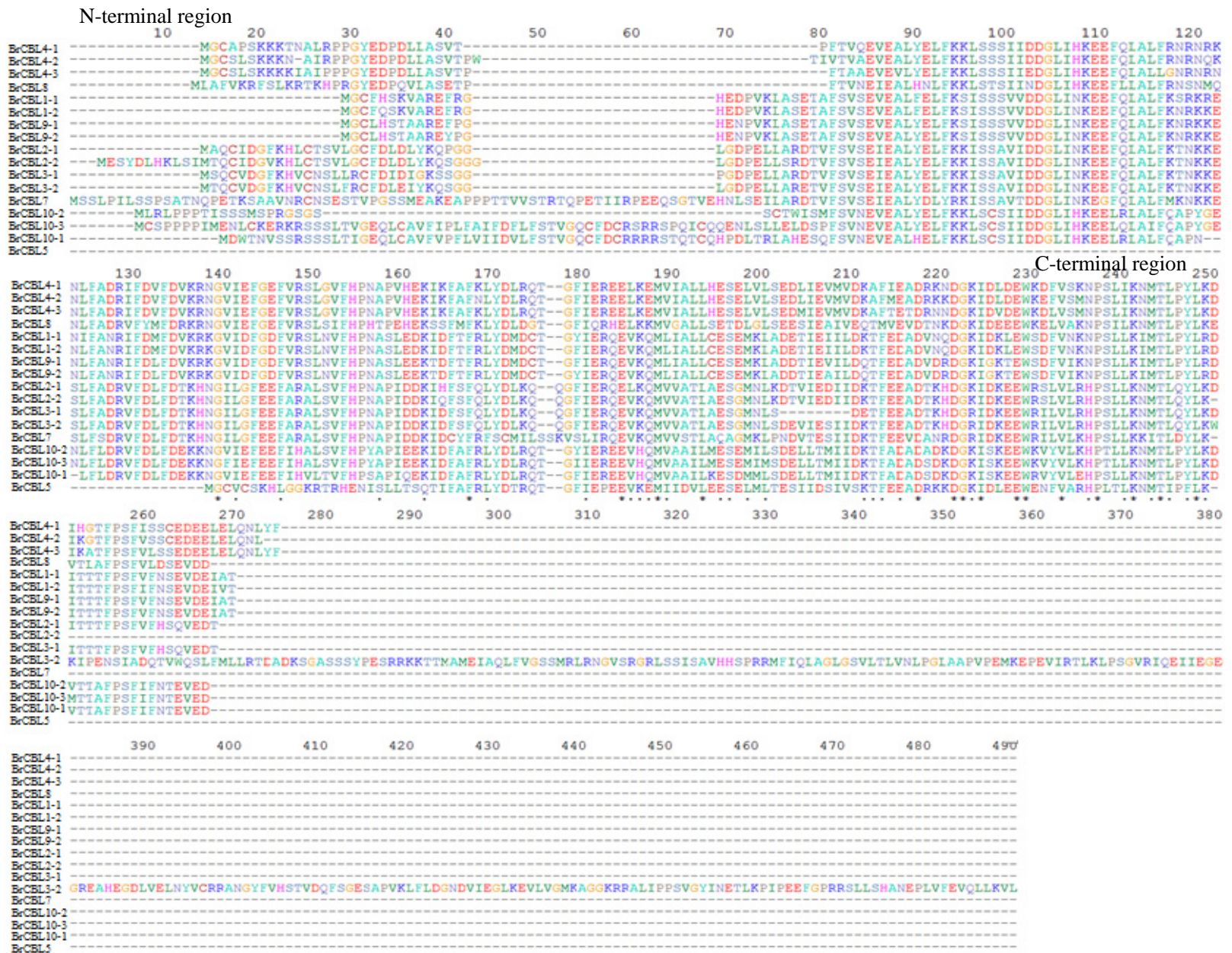| Gene name	Forward primer (5' → 3')	Reverse primer (5' → 3')	Product size (bp)
BrCBL1-1	TTCCGAGGACACGAAGACC	AATCGCTCCACTCTAGTTT	493
	TCGTGAACAAGAACCCATCA	TTGCAAACACTCGCTGGTC	150
BrCBL1-2	ACTGCCTTTAGTGTGAGTGAGG	ATCGCTCCACTCCAGTTTATC	453
	ACTGGAGTGGAGCGATTTTG	CGGAACTTGGTTTTGTTCGT	184
BrCBL2-1	TGCATTAAATCATGGCGC	AGCTTGGAAACGTAGTCGTG	660
	AAGCAGACACAAAACATGATGG	TCAACCTGAGAGTGGAACACA	151
BrCBL2-2	TTATCAATCATGACGCAG	TTCTTGAGAAGGCTAGGATGT	614
	ACAAGGAGGAGTTTCAGTTGG	GCATTGGGATGGAATACAGAGA	151
BrCBL3-1	ATTGATATAGGCAAATCTTCTG	TTATCGATCCTTCCGTCATG	470
	ACCAAACATGACGGAAGGA	GCCAAATTGCCTGCTCTAGT	183
BrCBL3-2	GAAGGAAGAAGACGACAATG	CATTGGTCCCAAGAAGATC	631
	TTTGGGTTCGGTCTTGACTC	CTTGAATCCTGACGCCACTT	116
BrCBL4-1	ACCATTTACGGTACAGGAAG	TAAATACGGTAACGTCATGTTC	502
	TGGAAAGATTTTGTGTCCAAGA	GCATGGATTACTCAGAAATATAGGTT	152
BrCBL4-2	AAGTGGAGGCTTTGTATGAA	GAAGCTGAGTCTTTTGATCG	618
	AGATGGTAATCGCGCTTCTT	CTTGCGATCAGCTTCCATAAAC	98
BrCBL4-3	CGTTTACGGCAGCAGAAGTTG	GGTTTTGCAACTCCAGTTC	562
	TGACGGGAAAATTGATGTAGA	ATTTTGGCAACCTGCATAGA	186
BrCBL5	CGGCTATATGATACTCGTCAGACTGG	AAGGATGCCTGGCCACAAAGTTCT	205
	GAGGTGAAAGAGATGATAATAGACG	GCCACAAAGTTCTCCCATTC	152
BrCBL7	TCGACTCGAACTCAGCCTGAAACA	AGAGAGCACGAGCAAACTCCTCAA	307
	GAAGCAAATGGTGGTTTCTACTC	CGCATCAACTTCCTCAAATGTC	100
BrCBL8	TTGAAGCGAACAAAGCATCCTCGC	TTGAGGTAGGGTAAAGTCATG	563
	GGAAACGAAACGGTGTGATTG	CCGGTTCCATCAAGGTCATAA	124
BrCBL9-1	CGAATAAGCTTCTTCTTGTTCG	GTGGTCGTTATGTCTCTCAG	635
	AACGTTAGCAACCAAGCTTTAC	CTCATGACCAGGAAACTCTCTG	149
BrCBL9-2	CAATCGTAGTAGTAAGCTTCTTC	TGGTCGTTATGTCCCTCAG	638
	AGCTTCTTCTTCGTTTTACTTGTCA	GAGGCTAGCTTGACAGGGTTC	100
BrCBL10-1	GACTGGACGAACGTTTCCTCTA	AGAAGTTCATCTGACAGCATC	551
	GCATCCCAGCTTGTTGAAG	ACAGCTAACAATGATCACCAACT	159
BrCBL10-2	GCTCCATATGGTGAGAACCTCT	GAGTCATATTCTTCAGCAAGG	376
	CCTTACCTCAAGGATGTGACG	GGAAACTGACAAAATCCAAAGC	103
BrCBL10-3	GCTTGATTCACAAGGAAGAG	TGTTGTTGTCTCAGTCCTCA	495
	AGCATCCGACCTTGTTGAAG	GCTACCTCACATTTACAACCTCA	167
BrActin	ATGGCCGAGGCTGATGACAT	AGCCTCGGTAAGAAGAACCG	410
	GGAATCCACGAGACAACCTATAA	TCCGCAATACCAGAGAACATAG	116

Table S2. Sequence relatedness of *Brassica rapa* CBL genes and *Arabidopsis thaliana* CBL genes amino acid sequence

Gene name	a	b	c	d	e	f	g	h	i	j	k	l	m	n	o	p	q	r	s	t	u	v	w	x	y	z	ab
AtCBL1 (a)	100																										
AtCBL2 (b)	61	100																									
AtCBL3 (c)	62	92	100																								
AtCBL4 (d)	59	53	53	100																							
AtCBL5 (e)	49	44	46	48	100																						
AtCBL6 (f)	51	70	69	46	40	100																					
AtCBL7 (g)	41	62	64	41	34	51	100																				
AtCBL8 (h)	53	52	53	61	44	45	34	100																			
AtCBL9 (i)	59	60	61	59	48	50	43	52	100																		
AtCBL10 (j)	53	57	57	53	41	46	45	52	56	100																	
BrCBL1-1 (k)	**98**	60	61	58	47	50	42	53	90	54	100																
BrCBL1-2 (l)	**95**	61	62	58	51	50	43	53	90	55	96	100															
BrCBL2-1 (m)	61	97	91	54	44	70	61	53	60	57	60	61	100														
BrCBL2-2 (n)	52	92	85	49	41	66	54	45	52	53	52	53	91	100													
BrCBL3-1 (o)	59	93	95	53	43	70	61	51	58	57	58	59	91	83	100												
BrCBL3-2 (p)	55	84	86	49	43	64	56	49	54	46	54	56	84	86	88	100											
BrCBL4-1 (q)	59	53	53	57	50	46	39	61	61	54	59	61	54	50	53	50	100										
BrCBL4-2 (r)	61	53	53	88	50	44	40	61	57	52	61	61	54	49	50	49	92	100									
BrCBL4-3 (s)	58	52	52	85	51	45	39	61	57	50	58	59	53	47	52	47	88	88	100								
BrCBL5 (t)	40	42	43	45	87	40	36	40	42	44	40	47	41	42	39	42	48	49	44	100							

BrCBL7 (u)	45	59	58	37	33	47	40	38	46	37	45	46	58	60	60	54	38	38	37	28	100					
BrCBL8 (v)	53	52	53	62	43	46	35	92	52	52	53	54	53	46	50	49	61	61	61	39	38	100				
BrCBL9-1 (w)	89	60	60	60	47	50	41	51	97	56	**90**	90	59	52	57	53	61	60	58	40	45	52	100			
BrCBL9-2 (x)	89	59	60	59	46	50	40	51	96	55	**90**	89	59	52	57	53	61	59	57	40	45	52	**98**	100		
BrCBL10-1 (y)	53	57	55	52	42	46	41	53	54	85	53	54	56	50	57	48	53	52	50	43	37	53	53	53	100	
BrCBL10-2 (z)	53	57	59	54	39	51	49	51	54	81	53	54	57	52	58	53	55	55	52	42	44	51	54	54	80	100
BrCBL10-3 (ab)	52	54	56	52	42	48	46	51	54	80	53	53	57	50	57	45	54	52	50	41	37	50	53	53	82	88	100

Fig. S1. Multiple alignment of all BrCBL proteins and Identical amino acids are asterisks. N and C terminal are indicated in figure.
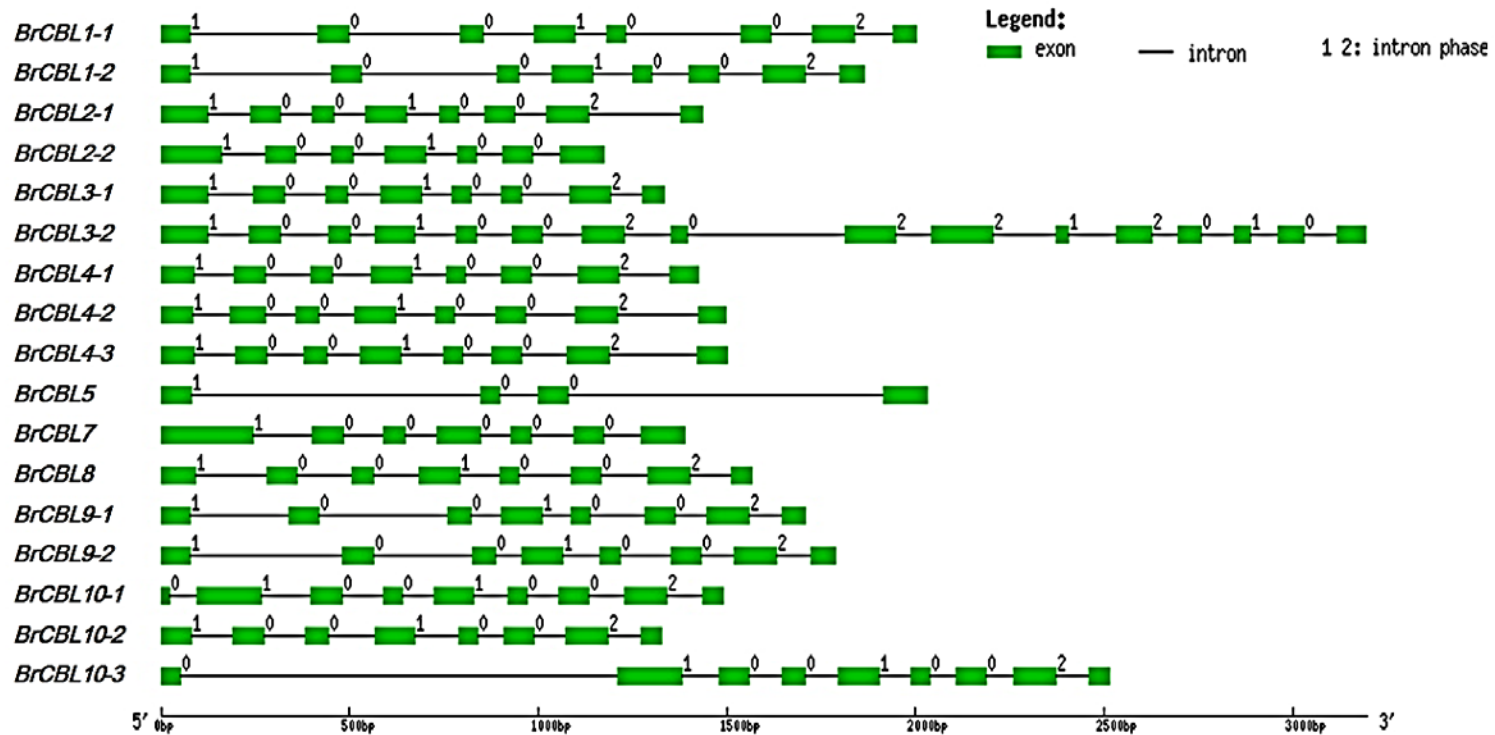
Fig. S2. Exon- intron structure of the 17 *CBL* genes in *Brassica rapa*. Horizontal bars indicate exons; horizontal lines indicate introns.
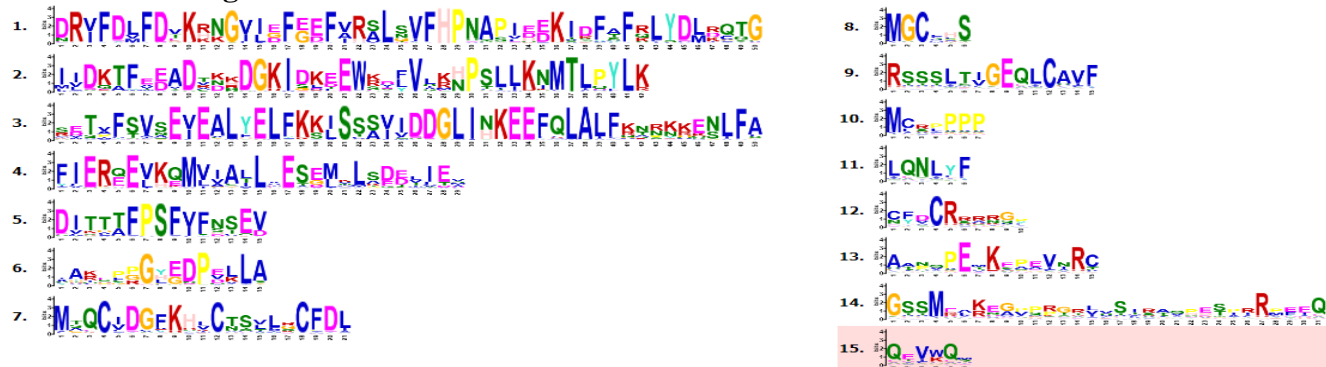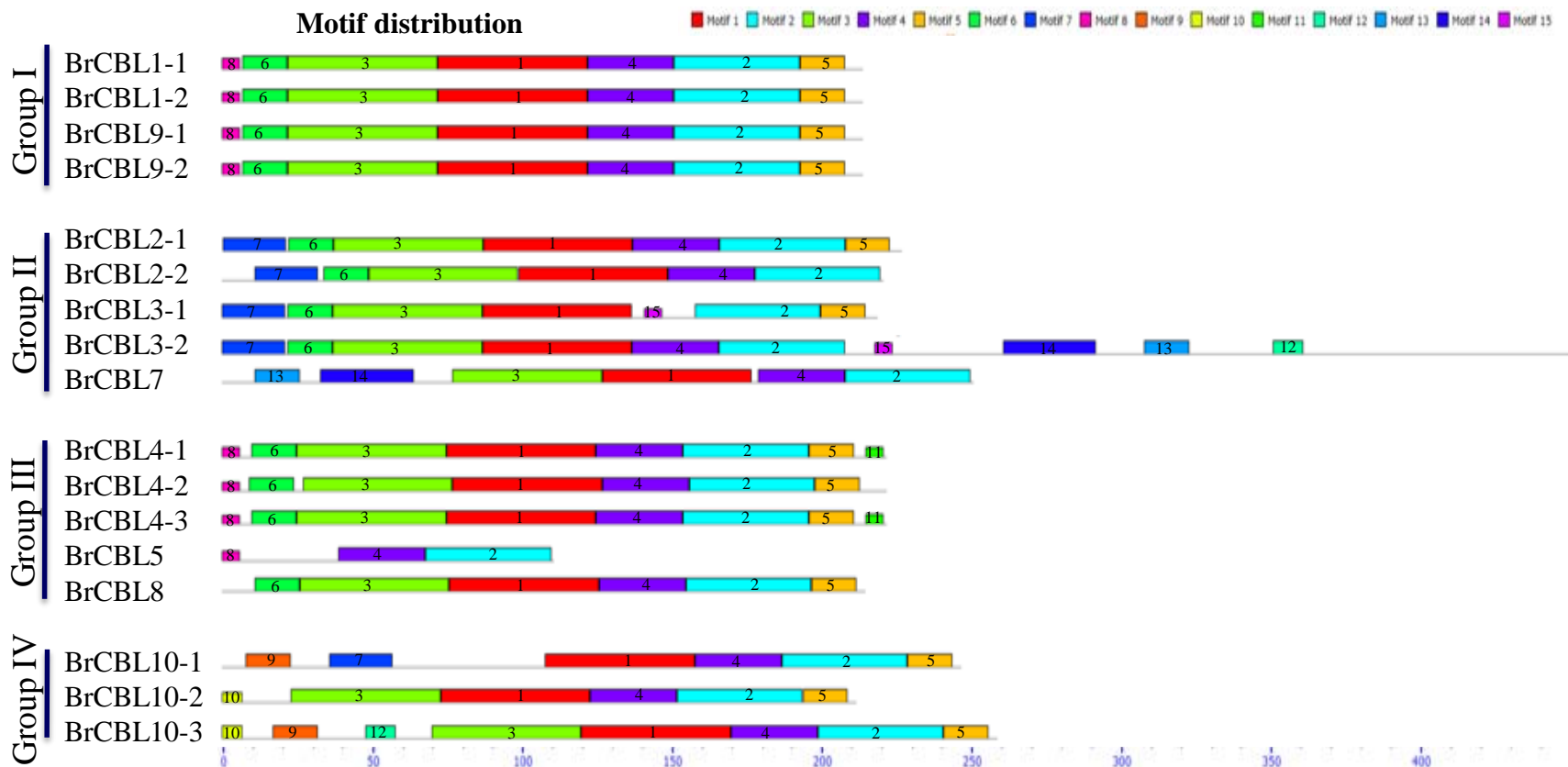
Fig. S3. Schematic representation of motif compositions in the BrCBL protein sequences. Different motifs, numbered 1–15, are displayed in different colored boxes. The names of all members are displayed on the left-hand side, while the length of motif is shown in scale at bottom of the figure and motif logo is shown in top of the figure.
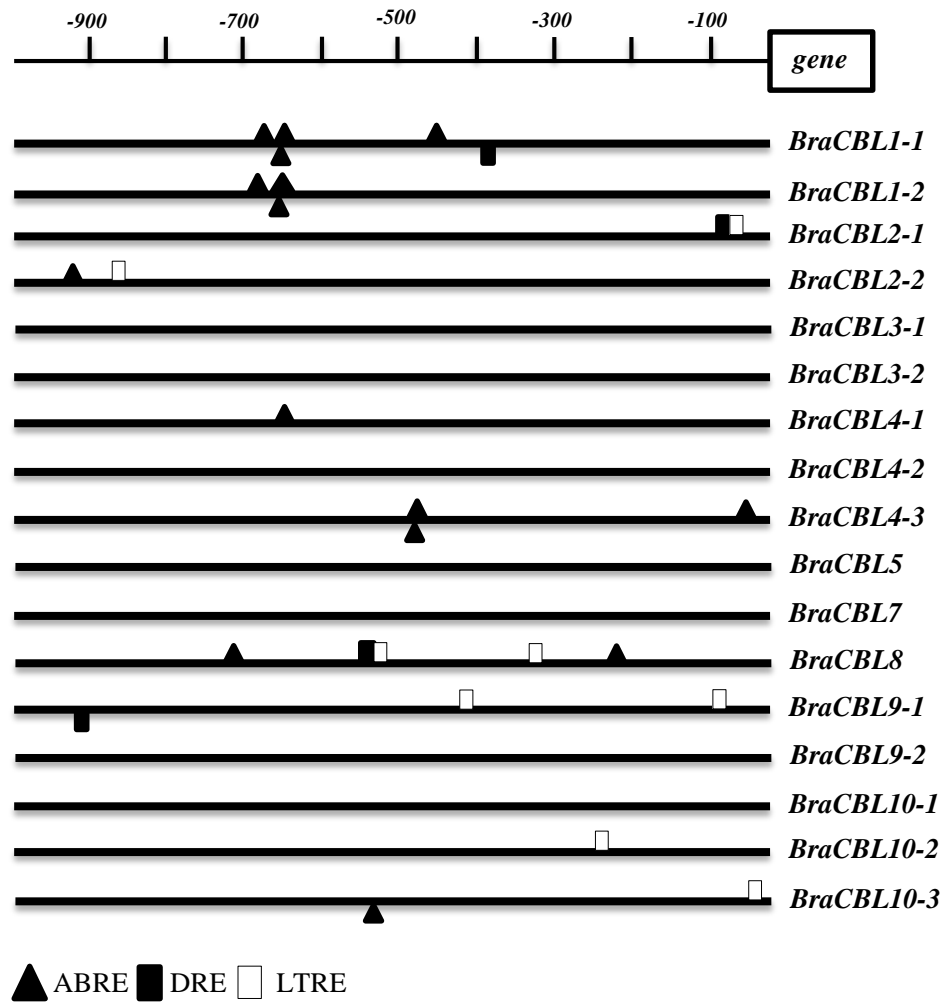
Fig. S4. Putative, ABRE, DRE and LTRE core sequences in the 1-kb promoter regions of the stress-inducible *BrCBL* genes. The lines represent promoter sequences. The elements located in the forward strand (sense strand of the gene) and the reverse strand, were indicated above and below the lines respectively.