Family name	Locus by	Gene symbol	Primer sequence(5'→3')						
Family name	ITAG 2.4	by NCBI	Forward	Reverse	temp.(°C)				
CAX	Solyc03g123790	LOC101267212	CCATTTTCAGAACAGCCGGC	AGTCGAGGTGCTCATTTGGC	68				
	Solyc06g006110	LOC101265339	GGGATTTGGAGCATAATGTTGG	CGGTTGATGACGTGTACCA	65				
			CCCCTATTAAATCAACATTTTCTAGTCC	GTTCAGTCAAGAAGCTGACACG	64				
			GGTACGATCGAGGCTGCATCAG	GCACCAATGACACAATAGGCAAGAC	69				
	Solyc07g056110	LOC101252790	CGTAAGCTACGCCAAAGCAA	CAGCTCAGAGTGGCCAAAAC	67				
	Solyc09g005260	LOC101254519	GGCTTCATCATCACCAGCA	GGAACTCTCAGCAACTATGGA	65				
			CCCCATACTCATACAAGATGAGA	TTGATGAGCCCAAATTGACA	64				
	Solyc12g011070	-	GCCAATATCATCTCGATTAATCTGC	GCGAGGGAGGAAACTTACG	64				
			ATGGCACTCTATTTAGCCAATATC	CTACCATATAATAATTGTATGAAGCGAG G	<del>6</del> 64				
	Solyc12g055750	LOC101250779	ACGATTCGATTCGCCCACTG	ACTGCCAGTTGTTGAGGAGTTC	68				
NCL	Solyc02g077270	LOC101251749	CTTTGGTAGTGATGCCAAGCC	TGAATGGGTTTGGGTTGGGTA	67				
			GCTCTCAACTCATTCGTTGGAAGGC	TGAATGGGTTTGGGTTGGGTA	68				
	Solyc03g006260	LOC101254062	TGTTACCAAGGTGCAAAGCAG	CCAAGAGGCTTGTCCAAAGTG	67				
			CAGTACTATACACTTCATTCTTCAATAA	TAATAGTCCCAACCAAACAATTAATTA	61				
	Solyc07g062700	LOC101263533	CCCAAATCGTTCTTCACTCTCC	AAACGACAGATGTGCACTGC	66				
			CGGCGAATAGTTCTAAACATGAGAA	CGGGCATAAACAATAGCCAA	65				
	Solyc12g014110	LOC101257045	AACTCCGATGGCATCTCTGG	CGACTAAAGTGTGCCGTAGC	67				
CCX	Solyc01g098800	LOC101261070	CAATATTCTGGAATGGCATGGC	GTTCCAGACCAGTGATGGATG	65				
	Solyc02g069710	LOC101265300	GGTGTTCAATCTTGTGTGTGTTCC	AAAGGAGTCGAAGAGCACATAC	65				
			GGGTTTTCGATGCGTTTTGCTG	CGCCCACGCACTTCCATTACAAC	69				
	Solyc07g006370	LOC101250521	CCAAACAACACTTTCACAATTCCC	TTCAGAGTCGACGTGCTTCC	66				
			${\tt CATCTCTCTCACTATTATTATTAAAAAAAAATGTC}$	GAGCTTCCTTTCAGAGTCGA	62				
	Solyc07g042000	LOC101250709	CCCTGTTTAGTTTGTGGAGGG	CCACTTTGTGTTGCAACAGTAC	65				
			CGCTTCCATGGCTCCCTATTTTC	CCCTGCTTTCACCCAAATGATGA	69				
	Solyc09g072690	LOC101248713	CCCATTCCGTTTCAAGCCAA	CAACAAGAGCCCATAGTAAGCC	67				
			CCTTATACATTTAGCTCTCTCTTCTCTTC	CATGTATACACTACATATAAACATCCTT GTC	64				
MHX	Solyc06g009130	_	AAGATGACCTCGCTTGGAAAC	GATATCGCTCCATTTAAGCCCA	65				

## **Table S1.** List of primers used for sequence analysis of *SlCaCA*.

## **Table S2.** List of primers used for expression analysis of SlCaCA.

Family name	Locus by	Gene symbol	Primer se	equence(5' $\rightarrow$ 3')	_ Annealing
	ITAG 2.4	by NCBI	Foward	Reverse	temp(°C)
CAX	Solyc03g123790	LOC101267212	GGAATTGCATTTTGGCAAGT	CACCCTCGATGGCATCTACT	56.1
	Solyc06g006110	LOC101265339	TGCCAATAGTGGGAAATGCAGCAG	TTGAGAAGCTGACCCCAATGCAAC	58.2
	Solyc07g056110	LOC101252790	GTTGGAAATGCAGCTGAACA	TGGGCTTGTCCTGTATAGCC	56.1
	Solyc09g005260	LOC101254519	GTGGTTCCCTTGTGTGTGATTG	TCCTGTAGAGTGAAAGCTGTGAC	58.2
	Solyc12g011070	-	GATGGCCGAGGAAGAGGATCATA	CGGATGCTCCTTCTACGGTATTAAC	57
	Solyc12g055750	LOC101250779	TGAGTCAGCTCATATGGCGTCGC	TGTAGCAGTATCGCCAATGGTCCA	62.7
NCL	Solyc02g077270	LOC101251749	GCTCTCAACTCATTCGTTGGAAGGC	TGCATGCCGTTGTACATGATGCAG	60.8
	Solyc03g006260	LOC101254062	CAAGCTACGTATGGCCAATGTGACC	AGAGTAGCCCCAAAGATGCCTGTAC	58.2
	Solyc07g062700	LOC101263533	AGGAAACAAGGAGAGAGCACAG	GAAGTTCCATGTTAGACCTCGGG	57
	Solyc12g014110	LOC101257045	GGTCGCCGTTTCATCAGTGACGA	GTTCACAACTCTCCTCTTCACCTCCG	58.2
CCX	Solyc01g098800	LOC101261070	CGACCAGCAATTTCACTGACTCCAA	TCTGGCTTGACCTCCCCTAACTG	58.2
	Solyc02g069710	LOC101265300	CGGGTCGGATGCTGATGATTTGG	CGCCCACGCACTTCCATTACAAC	58.2
	Solyc07g006370	LOC101250521	GGTGCCTTTGTTGGTGGATGAGG	CCCCACAACAAAGCCCAATAACACC	62
	Solyc07g042000	LOC101250709	TTAGGGATCGCGAGACTAGTTTG	CTTGTAGCTGCAGCAATCCATC	58.2
	Solyc09g072690	LOC101248713	ACTCCTATAGACGCGGCCTCAAC	CCTCCAAGAAGCCAAATCCACAAACA	60.8
MHX	Solyc06g009130	_	CCGGTCCATGGAGAGTGTTGTCA	CCAACGTTTGTCCTGTGCATAGGC	58.2
Ubiquitin 3	Solyc01g056940	_	ACTCTTGCCGACTACAACATCCA	AACTGCAACACAGCGAGCTTAAC	57





1.2

0.8

0.6



1.2



TMHMM posterior probabilities for WEBSEQUENCE

200

inside

250

300

350

outside

400

150







Figure S1. Transmembrane domains of SICAX searched using TMHMM. A) Solyc03g123790, B) Solyc06g006110, C) Solyc07g056110, D) Solyc09g005260, E) Solyc12g011070a, F) Solyc12g011070b, c, d, G) Solyc12g055750.



**Figure S2.** Transmembrane domains of SINCL searched using TMHMM. **A)** Solyc02g077270, **B)** Solyc03g006260, **C)** Solyc07g062700, **D)** Solyc12g014110.



**Figure S3.** Transmembrane domains of SICCX and SIMHX searched using TMHMM. **A)** Solyc01g098800, **B)** Solyc02g069710, **C)** Solyc07g006370, **D)** Solyc07g042000, **E)** Solyc09g072690, **F)** Solyc06g009130.

<u>CAX α1-repeat</u>		TM TM	
OsCAX1a	128	GNATELIIALFALLKGKIEVVKCSLLGSVLSNLL	163
OsCAX1b	136	GNVTEVIIALLALREGKIEVVKCSLLGSILSNLL	171 🔽
AtCAX1	137	GNATELIIAILALTNNKVAVVKYSLLGSILSNLL	172 🛿
AtCAX3	137	GNATELIIAILALANNKVAVVKYSLLGSILSNLL	172 🛿
Solyc09g005260	139	GNATELIIAIFALIEHKVDVVKYSLLGSILSNLL	174 🔽
Solyc06g006110	111	GNATEMIIGLFALYORKIHVLKYSLLGSILSNLL	146 🔽
OsCAX1c	143	GNVPELIIALFALHKNKMEILKWSLLGSILSNLL	178 🔽
AtCAX4	138	GNATEMIIAILAVGORKMRIVKLSLLGSILSNLL	173 🗗
Solyc03g123790	80	GNATEMIISLYALNNGMMRVVKQSLLGSILSNML	115 🔽
Solyc12g055750	141	GNATEMIISLYALNNGMMRVVKQSLLGSILSNML	176 🔽
OsCAX2	136	GNATEMIISLYALKNGMIRVVQQSLLGSILSNML	171 🔽
OsCAX3	115	GNATEMIIAIYALKNGMIRVVQQSLLGSILSNML	150 🔽
AtCAX5	139	GNVTELIISIFALKSGMIRVVQLTLLGSILSNML	174 🔽
AtCAX6	150	GNVIELIISIIALKNGMIRVVQLTLLGSILSNIL	185 🔽
AtCAX2	139	GNVTELIISIFALKNGMIRVVQLTLLGSILSNML	174 🔽
Solyc07g045110	144	GNATELIISMYALRRGMIRVVQQSLLGSILSNTL	179 🛿
Solyc12g011070	28	GNATELIISMYALKSGMIRVVQQSLLGSILSNTL	L <mark>V</mark> 63
OsCAX4	124	GSILSNLL	LV 133
		**** ** **	* *
<u>CAX α2-repeat</u>		TM TM	
OsCAX1a	325	GNAAEHAGAIIFALKNKLDITLGVALGSATQISME	<b>EV</b> 360
OsCAX1b	335	GNAAEHAGAVIFALKNKMDITLGVSLGSATQISM	<b>TV</b> 370
AtCAX1	333	GNAAEHAGAVIFAFKNKLDISLGVALGSATQIGLE	<b>EV</b> 368
AtCAX3	335	GNAAEHAGAIIFAFKNKLDISLGVALGSATQISLH	<b>EV</b> 370
Solyc09g005260	334	GNAAEHAGAIIFAFKNKLDISLGVALGSATQIAM	<b>EV</b> 369
Solyc06g006110	307	GNAAEHAGSIIFALKNKLDISLGVALGSASQISME	<b>FV</b> 342
OsCAX1c	339	GNAAEHAGAIIFAFKNKIDISLGITLGSATQISMI	LV 374
AtCAX4	337	GNAAEHAGAVIFAFRNKLDITLGIALGSATQIALH	<b>TV</b> 372
Solyc03g123790	275	GNAAEHASAIMFAMKDKLDITLGVAIGSSTQISME	<b>EV</b> 310
Solyc12g055750	326	GNAAEHASAIMFAMKDKLDITLGVAIGSSTQISME	<b>EV</b> 361
OsCAX2	328	GNAAEHASAIMFAMKDKLDITLGVAIGSSTQISMB	<b>EV</b> 363
OsCAX3	309	GNAAEHASAIMFAMKDKLDITLGVAIGSSTQISMB	<b>EV</b> 344
AtCAX5	333	GNAAEHAGAIMFAMKD <mark>KLDLSLGVAIGS</mark> SIQISMH	FA 368
AtCAX6	341	GNAAEHAGAIMFAMKD <mark>KLDLSLGVAIGS</mark> SIQISMH	<b>FA</b> 376
AtCAX2	333	GNAAEHAGAIMFAMKDKLDLSLGVAIGSSIQISM	FA 368
Solyc07g045110	339	GNAAEHAGAVMFAVKDKLDISLGVAIGSSTQIAM	<b>FG</b> 374
Solyc12g011070	223	GNAAEHAGAVMFACKDKLDISLGVAIGSSTQIAM	<b>FG</b> 258
OsCAX4	248	GNSAGHANAVMFAVKDKLDISLGVAIGSSIQISM	<b>FG</b> 283
		****	k

**Figure S4.** Multiple alignments of conserved  $\alpha$ 1-repeat and  $\alpha$ 2-repeat regions in CAX proteins. Amino acid sequence alignment was performed by ClustalW2 using CAX protein sequences from tomato, *Arabidopsis*, and rice. Asterisks and "TM" indicate identical amino acids among tomato CAXs and transmembrane domains, respectively.

CCX al-repeat	TM		TM	
OsCCX2 153	PPAIAGVT <mark>LL</mark> SL <mark>GNGA</mark> P	VFASVVSFAAGDGGGV	G <mark>LNSALGGALFVSTV</mark> VAG	204
OsCCX4 147	PPAIAGVTLLSLGNGAP	VLSSVVAFAAGARGGDGGGGGGGEDAGDV	GLSGVLGGALFVSTVVAG	210
OsCCX3 155	SPAIAGVTLLSLGNGAP	DALSTIASFASGGGEGETTAV	GLNGVLGSAMLVSSAVLG	210
AtCCX3/ CAX9 174	PPTVAGVT <mark>LL</mark> PL <mark>GNGA</mark> P	DVFASIAAFVGTDKGEV	GLNSVLGGAVFVTSVVVG	225
AtCCX4/ CAX10 173	PPTVAGVTLLPLGNGAP	DVFASIAAFVGSDKGEV	GLNSVLGGAVFVTCVVVG	224
OsCCX1 167	PPTVAGVTLLPFGNGAP	DVFASIAAFMGTGAGDV	GLNSVLGGAVFVTCVVVG	218
Solyc02g069710 172	SPTVAGVVLLPLGNGAP	VFASIAAFVGSGAGDV	GLNSVLGGAVFVTCVVG	223
Solyc07g042000 153	PPTVAGITLLPLGNGAP	VFASIAAFMGSDSGKV	GLNSVLGGAVFVTCIVVG	204
Solyc09g072690 137	SPAIAGTTLLPLGNGAN	VFSSIISFTRSSNSGTV	GLNSVLGGAFFISCFWVG	189
AtCCX1/ CAX7 138	SPTMAGVTLLSLGNGAP	LFSSVVSFTRSNNGDE	GLNSILGGAFFVSSFWVG	189
Solyc07g006370 142	SPITAGVTULSLGNGAP	FFSSIVSFMNDDTNDI	GLNSTIGGAFFVSSVVAG	193
AtCCX2/ CAX8a 128	SPTVAGVTILLSLGNGAP	DIFASLVSFMGESKGTYDV	CLNTVVGGSGFVTCVVVG	181
AtCCX5/ CCX11 129	SPSMAAVTILALGNGAP	VFASVAALRGGOYRT	GEGATLSAGTEVSAEWVG	179
Solyc01g098800 129	SPSMGAVTLLALGNGAP	VFASVAAVRGGOART	GEGATLSAGTEVSAEWUG	179
	* ** ****	* * *	* * * *	

<u>CCX</u> α2-repeat	$\mathrm{TM}$	TM
OsCCX2 439	VRASVLGVTVLAWGDSLGDLVSNVAMALHGGAGGAQTAVS	GCYAGPLENTVVGLGL 494
OsCCX4 453	VEAGVLGATVLAWGNSLGDLVADVALATRRGDGGAGAQTAVA	GCYAAPAPNTVVGLGL 510
OsCCX3 467	VDSAALGLTVLAWGNSLGDLVANLAVASRGGGGG-GAQVAVA	GCYGGPVFDVLVGLGV 523
AtCCX3/ CAX9 511	INPSILALTVLAWGNSMGDLVSNIALTMNGG-DGVQIALS	GCYAGPMENTLVGLGM 565
AtCCX4/ CAX10 512	INPSILGLTVLAWGNSMGDLVSNIALSMNGG-DGVQIALS	GCYAGPMENTLVGLGM 566
OsCCX1 505	INPSILGLTVLAWGNSMGDLMSNVALAMNGG-DGVOIAMS	GCYAGPMENTLAGLGI 559
Solyc02g069710510	VNPSILGITVMAWGNSMGDLVSNVALAMNGG-DGVOIALS	GCYAGPMENTLIGIGI 564
Solyc07g042000 488	VNPSTLALTVLAWGNSMGDLMSNVAIANNSA-DGVOIAMS	GCYAGPMENTLAGLGT 542
Solyc09g072690 441	TSPSTIGLTVLANCNSTCDLTSNVALALNGGKDGVOMALS	ACYAGPLENTLIGLEV 496
AtCCX1/ CAX7 437	TSPSVEGLTVLANCNSLODLLANVTVAFHGGNDGAOTALS	GOVAGPLENTVICE 492
Solyc07g006370432	TSPSTICLTVLAWCNSLCDLVANVTLAKTGGPTGAOVALC	GOVAGPTENTLYGIGS 487
AtCCX2/ CAX8a 429	VSPSTICITYLAWCNSTCDLTTNLTMAL HDCNFCA OVAVS	GOVACETENTIENT 484
AtCCX5/ CCX11 420	T DEATE GET VERNENSKODT VA DVAVAK	CCENCEMENTING 472
Solyc01g098800428	L DAA DI CI TULANCHSUCDI VADVAVAR ACODAMAMA	480
	* *** **** *** * *	* *** ** *

**Figure S5.** Multiple alignments of conserved  $\alpha$ 1-repeat and  $\alpha$ 2-repeat regions in CCX proteins. Amino acid sequence alignment was performed by ClustalW2 using CCX protein sequences from tomato, *Arabidopsis*, and rice. Asterisks and "TM" indicate identical amino acids among tomato CAXs and transmembrane domains, respectively.

MHX al-rep	<u>beat</u>	TM2	TM3	
OsMHX1	85	NYTIADVALLAFGTSFPQISLATIDAIRNLG	QLT <mark>AGGLGPGTLVGSAAFDLFPIHAV</mark>	141
Solyc06g009130	96	N <mark>YTIAD</mark> ITLLAFGTSFPQISLATIDAIRN <mark>I</mark> G	KLY <mark>AGGLGPGTLVGSAAFDLFPIHAV</mark>	152
AtMHX	95	NFTIAD <mark>IS</mark> LLAFGTSFPQISLATIDAIRNMG	ERYAGGLGPGTLVGSAAFDLFPIHAV	151

<u>MHX α2-rep</u>	<u>beat</u>	T	'M7			-TN	18	
OsMHX1	384 🟅	PYVIAFTALA	GTSWPDLV	ASKIAAERC	TADSAI	NITCSNSVNIY	V <mark>GIGV</mark>	436
Solyc06g009130	401 N	PYVIAFTALA <mark>S</mark>	GTSWPDLV	ASKIAAERO	LTADSAL	ANITCSNSVNIY	IGIGV	453
AtMHX	402 N	<b>PYVIAFTALA</b> S	GTSWPDLV	ASKIAAERO	LTADSAL	ANITCSNSVNIY	V <mark>GIGV</mark>	452

**Figure S6.** Multiple alignments of conserved  $\alpha$ 1-repeat and  $\alpha$ 2-repeat regions in MHX proteins. Amino acid sequence alignment was performed by ClustalW2 using MHX protein sequences from tomato, *Arabidopsis*, and rice. TM, transmembrane domains.

NCL conserved	l region	TM				_		TM					
Solyc02g077270	111 GII	GATVFQI	LMTLP	RIVMVIZ	AS <mark>G</mark> VSASE	KEKAQFC	ISSGI	STTVG	ATVF	NLTLMW(	GIC	168	
Solyc03g006260	96	GLLLPT	LKALE IGALDI	DALLVIA	ISCI.SCSI	RETAOSC	VI.TGM	GT.T.AC	STVE		STC	153	
OSEFCAX1/ NCL1	119 GI	GLFLPI	LGALPI	DALLIL	/SGLSGT	(EVA0SC	VLIGM	GLLAC	STVM		SSC	1/0	
Solvc07a062700	121 GLI	GLFLPI	LGALFI	DAMLILV	/S <mark>G</mark> ITGS/	AEAOSC	VSVGI	GLLA	STVM	LL <mark>T</mark> AIW(	GIC	178	
Solyc12g014110	111 <b>GI</b> I	GLFLPV	LGALPI	DAMLILV	75 <mark>G</mark> ISGS1	raa <mark>a</mark> qso	VSVGM	GLLA	STVM	LI <mark>TVI</mark> W(	GIC	168	
AtNCL1/ EFCAX1	114 🖭	GGLFLPM	LGALPI	DAMLIM	/S <mark>G</mark> LSGD/	ATAOSC	VSVGM	GLLAC	STVM	LL <mark>TVI</mark> W(	GIC	171	
AtNCL2a/ EFCAX2	a110 📳	GGIIFPL	LIMFPE	RIALILS	STGLVGS	REMASSE	VGNII	GVTVG	YSVF.	ALTIQUO	GAC	167	
AtNCL2b/ EFCAX2	b110 💵	Getter	LIMPE	RIALILS	oleries:	KE LANDP	II GNNV.	AVIVE	I SVE	ALLMOW	5AC	167	
NCL α2-repea	<u>at</u>		TM						TN	1			
Solyc02g077270	595 <b>PS</b> I	LIPFVMV	PLALN	ARMAIA	IFPASO	KSSITA	ITFSE	IYGG	IMNN	IMGMAT	LAV	VCIKD	658
Solyc03g006260	579 <b>PS</b> I	LIPFVIV	PLALN	ARMTIA	IYPASO	KCSKTA	5 LTFSE	IYVG	IRNN	IMGMTT	LIAI	VYAKD	642
OsEFCAX1/ NCL1	463 <b>PS</b> I	FISFIAL	PLATN	SSEAVS	IIFASR	KKLRTS	I TFSE	VYGG	TM <mark>NN</mark>	TLCLGV	R <mark>LA</mark> L	IYIRN	526
OsEFCAX2/ NCL2	455 <b>PS</b> I	FISFIVM	PLATN	SSEAVS	IIFASR	KKKRTL	5 LTFSE	VYGG	TMNN	TLCLAV	RLAL	VYVRG	517
Solyc07g062700	468 <b>PS</b> I	FISFIAL	PLATN	SSEAVS	IIFATR	KKQRSA	5 <mark>LTFSE</mark>	LYGA	TMNN	LLCLSV	R <mark>LA</mark> I	VYARG	531
Solyc12g014110	457 <b>PS</b> I	FISFIAL	PLATN	SSEAVS	IIFASR	KKLRSA	5 LTFSE	LYGA	TMNN	LLCLSV	<mark>PLA</mark> L	VYIRG	520
AtNCL1/ EFCAX1	464 <b>PS</b> I	FISFIAL	PLATN	SSEAVS	IIFASR	KKIRTA	5 <mark>LTFSE</mark>	LCGG	TMNN	ILCLSV	R <mark>LA</mark> I	VYVRG	527
AtNCL2a/ EFCAX2	a436 PSI	YVVFVVI	PLARN	LKNTLS	HFCRKK	DKAKIT	DTFSE	IYKD	TMNN	LMGISI	IAI	VYARE	499
AtNCL2b/ EFCAX2	b457 <b>PS</b> I	YVVFAVI	PLARN	LKNALS	HFCRKK	EKAKIT	DTFSE	IYRD	TLNN	LLGITI	ILAI	VYIRG	520

**Figure S7.** Multiple alignments of the conserved region, which may correspond to  $\alpha$ 1-repeat, and  $\alpha$ 2-repeat region in NCL proteins. Amino acid sequence alignment was performed by ClustalW2 using NCL protein sequences from tomato, *Arabidopsis*, and rice. Asterisks and "TM" indicate identical amino acids among tomato CAXs and transmembrane domains, respectively.