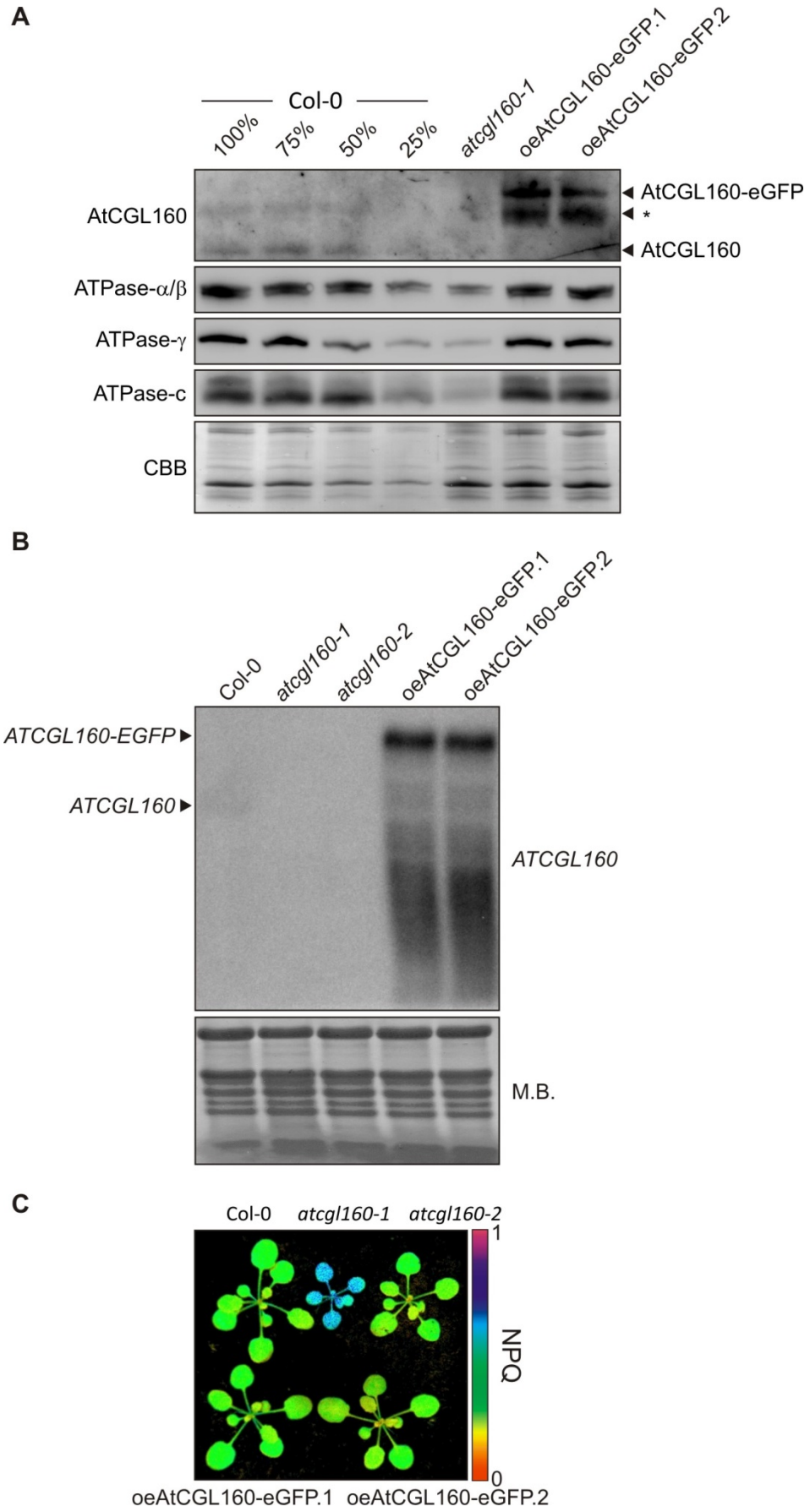

Supplemental Figure 1. AtCGL160-eGFP.1 complements the *atcgl160-1* mutation. A, Immunodetection of AtCGL160 and the cpATPase subunits α/β, γ and c in thylakoid

preparations from the two AtCGL160-eGFP overexpressor lines and from *atcgl160-1*, together with different amounts of similar WT (Col-0) extracts. After thylakoid extraction and fractionation on SDS gels, proteins on PVDF membranes were reversibly stained with Coomassie brilliant blue G250 (CBB) as a loading control. The asterisk marks a signal which might derive from degradation of the fusion protein AtCGL160-eGFP. B, *AtCGL160* transcript detection by Northern analyses in the same genotypes as in panel A. Total RNA was isolated from 4- to 6-week-old leaves and separated on a denaturing RNA gel. After transfer, the nitrocellulose membrane was stained with methylene blue (M.B.). After hybridization with a ^{32}P-labeled probe (see Supplemental Table 2 online for primer information) specific for the *AtCGL160* transcript, signals were detected using the Typhoon® (Amersham Biosciences) system. C, Restoration of WT NPQ levels in oeAtCGL160-eGFP lines. The two oeAtCGL160-eGFP lines, together with *atcgl160-1*, *atcgl160-2* and WT (Col-0) plants, were subjected to Imaging-PAM analyses for Y(NPQ) determination (see Methods). NPQ values are visualized in false color on a scale from 0 to 1 shown to the right of the panel.

Supplemental Table 1. *Coregulation of AtCGL160 with photosynthesis-related genes.*

Data were obtained from the ATTED database. Detailed information on the calculation of the coregulation factors New Rank (NR), Average Mutual Rank to Query Loci (AMR) and Average Correlation to Query Loci (AC) is available on the ATTED homepage (www.atted.jp). The other columns list the gene locus, the putative subcellular localization of the gene product (C, chloroplast; M, mitochondrion; Y, cytosol; O, others; according to TargetP and WoLF PSORT) and its function.

NR	AMR	AC	Gene locus	Target	Function
1	1	0.86	At4g27800	M, C	Chloroplast protein phosphatase TAP38/PPH1
7	4	0.83	At3g15840	C, M	PIFI (post-illumination chlorophyll fluorescence increase protein)
10	7	0.85	At1g20020	C, C	FNR2 (ferredoxin-$NADP^+$-oxidoreductase 2)
19	14	0.77	At1g08550	O, Y	NPQ1 (violaxanthin de-epoxidase)
63	57	0.78	At1g18730	C, Y	NDF6 (NDH dependent flow 6 protein)
92	76	0.72	At2g28800	C, C	ALB3 (ALBINO 3)
103	85	0.76	At5g66190	C, C	FNR1 (ferredoxin-$NADP^+$-oxidoreductase 1)
119	97	0.76	At3g16250	C, C	NDF4 (NDH-dependent cyclic electron flow 1)
126	103	0.75	At1g70760	C, C	CRR23 (chlororespiratory reduction 23)
138	111	0.75	At4g332260	C, C	cpATPase-b/b’
141	113	0.60	At4g11960	C, C	PGRL1B (PGR5-like1B)
143	114	0.75	At5g23120	C, C	HCF136
158	128	0.74	At2g20260	C, C	PsaE2 (PSI subunit E2);
171	138	0.67	At4g00895	C, C	cpATPase-δ
219	174	0.73	At1g15980	C, C	NDF1 (NDH-dependent cyclic electron flow 1/ NAD(P)H dehydrogenase subunit 48)
262	198	0.71	At4g04640	C, C	cpATPase-γ1 (or AtpC1)

Supplemental Table 2. *Primers used in this study.*

Overhangs which are necessary for cloning are underlined.

Gene	Forward primer	Reverse primer	Application
atcgl160-1 (T-DNA junction)	AAGTTAAGATTCCATTTTCGCATC	TCCCTAAACATCACATCCTGC	Genotyping
atcgl160-2 (T-DNA junction)	GAGTACAATCAATTTTCCTTGTGGACTTG	TGATCCATGTAGATTTCCCGGACATGAAG	Genotyping
AtCGL160	CTTTAGCAGAGTTATGAGTC	CAATAGCCTTACTCATTTGC	Amplicon 2 (see Figure 1)
AtCGL160	TACCCAATAAGAAACCTGAG	TAAGTCTGTGGAAGTAATGG	Amplicon 1 (see Figure 1)
AtCGL160	GGGGACAAGTTTGTACAAAAAAGCAGGCTCAATGGCGATTCTTAGTTACAT	GGGGACCACTTTGTACAAGAAAGCTGGGTGATCACTGGCCTGTGTGTCTG	*AtCGL160* cloning (pB7FWG2.0) for complementation
AtpC	CACCGCTTCCTCTGTTTCACCACTCCAAGCG	TCAAACCTGTGCATTAGCTCCAGCA	*AtpC* TOPO cloning (pET151) for overexpression in *E. coli*
AtCGL160	CACCGGAGAGTACGGTGGTCCTCC	TTATACTTCTGGGTCACCACGTG	*AtCGL160* TOPO cloning (pET151) for overexpression in *E. coli*
atpA	GACAGACAGACCGGTAAAAC	AAACATCTCCTGACTGGGTC	Northern probe
atpB	TTAGGTCCTGTCGATACTCG	ACCCAATAAGGCGGATACCT	Northern probe
atpE	GTGTACTGACTCCGAATCGA	TATTGAGAGCCTCGACTCGT	Northern probe
atpF	TCGTTTACTTGGGTCACTGG	TTGTTGGAAAACCCGTTCGC	Northern probe
atpH	GAATCCACTGGTTTCTGCTG	AGCGCTAATGCTACAACCAG	Northern probe
atpI	TATCCAGTTACCTCAAGGGGAGTTA	TTAATGATGACCTTCCATAGACTCA	Northern probe
AtCGL160	CACCGGAGAGTACGGTGGTCCTCC	CAATAGCCTTACTCATTTGC	Northern probe
AtCGL160	ATTAACAAGGCCATTACGGCCATGAAAATCATTCTACCCAATAAGA	AACTGATTGGCCGAGGCGGCCCCATCACTGGCCTGTGTGTCTGGAG	pAMBV4 cloning for split-ubiquitin assays,

			$AtCGL160_{29-350}$
AtCGL160	ATTAACAAGGCCATTACGGC CATGAAATTGTTTGATGATC CTAA	AACTGATTGGCCGAGGCGG CCCCATCACTGGCCTGTGTG TCTGGAG	pAMBV4 cloning for split-ubiquitin assays,
			$AtCGL160_{87-350}$
AtCGL160	ATTAACAAGGCCATTACGGC CATGGAAGCTAAAAAGCAA ATGAG	AACTGATTGGCCGAGGCGG CCCCATCACTGGCCTGTGTG TCTGGAG	pAMBV4 cloning for split-ubiquitin assays,
			$AtCGL160_{147-350}$
AtCGL160	ATTAACAAGGCCATTACGGC CATGAAAATCATTCTACCCA ATAAGA	CCGTTGCAACCGGTAAAAGT CAGCCCTGTCTTTAGCAGCT TGTA	Fusion PCR, N-terminus fragment $AtCGL160_{29-206}$
Atp1	TACAAGCTGCTAAAGACAG GGCTGACTTTTACCGGTTGC AACGG	AACTGATTGGCCGAGGCGG CCCCATCCGCTGCGGGCGTA AACA	Fusion PCR, C-terminus fragment $Atp1_{1-117}$
AtCGL160-Atp1	ATTAACAAGGCCATTACGGC CATGAAAATCATTCTACCCA ATAAGA	AACTGATTGGCCGAGGCGG CCCCATCCGCTGCGGGCGTA AACA	Fusion PCR for $AtCGL160_{29-206}$-$Atp1_{1-117}$