Supplementary Materials: Dual-Located WHIRLY1 Interacting with LHCA1 Alters Photochemical Activities of Photosystem I and is Involved in Light Adaptation in Arabidopsis

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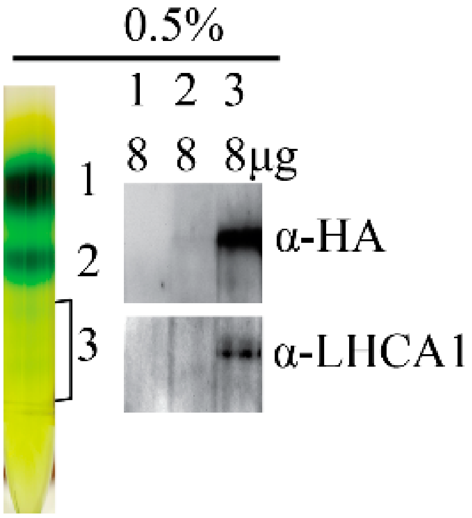

Figure S1. Sucrose density gradient ultracentrifugation of pigment protein complexes prepared from thylakoids solublized by 0.5% dodecyl-α- D-maltoside. Band 1 consists of free pigments. Band 2 contains LHCII and photosystem II complexes. Band 3 contains photosystem I complexes. Proteins from fractions 1–3 were used for immunological analysis. The blot was immunodecorated with the HA-tag antibody, followed by immunodecoration with an antibody specific for the LHCA1 (22 kD).

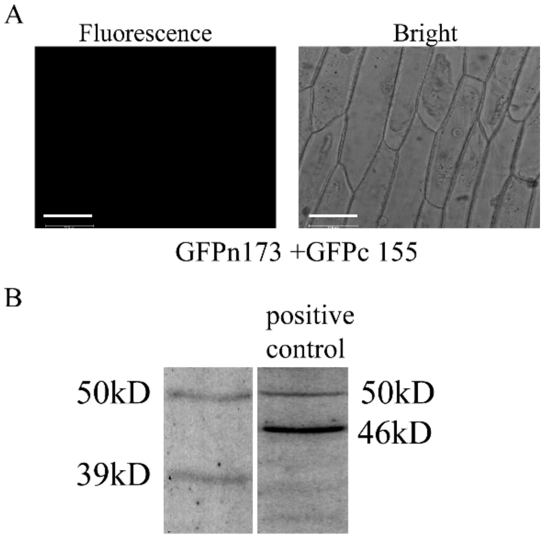

Figure S2. Negative controls for interaction of WHY1 and LHCA1. (**A**) Co-expression GFPn173 and GFPc155 without any fusions in onion epidermal cells. Fluorescence images are shown on the left and bright field images are shown on the right side, respectively. Scale bar 77.6 µm. (**B**) Immunodetection of the constructs (WHY1-GFPn173+LHCA4-GFPc155) or positive control (WHY1-GFPn173+WHY3-GFPc155) expression in the cells with the antibody against the full length GFP.

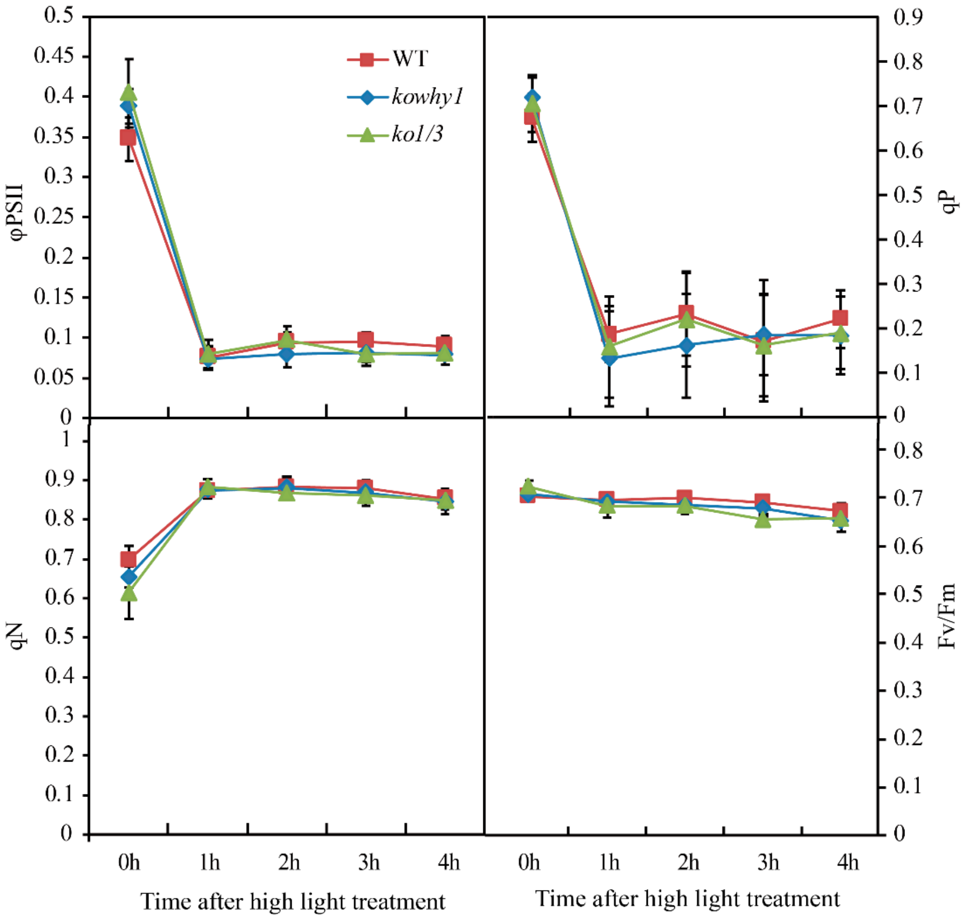

Figure S3. Photosynthetic parameters of *WHY1* mutants after high light treatment. Quantum efficiency of PSII(ΦPSII); photochemical quenching (qP); non-photochemical quenching(qN); maximum efficiency of PSII (Fv/Fm) in *WHY1* mutants under high light for 1, 2, 3, 4 hours. Means and SD of at least 10 independent measurements are shown.

Table S1. Primers for quantitative PCR.

TAIR number	Gene Name	Primer sequence (5'-3')
AT3G54890	*LHCA1*	FP:GCCGGGAATGTTGGTCGTATCAG RP:CAAACCCAAAGTCACCAGGAGCAG
AT3G61470	*LHCA2*	FP:GTCTTGAAGGTCAACAACGTCGAG RP:ACCACCCAAGAAACTTGGAGAAG
AT1G61520	*LHCA3*	FP:AAACCAGTTGCGTCTGCCTCAC RP:ATGGTCTGTTGGCTCCTTGCTTG
AT3G47470	*LHCA4*	FP:CCGCTTAACTTTGCTCCTACGC RP:AACATCGCCAACCTCCCGTTTG
AT1G45474	*LHCA5*	FP:AGAGCTTGTTCACTCTCGTTTCGC RP:TGTGGTCCGAAGGAGATCAGTG
AT1G19150	*LHCA6*	FP:GGTTTCGATCCTCTCGGTTTAGGG RP:ACCTAACCGCTCGAGACATTCTG
ATCG00350	*PsaA*	FP:AGCGAGCACCAGTTTGACTTGG RP:AAGCTACTTTGCCACCCACTGC

ATCG00340	*PsaB*	FP:AATTTCCTGGCGTGGTTATTGGC RP:CGTTCATGAGCCCACGCTAAAG
ATCG01060	*PSAC*	FP:TTCTGCTCCAAGAACCGAGGAC RP:GTTGGACAGGCGGATTCACATC
AT4G02770	*PSAD-1*	FP:AACACACCGTCTCCGATCTTCG RP:ACTCTTCCACTTGCGCTTTACG
AT1G03130	*PSaD-2*	FP:AGCCGTGAAAGAAGCTCCAGTTG RP:CTTCCGGCGAAGATTGGTGATG
AT4G28750	*PSaE-1*	FP:AGTTGTTGCCGTTGATCAGGAC RP:CCCATTTAAGCTGCAACTTCTTCG
AT2G20260	*PSaE-2*	FP:AGTTGTGGCCGTTGATCAGGAC RP:TTCTTCCACCTCGTCCAATGCG
AT1G31330	*PsaF*	FP:CTCTTGCTCTCAATGCTCAGATCG RP:ACTTCCCGTAGTTGTCGAACCTG
AT1G55670	*PsaG*	FP:CCATCTCATTCCATGGCCTTCGTC RP:TCCCGGTGGTTGATAGTTTGGG
AT3G16140	*PsaH*	FP:ACCCAAATCCATCCGGGCTAATG RP:AGAGCCGTATACGTCCCATTGAC
ATCG00510	*PsaI*	FP:TGACAACTTTCAATAACTTACCCTC RP:CCATTGCAATTGCCGGAAAGA
ATCG00630	*PSAJ*	FP:ATGGTTCGGTTCGTTAGCAG RP:GGGAAATGTTAATGCATCTGGAA
AT1G30380	*PsaK*	FP:GGAGCTTTGGGTGCAAAGTGTG RP:GGTCGTCGACGTTACCATTATCAG
AT4G12800	*PsaL*	FP:CCGAGCTGTTAAATCCGACAAGAC RP:AAGGTACCACGCGATCAATGGG
AT5G64040	*PsaN*	FP:GCCTGTGATCAAAGCTCAACGC RP:AAACCATGGCTGATCGTCTTCC
AT1G08380	*PsaO*	FP:CCGCTAAAGCCACTGCTTACTGTC RP:TAGTAGCTCTCGTCACAACGTTCC
AT2G46820	*PsaP*	FP:CCAACATTAAGCGCCAAGAACCC RP:TCAACCAGTTCCTCTCAAAGCAAG
ATCG01100	*NDHA*	FP:GGATGGAATTTGTGGCGTCAACC RP:ACGGTAACCTCTCGCATTCTGC
ATCG00890	*NDHB.1*	FP:CGGGGGAGAGATTGAGCTTC RP:TGGAGTGGGAGATCCTTCGT
ATCG00440	*NDHC*	FP:CAATTAGGAAGGGGCCGGAG RP:TTGTAACCAAGCATCCCCGA
ATCG01050	*NDHD*	FP:TTTCTCCTTGGTTGTTGGTAGTCG RP:TGACCGGGAGATGTTGAAGCTG
ATCG01070	*NDHE*	FP:TGGTTAGGGCTCTTATGTGTCT RP:CAGCGGCTGCAATTGCTATAA

ATCG01010	*NDHF*	FP:CCCTTTCATTCCACTTCCAGTACC
		RP:AAAGTCCACATGCGGCGAAG
ATCG01080	*NDHG*	FP:CGATACGTCATGGTACGGGG
		RP:CGAGCCACAGAAATTGCACC
ATCG01110	*NDHH*	FP:ATTCGAAGCTGCCACCGGTATG
		RP:TCAGCCGCTATTCCTCCAATACG
ATCG01090	*NDHI*	FP:TGGTCAACAAACCCTACGAGCTG
		RP:AATGGATTCGACCGCGGAAACG
ATCG00420	*NDHJ*	FP:TAGCCATCCACGACTGAAACGG
		RP:ACGTAAAGGCCACCCTATCCAAC
AT1G70760	*NDHL*	FP:ACAATCTTGGCAGCTCAACTCG
		RP:TGCTAAGGCTGGATGGTCAATCG
AT4G37925	*NDHM*	FP: AGCTGAACGTGAAGAGCAAGGG
		RP:TGACGTGTGACACTGCTTAGCC
AT5G58260	*NDHN*	FP:TATGGGTCCTCGAAGCAAAGGTC
		RP:GGACGAAGAGAGGGAAGTAAAGCG
AT1G74880	*NDHO*	FP:GACAGGAGAGTATGCACTTGTTGG
		RP:AGCATATCTGTTGGGAGCCAAGC
AT3G27690	*LHCB2*	FP:AGCAATGGCCACTTCAGCAA
		RP:CGGAGGAGATCGTTGGATGG
AT4G28660	*PSB28*	FP:TTCAGTCGACGGATGTGAACGC
		RP:TGTGCTTCGCCACAATCCCTTC
AT3G01440	*PNSL3*	FP:AAGCTTGAAGATGCAGCTAAGACG
		RP:ACCGAACCAGGATCATGCCATTC
AT1G70580	*AOAT2*	FP:AACAAGCCGGAAAAGTCCCT
		RP:CTGCTGGCAGAATTGTTGTCC
AT4G26530	*ATFBA5*	FP:AGGCACTCTGCTTAAACCGAAC
		RP:TATCACTTCCGGTGCAACCTTTG
AT2G05100	*LHCB2.1*	FP:CAACGCCTGGTCTTACGCTA
		RP:AACAGGGTGGTGTGGTTCA
AT5G52570	*BCH II*	FP:CCTGGTCTCTGCTTCGGTG
		RP:TGTGTGGTGTAGCTGGTGAG
AT2G36890	*MYB38*	FP:CCGTATAACCCATCAACAAACCA
		RP:GTTGTTGGCCCATCATTGTCA
AT3G49120	*PRXCB peroxidase*	FP:ACAATCTGTCACTTTGGCAGGAG
		RP:TGCATTAGCGAGTTCCAGGAATG
AT5G01820	*SR1*	FP:TAGACACGAATCCGCAGACGAG
		RP:TCGTCGTAGCCCTGTTTGAACC
AT 2G44840	*ERF13*	FP: AGCGACTTGCCGTTAAGTGTCG
		RP: AACGGCATCACGGAGAGTGTTG
AT4G34410	*ERF109*	FP: TGGGCCAAGGGCTAAACTCAAC
		RP: CAGCAGCAACAGGAGATGAAACTG

AT4G01250	*WRKY22*	FP: ACGGCGGAGCATAATCATCCAG RP: TGGTTTCTGACGTGTGCTTCCG