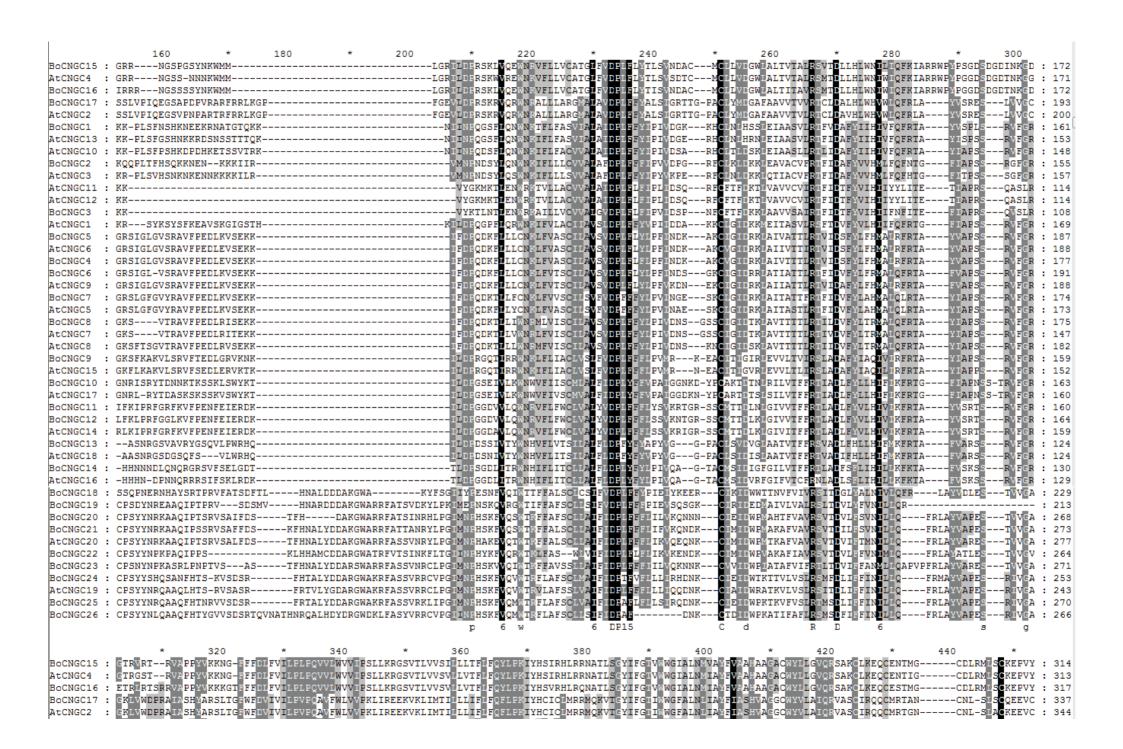
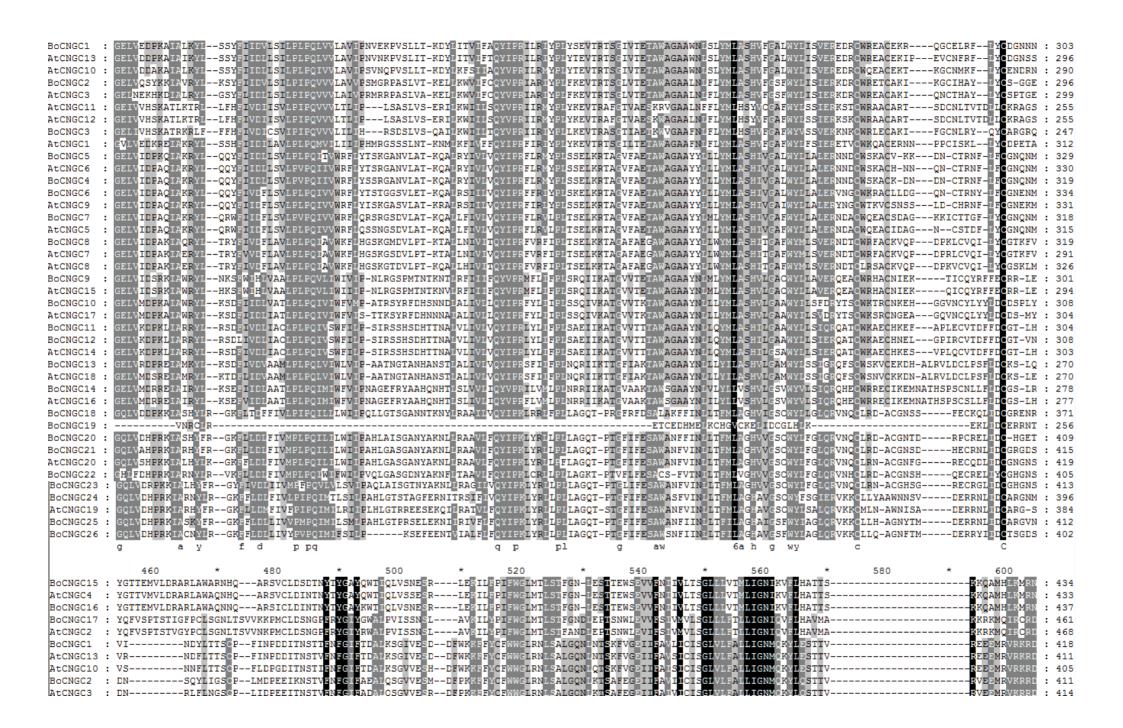
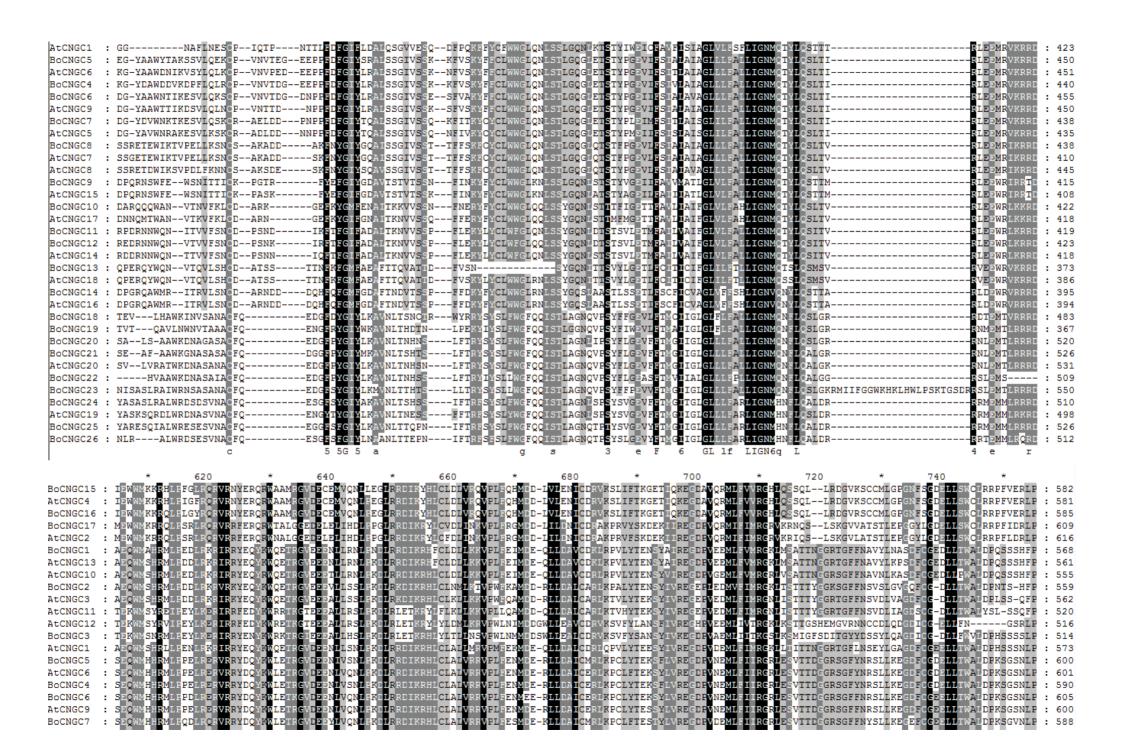
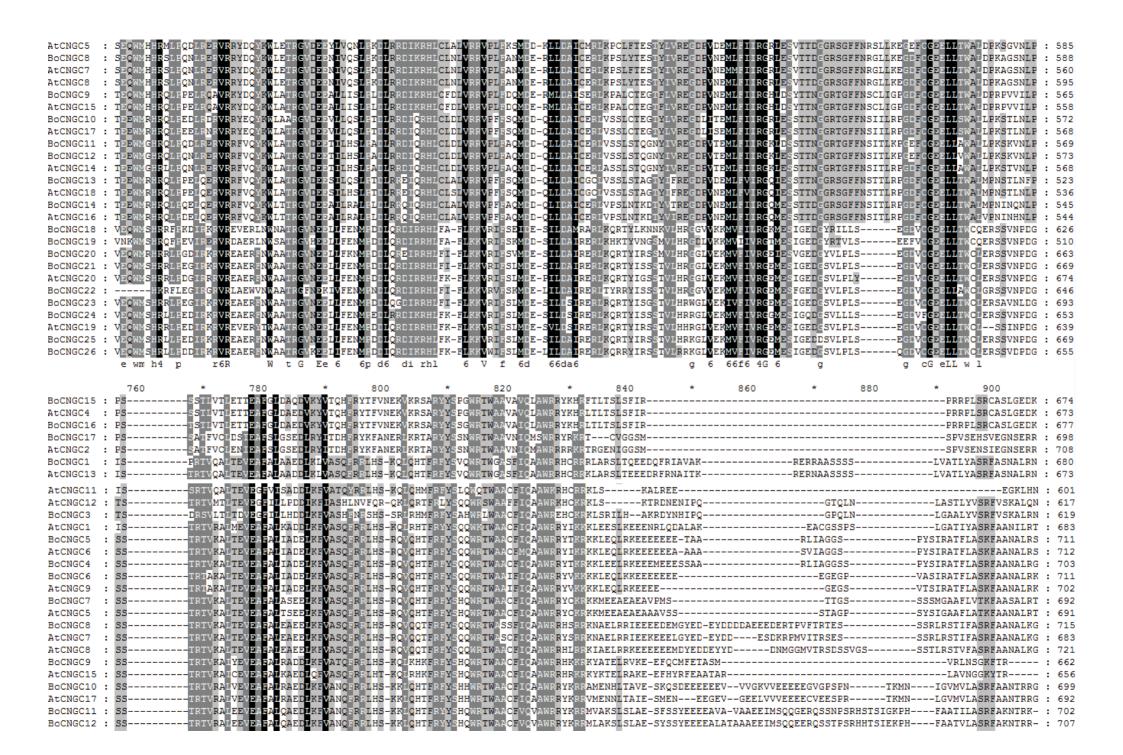
Additional file 9. Multiple sequence alignment of *CNGC***-encoded proteins of** *Arabidopsis* **and** *B. oleracea.* Multiple sequence alignment was performed by clustal X2 and viewed by GeneDoc software package.

D-CNCC4 F	* :MATECEFTI	20	*	40		50 SEEEEEEEEEE	*	80	*	100	*	120	*	140	*	
	:MATEQEFTH															: 61
PoCNCC16	:MATEQEFTH	KASK	TOKUSS	ercvv	SPEDNIEEEDE!	CEEEMEETEI							E		TUVCVICC	: 60
BoCNGC17	:MPSHTNFL	FDWTGT FSOR	TDDETTCICE	MNUCES	SCCDDTDIII	SCECTANCE,	×						UCVDAFU	TECEPEEEE	INVGVICG :	: 77
A+CNGC2	:MPSHPNFI	FRWIGLESON	FRECTTGISE	NSNLOTNEEDS	SSSCSDETEVI.	SSVECTACTO	2						VGVFAFII	STSCDQANA	DEWRASAG .	: 84
BoCNGC1	:	MGEGRDN	RVRWFKE-PS	SS-TEYGYGR	RARP	ST.NAVT.N	× 							NVRRGFE-KO	GSDKIRTE	: 51
AtCNGC13	· :	MAFGRNN	RVRFRDW-TS	SEGTEYGYGRN-	KARP	ST.NTVT.K								NVRRG	T.	: 43
AtCNGC10	:	MI	LFRFKDEGKE	LSSEYGYGR	KARP	SLDRVFK								NVKWG	F	: 38
BoCNGC2	:1															: 48
AtCNGC3	:	MMNPQRNK	FVRFNGN	DDEFSTK-	TTRP:	SVSSVMK								TVRRSFE-K	GSEKIRTF	: 49
AtCNGC11	:	MNLQRRK	FVRLDSTG			-VDGKLK								SVRGR	L	: 27
	:															: 27
	:															: 21
AtCNGC1	:	MNFRQEK	FVRFQDWKSI	OKTSSDVEYSGK	NEIQTGIFQ	RTISSISD								KFYRSFE-S	SSARIKLF	: 61
BoCNGC5	:MFD-CGTNGVKS	SQVISGHREK	FIRLESMDSF	RYSQSSDNTGLN	KCTLNIQ-APKI	RFAQGSK							TSSG	SFKNGFR-K	GSEGLWSI	: 78
	:MFDTCGPKGVKS	SQVISGQREN	FVRLDSMDSF	RYSQSSE-TGLN	KCTLNIQGGPKI	RFAQGSK							ASSG	SFKKGFR-K	GSEGLWSI	: 79
BoCNGC4	:MESKS	SQVISGHREK	FIRLDSMDPF	RSPEAGLN	RCTLNIQ-RPK	RFTQATK							ASSG	SFKKGFR-K	GSEGLWSI	: 68
BoCNGC6	:MFD-CVKKSVKS	SQVISGQREK	FVRLDSMDSF	RYSQGSE-AGLS	KCTLNLQ-GQSI	RANGGTGQGI	N						NNNASSG	SFKKGFR-RO	GSKGLWSL :	: 83
	:MLD-CGKKAVKS															: 79
	:															: 65
	:															: 64
BoCNGC8	:MYKS	SQYISGQREK	FVRLDDLDS-	SASHATGMMT	KRNCFG-FPVKI	NRGSEKKR							ASK	SFREGVK-I	JSEGLFSI :	: 69
	:MYKS															: 41
	:MYK:	SQYISGHREK	FVRLDDTDSF	RVSMSSNATGMK	KRSCFGLFNVT	SRGGGKTKN-							TSK	SEREGVK-10	SEGLKTI :	: 73
BoCNGC9 AtCNGC15	:															: 51
	:															: 44
	:															: 50
BoCNGC11	:	MEERDDM	TUDENCUERC	LONEANWAVN	DPM:	NGGYYI								-TESALKE-	-DNTTL :	: 49
BoCNGC11	:	MEEKDDN	TUDEVCEEK	SITEAIEVETE-	T DM1	RDSTTO								-rgrgerdi:	מדשאדששם סדשאדששם	: 53
A+CNGC14	:	METKEDN	TVRFIGEERS	TTENCERD	VDT	KESIIQ								-FMKOEVI DI	FREINGIA .	. 48
BoCNGC13	:	HETKKEN	I VKI IGDENÇ	ZIILVGERK	M1	IKIDSID								-FILEFTITS	51	: 18
	· :															: 20
BoCNGC14	· :			M-	SNT.	HT.HTSAR								-FRNFPTAF	SRR	: 22
AtCNGC16	:			M-	SNL	HLYTSAR								-FRNFPTTF	SLR	
	: MASPMENDDVPMLPASI															: 101
BoCNGC19	: MASSNGYDDVPMLPVS	CTSSSS-RTR	PFTFRSRSVS	SLSNTSSTIDVE	ENSSTVVLSYT	PLGTOROPO	O-LVOMGDP	ISSTRN	LELVS					КНАН	APYGTT	
	:MEKDDVPMLPVSI															
	: MASPKENDDVPMLPISI						-				~					
AtCNGC20	: MASHNENDDIPMLPIS	DPSSRT-RAR	AFTSRSRSVS	SLSNPTSSIEGE	-DTSTVVLGYT	SPLRTQRRPI	P-LVQMSGP	LTS-TRKHE	LFLPHPSS-	DSVGV	SSOPERYPSE	FAALEHKNSSE	DEFVLKHAN	LLRSGQLGMO	CNDPYCTT	: 141
BoCNGC22	: MAPPNEKDDVPMLPISS	SSSSS-RTR	SFTSRFRSTS	SLANTSSAIDGE	-DSSNVVLGYT	FLQTYGRPA	A-FVQMSAS	LPS-TLIPE	LFLHPTPTG	GSSHSIG-VS	SSQPESCP-E	FAALEHKNS-I	DELGLG	SGQLEVO	CNDPYCTT	: 138
	: MVSPNKNDKIHILPISI															
BoCNGC24	: MISPNENDQVSI	PEATSRAHTG	AFNFKNRSVS	SLSNSTYYIDGC	-DKSKVALGYT	PIRTQRRPI	PGP:	LYSTLRPE	SLLPPS	I	EPPDSS	STVDVRSEDE	svvknan	ILTSGQLGMO	CNEPYCTT :	: 120
	:															
	: MASPNEKDEFPILLPVS															
BoCNGC26	: MAYPNESDEFPMLRQVI	PEARSRAQSR	ALHSRNRSVS	SFSDSTYSTNRV	-ENSS	SPRRTQSRPS	SPSVHMSGP:	LYDTRRPPDÇ	SFFPPSP	V	QPPESSLSS	STTVDIPSEEV	VEALLKNAN	LLKSGQLGMO	CNDPYCTT :	: 133









At.CNGC14	: SSTRIVRALEEVEABALQAGDLKFMANQERIHS-KKLQHTERYYSHQWETWAACEVOVAWRRYKRSKLAK	SISLAE-SESSYDEEFAVA-VAATEEMSHEGFAGSGAKARHHTSNVKPHFAATILASREAKNTRR- : 7	01
BoCNGC13		ELSLHE-SSGYYYRDETGYNEEGDEENYYGSDDDDFEGERLSVDNTNNSQNLGATMLASKFAANTRRG : 6	
	: SSTRSVRALSEVEARAUSAEDUKEVAHQEKRIQS-KKIQHAERYYSHQNRAWGACEVQSAWRRYKREKLAK		
BoCNGC14	: LSTRIVETLSEVEARAL RAEDLKENANGERIHS-KKLCHAERYYSHCWEAWGTGFICABWRRYMKEKLAM		74
A+CNGC16	: LSTRIVETUSEVEARAURAEDUKFVANGERRIHS-KKUCHAFRYYSHOWRAWGTCFICAWWRYMKEKLAM		73
BoCNGC18			74
		· · · · · · · · · · · · · · · · · · ·	58
BoCNGC20	: TRIRMPSKGLLSNENVRCVTNVBAESISVADIEDVTSLESEFLRSNRVQGAIRYESPYWRLRAAMQIQVAWRYRRRELQRL		53
	: TRIRIFSKELLSYENVROVINVERSESVADDEDWITSLESSFLRNPRVCGAIRYESPYWELRAARCICVAWRYRREELCRL	YTAQS-SYSL:: 7	59
AtCNGC20	: TRIRMPSKGLLSSRNVRCVTNVBARSISVADIEDVTSLESRFLRSHRVQGAIRYDSPYWRLRAARQIQVAWRYRRRRLHRL	TIRKS SIST	64
BoCNGC22	: TRIRMPSKGLVSNENVRCVTDVEARSUSVAD EDUTSLELEFLRTHREQGAIRSPHNELRAARQIQVEWRHRRRELQRF	VSACS-SYSI	34
BoCNGC23	: MISKGLISSENVKCVINVEASSISAADEDVISLL-FIRSHRVCGAIRYESPYCELRAATCI VAWRYRKSQLRKI	STACKHOVSIFITKKUMAKT	89
BoCNGC24	: RSIKLPLKGLVSNRSVRCVTNVBARSISVAD EDVTSLESEFLRSHRVLGAIRYESPYNRLRAATQIQVAWRYRRRELHRL	VIACSISBR	43
AtCNGC19	: TRIKMPPKGLVSNENVROVTNVEARSISVAD EDVTSLESEFLRSHRVQGAIRYESPYNELRAAMQIQVANRYRKEQLQRL	NTAHSNSNR	29
BoCNGC25	: TRIKMPTKGLVSN:NVRCVTNVEARSISVALIEDVTSLES:FLRSHRVQGAIRYESPYNRLRAAMQIQVAWRYRKKELERL	ITONNEWKEMSDVPTGYRISWSGUVFGSGK	81
BoCNGC26	: TRIKMPTKGLVSNRSVRCVTNVEAESISVADIEDVTSLESRFLRSNRVQGAIRYESPYWELRAAMQIQVAWRYRKKRLERR		44
	r EaF6 6 6 r rsw aa gaw		
	* 920	*	
BoCNGC15	: LRLYTAILTSPKPNPDDFDDY	: 695	
	: LRLYAAILTSPKENPDDFDDY		
	: LRLYTAILTSPKENPDDFDDY		
	: LLCYAAMFMSIRPH-DHLE		
	: LLQYAAMFMSIRPH-DHLE		
	: LROHNTLPLLPPKPSEPDFGVDDD		
AtCNGC13	: LRTNN	MDET : 742	
	: LRHNISNLPPRYTLPLLPCKPTEPDFTANHTTDP		
BoCNGC2	: VRANAAARNSMLPHMLSLLPCKPADPEFPMDET	: 703	
AtCNGC3	:	: -	
	: TLQNDDSGGNKLNLGAAIYA		
AtCNGC12	: RRKDTADCSSSPDMSPPVPHKFADLEFAKAEA	: 649	(
BoCNGC3	: RQKNAANCSISPHMLPPIPHKPADPEFSKN	: 649	
	: IRRSGSVRKPRMPERMPPMLLQKFAEPDFNSDD		
	: VHKNRIRKSNLAPPSTKELVKFQKFPEPDFSADC		
	: VHKNRTAKSTLLLSSTKELVKFQKPPEPDFSAEDH		
	: VHKNRIEAKSTIELVKYCKPSEPDFSADDTS		
	: IHRNRNTRIRELVKLQKFPEPDFTAEDAD		
	: IHRNRNTKIRDLVKLQKPPEPDFTAD		
	: -HRLRSTESSKRLLNLQKFPEPDFDAE		
	: -HKLRVTESSKILINLQKFFEFDEDAE		
	: -GRIEVIESS		
	- SGSDSGMMSSIQKFVEPDFSSE		
BoCNGC10	: VAAORVKDVEMPREKKFEEPDFSAEPDD	727	
AtCNGC17	: VAAQRVKDVELPRFKKFEEPDFSAEHDD	: 720	
BoCNGC11	: -TAHKLKDVEVPMLPKFDEPDFSVDGD	: 728	
	: -ASRKIKDVDVPMLPKPEEPDFSVDAD		
	: -TAHKLKDVEIPMLPKPDEPDFSVDD		
	: TNQKASSSSTGKKDGSSNSLKMPQLFKPDEPDFSMDKEDV		
AtCNGC18	: TNQKASSSS-TGKKDGSSTSLKMPQLFKFDEPDFSIDKEDV	. 706	
	: VLGNQRGSSRIDPDDFTLKMPKMFKFEDPGFF		
	: VLGNQKGS1RIDPDHFILKMPKMFKFEDPGFF		
		· :: -	
	:	· : -	
BoCNGC21	:	: -	
AtCNGC20	:	: -	
	:		
	:		
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BOUNGU26	:	: -	