

Supplementary data

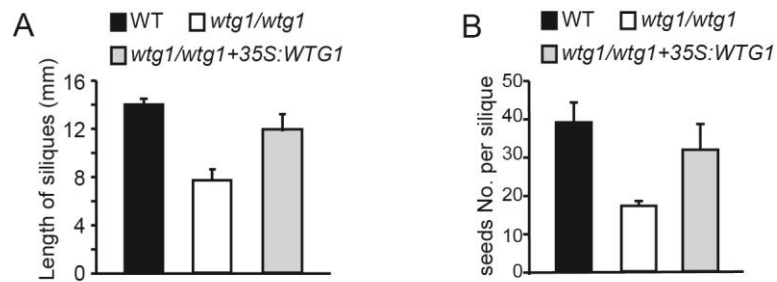


Figure S1. Loss of *WTG1* reduces the yield trait of *Arabidopsis*. (A) The length of siliques from wild-type, *wtg1*, and complementary lines. (B) Seed setting ability of wild type, *wtg1*, and complementary lines. Data are presented as mean \pm SD of triplicates.

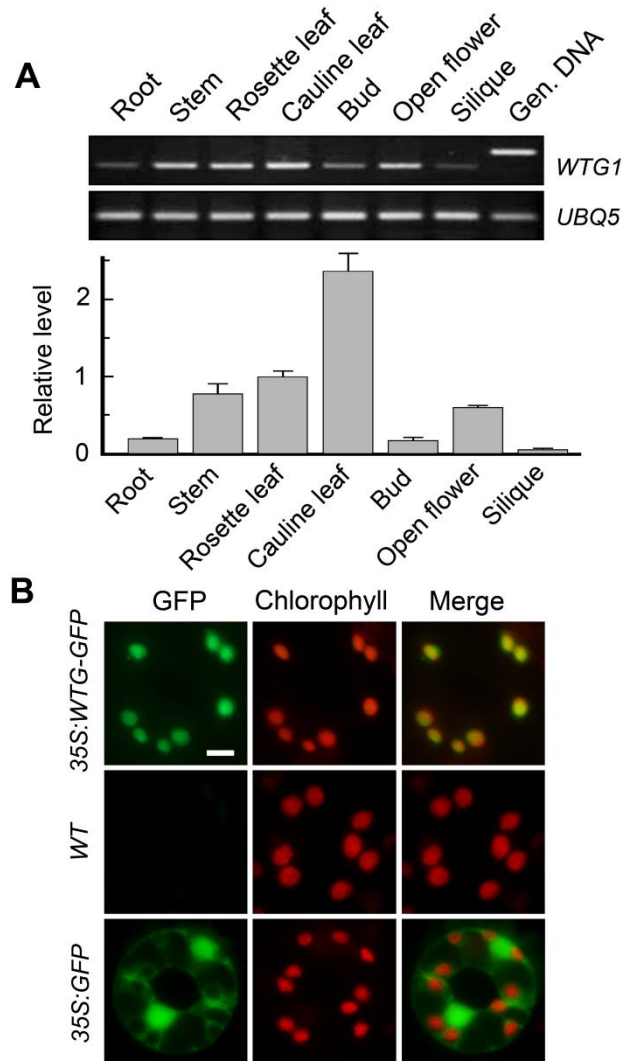


Figure S2. WTG1 is expressed ubiquitously in *Arabidopsis* and targeted to chloroplasts. (A) Reverse-transcriptase PCR (upper) and real-time PCR (bottom) assays of *WTG1*. *UBQ5* served as the loading control; data are presented as mean \pm SD of triplicates. (B) Subcellular localization of WTG1-GFP in transformed mesophyll cells. Chlorophyll autofluorescence is shown in red. The image appears yellow where the signals from GFP and chloroplasts overlap. Bars = 10 μ m.

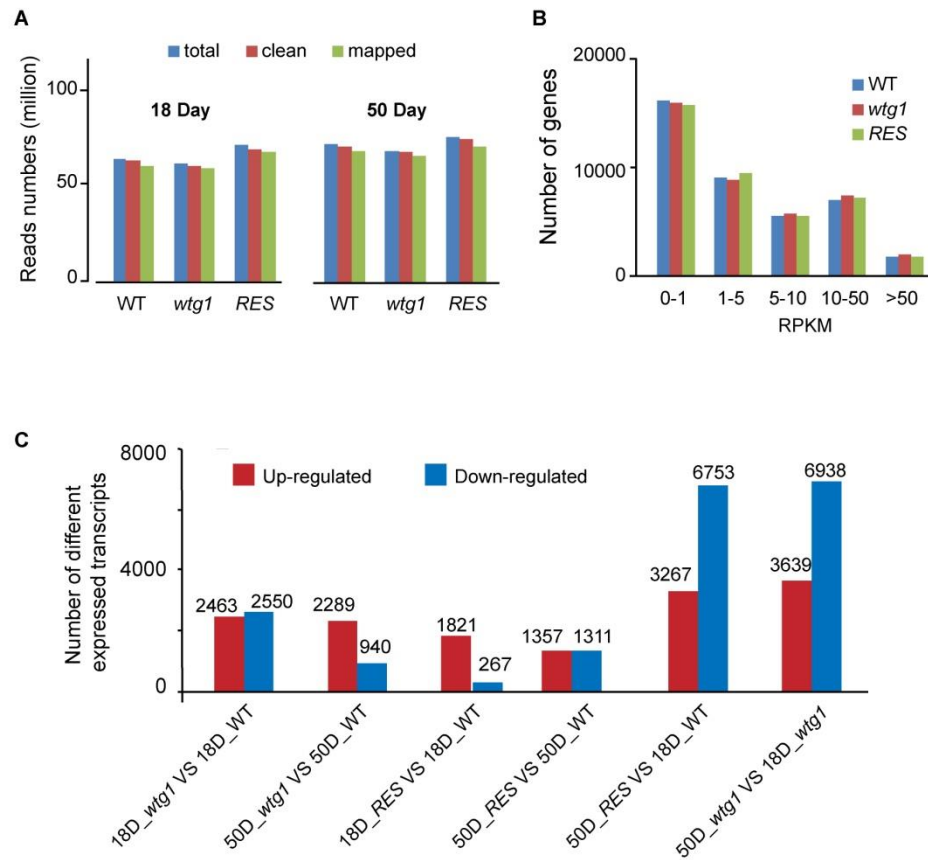


Figure S3. RNA-seq analysis of wild-type and *wtg1* leaves (A) Read numbers of sample sequences. (B) Frequencies of detected genes sorted according to their expression levels. (C) Number of differentially expressed transcripts.

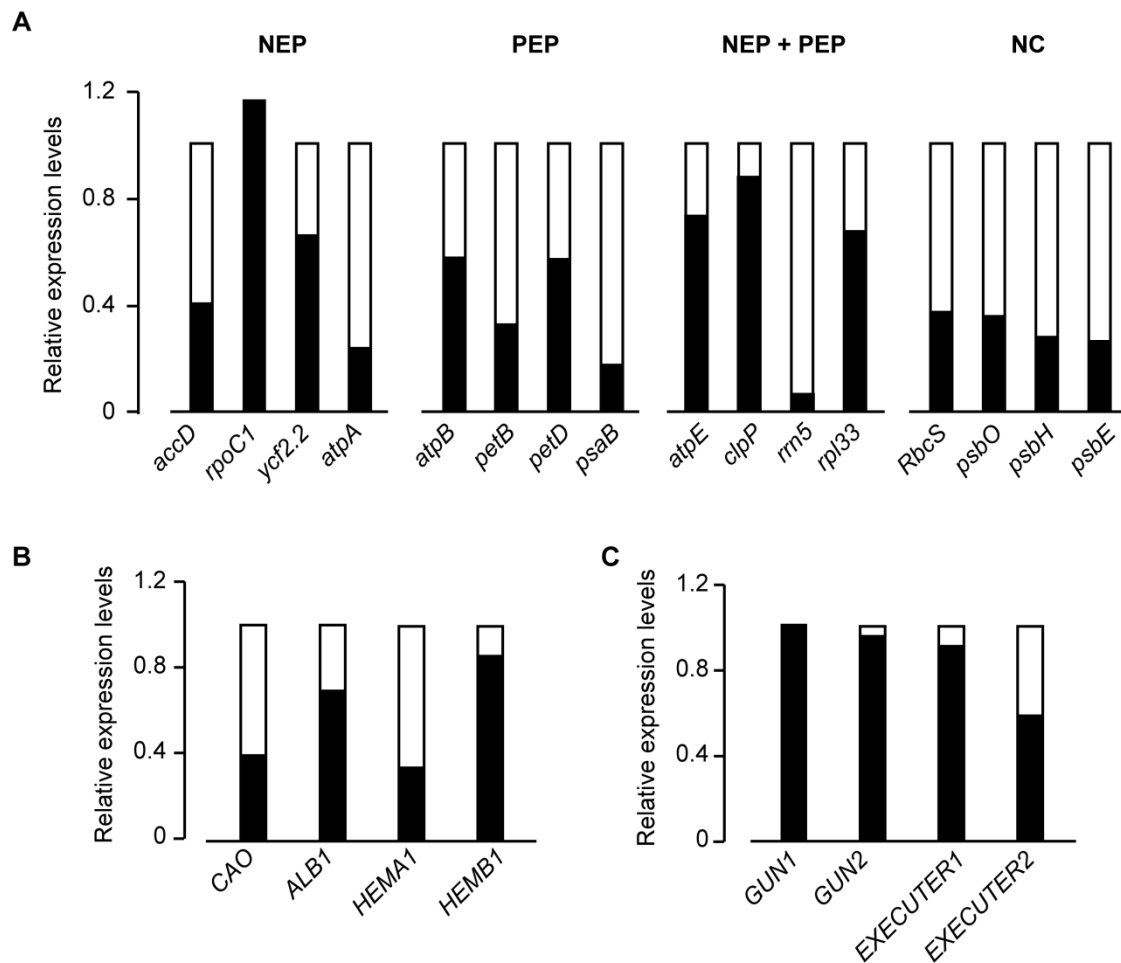


Figure S4. Transcript analysis of chloroplast-associated genes in 18-day-old *wtg1* by RNA-seq. The relative expression levels are represented by the RNA-seq fold change values with *wtg1* in black bars and WT in white bars (fold change value = 1). (A) The expression levels of plastid genes transcribed by nuclear-encoded polymerase (NEP), plastid-encoded polymerase (PEP), both nuclear-encoded and plastid-encoded polymerase (NEP + PEP) and nuclear-encoded chloroplast genes (NC). (B) The expression levels of chlorophyll biosynthesis genes. (C) The expression levels of genes involved in retrograde signaling.

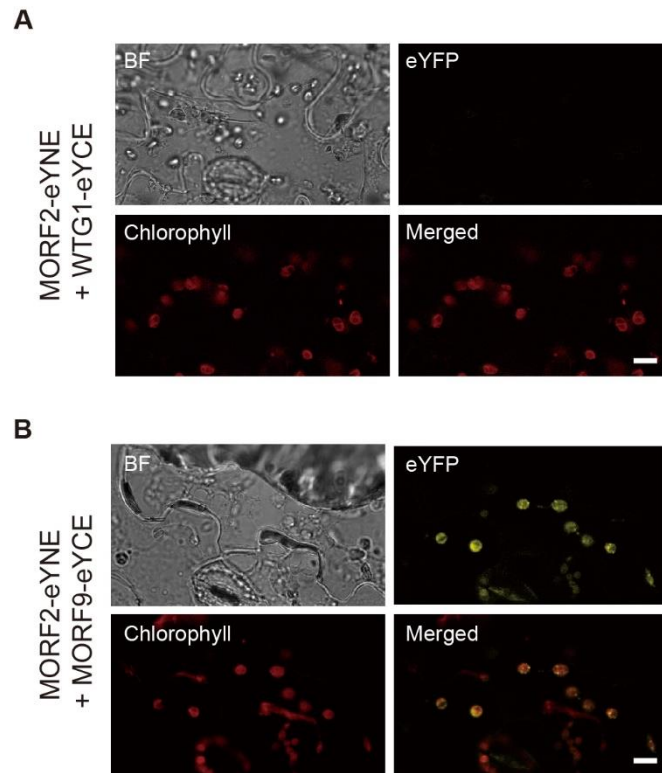


Figure S5. Controls for the Bimolecular fluorescence complementation assay. (A)

The negative control showed no interactions between WTG1 and MORF2. (B) The interaction between MORF2 and MORF9 was used as the positive control (Takenaka *et al.*, 2012). Chlorophyll autofluorescence is shown in red in (A) and (B). Bars = 5 μm .

Table S1 List of primers used in this study.

Primer name	Sequences (5'-3')	Purpose
53080cds_L1	CGCGGATCCATGGTGTCTCTAACTCTC	
53080link_R1	GACTAGACCTCCGCCGTAGCTAAGACTCTGCTTG	
linkGFP_L1	GCCGGCGGAGGTCTAGTCATGGTGAGCAAGGGCGAG	
linkGFP_R1	CGCGTCGACTTACTTGTACAGCTCGTCC	
BamHI-53080-F	CACGGATCC ATGGTGTCTCTAACTCTCTCC	
53080- EcoR1-R	CCCGAATTC CTAGTAGCTAAGACTCTGCTTG	
L1	TGGCAGTGTGTTTGTTCACG	
R1	TTGAGCAGAAGTTTACCGAG	
L2	TGTCCTTGTGCCTTCTCG	
R2	GAAGGAAGTTGAAAATGGAT	
071495-LP	CCTCAAAAGACGACAAACCTG	
071495-RP	GAAGCCGTTATTGAGGAGGAG	
006120-LP	TGCTTCAGCAGCTTTACCTTC	
006120-RP	TTTCAGGGCAAATCAATCAAG	
015164-LP	TCAGGATATAGCTGGTGGTGG	RT-PCR
015164-RP	GAGGTGGAAAACTCTGGCTC	
LBa1	TGGTTCACGTAGTGGGCCATCG	RT-PCR
UBQ5F	AAGGTTACGCGTTTGAGGAAGG	
UBQ5R	TCTTCTGGTAAACGTAGGTGAGTC	RT-PCR
Y2H-EcoRI-53080F	GCGAATTCATGGTGTCTCTAACTCTCT	
Y2H-53080-SalIR	GCGTCGACCTAGTAGCTAAGACTCTGCT	
Y2H-EcoRI-otp82F	GCGAATTCATGATGCTCT CGTGTCTCC	
Y2H-otp82-BamHIR	GCGGATCCCTACCAGTAGTCATTGCAGG	
Y2H-EcoRI-morf2F	GCGAATTCATGGCTTTGC CTTTGTCTGG	
Y2H-morf2-SacIR	GCGAGCTCTCATCTTGTGTTTTCTCTGC	
Y2H-EcoRI-morf8F	GCGAATTCATGGCGACGC ATACCATTTC	
Y2H-morf8-BamHIR	GCGGATCCTTAACCCTGGTAGGGGTTC	
Y2H-EcoRI-morf9F	GC GAATTCATGGCTTCCT TCACAACAAC	
Y2H-morf9-BamHIR	GCGGATCCTTAAGAGGAATCAGAGGCTG	
Y2H-EcoRI-orrm1F	GCGAATTCATGGAAGCTC TTATTGCTTC	
Y2H-orrm1-BamHIR	GCGGATCCCTAGAGCCCGAACTTGGTT	
Y2H-NdeI-OZ1F	GGCATATGATGAACAACCT CCACCAGACT	
Y2H-OZ1-BamHIR	GCGGATCCTCATTTATCTCCTTACCAG	
Y2H-EcoRI-ppo1-F	GCGAATTCATGGAGTTAT CTCTTCTCCG	
Y2H-ppo1-BamHI-R	GCGGATCCTTACTTGTAAAGCGTACCGTG	
BiFC-BamHI-53080F	CGCCACTAGTGGATCCATGGTGTCTCTAACTCTCT	

BiFC-53080-SalIR	TACCCTCGAGGTCGACGTAGCTAAGACTCTGCTTGT
BiFC-BamHI-morf2F	CGCCACTAGTATGGCTTTGC CTTTGTCTGG
BiFC-morf2-SalIR	TACCCTCGAGTCATCTTGTGTTTTCTCTGC
BiFC-BamHI-morf8F	CGCCACTAGTGGATCCATGGCGACGCATACCATTTC
BiFC-morf8-SalIR	TACCCTCGAGGTCGACACCCTGGTAGGGGTTGCCAC
BiFC-BamHI-morf9F	CGCCACTAGTGGATCCATGGCTTCCTTCACAACAAC
BiFC-morf9-SalIR	TACCCTCGAG GTCGACAGAGGAATCAGAGGCTGCTG
petL-pyro-F	AACATATTTTATTGAGTCCCTTC
petL-pyro-R (biotinylated)	TTGCTTAGACCAATAAACAGAAC
ndhG-pyro-F	GATTTTCTTTTAGTTTTTCTGGG
ndhG-pyro-R (biotinylated)	TACAAACAAGAACAAATCCTAAG
petLq-F	ATGCCTACTATAACTAGTTATTTTC
petLq-R	TCAAATAAGTCGTATTTTGCTTAG
ndhGq-F	TGGTACGGGGTTATTTGGACTAC
ndhGq-R	CACCTATCAAAGCAACTAAAAGAATT
18srRNA-F	AAACGGCTACCACATCCAAG
18srRNA-R	ACTCGAAAGAGCCCGGTATT
psaB-F	GGACCCCACTACTCGTCGTA
psaB-R	ATTGCTAATTGCCCGAAATG
psaD-F	GATCTTCAACTCCGCCATAA
psaD-R	ATCCCACGGGAGCTTCTTTC
Lhca1-F	CAGGAATGGGCAGCACTA
Lhca1-R	GCAATGGCTAAGAACTCAAT
Lhcb2-F	CTCCCCAAAGCATCTGGTAT
Lhcb2-R	CCCATCTGCTGTGGATTACTT
psbA-F	CCTATGGGGTCGCTTCTGTA
psbA-R	GAGCAGCAATGAATGCGATA
psbB-F	CGTGCGACTTTGAAATCTGA
psbB-R	TAGCACCATGCCAAATGTGT
atpC1-F	CGTGGATTATGTGGTGGAA
atpC1-R	GCTTCTTTAGCCGTAGGT
atpB-F	GAGCTCGTATGAGAGTTGGT
atpB-R	ACCCAATAAGGCGGATACCT
atpE-F	TCCACAAGAAGCTCAGCAAA
atpE-R	GTGTCCGAGCTCGTCTGAG
petC-F	CAAGTGGGTTGTTTGTGA

petC-R	AAGCATGTAGCCAGTAGGT	
petD-F	TCCTTTTGCAACTCCTTTGG	qPCR
petD-R	CCGCTGGTACTGAAACCATT	
rbcS-F	CTTCCTGACCTTACCGATTC	
rbcS-R	CGGGTGAGTTACCGTGCT	
rbcL-F	GTGTTGGGTTCAAAGCTGGT	
rbcL-R	CATCGGTCCACACAGTTGTC	
ndhB-F	GGCCTATATTTCTTGGTTTCAATAG	
ndhB-R	AATCGGGTTCATTGATATTCCTG	
ndhI-F	GTCAACAAACCCTACGAG	
ndhI-R	ACATACTTCACAAGCAAT	
rpoA-F	CAAGCCGACA CAATAGGCAT	
rpoA-R	AGCGCGTTGCGCGTTCCATA	
rpoB-F	GCAGGTTAGAATTAGAGATTGATA	
rpoB-R	GGGTAGCAAACATTCTCTAGAAT	
rpoC1-F	GCCTAGTATACTGCGATTTTTTC	
rpoC1-R	CTCGATTTCGAAATATATCGAAAC	
rrn16-F	CGGTATCTGGGGAATAAGCA	
rrn16-R	GATTTGACGGCGGACTTAAA	
rrn23-F	GGGCGACTGTTTACCAAAAA	
rrn23-R	TTACCCGACAAGGAATTTTCG	
rpl24-F	TTGTCGGTGCTACTTTGG	
rpl24-R	CTCGTCCTTGGTCTTCTTGATT	
rpl16-F	AACACTTGAACCCGCTTGG	
rpl16-R	GCGTTTCCGCAGGTCTTA	
rps17-F	CCCGAACCACAGAATGCC	
rps17-R	TCCACCGCCACAGTCTTG	
petL-A-F	AGTACTTTAAGAAACATATGTA	
petL-A-R	TCAAATAAGTCGTATTTTGCT	
ndhG-B-F	AAACAGCCTAATACTAATAA	
ndhG-B-R	TATATTATTAATAAAGAAAAATCG	
ndhG-C-F	TAATATAATGGATTTGCCTGGACCAATAC	
ndhG-C-R	GGGAAGTAATACCACTCCCAG	
ndhG-D-F	AACCCAATATTTTCAGCCTTTTC	
ndhG-D-R	GAAAAGGCTGAAAATATTGGGTT	
petB-nc-F	TTCATCGATGGTCGGCAAG	
petB-nc-R	TGCGGTCAATACACCCAGAA	

Table S2. Plastid RNA editing sites affected in the *wtg1* mutant plants.

All 34 reported editing sites in *Arabidopsis* plastid were detected by bulk sequencing. The affected sites, *petL-50* and *ndhG-5*, are shown in bold.

Editing site	Locus	Editing extent in wild-type (%)	Editing extent in <i>wtg1</i> (%)	Related editing factors	References
<i>matK-640</i>	2931	90	90	QED1 (PPR), MORF2, MORF9, ORRM1, OZ1	(Tillich <i>et al.</i> , 2005; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Sun <i>et al.</i> , 2015; Wagoner <i>et al.</i> , 2015)
<i>atpF-92</i>	12707	100	100	AEF1 (PPR), MORF2, MORF9	(Tillich <i>et al.</i> , 2005; Chateigner-Boutin & Small, 2007; Takenaka <i>et al.</i> , 2012)
<i>rpoC1-488</i>	21806	30	30	DOT4 (PPR), MORF2, MORF8, MORF9, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Hayes <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>rpoB-2432</i>	23898	90	90	QED1 (PPR), MORF2, MORF8, MORF9, ORRM1, OZ1	(Tillich <i>et al.</i> , 2005; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Sun <i>et al.</i> , 2015; Wagoner <i>et al.</i> , 2015)
<i>rpoB-551</i>	25779	90	90	CRR22 (PPR), MORF2, MORF9, ORRM1, OZ1	(Tillich <i>et al.</i> , 2005; Okuda <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>rpoB-338</i>	25992	90	90	YS1 (PPR), MORF2, MORF9, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Zhou <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)

<i>psbZ-50</i>	35800	100	100	OTP84 (PPR), MORF2, MORF9, OZ1, PPO1	(Chateigner-Boutin & Small, 2007; Hammani <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>rps14-80</i>	37161	100	100	MORF2, MORF9	(Tillich <i>et al.</i> , 2005; Takenaka <i>et al.</i> , 2012)
<i>rps14-149</i>	37092	100	100	OTP86 (PPR), MORF2, MORF9	(Tillich <i>et al.</i> , 2005; Hammani <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012)
<i>accD-794</i>	57868	100	100	RARE1/AtECB2 (PPR), MORF2, MORF8, MORF9, OZ1	(Tillich <i>et al.</i> , 2005; Robbins <i>et al.</i> , 2009; Yu <i>et al.</i> , 2009; Tseng <i>et al.</i> , 2010; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2015; Wagoner <i>et al.</i> , 2015)
<i>accD-3'UTR</i>	58642	80	80	QED1/AtECB2 (PPR), MORF2, MORF9, ORRM1, OZ1	(Chateigner-Boutin & Small, 2007; Robbins <i>et al.</i> , 2009; Tseng <i>et al.</i> , 2010; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Sun <i>et al.</i> , 2015; Wagoner <i>et al.</i> , 2015)
<i>psbF-77</i>	63985	100	100	LPA66 (PPR), MORF2, MORF9, OZ1	(Tillich <i>et al.</i> , 2005; Cai <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2015)
<i>psbE-214</i>	64109	100	100	CREF3 (PPR), MORF2	(Tillich <i>et al.</i> , 2005; Takenaka <i>et al.</i> , 2012; Yagi <i>et al.</i> , 2013)
<i>petL-5</i>	65716	100	40	MORF2, MORF8, MORF9, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>rps12-i58</i>	69553	30	30	OTP81/QED1 (PPR), MORF2, MORF8, MORF9, ORRM1, OZ1	(Chateigner-Boutin & Small, 2007; Hammani <i>et al.</i> , 2009; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Sun <i>et al.</i> , 2015; Wagoner <i>et al.</i> , 2015)

<i>clpP</i> -559	69942	80	80	CLB19 (PPR), MORF2, MORF9, ORRM1, OZ1	(Tillich <i>et al.</i> , 2005; Chateigner-Boutin <i>et al.</i> , 2008; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Sun <i>et al.</i> , 2015)
<i>rpoA</i> -200	78691	80	80	CLB19 (PPR), MORF2, MORF9, OZ1	(Chateigner-Boutin & Small, 2007; Chateigner-Boutin <i>et al.</i> , 2008; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2015)
<i>rpl23</i> -89	86055	80	80	OTP80 (PPR), MORF2, MORF9, OZ1, PPO1	(Chateigner-Boutin & Small, 2007; Hammani <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhB</i> -1481	94999	90	90	OTP84 (PPR), MORF2, MORF8, MORF9, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Hammani <i>et al.</i> , 2009; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhB</i> -1255	95225	100	100	CREF7 (PPR), MORF2, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Yagi <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhB</i> -872	95608	90	90	QED1 (PPR), MORF2, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015; Wagoner <i>et al.</i> , 2015)
<i>ndhB</i> -836	95644	100	100	OTP82 (PPR), MORF2, MORF8, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Hayes <i>et al.</i> , 2013; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhB</i> -830	95650	100	100	ELI1 (PPR), MORF2, MORF8, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Okuda <i>et al.</i> , 2009; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)

<i>ndhB</i> -746	96419	100	100	CRR22 (PPR), MORF2, MORF8, MORF9, OZ1	(Tillich <i>et al.</i> , 2005; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhB</i> -586	96579	100	100	MORF2, MORF8, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhB</i> -467	96698	90	90	CRR28 (PPR), MORF2, MORF8, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Okuda <i>et al.</i> , 2009; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhB</i> -149	97016	100	100	MORF2, MORF9, PPO1	(Tillich <i>et al.</i> , 2005; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014)
<i>ndhF</i> -290	112349	100	100	OTP84/AtECB2 (PPR), MORF2, MORF8, MORF9, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Hammani <i>et al.</i> , 2009; Tseng <i>et al.</i> , 2010; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhD</i> -887	116281	90	90	CRR22 (PPR), MORF2, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Okuda <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhD</i> -878	116290	80	80	CRR28 (PPR), MORF2, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Okuda <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhD</i> -674	116494	100	100	OTP85 (PPR), MORF2, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Hammani <i>et al.</i> , 2009; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)

<i>ndhD-383</i>	116785	100	100	CRR21 (PPR), MORF2, MORF8, MORF9, PPO1	(Tillich <i>et al.</i> , 2005; Okuda <i>et al.</i> , 2007; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014)
<i>ndhD-2</i>	117166	50	50	CRR4 (PPR), MORF2, MORF8, MORF9, OZ1, PPO1	(Kotera <i>et al.</i> , 2005; Tillich <i>et al.</i> , 2005; Okuda <i>et al.</i> , 2006; Bentolila <i>et al.</i> , 2012; Takenaka <i>et al.</i> , 2012; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)
<i>ndhG-50</i>	118858	100	50	OTP82 (PPR), MORF2, MORF9, ORRM1, OZ1, PPO1	(Tillich <i>et al.</i> , 2005; Okuda <i>et al.</i> , 2010; Takenaka <i>et al.</i> , 2012; Sun <i>et al.</i> , 2013; Zhang <i>et al.</i> , 2014; Sun <i>et al.</i> , 2015)

Table S3 *Trans*-factors involved in *petL-5* and/or *ndhG-50* editing

Trans-factor	Gene ID	Gene family	Editing extent in the mutant (%)		Editing level change mutant :: WT		Reference
			<i>petL</i>	<i>ndhG</i>	<i>petL</i>	<i>ndhG</i>	
			-5	-50	-5	-50	
							(Hammani <i>et al.</i> , 2009;
OTP82	AT1 G080 70	PPR	n/a	1	n/a	-99%	Okuda <i>et al.</i> , 2010; Kindgren <i>et al.</i> , 2015)
MORF2	AT2 G334 30	MORF	65	40	-35%	-60%	(Takenaka <i>et al.</i> , 2012)
MORF8	AT3 G150 00	MORF	35	72	-60%	-6%	(Bentolila <i>et al.</i> , 2012)
MORF9	AT1 G114 30	MORF	0	0	-100%	-100%	(Takenaka <i>et al.</i> , 2012)
ORRM1	AT3 G209 30	ORRM	66	8	+1%	-94%	(Sun <i>et al.</i> , 2013)
PPO1	AT4 G016 90	Protoporphyrinogen oxidase	65	85	-19%	-15%	(Zhang <i>et al.</i> , 2014)
OZ1	AT5 G177 90	RanBP2-type zinc finger	45	0	-42%	-100%	(Sun <i>et al.</i> , 2015)

+ indicates increased editing extent compared to that of wild-type plants; - indicates decreased editing extent compared to that of wild-type plants. n/a, not assayed.

References

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