Supplementary Material

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

Hee-Jeong Jung^A, Md. Abdul Kayum^A, Senthil Kumar Thamilarasan^A, Ujjal Kumar Nath^A, Jong-In Park^A, Mi-Young Chung^B, Yoonkang Hur^C and Ill-Sup Nou^{A,D}

^ADepartment of Horticulture, Sunchon National University, 255 Jungang-ro, Suncheon, Jeonnam 57922, South Korea.

^BDepartment of Agricultural Education, Sunchon National University, 255 Jungang-ro, Suncheon, Jeonnam 57922, South Korea.

^cDepartment of Biology, College of Biological Sciences and Biotechnology, Chungnam National University, Daejeon, South Korea.

^DCorresponding author. Email: nis@sunchon.ac.kr

Gene name	Forward primer $(5' \rightarrow 3')$	Reverse primer $(5' \rightarrow 3')$	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 S1. List of primers used in RT-PCR and Realtime PCR

Gene name	a	b	с	d	e	f	g	h	i	j	k	1	m	n	0	р	q	r	S	t	u	v	W	х	у	Z	ab
AtCBL1 (a)	10 0																										
AtCBL2 (b)	61	10 0																									
AtCBL3 (c)	62	92	10 0																								
AtCBL4 (d)	59	53	53	10 0																							
AtCBL5 (e)	49	44	46	48	$\begin{array}{c} 10\\ 0 \end{array}$																						
AtCBL6 (f)	51	70	69	46	40	10 0																					
AtCBL7 (g)	41	62	64	41	34	51	$\begin{array}{c} 10\\ 0 \end{array}$																				
AtCBL8 (h)	53	52	53	61	44	45	34	10 0																			
AtCBL9 (i)	59	60	61	59	48	50	43	52	10 0																		
AtCBL10 (j)	53	57	57	53	41	46	45	52	56	$\begin{array}{c} 10\\ 0 \end{array}$																	
BrCBL1-1 (k)	98	60	61	58	47	50	42	53	90	54	10 0																
BrCBL1-2 (1)	95	61	62	58	51	50	43	53	90	55	96	10 0															
BrCBL2-1 (m)	61	97	91	54	44	70	61	53	60	57	60	61	10 0														
BrCBL2-2(n)	52	92	85	49	41	66	54	45	52	53	52	53	91	10 0													
BrCBL3-1 (o)	59	93	95	53	43	70	61	51	58	57	58	59	91	83	10 0												
BrCBL3-2 (p)	55	84	86	49	43	64	56	49	54	46	54	56	84	86	88	10 0											
BrCBL4-1(q)	59	53	53	57	50	46	39	61	61	54	59	61	54	50	53	50	10 0										
BrCBL4-2 (r)	61	53	53	88	50	44	40	61	57	52	61	61	54	49	50	49	92	10 0									
BrCBL4-3 (s)	58	52	52	85	51	45	39	61	57	50	58	59	53	47	52	47	88	88	10 0								
BrCBL5 (t)	40	42	43	45	87	40	36	40	42	44	40	47	41	42	39	42	48	49	44	10 0							

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

BrCBL7(u)	45	59	58	37	33	47	40	38	46	37	45	46	58	60	60	54	38	38	37	28	10 0						
BrCBL8 (v)	53	52	53	62	43	46	35	92	52	52	53	54	53	46	50	49	61	61	61	39	38	10 0					
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	10 0				
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	10 0			
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	10 0		
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	10 0	
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	10 0

	N-terminal region									
	10	20	30 40	50	60	70	80	90	100 1	10 120
BrCBL4-1	MGC	APSKKKTNALRP	PGYEDPDLLAS	/T			PFTVQEV	EALYELFKKL	SSSIIDDGLIHK	EEFQLALFRNRNRK
BrCBL4-2 BrCBL4-3	MGC	SLSKKKN-AIRP	PGYEDPDLIAS	TPW			FTAREV	EALYELFKKI	SSSIIDDGLIHK	EEFQLALFENENQK EEFOLALLGNENEN
BrCBLS	MLAF	KRESLKRTKHP	RGYEDPOVLAS	TP			FTVNEI	EALHNLFKKL	STSIINDGLIHK	EEFLLALFRNSNMQ
BrCBL1-1			MGCFHSKVARE	RG		HEDPVKL	ASETAFSVSEV	EALFELFKSI	SSSVVDDGLINK	EEFQLALFKSRKRÊ
BrCBL1-2			MGCFQSKVARE	RG		HEDPVKL	ASETAFSVSEV	EALFELFKSI	SSSVVDDGLINK	EEFQLALFKNRKKE
BrCBL9-1 BrCBL9-2			MGCLHSTAARE	PG		HENPVKL	ASETAFSVSEV	EALYELFKSI	SSSVVDDGLINK	EEFOLALFKNRKKE
BrCBL2-1	MAQ	CIDGFKHLCTSV	LGCFDLDLYKQ	PGG		LGDPELL	ARDTVFSVSEI	EALYELFKKI	SSAVIDDGLINK	EEFQLALFKTNKKE
BrCBL2-2	MESYDLHKLSIMTQ	CIDGVKHLCTSV	LGCFDLDLYKQ	SGGG		LGDPELL	SRDTVFSVSEI	EALYELFKKI	SSAVIDDGLINK	EEFQLALFKTNKKE
BrCBL3-1 BrCBL3-2	MTO	CVDGFKHVCNSL	FRCFDIDIGKS	566		PGDPELL	ARDIVESUSEI	EALYELFKKI	SSAVIDDGLINK	EEFQLALFKTNKKE EEFOLALFKTNKKE
BrCBL7	MSSLPILSSPSATNOPE	TKSAAVNRCNSE	STVPGSSMEAK	APPPTTVVST	RTOPETIIRPEEC	SGTVEHNLSEIL	ARDTVFSVSEI	EALYDLYRKI	SSAVTDDGLINK	EGFQLALFMKNKKE
BrCBL10-2	MLRLPPPTIS:	SSMSPRGSGS				SC	TWISMFSVNEV	EALYELFKKL	SCSIIDDGLIHK	EELRLALFÇAPYGE
BrCBL10-3 BrCBL10-1	MCSPPPPIME	NLCKERKRSSSL NUTNUGGDGGGT	TIGEOLCAVEL	PLEATEDFLEST	PUGOCEDCRSRRS	TOTCOUPDLTPL	BHESOFSVNEV	FALYELFKKL	SCSIIDDGLIHK	EELQLAIFÇAPYGE
BrCBL5			11100 Xuchvi vi		VOXOL DORRAND	1X10XIII DDIRE	HILD XLOVIDA			Depertur Xuru
	130 140	150	160	170	180 19	200	210	220	230C-term	ninal region 250
BrCBL4-1	NLFADRIFDVFDVKRNGV	IEFGEFVRSLGV	FHPNAPVHEKIK	FAFKLYDLRQT-	GFIEREELKEM	IALLHESELVLS	DLIEVMVDKAF	IEADRKNDGK	IDLDEWKDFVSKN	PSLIKNMTLPYLKD
BrCBL4-2	NLEADRIEDVEDVKRNGV	IEFGEFVRSLGV	FHPNAPVHEKIK	FAFNLYDLRQT-	GFIEREELKEM	VIALLHESELVLS	DLIEVMVDKAF	MEADRKKDGK	IDLDEWKEFVSMN	PSLIKNMTLPYLKD
BrCBLS	NLFADRYFYMFDRKRNGV	IEFGEFVRSLGV IEFGEFVRSLSI	FHPHTPEHEKSS	FAFKLYDLROT-	-GFIERBELKEM	GALLSETDLGLS	SUMIEVMVDKAP	VEVDTNKDGK	IDVDEWKDLVSM)	PSLIKNMTLPYLKD
BrCBL1-1	NIFANRIFDMFDVKRKGV	IDFGDFVRSLNV	FHPNASLEDKID	FTFRLYDMDCT-	-GYIERQEVKQMI	LIALLCESEMKLAI	DETIEIILDETF	ECADVNQDGK	IDKLEWSDEVNKN	PSLLKIMTLPYLRD
BrCBL1-2	NLEANRIEDMEDVKRKGV	IDFGDFVRSLNV	FHPNASLEDKID	FTFRLYDMDCT-	GFIERQEVKQM	LIALLCESEMKLA	DETIEIILDKTE	ECADVNQDGK	IDKLEWSDEVNKN	PSLLKIMTLPYLRD
BrCBL9-1 BrCBL9-2	NLEANRIEDLEDVKKKGV	IDEGDEVESLOV	FHPNASLEEKTD	FTFRLYDMDCT-	-GYTEROEVKOM	LIALLCESEMKLA	DTIEVILDQTE	ECADVDRDGK	IGKTEWSDEVIKN IGKTEWSDEVIKN	IPSLLKIMTLPYLED
BrCBL2-1	SLEADRVFDLFDTKHNGI	LGFEEFARALSV	FHPNAPIDDKIH	FSFQLYDLKQ	QGFIERQELKQM	VATLAESGMNLKI	TVIEDIIDETF	EEADTKHDGK	IDKEEWRSLVLR	PSLLKNMTLQYLKD
BrCBL2-2 BrCBL3-1	SLEADRVFDLFDTKHNGI	LGFEEFARALSV	FHPNAPIDDKIQ	FSFQLYDLKQ	OGFIERQEVKOM	VATIAESGMNLKI	DTVIEDIIDKTF	EEADTKHDGK	IDKEEWRSLVLR	PSLLKNMTLQYLK-
BrCBL3-1 BrCBL3-2	SLFADRVFDLFDTKHNGI	LGFEEFARALSV	FHPNAPIDDKID	FSFQLYDLKQ	OGFIERQEVKQM	VATLAESGMNLS	DEVIESTIDETE	EEADTKHDGR	IDKEEWRILVLR	PSLLKNMTLQYLKD
BrCBL7	SLFSDRVFDLFDTKHNGI	LGFEEFARALSV	FHPNAPIDDKID	CYFRESCMILSS	KVSLIRQEVKQM	VSTLACAGMKLP	NDVTESIIDKTF	EEVLANRDGR	IDKEEWRILVLK	PSLLKKITLDYLK-
BrCBL10-2	NLFLDRVFDLFDEKKNGV	IEFEEFIHALSV	FHPYAPIEEKID	FAFRLYDLROT-	-GYIEREEVHOM	AAILMESEMILS	DELLTMIIDKTF	ACACADKDGK	ISKEEWKVYVLK	PTLLKNMTLPYLKD
BrCBL10-3	-LFLDRVFDLFDEKKNGP	IEFEEFIHVLTV	FHPSAPIOEKID	FAFRLYDLROT-	GFIEREEVHOM	VAAILMESEMIMSI	DELLTMIIDKTE	ALADSDKDGK	ISKEEWRVYVLEH	PILLKNMTLPILKD
BrCBL5	MGC	VCSKHLGGKRTR	HENISLLÍSQTI	FAFRLYDTROT-	-GFIEPEEVKEM	IIDVLEESELMLT	SIIDSIVSKTF	EEADRKKDGK	IDLEEWENFVAR	PLTLKNMTIPFLK-
	260 21	70 280	290	300	310	320 330	340	350	360	370 380
BrCBL4-1	IHGTFPSFISSCEDEELEI	LQNLYF								
BrCBL4-3	IKGTFPSFVSSCEDEELEI IKATFPSFVLSSEDEELEI	LONLYF								
BrCBLS	VTLAFPSFVLDSEVDD									
BrCBL1-1	TTTTTEPSEVENSEVDETA									
	THEFOLYENDERDER									
BrCBL9-1	ITTTFPSFIFNSEVDEIM									
BrCBL9-1 BrCBL9-2	ITTTFPSFIFNSEVDEIV ITTTFPSFVFNSEVDEIA ITTTFPSFVFNSEVDEIA									
BrCBL9-1 BrCBL9-2 BrCBL2-1 BrCBL2-2	ITTTFPSFIFNSEVDEIV ITTTFPSFVFNSEVDEIA ITTTFPSFVFNSEVDEIA ITTTFPSFVFNSEVDEIA									
BrCBL9-1 BrCBL9-2 BrCBL2-1 BrCBL2-2 BrCBL3-1	ITTTFPSFIFNSEVDEIV ITTTFPSFVFNSEVDEIA ITTTFPSFVFNSEVDEIA ITTTFPSFVFHSQVEDT									
BrCBL9-1 BrCBL9-2 BrCBL2-1 BrCBL2-2 BrCBL3-1 BrCBL3-2 BrCBL3-2	ITTTFPSFIFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSQVEDT- ITTTFPSFVFHSQVEDT- ITTTFPSFVFHSQVEDT- KIPENSIADQTVWQSLFMI	LLRTDADKSGASS	SSYPESRRKKTTM	AMEIAQLEVGS	MRLRNGVSRGRL:	SSISAVHHSPRRMI	IQLAGLGSVLT	LVNLPGLAAP	VPEMKEPEVIRTL	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-2 BrCBL2-1 BrCBL2-2 BrCBL3-1 BrCBL3-2 BrCBL3-2 BrCBL7 BrCBL10-2	ITTTFPSFIFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFHSQVEDT ITTTFPSFVFHSQVEDT KIPENSIADQTVWQSLFMI VTTAFPSFIFNTEVED	LLRTEADKSGASS	SSYPESRRKKTTM	AMEIAQLFVGS:	SMRLRNGVSRGRL	SSISAVHHSPRRMI	IQLAGLGSVLT	LVNLPGLAAP	VPEMKEPEVIRTL	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-2 BrCBL2-1 BrCBL2-2 BrCBL3-1 BrCBL3-2 BrCBL3-2 BrCBL7 BrCBL10-2 BrCBL10-3	ITTTFPSFIFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFHSQVEDT ITTTFPSFVFHSQVEDT KIPENSIADQTVWQSLFM VTIAFPSFIFNTEVED MTIAFPSFIFNTEVED	LRTEADKSGASS	55YP E SRRKKTTN	AMEIAQLEVGS	SMRLRNGVSRGRL	SSISAVHHSPRRMI	IQLAGLGSVLT	LVNLPGLAAP	VPEMKEPEVIRTL	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-2 BrCBL2-1 BrCBL3-1 BrCBL3-1 BrCBL3-2 BrCBL3-2 BrCBL10-3 BrCBL10-3 BrCBL10-1 BrCBL5	ITTTFPSFIFNSEVDEIA ITTTFPSFVFNSEVDEIA ITTTFPSFVFNSEVDEIA ITTTFPSFVFNSEVDEIA ITTTFPSFVFNSQVEDT- KIPENSIADQTVWQSLEMI VTTAFPSFIFNTEVED- WTTAFPSFIFNTEVED- VTTAFPSFIFNTEVED-	LRTEADKSGASS	SSYP E SRRKKTTN	AMEIAQLEVGS	MRLRNGVSRGRL	SSISAVHHSPRRM	IQLAGLGSVLT	LVNLPGLAAP	VPEMKEPEVIRTL	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-2 BrCBL2-1 BrCBL2-2 BrCBL3-1 BrCBL3-2 BrCBL3-2 BrCBL3-2 BrCBL10-2 BrCBL10-3 BrCBL10-1 BrCBL5	ITTTFPSFIENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSQVEDT- KIPENSIADQTVWQSLEM VTIAFPSFIENTEVED- VTIAFPSFIENTEVED- VTIAFPSFIENTEVED-	LRTEADKSGASS	SSYPESRRKKTIN	AMEIAQLEVGSS	MRLRNGVSRGRL	SSISAVHHSPRRM	FIQLAGLGSVLT	LVNLPGLAAP	VPEMKEPEVIRTL	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-2 BrCBL2-2 BrCBL2-2 BrCBL3-1 BrCBL3-2 BrCBL10-2 BrCBL10-3 BrCBL10-3 BrCBL10-1 BrCBL10-1 BrCBL5	ITTTFPSFIENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSQVEDT- KIPENSIADQTVWQSLEMI VTIAFPSFIENTEVED- WTIAFPSFIENTEVED- VTIAFPSFIENTEVED- 390 40	URTEADKSGASS	SSYPESRRKKTTM 420	AMEIAQLEVGS: 430	SMRLRNGVSRGRL 440 45	SSISAVHHSPRRMI 0 460	FIQLAGLGSVLT 470	LVNLPGLAAP 480	490	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-2 BrCBL2-2 BrCBL2-2 BrCBL3-2 BrCBL3-2 BrCBL10-2 BrCBL10-3 BrCBL10-3 BrCBL10-1 BrCBL10-1 BrCBL4-1 BrCBL4-2	ITTTFPSFIFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSQVEDT- ITTTFPSFVFNSQVEDT- KIPENSIADQTVWQSLFM VTIAFPSFIFNTEVED- WTIAFPSFIFNTEVED- VTIAFPSFIFNTEVED- 390 40	URTEADKSGASS	SSYPESRRKKTTM 420	AMEIAQLEVGSS 430	SMRLRNGVSRGRL 440 45	D 460	IQLAGLGSVLT 470	LVNLPGLAAP 480	4 90'	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-2 BrCBL2-2 BrCBL2-2 BrCBL2-2 BrCBL2-2 BrCBL2-2 BrCBL2-2 BrCBL10-3 BrCBL10-3 BrCBL10-3 BrCBL4-1 BrCBL4-3 BrCBL4-3	ITTTFPSFIFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVED- VTTAFPSFIFNTEVED- VTTAFPSFIFNTEVED- 390 40	LLRTEADKSGASS 0 410	SSYPESRRKKTTM 420	AMEIAQLEVGSS 430	SMRLRNGVSRGRL 440 45	SSISAVHHSPRRMI 0 460	IQLAGLGSVLT 470	LVNLPGLAAP 480	4 90'	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-1 BrCBL2-1 BrCBL2-1 BrCBL3-1 BrCBL3-2 BrCBL3-2 BrCBL10-3 BrCBL10-3 BrCBL10-3 BrCBL10-3 BrCBL10-3 BrCBL1-1 BrCBL4-1 BrCBL4-1 BrCBL4-3 BrCBL2-3 BrCBL10-3 B	ITTTFPSFIFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSQVEDT- ITTTFPSFVFNSQVEDT- VTTAFPSFIFNTEVED- VTTAFPSFIFNTEVED- VTTAFPSFIFNTEVED- 390 40	0 410	SSYPESRRKKTTN 420	AMEIAQLEVGS	MRLRNGVSRGRL 440 45	SSISAVHHSPRRM 0 460	IQLAGLGSVLT 470	LVNLPGIAAP 480	4 90'	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-1 BrCBL2-1 BrCBL2-1 BrCBL2-2 BrCBL3-1 BrCBL3-2 BrCBL10-2 BrCBL10-2 BrCBL10-2 BrCBL10-1 BrCBL4-3 BrCBL4-3 BrCBL4-3 BrCBL4-3 BrCBL4-3 BrCBL4-3 BrCBL4-3 BrCBL1-1 BrCBL1-2	ITTTFPSFIFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFNSEVDEIN ITTTFPSFVFHSQVEDT- ITTTFPSFVFHSQVEDT- VTTAFPSFIFNTEVED- VTTAFPSFIFNTEVED- VTTAFPSFIFNTEVED- VTTAFPSFIFNTEVED- 390 40	0 410	420	AMEIAQLEVGS	MRLRNGVSRGRL	SSISAVHHSPRRM 0 460	IQLAGLGSVLT 470	LVNLPGIAAP 480	490'	KLPSGVRIQEIIEGE
BCBL9-1 BCBL9-1 BCBL2-1 BCBL2-1 BCBL2-1 BCBL3-1 BCBL3-1 BCBL3-1 BCBL3-1 BCBL3-1 BCBL3-1 BCBL3-1 BCBL3-1 BCBL10-1 BCBL4-1 BCBL4-1 BCBL4-2 BCBL4-2 BCBL4-3 BCBL4-2 BCBL4-1 BCBL4	ITTTFPSFIENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSQVEDT- KIPENSIADQTVWQSLEM VTIAFPSFIENTEVED- VTIAFPSFIENTEVED- VTIAFPSFIENTEVED- 390 40	0 410	420	AMEIAQLEVGS 430	MRLRNGVSRGRL	D 460	IQLAGLGSVLT 470	LVNLPGLAAP 480	490 [']	KLPSGVRIQEIIEGE
BrCBL9-1 BrCBL9-1 BrCBL9-1 BrCBL2-1 BrCBL2-1 BrCBL3-1 BrCBL3-2 BrCBL10-2 BrCBL10-2 BrCBL10-1 BrCBL10-1 BrCBL10-1 BrCBL9-2 BrCBL4-1 BrCBL4-2 BrCBL4-2 BrCBL4-1 BrCBL4-2 BrCBL4-1 BrCBL9-1 BrCBL9-1 BrCBL9-2 BrCBL9-1 BrCBL9-2 BrCBL9-1 BrCBL9-2 BrCBL9-1 BrCBL9-2 BrCBL9-1 BrCBL9-2 BrCBL9-1 BrCBL9-2 BrCBL9-1 BrCBL9-2 BrCBL9-	ITTTFPSFIENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSEVDEIN ITTTFPSFVENSQVEDT- KIPENSIADQTVWQSLEM VTIAFPSFIENTEVED- VTIAFPSFIENTEVED- 390 40	0 410	420	AMEIAQLEVGS: 430	SMRLRNGVSRGRL 440 45	D 460	470	LVNLPGLAAP 480	490'	KLPSGVRIQEIIEGE
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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.

Motif logo

- 4. FIEREEVKONVAALLESEM LSPEALES
- 5. DITTIEPSEYE№SEX
- 7. MEQCYDGEKHECTSELECEDL

- в. **MGC**, S
- 9. Reselt.GEQLCAYF

- a PEKKERYRC
- ^₄⋰<mark>GssM_{FS}₭₣%₽₽₽₽₽₽</mark>₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽
- 15. **Q. ⊻**wQ.



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.