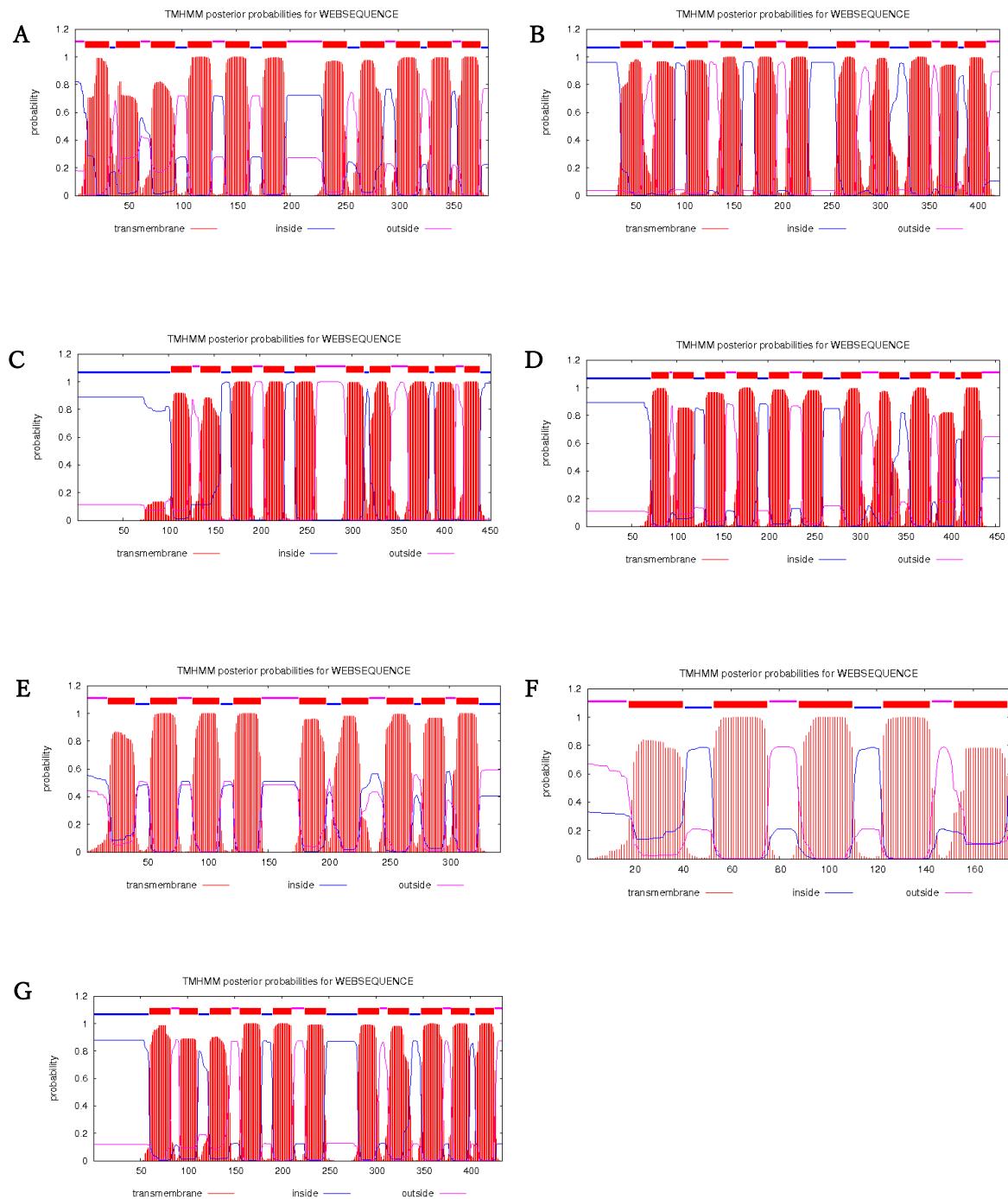


**Table S1.** List of primers used for sequence analysis of *SlCaCA*.

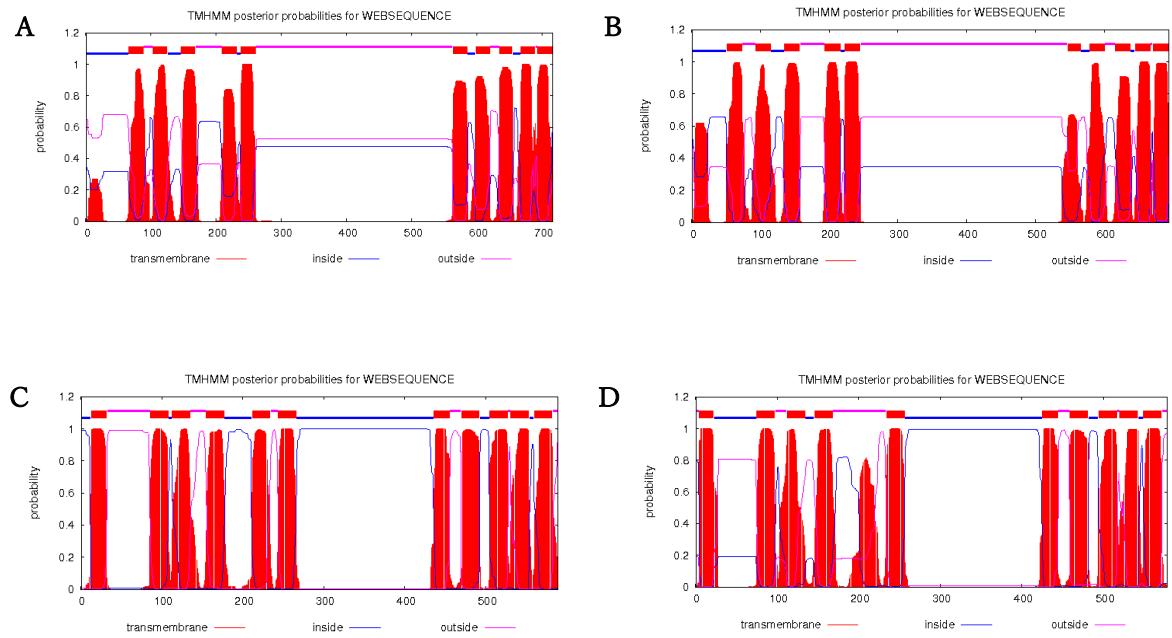
Family name	Locus by ITAG 2.4	Gene symbol by NCBI	Primer sequence(5'→3')		Annealing temp.(C)
			Forward	Reverse	
CAX	<i>Soly03g123790</i>	LOC101267212	CCATTTTCAGAACACAGCCGC	AGTCGAGGTGCTCATTTGGC	68
	<i>Soly06g006110</i>	LOC101265339	GGGATTGGAGCATAATGTTGG CCCCTATTAAATCAACATTCTAGTCC GGTACGATCGAGGCTGCATCG	CGGTTGATGACGCTGTACCA GTTCAGTCAGAACAGTGACACG GCACCAATGACACAATAGGAAGAC	65 64 69
	<i>Soly07g056110</i>	LOC101252790	CGTAAGCTACGCCAAGCAA	CAGCTCAGAGTGGCCAAAAC	67
	<i>Soly09g005260</i>	LOC101254519	GGCTTCATCATCACCAAGCA CCCCATACTCATACAAAGATGAGA	GGAACCTCTCAGCAACTATGGA TTGATGAGCCAAATTGACA	65 64
	<i>Soly12g011070</i>	—	GCCAATATCATCTCGATTAATCTGC ATGGCACTCTATTTAGCCAATATC	GCGAGGGAGGAAACTTACG CTACCATATAATAATTGTATGAAGCGAG	64
	<i>Soly12g055750</i>	LOC101250779	ACGATTCGATTGCCCACTG	ACTGCCAGTTGTTGAGGAGTC	68
	<i>Soly02g077270</i>	LOC101251749	CTTGGTAGTGTGCAAGCC GCTCTCAACTATTCTGGAAAGGC	TGAATGGGTTGGGTTGGGTA TGAATGGGTTGGGTTGGGTA	67 68
	<i>Soly03g006260</i>	LOC101254062	TGTTACCAAGGTGCAAAGCAG CAGTACTATACACTTCAATTCTCAATAA	CCAAGAGGCTGTGCAAAAGTG TAATAGTCCAACCAAACAATTAAATA	67 61
NCL	<i>Soly07g062700</i>	LOC101263533	CCCAAATCGTCTTCACCTCTCC CGCGAATAGTCTAAACATGAGAA	AAACGACAGATGTCGACTGC CGGGCATAAACAATAGCCAA	66 65
	<i>Soly12g014110</i>	LOC101257045	AACTCCGATGGCATCTCTGG	CGCTAAAGTGTGCCGTAGC	67
	<i>Soly01g098800</i>	LOC101261070	CAATATTCTGGAATGGCATGGC	GTTCCAGACAGTGATGGATG	65
	<i>Soly02g069710</i>	LOC101265300	GGTGTTCATCTGTGTGTTCC GGGTTTCGATCGGTTTGTCTG	AAAGGAGTCGAAGAGCACATAC CGCCACGCACTCCATTACAAC	65 69
CCX	<i>Soly07g006370</i>	LOC101250521	CCAAACAAACACTTCAATTCTCC CATCTCTCTACTATTATTAAAAAAATGTC	TTCAGAGTCGACGTGCTTCC GAGCTTCTCTTCAGAGTCGA	66 62
	<i>Soly07g042000</i>	LOC101250709	CCCTGTTTAGTTGTGGAGGG CGCTTCATGGCTCCCTATTTC	CCACTTTGTTGCAACAGTAC CCCTGCTTCACCAAATGATGA	65 69
	<i>Soly09g072690</i>	LOC101248713	CCCATTCGTTCAAGCCAA CCTTATACATTTAGCTCTCTCTTC	CAACAAGAGCCATAGTAAGCC CATGTATACACTACATATAAACATCCTT	67 64
	<i>Soly06g009130</i>	—	AAGATGACCTCGCTTGGAAAC	GATATCGCTCCATTTAAGCCCA	65
MHX					

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

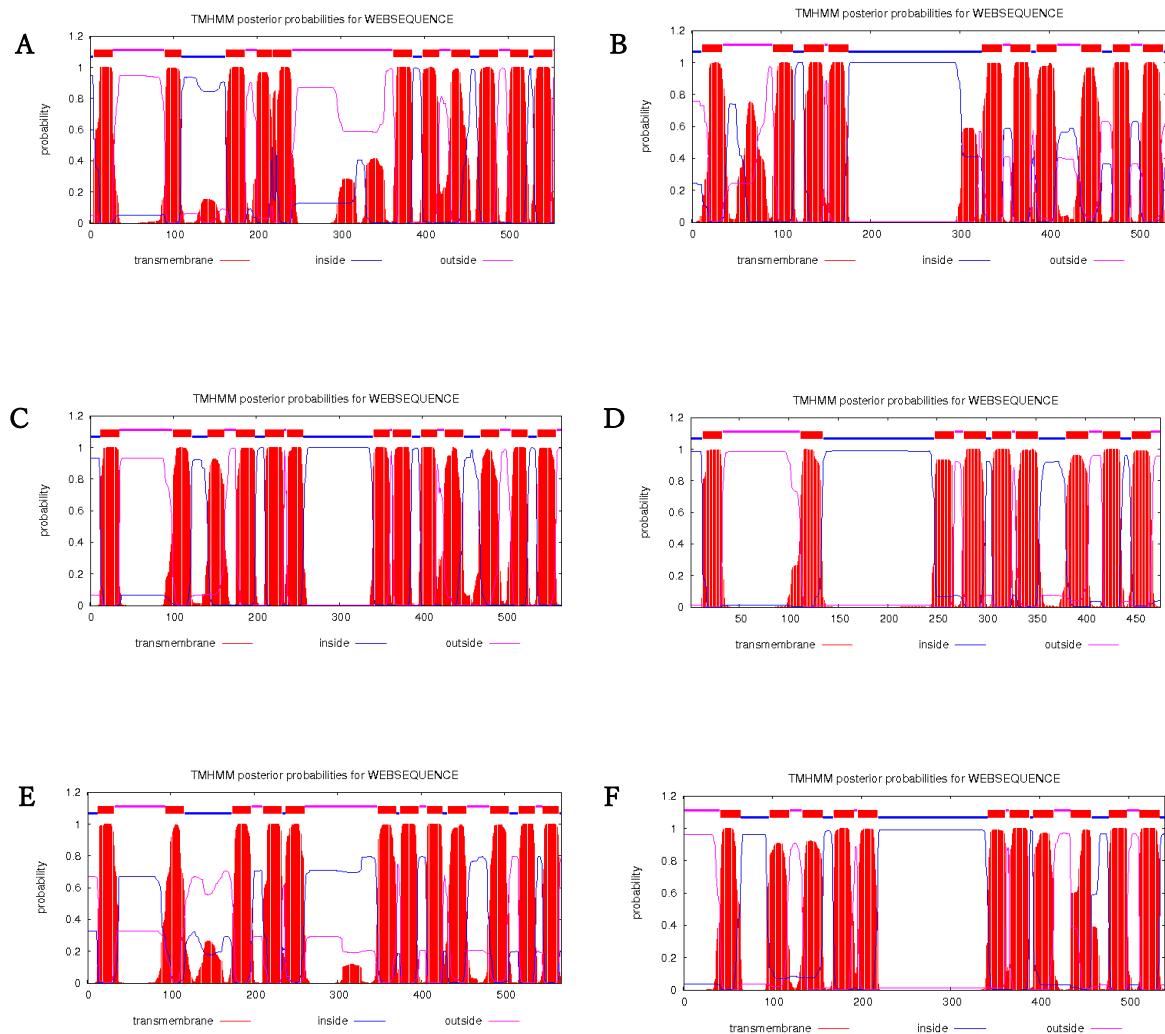
Family name	Locus by ITAG 2.4	Gene symbol by NCBI	Primer sequence(5'→3')		Annealing temp(°C)
			Forward	Reverse	
CAX	<i>Soly03g123790</i>	LOC101267212	GGAATTGCATTTGGCAAGT	CACCCCTCGATGGCATCTACT	56.1
	<i>Soly06g006110</i>	LOC101265339	TGCCAATAGTGGGAAATGCAGCAG	TTGAGAACGCTGACCCAAATGCAAC	58.2
	<i>Soly07g056110</i>	LOC101252790	GTTGGAAATGCGAGCTGAACA	TGGGCTTGTCTGTATAGCC	56.1
	<i>Soly09g005260</i>	LOC101254519	GTGGTCCCTTGTGTGATTG	TCCTGTAGAGTGAAGCTGTGAC	58.2
	<i>Soly12g011070</i>	—	GATGGCCGAGGAAGAGGATCATA	CGGATGCTCTCTACGGTATTAAC	57
	<i>Soly12g055750</i>	LOC101250779	TGAGTCAGCTCATATGGCGTCGC	TGTAGCAGTATGCCAATGGTCCA	62.7
NCL	<i>Soly02g077270</i>	LOC101251749	GCTCTCAACTATTCTGGAAAGGC	TGCATGCCGTTGTACATGATGCAG	60.8
	<i>Soly03g006260</i>	LOC101254062	CAAGCTACGTATGGCAATGTGACC	AGAGTAGCCCCAAAGATGCCGTGAC	58.2
	<i>Soly07g062700</i>	LOC101263533	AGGAAACAAAGGAGAGCACAG	GAAGTTCCATGTTAGACCTCGGG	57
	<i>Soly12g014110</i>	LOC101257045	GGTCGCCGTTCATCAGTGACGA	GTTCACAACTCTCTCTCACCTCCG	58.2
CCX	<i>Soly01g098800</i>	LOC101261070	CGACCAGCAATTTCACTGACTCCAA	TCTGGCTTGACCTCCCTAACTG	58.2
	<i>Soly02g069710</i>	LOC101265300	CGGGTCGGATGCTGATTTGG	CGCCCCACGGACTTCATACAAC	58.2
	<i>Soly07g006370</i>	LOC101250521	GGTCCTTGTGGATGAGG	CCCCACAAACAGGCCAATAACACC	62
	<i>Soly07g042000</i>	LOC101250709	TTAGGGATCGCGAGACTAGTTG	CTTGTAGCTGCGACATCCATC	58.2
	<i>Soly09g072690</i>	LOC101248713	ACTCCTATAGACGCCCTCAAC	CCTCCAAGAAGCCAAATCCACAAACA	60.8
MHX	<i>Soly06g009130</i>	—	CCGGTCCATGGAGAGTGTGTCA	CCAACGTTGTCCTGTGCATAGGC	58.2
<i>Ubiquitin 3</i>	<i>Soly01g056940</i>	—	ACTCTGCCGACTACACATCCA	AACTGCAACACAGCGAGCTAAC	57



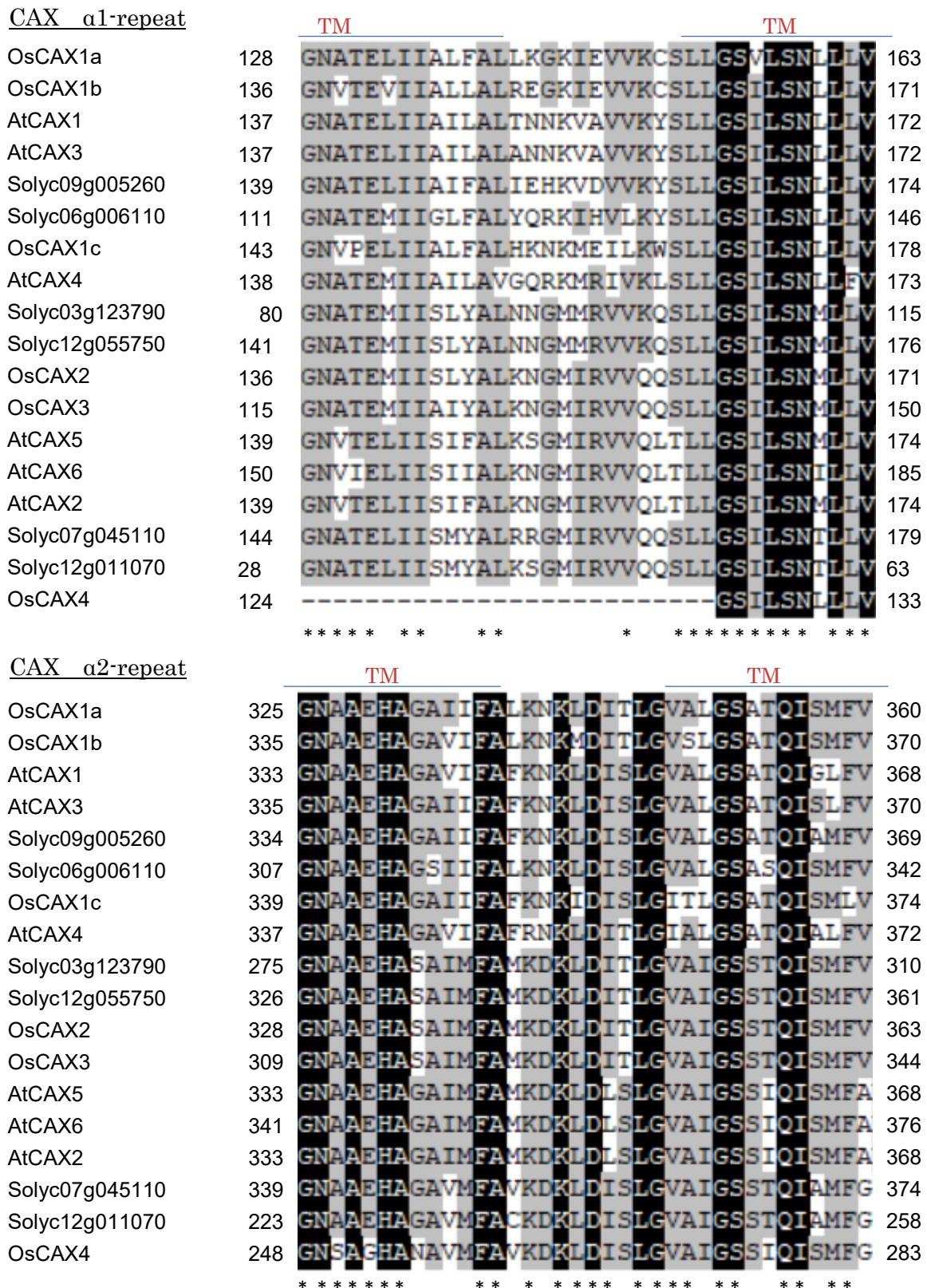
**Figure S1.** Transmembrane domains of SICAX searched using TMHMM. **A)** Solyc03g123790, **B)** Solyc06g006110, **C)** Solyc07g056110, **D)** Solyc09g005260, **E)** Solyc12g011070a, **F)** Solyc12g011070b, c, d, **G)** Solyc12g055750.



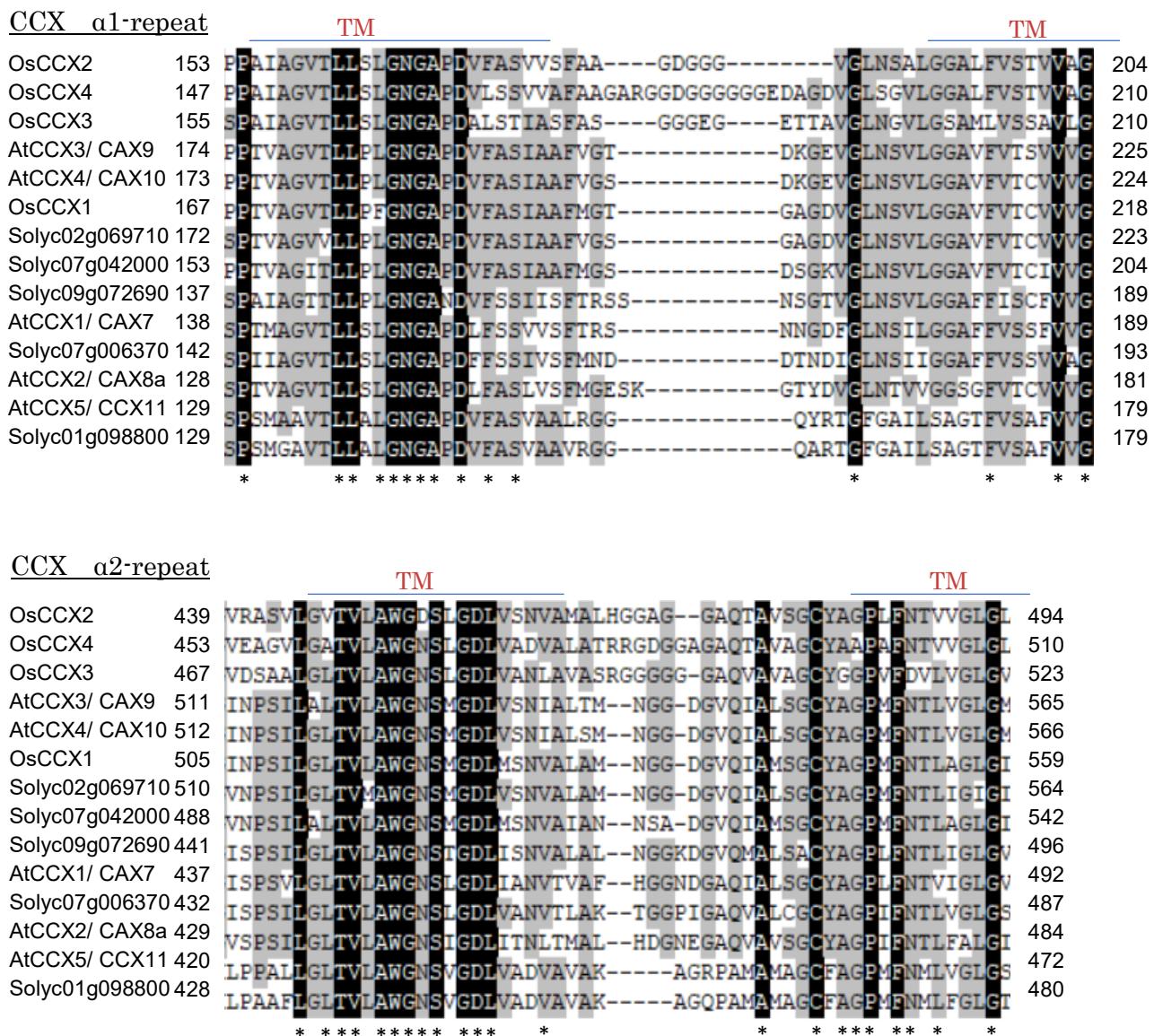
**Figure S2.** Transmembrane domains of SINCL searched using TMHMM. **A)** Solyc02g077270, **B)** Solyc03g006260, **C)** Solyc07g062700, **D)** Solyc12g014110.



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



**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.



**Figure S5.** Multiple alignments of conserved α1-repeat and α2-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	$\alpha$ 1-repeat	TM2	TM3	
OsMHX1	85	NYTIADVALLAFGTSFPQISLATIDAIRNLGQLTAGGLGPGLVGSAAFDLFFPIHAV		141
Solyc06g009130	96	NYTIADITLLAFTSFPQISLATIDAIRNIGLYAGGLGPGLVGSAAFDLFFPIHAV		152
AtMHX	95	NETIADISLLAFTSFPQISLATIDAIRNMGERYAGGLGPGLVGSAAFDLFFPIHAV		151

MHX	$\alpha$ 2-repeat	TM7	TM8	
OsMHX1	384	SPYVIAFTALAPGT SWPDLVASKIAAERQITADSAITNITCSNSVNIYVGIGV		436
Solyc06g009130	401	NPYVIAFTALASGT SWPDLVASKIAAERQITADSAIANITCSNSVNIYIGIGV		453
AtMHX	402	NPYVIAFTALASGT SWPDLVASKIAAERQITADSAIANITCSNSVNIYVGIGV		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 region	TM	TM	
Solyc02g077270	111	GIFGATVFQILMTLPRIVMVIASGVASASKEKAQFQISSGISTTVGATVFNLTLMWGIC		168
Solyc03g006260	96	GIFGATLFQILKAFPRIILVIASGVFTSKDKAQNQVSTGVSTNVGATVFNLTLMWGIC		153
OsEFCAX1/ NCL1	119	GLVGGLLLPILGALPDALLVLVSGLGSRETAQSQVLIQMGLLAGSTVFLTLWGTC		176
OsEFCAX2/ NCL2	111	GIVCGGLFLPILGALPDALLLILVSGLSGTKEVAQSQVLIQMGLLAGSTVMLLTWGSC		168
Solyc07g062700	121	GLIGGLFLPILGALPDAMLLILVSGITGSAAEAQSQVSVGIGLLAGSTVMLLTWGTC		178
Solyc12g014110	111	GIIGGLFLPVGLGALPDAMLLILVSGISGSTAQQSQVSVGMGLLAGSTVMLLTWGTC		168
AtNCL1/ EFCAX1	114	GIVGGGLFLPMGLGALPDAMLLIMVSGLSDAATAQSQVSVGMGLLAGSTVMLLTWGTC		171
AtNCL2a/ EFCAX2a110		GFYGGIIFPLLTMFPRIALILSTGLVGSREMASSRVGNIIIGVTVGYSVFAITIOWGAC		167
AtNCL2b/ EFCAX2b110		GFFGGIIFPLLTMFPRIALILSTGLIGSREIANSMTGNNAVTVGYSVFAITMOWGAC		167

NCL	$\alpha$ 2-repeat	TM	TM	
Solyc02g077270	595	PSFLIPFVMVPLAINARMAIAIFPASQKSSITASLTFS*EYGGVIMNNIMGMATLLAVVCIKD		658
Solyc03g006260	579	PSFLIPFVIVPLAINARMTIAAIYPASQKCSKTASLTFS*EYVGVI>NNIMGMTLLAIVYAKD		642
OsEFCAX1/ NCL1	463	PSFFISFIALPLATNSSEAVSAIIFASRKKLRTSSLTFSEVYGGVIMMNNTLCLGFLALIYIRN		526
OsEFCAX2/ NCL2	455	PSFFISFIVMPLATNSSEAVSAIIFASRKKKRTLSLTFS*EYVGVIMMNNTLCLGFLALVYVRG		517
Solyc07g062700	468	PSFFISFIALPLATNSSEAVSAIIFATRKKQRSASLTFS*EYGAUTMNNLLCSVFLALIVYARG		531
Solyc12g014110	457	PSFFISFIALPLATNSSEAVSAIIFASRKKLRSASLTFS*EYGAUTMNNLLCSVFLALVYIRG		520
AtNCL1/ EFCAX1	464	PSFFISFIALPLATNSSEAVSAIIFASRKKIRTASLTFS*ELCGGVIMNNILCSVFLALIVYVRG		527
AtNCL2a/ EFCAX2a436		PSFYVVVFVVIPLARNLKNTLSAHFCRKDKAKITSDFSEIYKDUTMNNLMGISIILAIIVYARE		499
AtNCL2b/ EFCAX2b457		PSFYVVFAVAPIPLARNLKNTLSAHFCRKKEKAKITSDFSEIYRDVTLNNLGITIILAIIVYIRG		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.