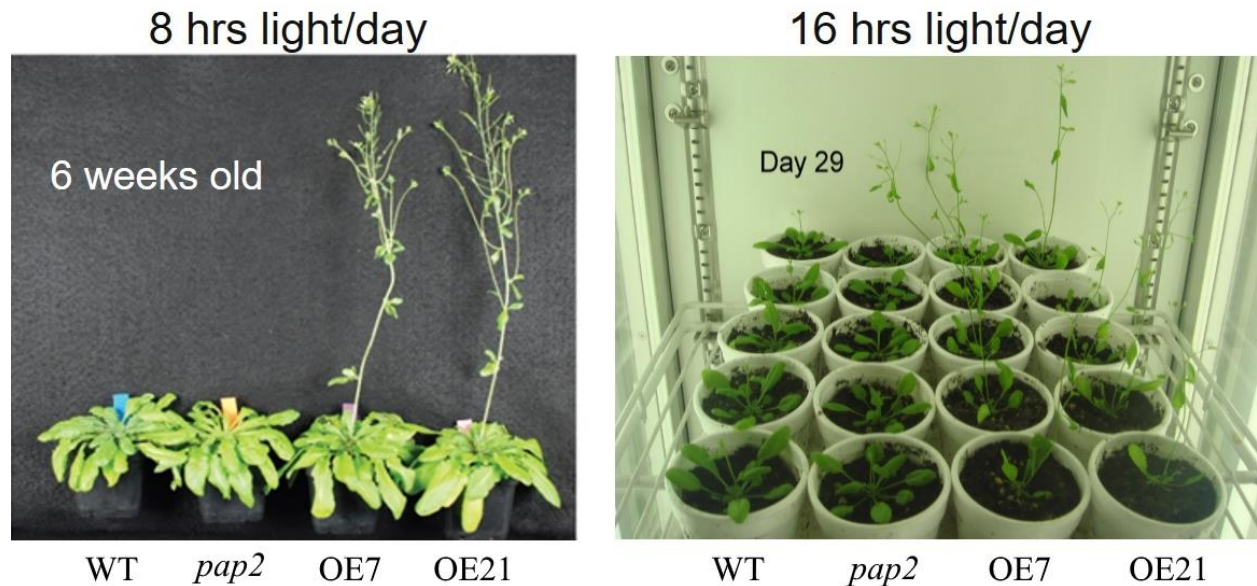
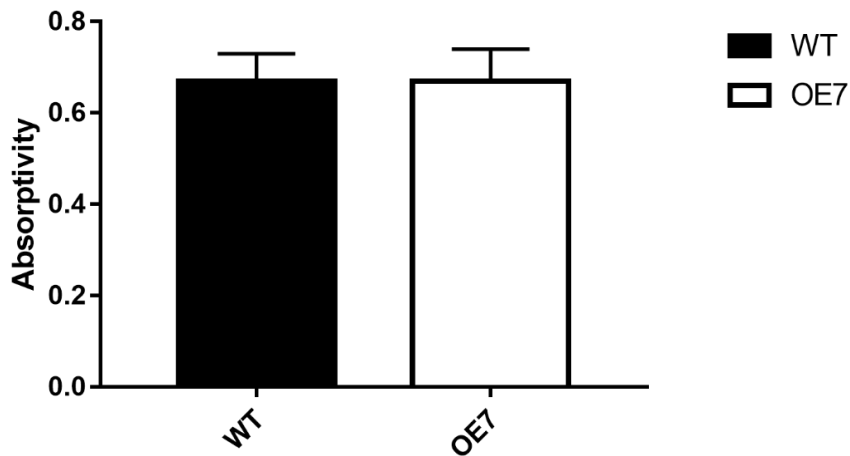


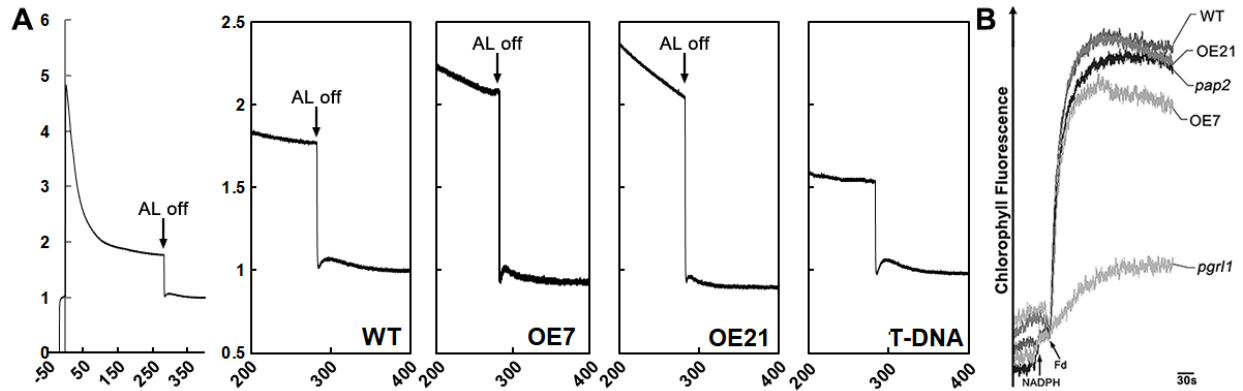
Supplemental Figures and Tables



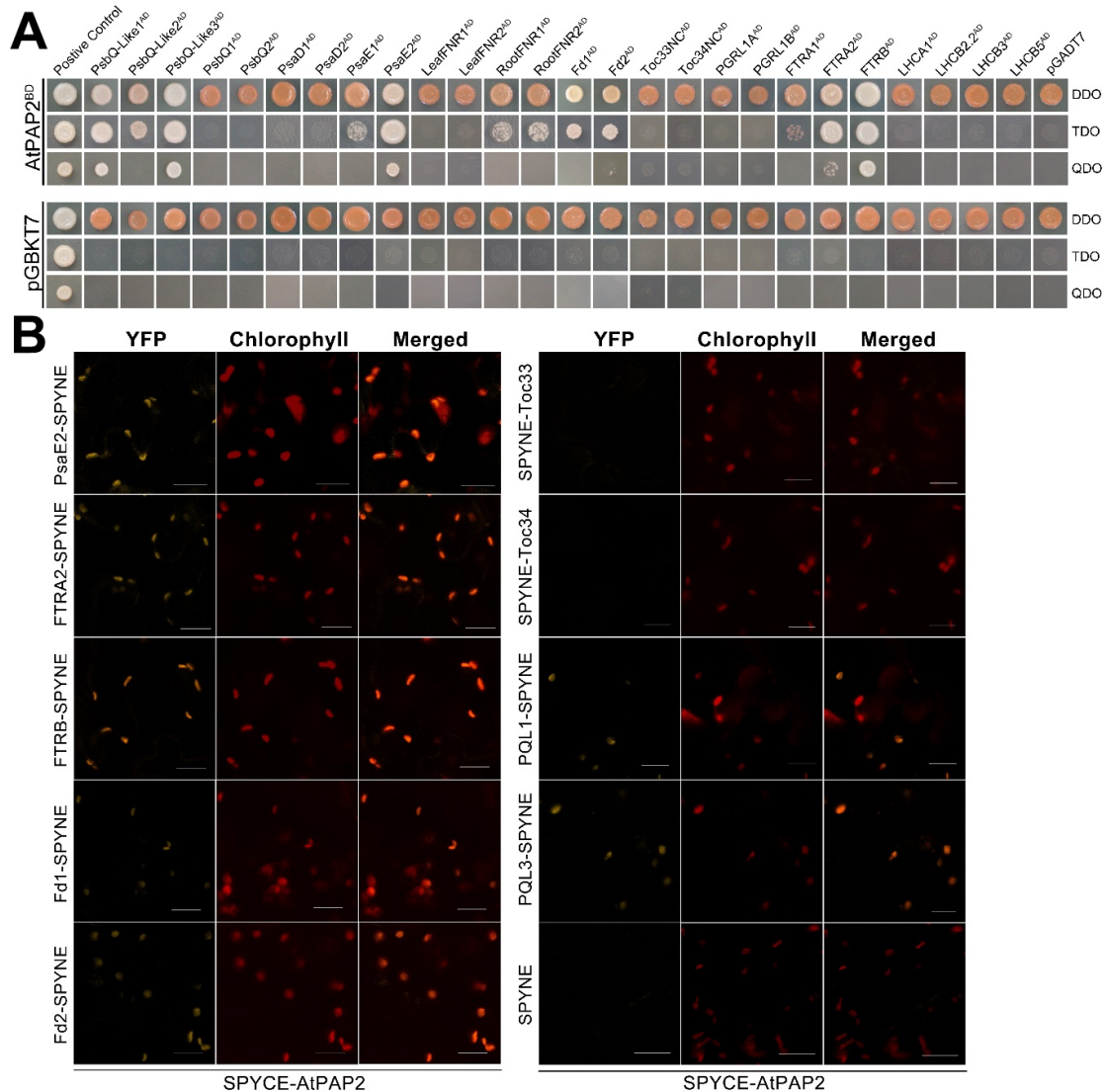
**Supplemental Figure 1. The OE lines grew faster under both SD (8h/16h) and LD (16h/8h) conditions.**



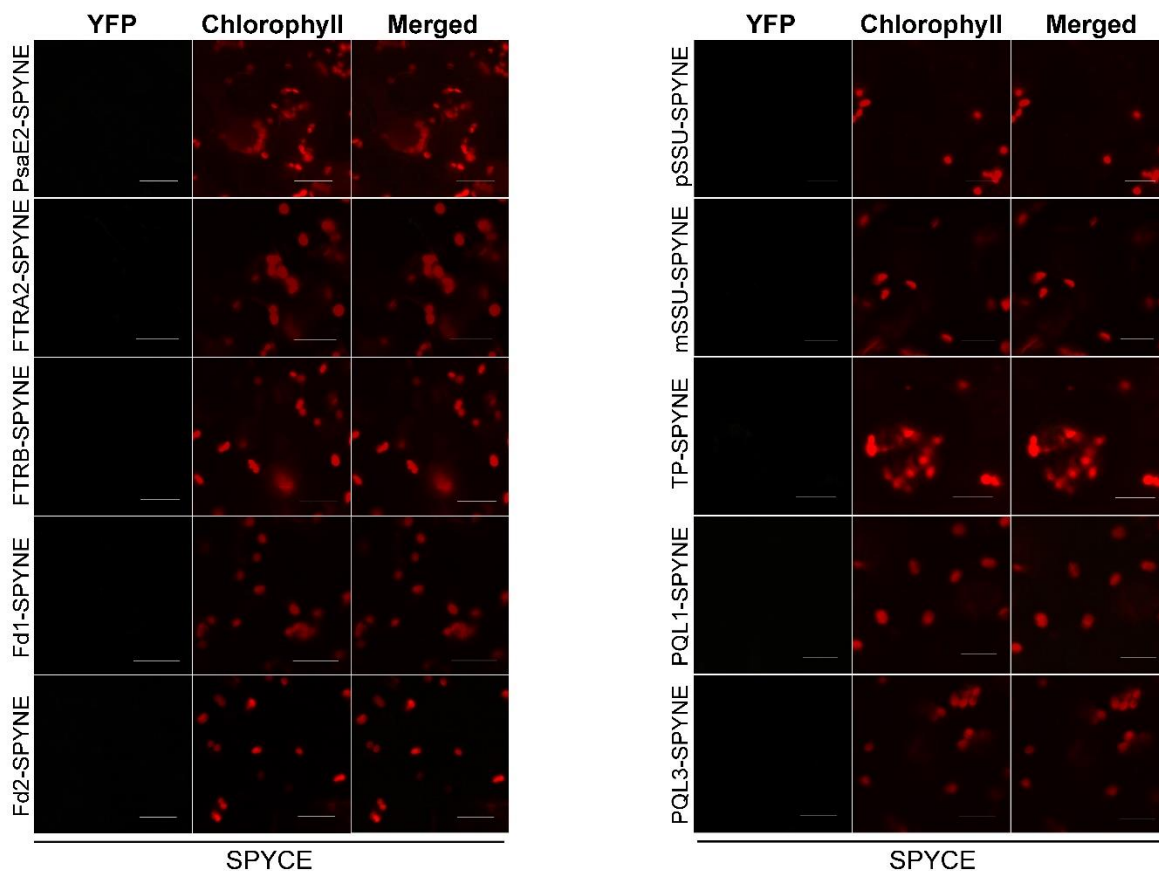
**Supplemental Figure S2. Leaf absorptivity is similar between WT line and AtPAP2 overexpression line (OE7).** Absorptivity of 20-day-old leaves were determined by IMAGING-PAM M-Series Maxi Version (WALZ, Germany). First an NIR (near-infrared)-remission image and then a R (red)-remission image was measured, the absorptivity was automatically calculated pixel by pixel according to the equation  $\text{absorptivity} = 1 - R/\text{NIR}$ . This approach is based on the empirical fact that pigments that contribute to the absorption of PAR (photosynthetic active radiation) do not show significant absorption bands in the NIR spectral region. On the other hands, pigments that absorb NIR are likely to also absorb Red light. Bar graph represents the mean value of absorptivity with SD (n = 63).



**Supplemental Figure S3. *In vivo* analysis of the cyclic electron flow rate.** **A.** Post-illumination chlorophyll fluorescence transient for the measuring of NAD(P)H dehydrogenase (NDH)-CEF. Typical induction kinetics of chlorophyll fluorescence in a dark-acclimated leaf of WT *Arabidopsis* under illumination with actinic light (AL,  $50 \mu\text{mol photon m}^{-2} \text{s}^{-1}$ ) were shown. Changes in chlorophyll fluorescence after the cessation of the actinic illumination were compared at a higher time resolution. Chlorophyll fluorescence was normalized to the original level in the dark ( $F_0$ ). **B.** Ruptured chloroplast assay for the quantification of antimycin A-sensitive Fd-dependent CEF. After the addition of NADPH and Fd to freshly ruptured chloroplasts, the increase in chlorophyll fluorescence was measured ( $n = 3$ ). The *pgr1* mutant served as a negative control.



**Supplemental Figure S4. AtPAP2 selectively interacts with certain photosystem proteins. A.** Mature AtPAP2 protein without the signal peptide and C-terminus (a.a. 25–613, P2NC) interacted with several photosystem proteins (PQL1-AD, PQL2-AD, PQL3-AD, PsaE2-AD, FTRA2-AD and FTRB-AD). Blank vectors of BD (pGBKT7) and AD (pGADT7) were co-transformed with bait and prey, respectively, to assess auto-activation. The assays were carried on dropout medium of DDO (SD/-Leu/-Trp), TDO (SD/-Leu/-Trp/-His) and QDO (SD/-Ade/-His/-Leu/-Trp). **B.** BiFC assay of the interaction between AtPAP2 and candidate proteins. YFP<sup>N</sup>-fused photosystem proteins (PsaE2, FTRA2, FTRB, Fd1, Fd2, PQL1, PQL3, Toc33 and Toc34) and YFP<sup>C</sup>-AtPAP2 were transiently expressed in tobacco leaves. Empty SPYNE vectors were used as controls. Reconstituted YFP fluorescence was monitored at 514 nm (left panel with PMT detector emission bandwidth of 488–550 nm). Chlorophyll autofluorescence was excited at 458 nm (middle panel with PMT detector emission bandwidth of 650–710 nm). An overlay of the YFP signal and the chlorophyll autofluorescence is shown in the right panel. Scale bars: 20  $\mu$ m. All images were captured using the same gain settings as the corresponding PMT channels. The representative images of 3 biological replicates are presented.



**Supplemental Figure S5. Results of BiFC negative controls.** YFPN-fused photosynthetic apparatus subunits (PsaE2, FTRA2, FTRB, PQL1, PQL3, Fd1, Fd2, SP, mSSU and pSSU) and empty SPYCE vector were transiently expressed in tobacco leaves as controls. Reconstituted YFP fluorescence was monitored at 514 nm (left panel with PMT detector emission bandwidth of 488–550 nm). Chlorophyll autofluorescence was excited at 458 nm (middle panel with PMT detector emission bandwidth of 650–710 nm). An overlay of the YFP signal and the chlorophyll autofluorescence is shown in the right panel. Scale bars: 20  $\mu$ m. All of the images were captured at the same gain settings as the corresponding PMT channels.

**Supplemental Table S1. Photosynthetic pigment content.**

	WT	<i>pap2</i>	OE7	OE21
Chlorophyll a	8.43 + 0.44 <sup>a</sup>	10.62 + 0.18 <sup>b</sup>	6.53 + 1.12 <sup>c</sup>	5.55 + 0.29 <sup>c</sup>
Chlorophyll b	3.35 + 0.21 <sup>a</sup>	3.96 + 0.87 <sup>b</sup>	2.81 + 0.36 <sup>ac</sup>	2.16 + 0.16 <sup>c</sup>
$\beta$ -Carotene	0.28 + 0.02 <sup>a</sup>	0.30 + 0.07 <sup>b</sup>	0.22 + 0.03 <sup>c</sup>	0.18 + 0.00 <sup>ac</sup>
Lutein	1.09 + 0.06 <sup>a</sup>	1.28 + 0.07 <sup>b</sup>	0.83 + 0.15 <sup>c</sup>	0.68 + 0.02 <sup>c</sup>
Violaxanthin	0.28 + 0.02 <sup>a</sup>	0.29 + 0.08 <sup>a</sup>	0.26 + 0.07 <sup>a</sup>	0.18 + 0.01 <sup>a</sup>

Pigments were extracted 8 hours after the light period from the leaves of 20-day-old *Arabidopsis* under LD regime. Values ( $\text{mg g}^{-1}$  DW of tissues) marked by different letters are significantly different ( $p < 0.05$ ) in the same row by one-way ANOVA analysis followed by HSD test. DW, dry weight.

**Supplemental Table S2. Chloroplast proteins identified in 2D BN PAGE.**

<b>Spot ID</b>	<b>Peptides (95%)</b>	<b>Unused peptide</b>	<b>Protein Name</b>	<b>Accession</b>	<b>Function</b>	<b>Average Ratio (OE/WT)</b>
1	103	162.86	PsaA	ATCG00350	PS I core protein	1.00
1	80	98.48	PsaB	ATCG00340	PS I core protein	1.00
2	38	69.11	PsaA	ATCG00350	PS I core protein	0.82
2	38	62.91	PsaB	ATCG00340	PS I core protein	0.82
23	72	78.56	PsaD1	AT4G02770	PS I core protein	0.97
12	23	29.77	PsbA, D1	ATCG00020	PS II core protein	0.78*
6	95	82.02	PsbB, CP47	ATCG00680	PS II core protein	0.63**
7	58	96.16	PsbB, CP47	ATCG00680	PS II core protein	0.72*
8	51	64.74	PsbC, CP43	ATCG00680	PS II core protein	0.65**
9	181	249.7	PsbC, CP43	ATCG00280	PS II core protein	0.80
12	41	58.68	PsbD, D2	ATCG00270	PS II core protein	0.78*
13	108	136.85	PsbO1, OE33	AT5G66570	PS II core protein	6.83**
14	59	83.54	PsbO1, OE33	AT5G66570	PS II core protein	8.64**
15	15	26.96	PsbO1, OE33	AT5G66570	PS II core protein	3.02**
21	22	25.47	PsbS, NPQ4	AT1G44575	PS II core protein	1.06
22	25	39.68	PsbS, NPQ4	AT1G44575	PS II core protein	1.01
16	145	173.1	Lhcb1.4	AT2G34430	LHC II protein	0.88
16	57	27.88	Lhcb2.2	AT2G05070	LHC II protein	0.88
17	91	140.01	Lhcb4.1, CP29	AT5G01530	LHC II protein	1.44
18	59	63.18	Lhcb4.1, CP29	AT5G01530	LHC II protein	0.79
18	33	33.7	Lhcb1.4	AT2G34430	LHC II protein	0.79
19	92	10.33	Lhcb1.1	AT1G29920	LHC II protein	0.92
19	93	129.87	Lhcb1.4	AT2G34430	LHC II protein	0.92
19	47	33.61	Lhcb2.2	AT2G05070	LHC II protein	0.92
19	37	52.97	Lhcb5, CP26	AT4G10340	LHC II protein	0.92
20	129	12.78	Lhcb1.3	AT1G29930	LHC II protein	0.84
20	125	190.01	Lhcb1.4	AT2G34430	LHC II protein	0.84
20	57	47.46	Lhcb2.2	AT2G05070	LHC II protein	0.84
20	56	92.39	Lhcb5, CP26	AT4G10340	LHC II protein	0.84
21	29	35.92	Lhcb6, CP24	AT1G15820	LHC II protein	1.06
22	71	99.62	Lhcb6, CP24	AT1G15820	LHC II protein	1.01
24	32	45.98	PetC	AT4G03280	Cytochrome B6f complex	1.1
25	3	3.36	PetD	ATCG00730	Cytochrome B6f complex	0.25**
4	306	320.72	atpA	ATCG00120	ATP synthase	0.32**
5	325	381.21	atpB	ATCG00480	ATP synthase	0.36**
10	64	87.68	atpC1	AT4G04640	ATP synthase	0.60**
11	58	62.97	atpC1	AT4G04640	ATP synthase	0.66**
3	271	405.15	RBCL	ATCG00490	Calvin cycle	4.07**

Isolated chloroplast proteins from WT and OE7 were resolved by 2D BN/SDS-PAGE and the protein spots were extracted for MS/MS analysis. Protein candidates with the highest unused score and at least 2 unique peptides (95%) were shown. Average ratio is the mean of the value (OE/WT) from three biological replicates. Spots with fold change of  $\pm 1.2$  or  $\pm 1.5$  folds and  $p < 0.05$  by one-way ANOVA are denoted by \* and \*\*, respectively.

**Supplemental Table S3. Summary of identified mitochondrial protein spots.**

Spot ID	Peptides (95%)	Unused peptide	Protein name	Accession	Protein complex	Ratio (OE/WT)
1	327	328.85	Heat Shock Protein 60-3B	AT3G23990.1	HSP60	1.07
1	262	158.77	Heat Shock Protein 60-2	AT2G33210.1	HSP60	1.07
2	244	288.80	MPPbeta	AT3G02090.1	Complex III	0.99
3	295	358.38	ATP synthase beta-subunit	AT5G08690.1	Complex V	0.52**
3	292	4.48	ATP synthase beta-subunit	AT5G08680.1	Complex V	0.52**
3	239	312.37	ATP synthase alpha-subunit	AT2G07698.1	Complex V	0.52**
4	217	287.35	ATP synthase beta-subunit	AT5G08690.1	Complex V	0.43**
4	209	6.00	ATP synthase beta-subunit	AT5G08680.1	Complex V	0.43**
4	8	234.30	ATP synthase alpha-subunit	AT2G07698.1	Complex V	0.43**
5	622	637.08	RBCL	ATCG00490.1		2.33**
6	342	349.23	ATP synthase beta-subunit	AT5G08690.1	Complex V	0.56**
6	335	6.00	ATP synthase beta-subunit	AT5G08680.1	Complex V	0.56**
6	204	220.55	ATP synthase alpha-subunit	AT2G07698.1	Complex V	0.56**
7	245	315.84	Insulinase protein	AT1G51980.1	Complex III	1.08
7	73	11.84	MPPalpha	AT3G16480.1	Complex III	1.08
7	14	22.21	MPPbeta	AT3G02090.1	Complex III	1.08
8	242	335.95	ATP synthase gamma-subunit (ATP3)	AT2G33040.1	Complex V	0.64**
8	25	41.00	ATP Synthase subunit 1 (ATP1)	ATMG01190.1	Complex V	0.64**
8	20	35.36	ATP synthase beta-subunit	AT5G08690.1	Complex V	0.64**
9	19	28.61	ATP synthase alpha-subunit	AT2G07698.1	Complex V	0.65**
9	32	56.70	ATP synthase gamma-subunit (ATP3)	AT2G33040.1	Complex V	0.65**
9	29	50.43	ATP synthase beta-subunit	AT5G08690.1	Complex V	0.65**
10	87	131.85	ATP synthase gamma-subunit (ATP3)	AT2G33040.1	Complex V	0.64**
10	49	72.64	ATP synthase beta-subunit	AT5G08670.1	Complex V	0.64**

Isolated mitochondrial proteins from WT and OE7 were resolved by 2D BN/SDS-PAGE and the mitochondrial protein spots were extracted for MS/MS analysis. Protein candidates with the highest unused score and at least 2 unique peptides (95%) were shown. Average ratio is the mean



of the value (OE/WT) from three biological replicates. Spots with fold change of  $\pm 1.2$  or  $\pm 1.5$  folds and  $p < 0.05$  by one-way ANOVA are denoted by \* and \*\*, respectively.

**Supplemental Table S4. AtPAP2-interacting proteins identified by Y2H library screening.**

AGI code	No. of clones	a.a. residues	Sequence in clone	Phosphorylation sites (1-50)	pI	Proteins	Experimental location
At1g14150	5	190	All are full length	T9,Y13,T46	8.93	PsbQ-like (PQL1)	Plastid
At1g18640	5	695	All are full length	T6	6.29	3-Phosphoserine phosphatase	Plastid
At1g26220	1	197	Full length	T9,T27,S31,Y46,S47,S49	9.79	Acyl-CoA N-acyltransferases superfamily protein	Plastid
At1g29900	2	1187	aa.771-End	S18,S19,S26,S31,S33	5.45	Carbamoyl phosphate synthetase B (CARB)	Plastid
At1g30510	1	382	aa.135-End	S15,T49	8.85	Ferredoxin--NADP+ reductase (RFNR2)	Plastid
At2g04700	5	146	All are full length	S15,T20,T34,S48	7.98	Ferredoxin-thioredoxin reductase B	Plastid
At2g05990	1	390	aa.149-End	S17,S19,S20,Y30	9.36	Enoyl-ACP reductase	Plastid
At2g20260	1	145	Full length	S24,S25	10.54	Subunit E of photosystem I (PsaE2)	Plastid
At2g22360	1	442	aa.228-End	Y25,S32	9.49	DNAJ heat shock family protein A6	Plastid
At2g34860	1	186	Full length	S16,S39,S42,S45,S47,S49	9.25	DnaJ/Hsp40 cysteine-rich domain protein	Plastid
At2g35500	1	387	Full length	S14,S34,S35	6.19	Shikimate kinase-like 2 (SKL2)	Plastid
At4g20760	1	298	Full length	S14,S34,S37,T32	10.24	NAD(P)-binding Rossmann-fold protein	Plastid
At4g21860	1	202	Full length	T7,S34,S45,S46	8.68	Methionine sulfoxide reductase B2	Plastid
At4g25370	1	238	Full length	S26,S28,S29,T36	9.78	Double Clp-N motif protein	Plastid
At4g35860	1	211	Full length	T49	7.03	GTP-binding protein GB2 (GB2)	Plastid
At5g06340	3	227	All are full length	S37,S50	8.77	Nudix hydrolase 27 (NUDX27)	Plastid
At5g08280	1	382	Full length	T26,S44	8.62	Hydroxymethylbilane synthase	Plastid
At5g11450	4	297	All are full length	S20,Y27,T43,S45,S47	9.06	PPD5	Plastid

At5g11650	1	390	aa.323-End	T12	8.73	Alpha/beta fold hydrolase family protein Rhodanese-like	Plastid
At5g19370	4	299	All are full length	T7,S9,S13,T30	8.62	Peptidyl-prolyl cis-trans isomerase	Plastid
At5g21222	1	831	aa.523-End	Y13,T33,T35	8.01	Serine/threonine protein kinase	Plastid
At5g38430	2	181	Full length	S14,S32,T36	7.83	Ribulose biphosphate carboxylase small chain 1B	Plastid
At5g66120	2	442	aa.1-344 and 1-343	T14,T31,Y50	7.53	3-dehydroquinate synthase	Plastid
At4g33520	1	949	Full length	T14	9.02	Copper-transporting ATPase PAA1 (PAA1)	Plastid inner membrane
At1g53670	1	202	Full length	Y23,Y48	9.20	Methionine sulfoxide reductase B1	Plastid stroma
At2g20270	1	206	Full length	T45	8.94	Monothiol glutaredoxin-S12	Plastid stroma
At2g38270	4	293	All are full length	S15,T31,T37,S41	8.07	Monothiol glutaredoxin 16	Plastid stroma
At2g36460	2	358	aa.76-End and aa.112-End	S32,T33,T35,S42	7.46	Fructose-bisphosphate aldolase, class I	Plastid, cytosol, PM, extracellular
At1g18080	1	327	aa.53-End	T19,T23	7.81	RACK1A	Plastid, cytosol, PM, nucleus
At1g70580	1	481	aa.145-End	Y8,Y27	6.52	Alanine-2-oxoglutarate aminotransferase 2	Plastid, Peroxisome
At5g16370	1	552	aa. 871-1766	S11,T15	6.97	Acyl activating enzyme 5 (AAE5)	Plastid, Peroxisome
At4g25130	3	258	All are full length	S7	8.92	Methionine sulfoxide reductase	Plastid, stroma
At2g35240	1	232	Full length	S19,S26,S40,Y49	9.14	pMORF6	Mitochondria
At5g40770	1	277	aa.47-End	T34	7.89	Prohibitin 3 (PHB3)	Mitochondria
At4g35830	1	898	aa.467-End	Y41	6.35	Aconitate hydratase 1 (ACO1)	Mitochondria and cytosol
At1g05060	1	253	Full length	Y16,S32,T35,S41,S42	10.02	Uncharacterized protein	N/A
At1g29810	1	187	Full length	T42,S47,T49,T50	10.37	Transcriptional coactivator/pterin dehydratase	N/A

At1g31817	1	314	aa.48-End	S31,S33,S37,S48	11.15	30S ribosomal protein S11	N/A
At1g53140	1	817	aa.620-End	Y7,T10,T14	7.47	Dynamin related protein 5A (DRP5A)	N/A
At2g38080	1	558	aa.172-534	T49	9.60	Laccase/Diphenol oxidase family protein	N/A

Experimental location: determined by GFP or MS analysis (SUBA3, <http://suba.plantenergy.uwa.edu.au/>)

Phosphorylation sites (1-50): Experimental determined phosphorylation sites in the first 50 a.a. residues were retrieved from Phosphat 4.0 (<http://phosphat.uni-hohenheim.de/phosphat.html>)

Predicted location: predicted by SUBA3 (<http://suba.plantenergy.uwa.edu.au/>)

Predicted phosphorylation sites (1-50) are shown in italics. The prediction was carried out at Phosphat 4.0 or NetPhos 2.0 (<http://www.cbs.dtu.dk/services/NetPhos/>)

**Supplemental Table S5. Primer list.**

<b>Vector (Purpose)</b>	<b>Primer Name (AGI code)</b>	<b>Primer Sequence (5'-3')<sup>1</sup></b>
pGBKT7 (Yeast two-hybrid)	25-613aaAtPAP2 (AT1G13900)	F: TTCTCATATGACCATTTCAATTTCCCC R: GCATGTCGACCAGCATTAGATTCTGATTTTC
pGADT7 (Yeast two-hybrid)	42-181aaSSU1B (AT5G38430)	F: ATTCCATATGGACATTACTTCCATCACAAGC R: ATTACTCGAGAGCATCAGTGAAGCTTGGGG
pGADT7 (Yeast two-hybrid)	1-50aaSSU1B (AT5G38430)	F: ATTACATATGGCTTCTCTATGCTCTCCT R: ATTACTCGAGCCCATTGCTTGTGATGGAAG
pGADT7 (Yeast two-hybrid)	PsbQ1 (AT4G21280)	F: ATTAGAATTCATGGCTTCGATGGGTGGATT R: CTAGCTCGAGTTAACCAAGCTTGGCAAGAACT
pGADT7 (Yeast two-hybrid)	PsbQ2 (AT4G05180)	F: TTAGCATATGATGGCTCAAGCAGTGACTTC R: ATTAGAGCTCTTAACCGAGCTTGGCAAGAAC
pGADT7 (Yeast two-hybrid)	PsbQ-Like1 (AT1G14150)	F: ATTGCATATGATGAGCTCCTTCACCACCAC R: ATCGCTCGAGTTAAGCAAGAACTCCACAAC
pGADT7 (Yeast two-hybrid)	PsbQ-Like2 (AT3G01440)	F: TGTCCATATGATGGCTCACTTCATAGACCT R: TAATCTCGAGTCATGCCATTCTGGTCATTAC
pGADT7 (Yeast two-hybrid)	PsbQ-Like3 (AT2G01918)	F: TAATCATATGATGGCGATTTCAAAGCCACC R: ACCGCTCGAGTTAAATTCGAGGGAAGATATC
pGADT7 (Yeast two-hybrid)	PsaD1 (AT4G02770)	F: ATTACATATGATGGCAACTCAAGCCGCCGG R: GCTACTCGAGTTACAAATCATAACTTTGTTTGCCAG
pGADT7 (Yeast two-hybrid)	PsaD2 (AT1G03130)	F: ATTACATATGATGGCAACTCAAGCCGCCGG R: GTCTCGAGTTACAAATCATAAGATTGTTTCCAGTG
pGADT7 (Yeast two-hybrid)	PsaE1 (AT4G02770)	F: ATTACATATGATGGCGATGACGACAGCATC R: CTTACTCGAGTTAAGCTGCAACTTCTTCGACCT
pGADT7 (Yeast two-hybrid)	PsaE2 (AT2G20260)	F: ATTACATATGATGGCGATGACGTCAGCAGC R: GTTACTCGAGTCATTTTACTTCTTCCACCTCGTCC
pGADT7 (Yeast two-hybrid)	LeafFNR1 (AT5G66190)	F: TTAGCATATGATGGCTGCTGCTATAAGTGC R: TACGCTCGAGTTAGTAGACTTCAACATTCCACTG
pGADT7 (Yeast two-hybrid)	LeafFNR2 (AT1G20020)	F: ATTACATATGATGGCGACTACCATGAATGC R: TCTACTCGAGTCAGTAGACTTCAACGTTCCATT
pGADT7 (Yeast two-hybrid)	RootFNR1 (AT3G05390)	F: ATTGCATATGATGGCTCTCTCAACTACTCC R: GCTACTCGAGTCAATACACTTCAACATGCC
pGADT7 (Yeast two-hybrid)	RootFNR2 (AT1G30510)	F: ATTGCATATGATGTCTCACTCTGCTGTTTCT R: CTTACTCGAGTCAATAGACTTCAACGTGCC
pGADT7 (Yeast two-hybrid)	LeafFd1 (AT1G10960)	F: ATTACATATGATGGCTTCCACTGCTCTCTCC R: ATTACTCGAGTTACATAATGGCTTCTTCTTTGTGG
pGADT7 (Yeast two-hybrid)	LeafFd2 (AT1G60950)	F: ATTGCATATGATGGCTTCCACTGCTCTCTC R: GTCACTCGAGTTAAACAATGTCTTCTTCTTTGTGG
pGADT7 (Yeast two-hybrid)	1-251aaToc33 (AT1G02280)	F: ATTACATATGATGGGGTCTCTCGTTTCGTG R: ATTACCCGGGTTAGTCTACATGAATTGCTTTCCTC
pGADT7 (Yeast two-hybrid)	1-254aaToc34 (AT5G05000)	F: ATTACATATGATGGCAGCTTGGCAAACGCT R: ATTACCCGGGTTACTTGTCAACATGAATCGCCTT
pGADT7 (Yeast two-hybrid)	PGR5-Like1A (AT4G22890)	F: ATTGCATATGATGGGTAGCAAGATGTTGTT R: TAATCTCGAGTTAAGCTTGGCTTCCCTTCTG
pGADT7 (Yeast two-hybrid)	PGR5-Like1B (AT4G11960)	F: ATTGCATATGATGGCTTTTACTCTAACAATCC R: AACTGAGCTCTTAAGCTTTCCCTCCTTCTG
pGADT7 (Yeast two-hybrid)	FTRA1 (AT5G23440)	F: ATTGCATATGATGAGTAGCCAAATCGCTTTGT R: TACTGAGCTCTCACTGATCAATGAACCTCGAACTC
pGADT7 (Yeast two-hybrid)	FTRA2 (AT5G08410)	F: ATTGCATATGATGACTAACAGTTACGCTCTGTC R: ATTACTCGAGTCACGGATCAATTAACCTCGAAC
pGADT7 (Yeast two-hybrid)	FTRB (AT2G04700)	F: AGCTGAATTCATGAATCTTCAAGCTGTTTC R: ATCGCTCGAGTCACATGTTAGCTGTAGTTTC

pGADT7 (Yeast two-hybrid)	LHCA1 (AT3G54890)	F: TAAT <u>CATAT</u> G GCGTCGAACTCGCTTAT R: TAAT <u>CATATG</u> T TAGTTGAAAGGGATAACAAT
pGADT7 (Yeast two-hybrid)	LHCB2.2 (AT2G05070)	F: TAAT <u>CATATG</u> GCCACATCAGCTATCCAAC R: TAAT <u>CTCGAG</u> T TACTTTCCGGGGACAAAGTT
pGADT7 (Yeast two-hybrid)	LHCB3 (AT5G54270)	F: TAAT <u>CATATG</u> G CATCAACATTCACGAGC R: TAAT <u>CTCGAG</u> T TAAGCTCCAGGTGCAAAC
pGADT7 (Yeast two-hybrid)	LHCB5 (AT4G10340)	F: TAAT <u>CATATG</u> GCGTCTTTGGGTGTGTC R: TAAT <u>CTCGAG</u> T TAGAGAGTGGGAGCTCTCTC
SPYCE (BiFC)	AtPAP2 (AT1G13900)	F: ATCG <u>ACTAGT</u> ATGATCGTTAATTTCTCTTTCTTC R: GAAT <u>ACTAGT</u> TTATGTCTCCTCGTTCTTGACTG
SPYCE (BiFC)	Multiple cloning site	F: ATTAG <u>GAGCTC</u> GTTAACCGGGCTCAGGCCT R: ATTAG <u>GAGCTC</u> CCCCGGGAGCGGTACCCTC
SPYCE (BiFC)	YFP <sup>C</sup>	F: TAACT <u>CTAGA</u> ATGTACCCATACGATGTTCCAG R: ATTAG <u>GAGCTC</u> CTTGTACAGCTCGTCCATG
SPYNE (BiFC)	PsaE1 (AT4G28750)	F: GAAC <u>TCTAGA</u> ATGGCGATGACGACGACAT R: ATTAG <u>CTGAGAG</u> CTGCAACTTCTTCGACCTC
SPYNE (BiFC)	PsaE2 (AT2G20260)	F: ATTAT <u>CTAGA</u> ATGGCGATGACGTCAGCAGC R: TAAT <u>CTCGAG</u> T TTTTACTTCTTCCACCTCGTCCAAT
SPYNE (BiFC)	FTRA1 (AT5G23440)	F: ATTAT <u>CTAGA</u> ATGAGTAGCCAAATCGCTTT R: ATTAG <u>CTGAGCT</u> GATCAATGAACTCGAACTC
SPYNE (BiFC)	FTRA2 (AT5G08410)	F: CTAG <u>TCTAGA</u> ATGACTAACAGTTACGCTCTGTC R: ATTAG <u>CTGAGCG</u> GATCAATTAACCTCGAACTC
SPYNE (BiFC)	FTRB (AT2G04700)	F: ATTAT <u>CTAGA</u> ATGAATCTTCAAGCTGTTTCTTG R: ATTAG <u>CTGAGCAT</u> GTTAGCTGTAGTTTCTTTTATT
SPYNE (BiFC)	LeafFd1 (AT1G10960)	F: ATTAT <u>CTAGA</u> ATGGCTTCCACTGCTCTCTCC R: TAAT <u>CTCGAG</u> CATAATGGCTTCTTCTTTGTGG
SPYNE (BiFC)	LeafFd2 (AT1G60950)	F: ATT <u>GCTAGA</u> ATGGCTTCCACTGCTCTCTC R: ATTAG <u>CTGAGA</u> ACAATGTCTTCTTCTTTGTGGG
SPYNE (BiFC)	Toc33 (AT1G02280)	F: ATTAT <u>CTAGA</u> ATGGGGTCTCTCGTTTCGTGAAT R: CCTAT <u>CTAGAA</u> AGTGGCTTTCCACTTGTCTTGAT
SPYNE (BiFC)	Toc34 (AT5G05000)	F: ATTAT <u>CTAGA</u> ATGGCAGCTTTGCAAACGCT R: GAAT <u>TCTAGA</u> AGACCTTCGACTTGCTAAACCG
SPYNE (BiFC)	PsbQ-Like1 (AT1G14150)	F: ATT <u>GACTAGT</u> ATGAGCTCCTTACCACCAC R: ATTAG <u>CTGAGAG</u> CAAGAACTCCACAACATT
SPYNE (BiFC)	PsbQ-Like3 (AT2G01918)	F: ATT <u>CACTAGT</u> ATGGCGATTTCAAAGCCACC R: ATTAG <u>CTGAGA</u> AATTCGAGGGAAGATATCATCGAG
SPYNE (BiFC)	42-181aaSSU1B (AT5G38430)	F: ATT <u>CTCTAGA</u> ATGGACATTACTTCCATCACAAGC R: ATTAG <u>CTGAGAG</u> CATCAGTGAAGCTTGGGG
SPYNE (BiFC)	1-50aaSSU1B (AT5G38430)	F: ATTAT <u>CTAGA</u> ATGGCTTCTCTATGCTCTCCT R: ATTAG <u>CTGAG</u> CCCATTGCTTGTGATGGAAG
pCXSN (Transgenic line)	TOC33overlap (At1g02280)	F: ATCAGTGGGAGCAAAGTAGATGGATCTTACTCT R: GTAAGATCCATCTACTTTGCTCCCACTGATTAC

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<sup>1</sup> Restricted sites are indicated by underline.