Supporting Information

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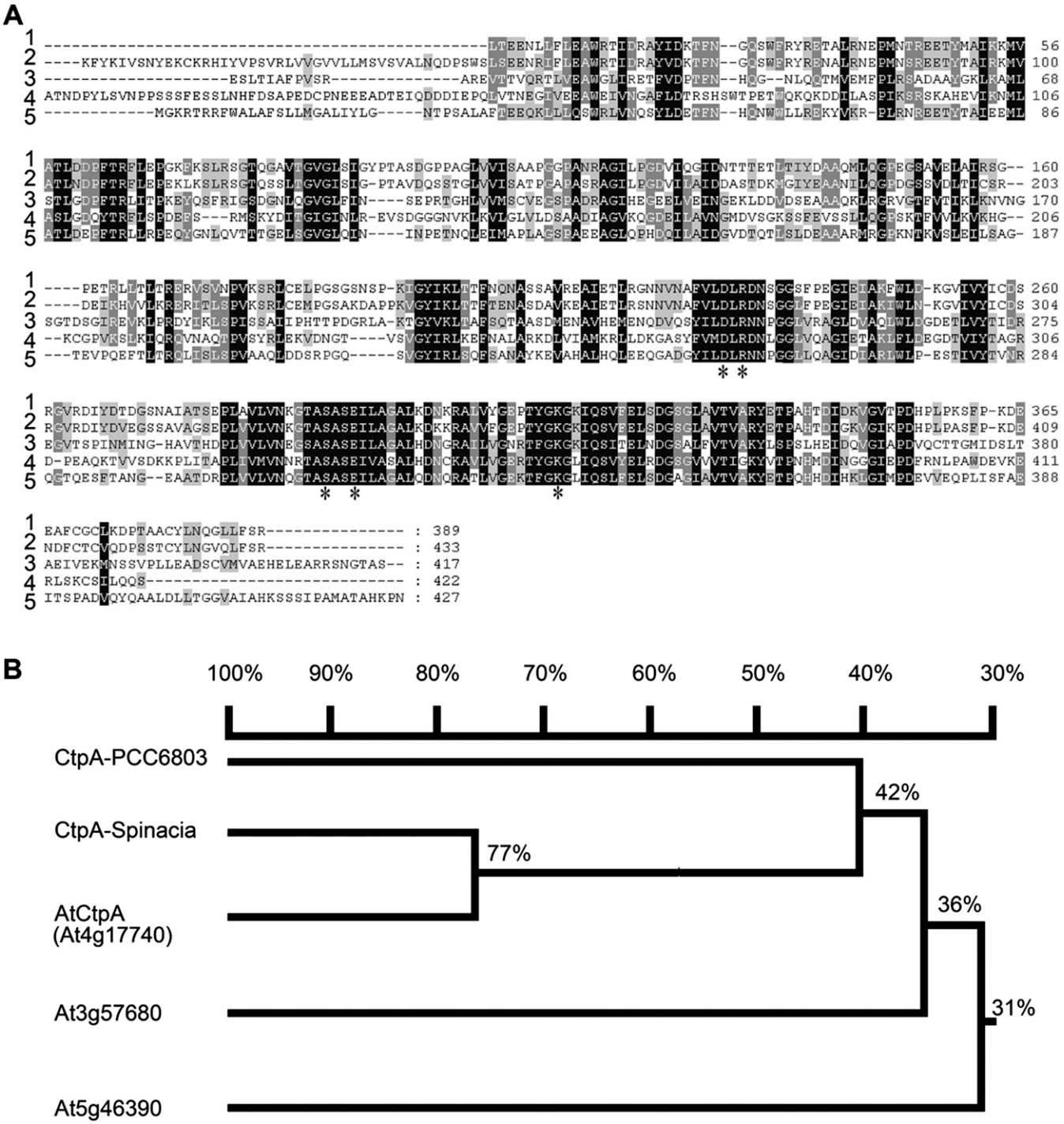

Fig. S1. Sequence analyses of carboxyl-terminal peptidase A (AtCtpA) and related protein sequences. (*A*) Comparison of amino acid sequences of mature proteins: (1) *Arabidopsis* carboxyl-terminal peptidase (CtpA; At4g17740); (2) *Spinacia* CtpA; (3) *Arabidopsis* At3g57680; (4) *Arabidopsis* At5g46390; and (5) *Synechocystis* PCC 6803 CtpA. *Conserved residues essential for catalytic activity of CtpA. Identical and similar amino acids are highlighted by black and gray shading, respectively. Alignment of protein sequences was performed with ClustalX program (www.ch.embnet.org/software/ClustalW.html). (*B*) Phylogeny of mature protein sequences from *Arabidopsis* CtpA, *Spinacia* CtpA, *Arabidopsis* At3g57680, *Arabidopsis* At5g46390, and *Synechocystis* PCC 6803 CtpA. The percentage indicates the similarity among different amino acid sequences. DNAMAN program was used in this analysis.

C-terminal sequence in wild type

1451 CAAAGTCGTT TCCGAAAGAT GAAGAGGCGT TCTGTGGATG CCTTAAGGAT
1501 CCTACAGCTG CTTGTTATCT CAATCAAGGC CTACTTTTTT CTAGATGA

451 LSDGSGLAVT VARYETPAHT DIDKVGVTPD HPLPKSFPKD EEAFCGCLKD
501 PTAACYLNQG LLFSR

C-terminal sequence in *atctpa-2*

1451 CAAAGTCGTT TCCGAAAGAT GAAGAGGCGT TCTGTGGATG CTTAGACAAC
1501 TTAATAACAC ATTGCGGACG TTTTTAA

451 LSDGSGLAVT VARYETPAHT DIDKVGVTPD HPLPKSFPKD EEAFCGCLDN
501 L I THCGRF

Fig. S2. Flanking sequences of transfer DNA (T-DNA) insertion in the *atctpa-2* mutant compared with *AtCtpA* sequence in WT. The T-DNA insertion sequence and corresponding amino acid sequence are underlined. The mutated version of AtCtpA in the *atctpa-2* mutant contains 497 aa of AtCtpA plus 11 aa from the T-DNA sequence.

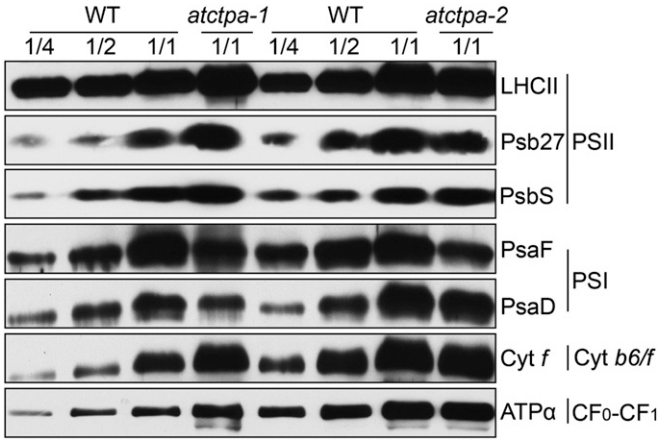

Fig. S3. Immunoblot analysis of representative subunits of photosynthetic complexes from wild-type (WT), *atctpa-1*, and *atctpa-2* plants. Chloroplast thylakoid protein samples equivalent to 2 μg chlorophyll were resolved by 10% SDS/PAGE containing 8M urea; blots were probed with the indicated antibodies. The sample preparation and plant growth conditions were the same as that in Fig. 3.

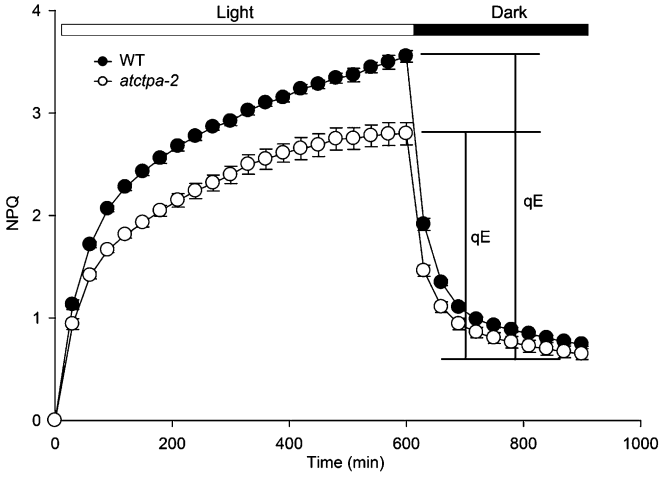

Fig. S4. Nonphotochemical quenching (NPQ) analyses. NPQ kinetics after rapid induction and dark relaxation were measured using intact leaves from 4-wk-old WT and *atctpa-2* plants grown in soil (350 μE) under long-day condition. Actinic light intensity, 1,800 μE. Data are presented as means ± SD ($n = 4$). WT and *acctpa-2* data are significantly different except for the last three time points ($P < 0.05$).

Fig. S5. Complementation of *atctpa-2* mutant. (*A*, *Upper*) Immunoblot analysis of AtCtpA in WT, *atctpa-2*, and two independent lines of *atctpa-2* mutant plants complemented with *35S::AtCtpA* construct. (*A*, *Lower*) Photographs of corresponding plants of WT, *atctpa-2*, and complemented lines. Plants were grown under 350 μE for 4 wk in soil with long-day cycle. (*B*) D1 status in WT, *atctpa-2*, and *35S::AtCtpA/atctpa-2* plants after 2 h high light treatment (1,800 μE). Immunoblot analysis was carried out as that in Fig. 3.

Table S1. Primers used in this study

Primer name	Primer sequence
atctpa-1 left board	GCCTCGAGGAAGAGAAGATTC
atctpa-1 right board	TTCCTTGATGGTGGTTCAGTC
atctpa-2 left board	GTGGAGGTTCTTTCCCAGAAG
atctpa-2 right board	GCTTGCTCTTGGTGATTTTTG
LBb1.3	ATTTTGCCGATTTCGGAAC
P1 F	AGAGTTGGAATTTTCCCGGGGAA
P1 R	GAAATTTCTGGTTTCGATTAGCTAAAGCTAT
P2 F	ATGGAGGTCCTTGCGAGCTCTTCAT
P2 R	GCATCCACAGAACGCCTCTT
AtCtpA CDS F	ATGGAGGTCCTTGCGAGCTCTTCAT
AtCtpA CDS R	TCATCTAGAAAAAAGTAGGCCTTGATTGAGATAACAAG
Actin2 F	GGAAGGATCTGTACGGTAAC
Actin2 R	TGTGAACGATTCCTGGACCT