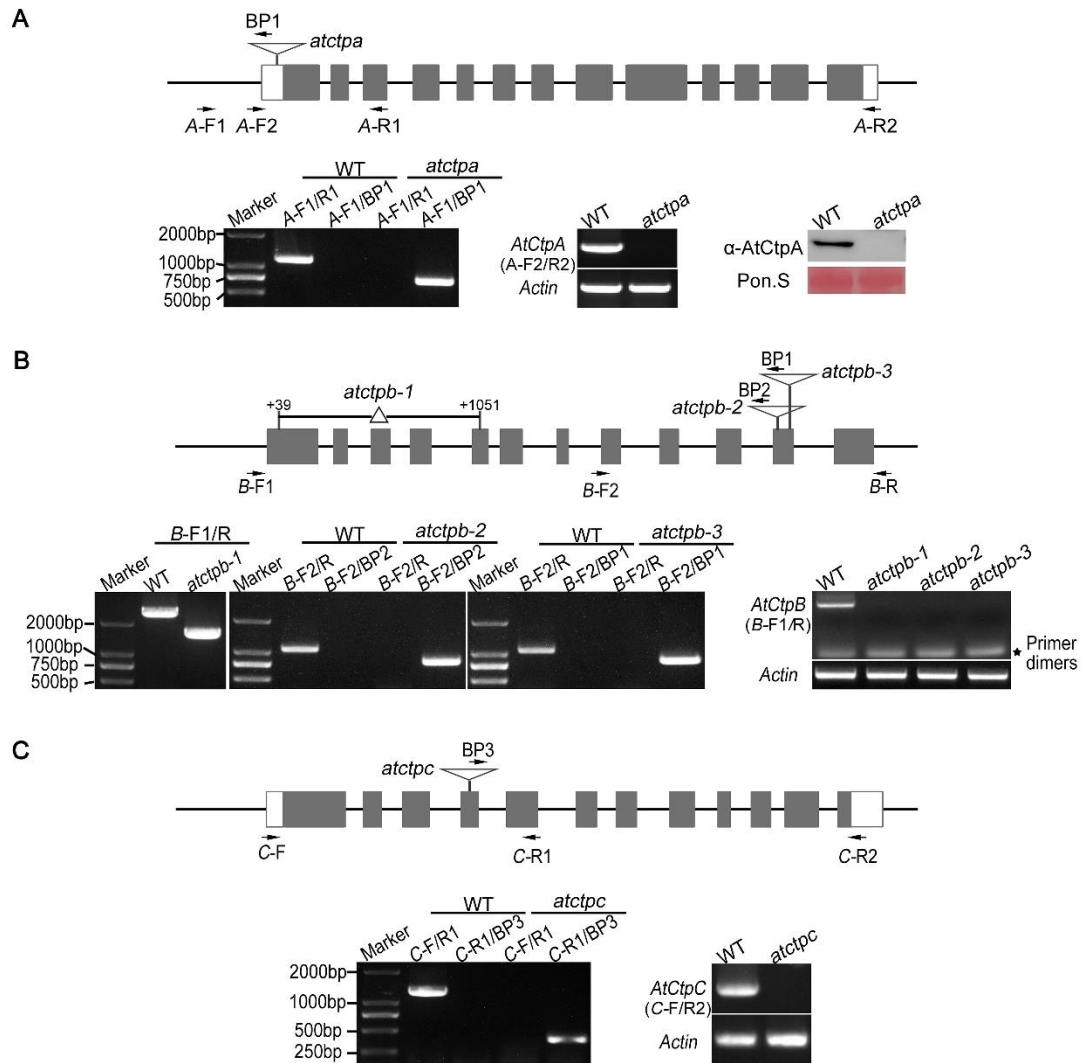


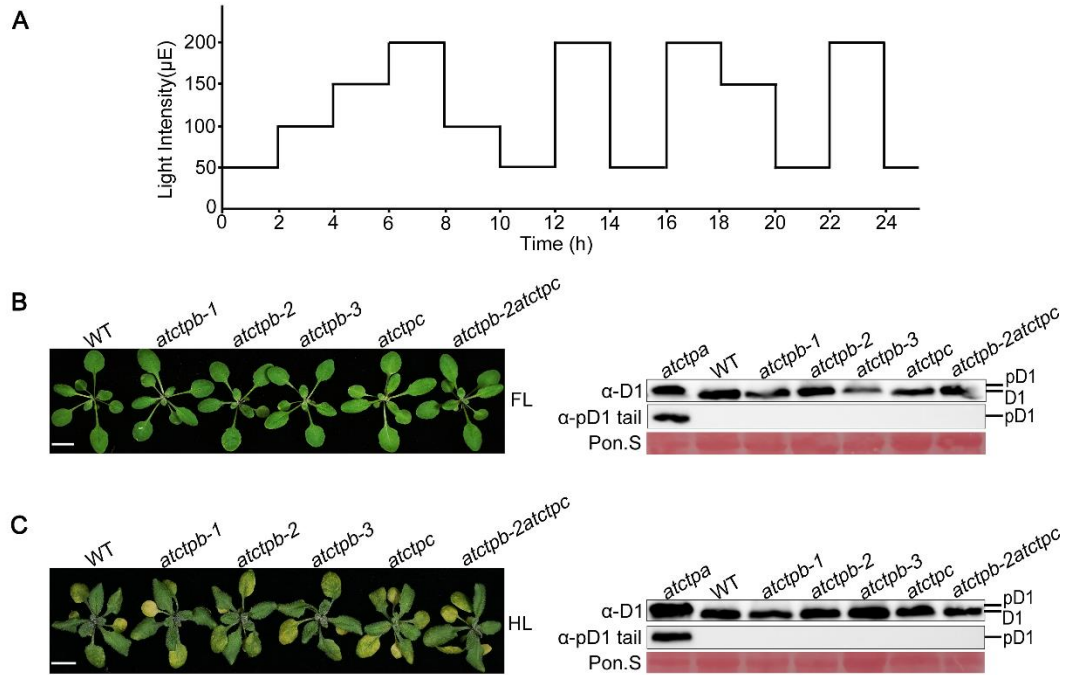
Supplementary Figure S1. Phylogenetic tree constructed by Maximum-Likelihood method.

To make the relationships of Ctp clades in Figure 1 more trustworthy, 286 Ctp proteins analyzed in figure 1 were also used to construct phylogenetic tree by MAGA6 using the method of Maximum-Likelihood, with the bootstrapping value set at 500 replications. The new tree displays the same topology as in figure 1.



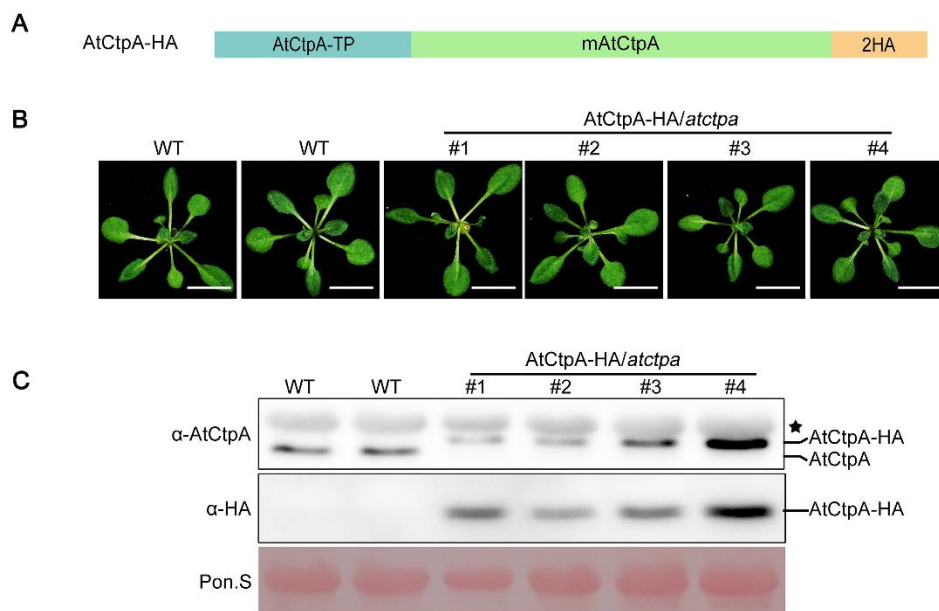
Supplementary Figure S2. Molecular characterizations of *atctpa* (A), *atctpb* (B), and *atctpc* (C) mutants.

Upper panels in (A), (B), and (C) are schematic representations of different alleles of *atctpa*, *atctpb*, and *atctpc*. White boxes, the 5'- and 3'-UTR of genes; grey boxes, exons; black lines through boxes, the flanking regions and introns of genes; inverted triangles, T-DNA insertions; Δ , DNA deletions; horizontal arrows, PCR primers used for characterizing mutants. Molecular characterizations of mutants were placed below the schematics, including genotyping by PCR (left) and transcription level analyses by RT-PCR (right in (B) and (C) or middle in (A)), of which the forward primer (*A-F2*) for analysis of *AtCtpA* transcription level is located in the 5'-UTR region before the T-DNA insertion site. For *atctpa* mutant, *AtCtpA* protein level was further analyzed by immunoblot against α -*AtCtpA* antibody (right). The filters stained with Ponceau S (Pon. S) were used as loading controls.



Supplementary Figure S3. Analyses of *atctpb* and *atctpc* mutants under FL and HL light conditions.

(A) Schematic diagram of light intensity changes during a 24-hour period (Fluctuating light, FL). (B) and (C) Characterizations of the phenotypes (left) and pD1 processing statuses (right) of *atctpb* and *atctpc* mutants under FL and HL conditions. The plants were grown in soil for three weeks as the following continuous light conditions: FL, under normal light (NL, 80 $\mu\text{mol/s/m}^2$) for one week and then under FL for two weeks; high light (HL, 350 $\mu\text{mol/s/m}^2$), under NL for two weeks and then under HL for one week. Scale bars denote 1 cm. After photographed, the pD1 processing statuses in plants were analyzed by immunoblot against α -D1 (for D1 and pD1) and α -pD1 tail (for pD1). The filters stained with Ponceau S (Pon. S) were used as loading controls.

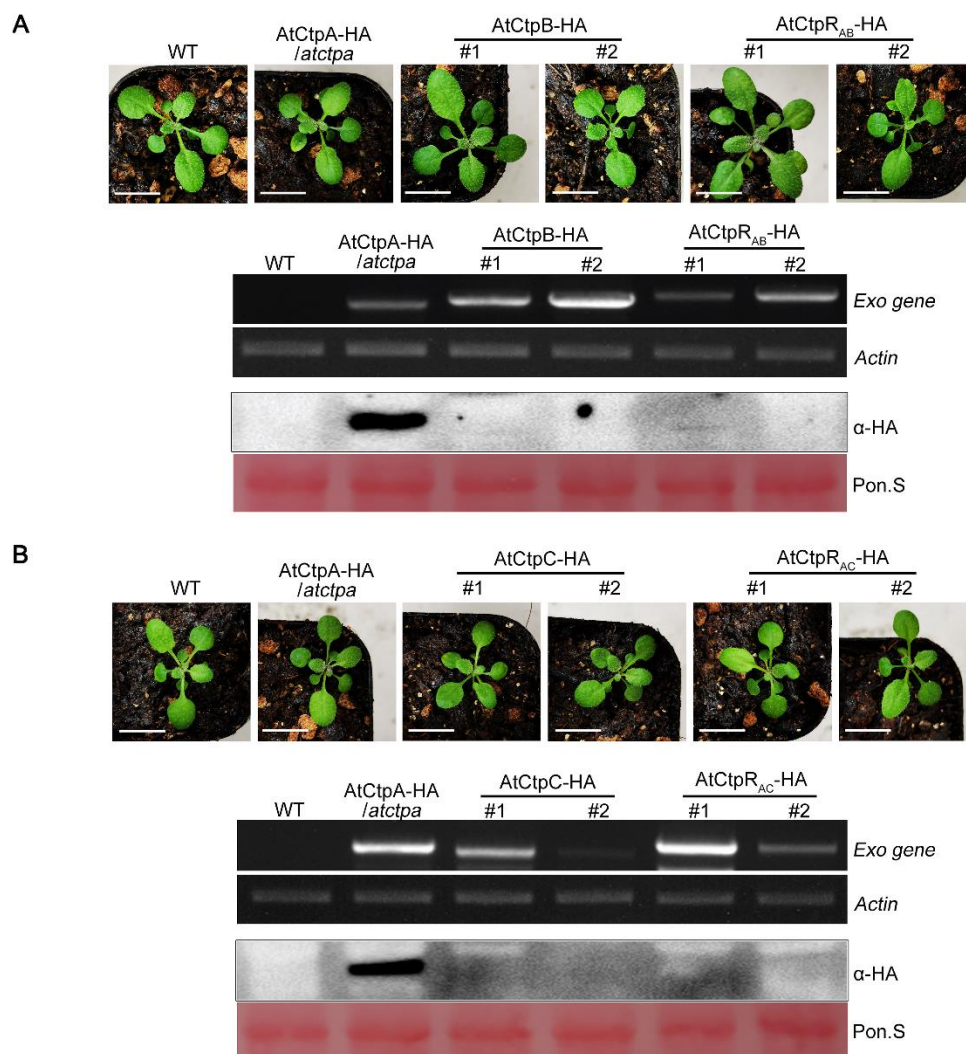


Supplementary Figure S4. Complementation of *atctpa* mutant phenotypes with *AtCtpA*.

(A) Schematic diagram of AtCtpA-HA for the complementation analysis. AtCtpA-TP is the chloroplastic transit peptide, mAtCtpA is the mature peptide; the 2HA indicates a double hemagglutinin tag.

(B) The phenotypes of transgenic *atctpa* plants carrying CaMV 35S promoter-driven *AtCtpA-HA*. The plants were grown on 1/2 MS medium with 1% sucrose under continuous low light (LL, 25 $\mu\text{mol/s/m}^2$) for three weeks. AtCtpA-HA #1-4 indicate different independent transgenic lines. Scale bars represent 1cm.

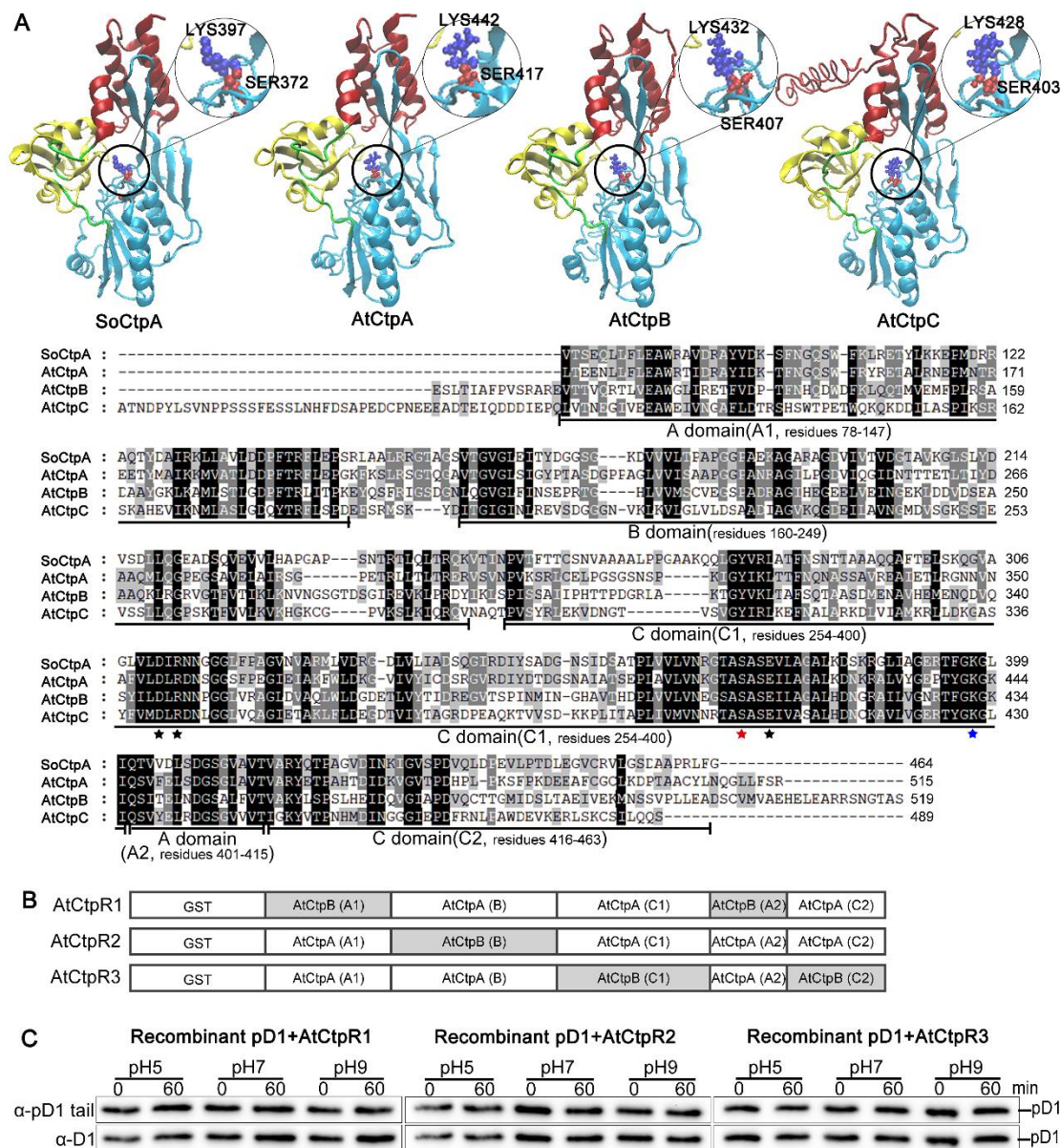
(C) The AtCtpA proteins levels of the plants in (B) were analyzed by immunoblot with α -AtCtpA and α -HA antibodies. The filter stained with Ponceau S (Pon. S) was used as loading control. Asterisk indicates unspecific bands.



Supplementary Figure S5. Characterizations of transgenic plants carrying *AtCtpB* or *R_{AB}* and *AtCtpC* or *R_{AC}* driven by 35S promoter in wild type background.

AtCtpB-HA or *AtCtpR_{AB}-HA* and *AtCtpC-HA* or *AtCtpR_{AC}-HA*, driven by CAMV 35S, were transformed into wild type (WT) Columbia through agrobacteria mediated method, and the diagrams for them were the same as Figure 6A. The upper panels in (A) and (B): T2 transgenic plants grown in soil under NL light (80 $\mu\text{mol/s/m}^2$) for two weeks. #1 and #2 represent two independent lines. Scale bars indicate 1 cm. The lower panels in (A) and (B): the expressions of exogenous transgenes (*Exo*) in transgenic

plants were analyzed at RNA (top two images) and protein (bottom two images) levels by semi qRT-PCR and immunoblot. Native *Actin 2* (*AT3G18780*) and the filters stained with Ponceau S (Pon. S) were used as quantity controls, respectively.



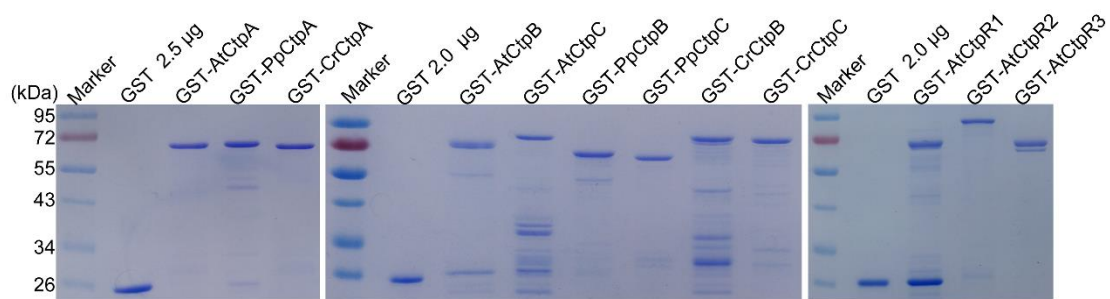
Supplementary Figure S6. Domain swapping Analysis of AtctpA and ActpB.

(A) The structure (upper) and sequence (lower) comparisons of SoCtpA, AtCtpA, AtCtpB, and AtCtpC. The tertiary structure of *Scenedesmus obliquus* CtpA (SoCtpA) was obtained from PDB database (<https://www.rcsb.org/structure/1fcf>). The 3D structures of AtCtpA, AtCtpB, and AtCtpC were predicted by I-TASSER (Roy et al., 2012; Yang and Zhang, 2015; Zhang et al., 2017; Zhang, 2009). These four pdb files were uploaded in the Visual Molecular Dynamics program (Humphrey et al., 1996) to generate the presented structures. A domain is colored in red, B domain in yellow, C domain in blue, and loops between domains in green. The amino acids of catalytic dyad in structures were colored in blue (Lys) and red (Ser) as showed by magnification. Sequence comparisons were performed with ClustalW program in MEGA6. The structural domains are marked with black straight lines below the

corresponding sequences. The conserved amino acids essential for catalytic activity of CtpA (Inagaki et al., 2001; Che et al. 2013) are indicated by asterisks, in which Lys and Ser composing the catalytic dyad are marked with blue and red asterisks, respectively.

(B) Schematic diagrams for domain swapping experiment between AtCtpA and AtCtpB. The A, B, and C domains in GST fused AtCtpA were respectively replaced by their counterparts in AtCtpB (grey boxes) to form recombinant proteins AtCtpR1, AtCtpR2, and AtCtpR3. Un-swapped domains in each protein were drawn in white boxes.

(C) *In vitro* protease activity tests of AtCtpR1, AtCtpR2, and AtCtpR3 were carried out by using synthesized pD1 substrate as that in figure 4.



Supplementary Figure S7. SDS-PAGE analyses of Ctp proteins used in the protease activity assays.

After purification, the amounts of GST-Ctps in eluents were evaluated by SDS-PAGE analyses relative to standard GST protein. Ten µg of Ctp proteins were used in subsequent protease activity assays.

Supplementary Table 1 Protein accession numbers in phylogenetic tree analyses.

pD1 Type	Organism	CtpA				CtpB				CtpC				Database
		Accession number	coverage (%)	Score	E-value	Accession number	coverage (%)	Score	E-value	Accession number	coverage (%)	Score	E-value	
Group I	Cyanophyta													
(16)	(Prokaryotic)													
	<i>Synechocystis sp.</i> <i>PCC 6803</i>	WP_010873417	—	—	—	WP_010871361	—	—	—	WP_010872128	—	—	—	NCBI
	<i>Synechococcus</i> <i>elongatus PCC 7942</i>	ABB58360.1	88	480	3E-170	ABB56548.1	82	365	4E-124	ABB56744.1	100	543	0	NCBI
	<i>Leptolyngbya</i> <i>boryana</i>	WP_017287738.1	86	458	3E-161	WP_017289088.1	84	417	5E-144	WP_026148389.1	98	567	0	NCBI
	<i>Geitlerinema sp. PCC</i> <i>7407</i>	WP_015173572.1	97	494	2E-176	WP_015172436.1	93	431	1E-150	WP_015170194.1	98	536	0	NCBI
	<i>Leptolyngbya ohadii</i>	WP_088893494.1	96	474	2E-167	WP_088894311.1	82	390	2E-133	WP_088892848.1	97	531	0	NCBI
	<i>Pleurocapsa minor</i>	WP_015144827.1	95	565	0	WP_015143772.1	84	532	0	WP_015142506.1	99	639	0	NCBI
	<i>Limnoraphis robusta</i> <i>CS-951</i>	KKD37180.1	95	499	1E-177	KKD35691.1	85	412	5E-142	KKD37108.1	98	545	0	NCBI
	<i>Rippkaea orientalis</i>	WP_012593970.1	96	564	0	WP_012594914.1	88	563	0	WP_15957337.1	98	634	0	NCBI
	<i>Gloeocapsa sp. PCC</i> <i>7428</i>	WP_015188917.1	90	493	7E-175	WP_015186501.1	82	419	5E-145	WP_015190966.1	98	557	0	NCBI
	<i>Oscillatoriales</i> <i>cyanobacterium</i> <i>JSC-12</i>	WP_009555551.1	95	471	2E-166	WP_009555425.1	82	425	2E-147	WP_009557210.1	98	559	0	NCBI
	<i>Leptolyngbya sp.</i> <i>PCC 6406</i>	WP_027268870.1	96	471	1E-166	WP_071992215.1	82	367	9E-125	WP_008316952.1	99	530	0	NCBI

<i>Chroogloeocystis siderophila</i>	WP_073548808.1	90	489	8E-174	WP_073549695.1	82	419	4E-145	WP_073548177.1	98	559	0	NCBI
<i>Planktothrix tepida</i>	WP_072717855.1	95	503	5E-179	WP_072717382.1	82	420	2E-145	WP_083580024.1	95	551	0	NCBI
<i>Oscillatoria sp. PCC 10802</i>	WP_017716499.1	95	495	8E-176	WP_017717799.1	82	430	2E-149	WP_026098110.1	97	555	0	NCBI
<i>Oscillatoriales cyanobacterium CG2_30_40_61</i>	OIP73180.1	95	500	4E-178	OIP67295.1	82	419	2E-145	OIP68024.1	99	561	0	NCBI
<i>Planktothrix sp. PCC 11201</i>	WP_079679774.1	95	507	1E-180	WP_079678415.1	82	416	9E-144	WP_079680804.1	95	547	0	NCBI
<i>Planktothrix agardhii</i>	WP_042153271.1	95	490	4E-173	WP_042155587.1	82	417	7E-144	WP_042154560.1	99	558	0	NCBI
<i>Planktothrix paucivesiculata PCC 9631</i>	VXD20545.1	95	502	1E-178	VXD25008.1	82	425	2E-147	VXD16497.1	99	560	0	NCBI
<i>Roseofilum reptotaenium AO1-A</i>	OJJ24040.1	93	472	6E-167	OJJ25102.1	94	406	3E-140	OJJ25011.1	95	524	0	NCBI
<i>Phormidium ambiguum</i>	WP_073593457.1	90	490	5E-174	WP_073591607.1	82	364	2E-123	—	—	—	—	NCBI

Group II
(9)

Chlorophyta (Eukaryotic)													
<i>Chlamydomonas reinhardtii</i>	Cre10.g420550.t1.1	96	357	1.4E-118	Cre10.g453807.t2.1	96	355	4E-116	Cre06.g265850.t1.1	93	267	1.2E-80	JGI
					Cre10.g426050.t1.2	79	229	3E-40	Cre17.g739150.t1.2	83	261	5E-30	JGI
<i>Dunaliella salina</i>	Dusal.0111s00010.1	96	359	1.1E-119	Dusal.0015s00042.1	83	241	1.4E-74	Dusal.1339s00002.1	88	289	4E-91	JGI
	1				1				1				
<i>Volvox carteri</i>		96	372	5.3E-124	Vocar.0030s0105.1	96	355	3E-116	Vocar.0002s0139.1	93	241	9E-71	JGI

	Vocar.0016s0059.2												
					Vocar.0005s0358.1	76	278	4E-41	Vocar.0003s0289.1	74	183	3E-32	JGI
<i>Coccomyxa</i>	XP_005648207.1	94	413	1.3E-141	XP_005645927.1	98	372.9	2E-125	XP_005652247.1	98	292	3.6E-94	NCBI
<i>subellipsoidea C-169</i>													
					XP_005648181.1	94	197	4.9E-58	XP_005647465.1	85	125	1.3E-32	NCBI
<i>Micromonas pusilla</i>	XP_003056496.1	94	364	1.1E-121	—	—	—	—	XP_003063156.1	87	271	4.5E-87	NCBI
<i>Micromonas sp.</i>	XP_002502055.1	95	364	1.2E-121	—	—	—	—	XP_002506449.1	94	310	9.1E-101	NCBI
<i>RCC299</i>													
<i>Ostreococcus</i>	XP_001415400.1	96	352	1.5E-118	—	—	—	—	XP_001417628.1	89	305	5.1E-99	NCBI
<i>lucimarinus</i>													
<i>Scenedesmus</i>	O04073.1	95	392	1E-136	—	—	—	—	—	—	—	—	NCBI
<i>obliquus</i>													
<i>Monoraphidium</i>	XP_013900651.1	97	388	1E-133	XP_013901188.1	85	298	1E-97	—	—	—	—	NCBI
<i>neglectum</i>													
<i>Micractinium</i>	PSC76991.1	94	386	6E-132	PSC70752.1	93	315	2E-100	PSC70735.1	88	328	1E-108	NCBI
<i>conductrix</i>													
<i>Chlorella sorokiniana</i>	PRW34015.1	91	382	1E-126	PRW57074.1	99	323	3E-106	PRW57137.1	86	320	3E-98	NCBI
<i>Chlorella variabilis</i>	XP_005849285.1	94	363	1E-124	XP_005847884.1	97	341	2E-113	XP_005847877.1	83	282	5E-91	NCBI
<i>Chlamydomonas</i>	GAX73199.1	96	365	9E-124	GAX76907.1	88	332	3E-109	GAX80856.1	90	290	1E-92	NCBI
<i>eustigma</i>													
<i>Raphidocelis</i>	GBF95448.1	85	356	3E-120	GBF96323.1	88	306	1E-99	GBF93599.1	86	267	9E-83	NCBI
<i>subcapitata</i>													
									GBF93173.1	83	184	5E-51	NCBI
<i>Ostreococcus tauri</i>	XP_003074135.1	95	347	5E-117	—	—	—	—	XP_022838876.1	93	314	5E-104	NCBI
<i>Bathycoccus prasinos</i>	XP_007515489.1	92	326	1E-109	—	—	—	—	XP_007511360.1	90	321	1E-104	NCBI
<i>Auxenochlorella</i>	XP_011396732.1	94	308	1E-102	XP_011397739.1	96	286	2E-86	XP_011399412.1	86	237	2E-70	NCBI

protothecoides

Gonium pectorale — — — — KXZ54634.1 88 337 1E-111 KXZ42218.1 86 273 5E-86 NCBI

Embryophyte

(Eukaryotic)

Bryophyta

Physcomitrella patens XP_024385318.1 100 548 0 XP_024391049.1 97 520 0 XP_024398460.1 97 437 1.2E-148 NCBI

XP_024376785.1 93 440 2.5E-149 NCBI

XP_024384517.1 82 212 1.7E-54 NCBI

Marchantia PTQ45047.1 94 542 0 OAE24478.1 97 510 9E-177 PTQ38413.1 95 453 7E-154 NCBI

polymorpha

PTQ29718.1 84 211 2.1E-47 NCBI

Sphagnum fallax Sphfalx0044s0010. 100 535 0 Sphfalx0008s0198. 97 539 0 Sphfalx0014s0014. 94 457 4.4E-158 JGI

1

1

2

Sphfalx0162s0014. 97 513 2E-178 Sphfalx0020s0021. 83 166 3.3E-45 JGI

1

1

Tracheophyte

Selaginella XP_002979781.1 100 509 6.6E-180 XP_024540786.1 96 485 7E-170 XP_002965587.1 86 448 4E-160 NCBI

moellendorffii

Angiosperm

Amborella trichopoda XP_011625922.1 100 619 0 XP_006850171.1 100 659 0 XP_011621275.1 83 429 2.2E-147 NCBI

Monocots

Ananas comosus XP_020112923.1 100 608 0 XP_020090596.1 100 498 1E-171 XP_020098589.1 86 393 4.5E-133 NCBI

Musa acuminata XP_009407843.1 100 630 0 XP_009383212.1 100 630 0 XP_009406283.1 97 542 0 NCBI

Spirodela polyrhiza Spipo1G0011200 100 635 0 Spipo12G0033700 100 637 0 Spipo14G0041900 94 529 0 JGI

Zostera marina KMZ68881.1 100 602 0 KMZ60132.1 98 577 0 KMZ70100.1 92 516 0 NCBI

Brachypodium XP_003578617.1 100 632 0 XP_003563904.1 100 618 0 XP_003569507.1 90 513 0 NCBI

distachyon3

<i>Brachypodium</i>	Brast05G210100.1	100	632	0	Brast07G109600.1	100	617	0	Brast01G192500.1	90	515	1.4E-180	JGI
---------------------	------------------	-----	-----	---	------------------	-----	-----	---	------------------	----	-----	----------	-----

stacei3

<i>Oryza sativa</i>	XP_015626598.1	100	622	0	XP_015643584.1	100	620	0	XP_015622457.1	92	552	0	NCBI
---------------------	----------------	-----	-----	---	----------------	-----	-----	---	----------------	----	-----	---	------

Japonica Group

<i>Oropetium thomaeum</i>	Oropetium_201501 05_04627A	75	446	2.7E-156	Oropetium_201501 05_23514A	100	618	0	Oropetium_201501 05_11691A	82	369	1.6E-124	JGI
---------------------------	-------------------------------	----	-----	----------	-------------------------------	-----	-----	---	-------------------------------	----	-----	----------	-----

<i>Panium hallii</i>	Pahal.A03864.2	100	634	0	Pahal.D02099.1	100	625	0	Pahal.E02231.1	92	529	0	JGI
----------------------	----------------	-----	-----	---	----------------	-----	-----	---	----------------	----	-----	---	-----

<i>Panicum virgatum</i>	Pavir.Ab03278.1 Pavir.Aa00118.1	100 91	637 637	0 0	Pavir.Da01617.1	100	623	0	Pavir.Eb02683.1 Pavir.Ea02341.1	90 71	521 353	0 7.9E-120	JGI
-------------------------	------------------------------------	-----------	------------	--------	-----------------	-----	-----	---	------------------------------------	----------	------------	---------------	-----

<i>Setaria italica</i>	Seita.1G364200.1	100	630	0	Seita.4G138700.1	100	621	0	—	—	—	—	JGI
------------------------	------------------	-----	-----	---	------------------	-----	-----	---	---	---	---	---	-----

<i>Sorghum bicolor</i>	Sobic.004G343500. 1	100	626	0	Sobic.010G131700. 1	100	618	0	Sobic.003G247400. 2	92	515	0	JGI
------------------------	------------------------	-----	-----	---	------------------------	-----	-----	---	------------------------	----	-----	---	-----

<i>Zea mays PH207</i>	Zm00008a023329_ T01	100	630	0	Zm00008a034149_ T01	100	591	0	Zm00008a032213_ T01	90	519	0	JGI
-----------------------	------------------------	-----	-----	---	------------------------	-----	-----	---	------------------------	----	-----	---	-----

Eudicot

<i>Aquilegia coerulea</i>	Aqcoe5G010500.1	100	662	0	Aqcoe1G023500.1	100	671	0	Aqcoe1G203500.1	94	538	0	JGI
---------------------------	-----------------	-----	-----	---	-----------------	-----	-----	---	-----------------	----	-----	---	-----

<i>Amaranthus hypochondriacus</i>	AHYPO_003918-R A	100	582	0	AHYPO_000094-R A	100	589	0	AHYPO_004375-R A	94	519	0	JGI
-----------------------------------	---------------------	-----	-----	---	---------------------	-----	-----	---	---------------------	----	-----	---	-----

<i>Daucus carota</i>	DCAR_002290	100	642	0	DCAR_013578	100	673	0	DCAR_031456	95	480	5E-163	JGI
----------------------	-------------	-----	-----	---	-------------	-----	-----	---	-------------	----	-----	--------	-----

<i>Mimulus guttatus</i>	—	—	—	—	Migut.J01789.1	100	659	0	Migut.M00953.1	70	351	2.4E-117	JGI
-------------------------	---	---	---	---	----------------	-----	-----	---	----------------	----	-----	----------	-----

<i>Solanum lycopersicum</i>	Solyc12g097030.1 1	100	651	0	Solyc03g059260.2 1	100	663	0	Solyc02g071190.2 1	87	512	2.8E-179	JGI
-----------------------------	-----------------------	-----	-----	---	-----------------------	-----	-----	---	-----------------------	----	-----	----------	-----

<i>Solanum tuberosum</i>	PGSC0003DMT40 0022218	100	651	0	PGSC0003DMT40 0084308	100	670	0	PGSC0003DMT40 0007927	91	534	0	JGI
--------------------------	--------------------------	-----	-----	---	--------------------------	-----	-----	---	--------------------------	----	-----	---	-----

<i>Kalanchoe</i>	Kaladp0024s0051.1	100	675	0	Kaladp0087s0188.1	100	672	0	—	—	—	—	JGI
------------------	-------------------	-----	-----	---	-------------------	-----	-----	---	---	---	---	---	-----

fedtschenkoii

<i>Kalanchoe laxiflora</i>	Kalax.0130s0052.1	100	673	0	Kalax.0322s0004.1	100	665	0	Kalax.0835s0023.1	93	536	0	JGI
	Kalax.1447s0004.1	84	554	0	Kalax.0637s0013.1	99	660	0	Kalax.0164s0012.3	93	535	0	JGI
<i>Eucalyptus grandis</i>	Eucgr.H02885.1	89	604	0	Eucgr.A02402.1	96	651	0	Eucgr.E02360.3	98	471	1.2E-163	JGI
<i>Vitis vinifera</i>	GSVIVT01001855	100	677	0	GSVIVT01033332	100	691	0	GSVIVT01021388	90	563	0	JGI
<i>Genoscope</i>	001				001				001				
<i>Linum usitatissimum</i>	Lus10004402	99	600	0	Lus10040494	100	676	0	Lus10004601	88	571	0	JGI
	Lus10023704	99	594	0					Lus10004545	95	439	2.1E-150	JGI
<i>Manihot esculenta</i>	Manes.03G156100.	100	688	0	Manes.09G029500.	100	691	0	Manes.17G065400.	92	575	0	JGI
	1				1				1				
<i>Populus trichocarpa</i>	Potri.008G173900.	100	679	0	Potri.006G055400.	100	674	0	Potri.011G078700.	95	572	0	JGI
	4				1				1				
<i>Ricinus communis</i>	29904.m003051	100	671	0	27810.m000652	85	445	2E-152	29693.m002070	88	556	0	JGI
<i>Salix purpurea</i>	SapurV1A.0021s02	100	683	0	SapurV1A.0133s02	100	664	0	SapurV1A.0031s02	95	560	0	JGI
	90.1				20.1				80.1				
<i>Citrus sinensis</i>	orange1.1g009668	100	677	0	orange1.1g047092	100	662	0	orange1.1g012084	89	579	0	JGI
	m				m				m				
<i>Citrus clementina</i>	Ciclev10004718m	100	677	0	Ciclev10004757m	100	679	0	Ciclev10018134m	89	557	0	JGI
<i>Carica papaya</i>	evm.model.superco	100	681	0	evm.model.superco	100	693	0	—	—	—	—	JGI
	ntig_59.36				ntig_85.132								
<i>Gossypium raimondii</i>	Gorai.006G253900.	100	664	0	Gorai.002G229800.	100	687	0	Gorai.009G157600.	89	547	0	JGI
	1				1				3				
	Gorai.001G131500.	75	299	6.4E-99									JGI
	1												
<i>Theobroma cacao</i>	Thecc1EG021046t1	100	667	0	Thecc1EG024797t1	100	680	0	Thecc1EG029558t1	98	572	0	JGI
<i>Arabidopsis thaliana</i>	AT4G17740.1	—	—	—	AT3G57680.1	—	—	—	AT5G46390.1	—	—	—	JGI

<i>Boechera stricta</i>	Bostr.30275s0238.1	100	783	0	Bostr.20903s0020.1	100	820	0	Bostr.8819s0177.1	100	759	0	JGI
<i>Brassica oleracea capitata</i>	Bol037109	100	759	0	Bol045512	100	763	0	Bol032116	95	676	0	JGI
<i>Brassica rapa FPsc</i>	Brara.K00491.1	100	757	0	Brara.I03985.1	100	786	0	Brara.I01932.1	100	714	0	JGI
<i>Capsella grandiflora</i>	Cagra.3356s0066.1	100	779	0	Cagra.0210s0005.1	100	817	0	Cagra.0569s0015.1	95	737	0	JGI
<i>Capsella rubella</i>	Carubv10007107m	100	778	0	Carubv10018381m	100	808	0	Carubv10026297m	95	735	0	JGI
<i>Eutrema salsugineum</i>	Thhalv10024882m	100	764	0	Thhalv10005897m	98	802	0	Thhalv10001155m	100	727	0	JGI
<i>Cucumis sativus</i>	Cucsa.383050.2	100	647	0	Cucsa.357250.2	100	683	0	Cucsa.212480.1	95	537	0	JGI
<i>Fragaria vesca</i>	mrna28308.1-v1.0-hybrid	97	659	0	mrna14365.1-v1.0-hybrid	100	687	0	mrna24893.1-v1.0-hybrid	93	553	0	JGI
<i>Glycine max Wm82</i>	Glyma.20G199000.1	100	652	0	Glyma.10G094900.1	100	681	0	Glyma.05G165100.5	94	557	0	JGI
<i>Malus domestica</i>	MDP0000219700	99	661	0	MDP0000305189	100	649	0	—	—	—	—	JGI
	MDP0000251269	100	654	0									JGI
<i>Medicago truncatula</i>	Medtr1g073130.1	100	653	0	Medtr1g052135.1	100	676	0	Medtr8g088150.1	96	555	0	JGI
<i>Phaseolus vulgaris</i>	Phvul.L001972.1	99	644	0	Phvul.007G255600.1	100	684	0	Phvul.002G245300.1	93	555	0	JGI
<i>Prunus persica</i>	Prupe.1G052500.2	100	664	0	Prupe.7G068000.1	100	702	0	Prupe.4G074500.1	94	561	0	JGI
<i>Trifolium pratense</i>	Tp57577_TGAC_v2_mRNA19200	100	663	0	Tp57577_TGAC_v2_mRNA23564	100	664	0	Tp57577_TGAC_v2_mRNA6999	94	503	4.7E-176	JGI

Group III Chlorarachniophyta

(0) (Eukaryotic)

<i>Bigeloviella natans</i>	—	—	—	—	—	—	—	—	Bigna1 87480	C-87	173	1E-45	JGI
									Bigna1 133319	A-94	125	6E-37	JGI

Dinophyta

(Eukaryotic)

	<i>Symbiodinium</i>	—	—	—	—	—	—	—	—	OLP86183.1	A-89	236	3E-52	NCBI
	<i>microadriaticum</i>													
Outgroup	<i>Escherichia coli</i>	WP_096246988								MRF42352.1				NCBI

Supplementary Table S2. Primers used in this study.

Names	Primer sequences (5'-3')	Purposes
A-F1	TTCCTTGATGGTGGTTCAGTC	<i>atctpA</i> genotyping
A-R1	GCCTCGAGGAAGAGAAGATTC	<i>atctpA</i> genotyping
A-F2	AGAGTTGGAATTTTCCCGGGGAA	<i>AtCtpA</i> full length cDNA amplification
A-R2	TCATCTAGAAAAAAGTAGGCCTTGATTG	<i>AtCtpA</i> full length cDNA amplification
B-F1	ATGGAAAAAGTTGTAACCCTAAATCATG	<i>AtCtpB</i> CDS amplification and <i>atctpb-1</i> genotyping
B-F2	TGATGGACGTTTAGCGAAGAC	<i>atctpb-2/-3</i> genotyping
B-R	TCAAGAAGCTGTTCCATTAGATCGTC	<i>AtCtpB</i> CDS amplification and <i>atctpb</i> genotyping
C-F	ATGAGGCTTTTGCTTCCATTTCTCTCGC	<i>AtCtpC</i> CDS amplification and <i>atctpc</i> genotyping
C-R1	GAAACTGGGGTCTGTGCATTA	<i>atctpc</i> genotyping
C-R2	TCATCAACTTTGTTGGAGAATACTGCAC	<i>AtCtpC</i> CDS amplification
BP1	ATTTTGCCGATTTCCGGAAC	SALK line genotyping
BP2	GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC	SAIL line genotyping
BP3	ATAATAACGCTGCGGACATCTACATTTT	GABI line genotyping
pRI101-AN-F	GATCAAAAGCAAGTTCTTCACTG	Transgene amplification
pRI101-AN-R	AAATTCGAGCTCGGTAGCAATTC	Transgene amplification
TP _{<i>AtCtpA</i>} -R	ACCCCATGATGGTGGTGAATCAG	Transgene amplification
<i>Actin</i> -F	CTCTCCCGCTATGTATGTCGCCATCC	<i>Actin</i> gene amplification
<i>Actin</i> -R	CTGTGAACGATTCCTGGACCTGCCTC	<i>Actin</i> gene amplification
<i>GAPDH</i> -F	CCATGGCTTCGGTTACTTTC	qRT-PCR of internal control gene
<i>GAPDH</i> -R	CACCTTAAGCTTGGCCTCAG	qRT-PCR of internal control gene
qPCR (CtpA)-F	TTCTGTTCTGCTTGCTCTTCC	qRT-PCR of <i>AtCtpA</i>
qPCR (CtpA)-R	CTCTGTAACGAAACCAGCTTTG	qRT-PCR of <i>AtCtpA</i>
qPCR (CtpB)-F	TCGTGAGGTTACTACAGTACAG	qRT-PCR of <i>AtCtpB</i>
qPCR (CtpB)-R	AAGCAGCATCTGCTGATCTTAG	qRT-PCR of <i>AtCtpB</i>
qPCR (CtpC)-F	GTAGTTCTCAAGGTGAAGCATG	qRT-PCR of <i>AtCtpC</i>
qPCR (CtpC)-R	ATCTTTTCTAGCCAGCGCATTG	qRT-PCR of <i>AtCtpC</i>