

Supplemental Data

Table S1. List of CIA2 and CIL homologous proteins.

The N-terminal 1-200 amino acid sequences of Arabidopsis CIA2 and CIL were subjected to BLAST analysis to identify homologous proteins in the NCBI and Gramene databases. Information on 72 full-length CIA2 and CIL homologues is summarized below.

Protein name ^a	Gene symbol / Gene locus ^{bc}	Amino acid	Species	Sequence ID	Description ^d	Percentage identity to CIA2 FL (%) ^e	E-value ^e	Percentage identity to CIL FL (%) ^e	E-value ^e
Aegta_CIL-I	LOC109759413 AET6Gv20305800 ^c	494	<i>Aegilops tauschii subsp. tauschii</i>	XP_020173826.1	CCT(440-483aa)	32.15	2.00E-47	31.39	9.00E-49
Aegta_CIL-II	LOC109734132	457	<i>Aegilops tauschii subsp. tauschii</i>	XP_020148948.1	CCT(401-445aa)	27.4	4.00E-23	28.64	3.00E-25
Aegta_Uncharacterized protein	AET7Gv21020300 ^c	267	<i>Aegilops tauschii subsp. tauschii</i>	UniProtKB-M8BAB9	-	39.39	6.00E-11	38.95	2.00E-09
Ambtr_CIA2	LOC18440680 ^b AMTR_s00025p00156240 ^c	436	<i>Amborella trichopoda</i>	XP_006850881.1	CCT(382-425aa)	32.53	3.00E-44	32.39	8.00E-43
Araly_CIA2-I	LOC9305708 ^b	392	<i>Arabidopsis lyrata</i>	XP_002867585.1	CCT(339-382aa)	55.48	2.00E-132	85.71	0
Araly_CIA2-II	LOC9302264 ^b	438	<i>Arabidopsis lyrata</i>	XP_020866733.1	CCT(386-429aa)	87.97	0	56.36	1.00E-131
CIL (CMF9 ^a)	AT4G25990 ^b	394	<i>Arabidopsis thaliana</i>	NP_567737.1	CCT(341-384aa)	55.98	1.00E-129	100	0
CIA2 (CMF14 ^a)	AT5G57180 ^b	435	<i>Arabidopsis thaliana</i>	NP_568852.2	CCT(383-426aa)	100	0	54.5	2.00E-129
Bradi_CMF7 ^a	LOC100822180 ^b BRADI_1g34060 ^c	448	<i>Brachypodium distachyon</i>	XP_003560511.1	CCT(398-436aa)	40	4.00E-10	28.5	5.00E-26
Bradi_CMF3 ^a	LOC100822550 ^b BRADI_3g03770 ^c	459	<i>Brachypodium distachyon</i>	XP_014756479.1	CCT(416-452aa)	32.48	5.00E-38	33	3.00E-38
Bran_CIA2-I	LOC106444616 ^b BnaA01g15160D ^c	382	<i>Brassica napus</i>	XP_013741528.1	CCT(327-372aa)	53.29	3.00E-130	64.25	1.00E-164
Bran_CIL-I	LOC106388956 ^b BnaA02g08300D ^c	392	<i>Brassica napus</i>	XP_013684589.1	CCT(340-383aa)	64.03	9.00E-164	50.99	2.00E-113
Bran_CIL-II	LOC106371508 ^b BnaA10g11220D ^c	397	<i>Brassica napus</i>	XP_013667045.1	CCT(345-388aa)	62.5	1.00E-150	56.18	5.00E-114
Bran_CIL-III	LOC106376068 ^b BnaC01g17920D ^c	391	<i>Brassica napus</i>	XP_013671573.1	CCT(336-381aa)	53.02	5.00E-131	64.51	3.00E-163
Bran_CIA2-II	LOC106377535 ^b	386	<i>Brassica napus</i>	XP_013673245.1	CCT(334-377aa)	60.22	5.00E-153	50.37	7.00E-109

	BnaC02g11770D ^c								
Brana_CIA2-III	LOC106409124 ^b BnaC07g39980D ^c	397	<i>Brassica napus</i>	XP_013705259.1	CCT(344-389aa)	50.66	1.00E-96	63.1	5.00E-127
Brana_CIL-IV	LOC106418421 ^b BnaC09g53340D ^c	398	<i>Brassica napus</i>	XP_013714579.1	CCT(346-389aa)	63.98	3.00E-159	56.61	7.00E-121
Capru_CIA2-I	LOC17879835	392	<i>Capsella rubella</i>	XP_006283882.1	CCT(339-382aa)	53.54	1.00E-117	78.3	0
Capru_CIA2-II	LOC17876953	436	<i>Capsella rubella</i>	XP_006280489.1	CCT(384-427aa)	71.71	0	51.05	8.00E-115
Capru_CIL	LOC107877814	441	<i>Capsicum annuum</i>	XP_016580048.1	CCT(375-417aa)	43.76	4.00E-86	42.4	9.00E-79
Capba_CCT protein	CQW23_16970	415	<i>Capsicum baccatum</i>	PHT42945.1	CCT(364-407aa)	43.74	6.00E-88	43.44	2.00E-80
Capch_CCT protein	BC332_18791	442	<i>Capsicum chinense</i>	PHU11861.1	CCT(376-434aa)	43.76	9.00E-87	42.65	6.00E-79
Cicar_CIL-I	LOC101508698	400	<i>Cicer arietinum</i>	XP_004507897.1	CCT(354-396aa)	46.56	2.00E-91	42.33	2.00E-78
Cicar_CIL-II	LOC101511273	303	<i>Cicer arietinum</i>	XP_004487994.2	-	32.34	2.00E-30	30.77	8.00E-25
Ginbi_COL16	N/A	436	<i>Ginkgo biloba</i>	ASW41094.1	CCT(381-424aa)	44.62	1.00E-23	42.64	6.00E-22
Glyma_CIA2-I	LOC100783619 GLYMA_09G059800 ^c	374	<i>Glycine max</i>	XP_006586995.1	CCT(344-373aa)	34.18	2.00E-46	35.75	3.00E-40
Glyma_CIA2-II	LOC100784788 GLYMA_13G100700 ^c	399	<i>Glycine max</i>	XP_003543009.1	CCT(349-391aa)	43.58	2.00E-76	44.16	6.00E-78
Glyma_CIA2-III	LOC102670319 GLYMA_15G166500 ^c	395	<i>Glycine max</i>	XP_006597800.1	-	34.34	4.00E-46	32.64	2.00E-36
Glyma_CIA2-IV	LOC100810303 GLYMA_17G059100 ^c	398	<i>Glycine max</i>	XP_003549301.1	CCT(347-389aa)	45.11	5.00E-79	45.29	5.00E-77
Horvu_CMF3 ^a	HORVU6Hr1G021460 ^c	480	<i>Hordeum vulgare subsp. Vulgare</i>	UniProtKB-A0A287TJQ3	CCT(436-478aa)	32.34	1.00E-44	32.44	7.00E-47
Horvu_CIA2 (Horvu_CMF7 ^a)	HORVU7Hr1G097630 ^c	459	<i>Hordeum vulgare subsp. Vulgare</i>	SNU42600.1	CCT(403-448aa)	29.59	2.00E-23	27.89	2.00E-25
Medtr_CIA2-I	LOC11443621 MTR_2g038010 ^c	313	<i>Medicago truncatula</i>	XP_003595074.1	-	32.04	6.00E-31	30.32	6.00E-26
Medtr_CIA2-II	LOC11441754 MTR_4g127420 ^c	379	<i>Medicago truncatula</i>	XP_003610054.1	CCT(342-378aa)	45.33	3.00E-70	42.33	4.00E-63
Medtr_COL	MTR_4g0071811 ^b	393	<i>Medicago truncatula</i>	RHN64690.1	CCT(342-384aa)	45.78	2.00E-75	42.64	3.00E-68
Nicat_CIL-I	LOC109238457 A4A49_06707 ^c	428	<i>Nicotiana attenuata</i>	XP_019260475.1	CCT(373-415aa)	43.82	2.00E-85	42.59	7.00E-82
Nicat_CIL-II	LOC109238456 A4A49_06709 ^c	385	<i>Nicotiana attenuata</i>	XP_019260474.1	-	39.91	1.00E-66	41.36	2.00E-67
Nicsy_CIL-I	LOC104229215	399	<i>Nicotiana glauca</i>	XP_009780110.1	-	42.28	5.00E-67	40.83	3.00E-68
Nicsy_CIL-II	LOC104246955	424	<i>Nicotiana glauca</i>	XP_009801175.1	CCT(373-416aa)	43.31	3.00E-83	42.35	8.00E-81
Nicta_CIL	LOC107760235	425	<i>Nicotiana tabacum</i>	XP_016433772.1	CCT(370-412aa)	44.62	3.00E-88	43.5	2.00E-86

Nicto_CIL	LOC104090569	425	<i>Nicotiana tomentosiformis</i>	XP_009593986.1	CCT(370-413aa)	44.84	6.00E-89	43.74	4.00E-87
Orybr_CIA2-I	LOC102710464 OB02G13170 ^c	480	<i>Oryza brachyantha</i>	XP_006646882.1	CCT(426-469aa)	37.55	1.00E-34	39.74	9.00E-37
Orybr_CIA2-II	LOC102703227 OB06G33920 ^c	432	<i>Oryza brachyantha</i>	XP_015693696.1	CCT(371-415aa)	29.02	2.00E-28	31.28	2.00E-32
Orygla_CCT protein-I	ORGLA02G0034600 ^e	484	<i>Oryza glaberrima</i>	UniProtKB-I1NX90	CCT(430-472aa)	61.61	7.00E-34	33.19	8.00E-47
Orygla_CCT protein-II	ORGLA06G0219500 ^e	466	<i>Oryza glaberrima</i>	UniProtKB-I1Q4Y2	CCT(412-454aa)	29.3	7.00E-31	29.64	6.00E-28
OsI_CMF3 ^a	OsI_05849 BGIOGA007536 ^c	474	<i>Oryza sativa (Indica Group)</i>	EAY84475.1	CCT(430-463aa)	54.46	3.00E-25	31.5	1.00E-37
OsI_CMF7 ^a	OsI_24346 BGIOGA023549 ^c	466	<i>Oryza sativa (Indica Group)</i>	EEC81257.1	CCT(416-454aa)	29.3	7.00E-31	29.64	6.00E-28
OsJ_CMF3 ^a	LOC4328296 Os02g0148000 ^c	482	<i>Oryza sativa (Japonica Group)</i>	XP_015624719.1	CCT(428-471aa)	61.61	7.00E-34	33.41	2.00E-46
OsJ_CMF7 ^a	LOC4341958 Os06g0699600 ^c	466	<i>Oryza sativa (Japonica Group)</i>	XP_015644406.1	CCT(416-454aa)	29.07	8.00E-30	29.4	6.00E-27
Phavu_CCT protein	PHAVU_003G141200g	380	<i>Phaseolus vulgaris</i>	XP_007154712.1	CCT(340-378aa)	42.47	2.00E-72	43.48	7.00E-69
Phavu_hypothetical protein	PHAVU_009G236100g	264	<i>Phaseolus vulgaris</i>	XP_007138773.1	-	29.19	4.00E-23	27.93	4.00E-16
Setit_CIA2	LOC101763382 SETIT_006393mg ^c	459	<i>Setaria italica</i>	XP_004966116.1	-	25.6	4.00E-15	45.21	1.00E-13
Setit_CMF3 ^a	LOC101777609 SETIT_017125mg ^c	483	<i>Setaria italica</i>	XP_012698033.2	CCT(429-472aa)	34.75	2.00E-54	33.61	2.00E-51
Solch_CCT protein	EJD97_009489	432	<i>Solanum chilense</i>	TMW95010.1	CCT(381-423aa)	44.16	8.00E-91	43.35	8.00E-85
Solly_CIA2	LOC101255506 Solyc07g008540.3 ^c	432	<i>Solanum lycopersicum</i>	XP_004242804.1	CCT(381-424aa)	44.35	5.00E-91	43.12	2.00E-84
Solpe_CIA2	LOC107026098	431	<i>Solanum pennellii</i>	XP_015082438.1	CCT(380-423aa)	44.01	5.00E-92	43.22	6.00E-87
Soltu_CIL	LOC102605364 ^b PGSC0003DMG400022983 ^c	432	<i>Solanum tuberosum</i>	XP_006362450.1	CCT(381-424aa)	45.72	9.00E-92	42.2	6.00E-82
Sorbi_CMF3 ^a	LOC8074627 SORBI_3004G040100 ^c	486	<i>Sorghum bicolor</i>	XP_002451540.1	CCT(432-475aa)	33.8	4.00E-52	44.29	4.00E-11
Sorbi_CIA2	LOC8065562 SORBI_3010G250100 ^c	454	<i>Sorghum bicolor</i>	XP_021304472.1	-	40.3	3.00E-09	34.38	2.00E-51
Triae_CCT protein-I	TraesCS6A02G118000 ^c	492	<i>Triticum aestivum</i>	UniProtKB-A0A3B6NM01	CCT(438-480aa)	32.48	2.00E-46	32.45	7.00E-48
Triae_CCT protein-II	TraesCS6B02G146200 ^c	484	<i>Triticum aestivum</i>	UniProtKB-A0A3B6PIL6	CCT(440-482aa)	30.57	8.00E-38	31.3	3.00E-39
Triae_CCT protein-III	TraesCS6D02G108000 ^c	494	<i>Triticum aestivum</i>	UniProtKB-A0A3B6QBQ3	CCT(440-482aa)	32.15	2.00E-47	31.39	9.00E-49
Triae_CCT protein-IV	TraesCS7A02G422200 ^c	458	<i>Triticum aestivum</i>	UniProtKB-A0A3B6RKZ5	CCT(404-446aa)	29.12	5.00E-25	28.68	7.00E-28
Triae_CCT protein-V	TraesCS7B02G322600 ^c	457	<i>Triticum aestivum</i>	UniProtKB-A0A3B6SPQ1	CCT(403-445aa)	27.69	1.00E-23	27.76	5.00E-26

Triae_CCT protein-VI	TraesCS7D02G414400 ^c	457	<i>Triticum aestivum</i>	UniProtKB - A0A3B6TPS5	CCT(403-445aa)	27.4	5.00E-23	28.64	2.00E-25
Tritu_CCT protein-I	TRITD_6Av1G037420 ^{bc}	482	<i>Triticum turgidum subsp. duru</i>	VAI43762.1	CCT(438-480aa)	31.67	6.00E-42	31.62	2.00E-43
Tritu_CCT protein-II	TRITD_6Bv1G050550 ^{bc}	501	<i>Triticum turgidum subsp. duru</i>	VAI55361.1	CCT(440-482aa)	31.46	9.00E-42	32.23	3.00E-43
Tritu_CCT protein-III	TRITD_7Av1G227500 ^{bc}	453	<i>Triticum turgidum subsp. duru</i>	VAI79113.1	CCT(399-441aa)	29.12	5.00E-25	28.68	6.00E-28
Tritu_CCT protein-IV	TRITD_7Bv1G176630 ^{bc}	457	<i>Triticum turgidum subsp. duru</i>	VAI91171.1	CCT(403-445aa)	27.69	1.00E-23	27.76	5.00E-26
Zeama_Uncharacterized protein-I	LOC100501277 Zm00001d014664 ^e	435	<i>Zea mays</i>	NP_001353852.1	-	26.7	4.00E-14	26.91	5.00E-18
Zeama_CIA2-I	LOC103626617 Zm00001d015268 ^e	485	<i>Zea mays</i>	XP_008645243.1	CCT(431-474aa)	33.74	5.00E-50	33.96	1.00E-50
Zeama_Uncharacterized protein-II	LOC100384273 Zm00001d036485 ^e	443	<i>Zea mays</i>	NP_001170309.2	-	26.24	2.00E-17	26.37	5.00E-17
Zeama_CIA2-II	LOC100281423 Zm00001d053880 ^e	459	<i>Zea mays</i>	XP_008677196.1	CCT(405-448aa)	63.72	6.00E-35	25.11	2.00E-12

^a CMF proteins, as per Cockram et al. (2012).

^{b,c} Gene symbol and locus refer to the NCBI or Gramene databases.

^d CCT-motif fragment, as predicted by PROSITE (prosite.expasy.org).

^e Identity value and E-value from the NCBI database.