

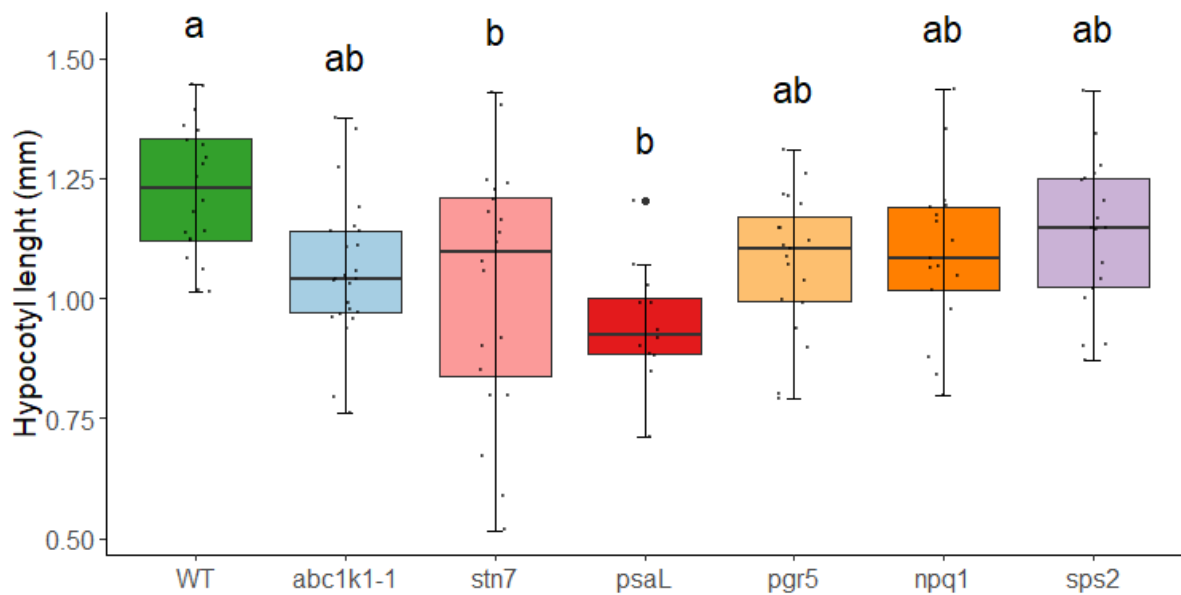


Figure S1: Length of the hypocotyl by genotype of seedlings grown under continuous white light (80 μ E). The whiskers and box plot shows the minimum, first quartile, median, average, third quartile and maximum of each dataset, points indicate individual samples, outliers are indicated by a bigger point. (WT n=20, *abc1k1-1* n=24, *stn7* n=20, *psaL* n=12, *pgr5* n=19, *npq1* n=17 and *sps2* n=18). The letters identify statistically different groups obtained by a Tukey-HSD post-hoc test ($\alpha = 0.01$).

Identified Proteins	Accession Number	Alternate ID	CTL WL	K1 WL	CTL RL	K1 RL	Localization
Found in the eluate of ABC1K1 in normal light and red light							
AT3g24190/MU8_17 OS=Arabidopsis thaliana OX=3702 GN=At3g24190 PE=2 SV=1	Q9LRNO	At3g24190	0	2	0	15	Chloroplast
LETM1-like protein OS=Arabidopsis thaliana OX=3702 GN=MBL20.10 PE=4 SV=1	A0A1P8B9X6	At5g06220	0	5	0	11	Chloroplast, chloroplast envelope, mitochondrial inner membrane
Oligouridylate-binding protein 1C OS=Arabidopsis thaliana OX=3702 GN=UBP1C PE=1 SV=1	Q9LH8	At3g14100	0	5	0	11	Cytoplasm, nucleus
Amino acid kinase family protein OS=Arabidopsis thaliana OX=3702 GN=At3g18680 PE=1 SV=1	A0A1P9L1R3 (+1)	At3g18680	0	3	0	11	Chloroplast
NAD(P)H-quinone oxidoreductase subunit K, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ndhK PE=3 SV=1	P56756	Atg00430	0	12	0	10	Chloroplast, plastid
NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ndhA PE=3 SV=2	Q37165	Atg01100	0	11	0	10	Chloroplast
Probable plastid-lipid-associated protein 10, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PAP10 PE=1 SV=1	Q8W4F1	At2g46910	0	7	0	10	Chloroplast, cytosol, plastoglobule
Protein MITOFERRINLIKE 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=MF11 PE=2 SV=1	Q9FHX2	At5g42130	0	4	0	10	Chloroplast, chloroplast envelope, mitochondrion, plastid
Thioredoxin family protein OS=Arabidopsis thaliana OX=3702 GN=At4g10000 PE=4 SV=1	F4JKW0	At4g10000	0	3	0	9	Chloroplast
Thioredoxin-like protein HCF164, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=HCF164 PE=1 SV=2	Q23166	At4g37200	0	4	0	9	Chloroplast thylakoid membrane
Jaracalin-related lectin 8 OS=Arabidopsis thaliana OX=3702 GN=JAL8 PE=3 SV=1	F4IB94	At1g52050	0	4	0	8	Extracellular regions
Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana OX=3702 GN=At1g74640 PE=2 SV=1	BL8475	At1g74640	0	4	0	8	Chloroplast, chloroplast envelope, chloroplast thylakoid membrane
NAD(P)H-quinone oxidoreductase subunit M, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ndhM PE=2 SV=1	Q2V257	At4g37925	0	7	0	7	Chloroplast, chloroplast thylakoid membrane, plasma membrane
CBS domain-containing protein CBSCBSP85 OS=Arabidopsis thaliana OX=3702 GN=CBSCBSP85 PE=1 SV=1	P0DH79 (+1)	At5g0640	0	3	0	7	Plastid
Mitochondrial transcription termination factor family protein OS=Arabidopsis thaliana OX=3702 GN=At5g07900 PE=2 SV=1	Q9SD94	At5g07900	0	5	0	7	Chloroplast
GDP-L-fucose synthase 1 OS=Arabidopsis thaliana OX=3702 GN=GER1 PE=1 SV=3	O49213	At1g73250	0	2	0	7	Cytoplasm
Protein kinase superfamily protein OS=Arabidopsis thaliana OX=3702 GN=At3g61080 PE=4 SV=1	A0A1P9LR17 (+1)	At3g61080	0	4	0	6	Chloroplast, mitochondrion
Conserved oligomeric Golgi complex subunit 4 OS=Arabidopsis thaliana OX=3702 GN=COG4 PE=1 SV=1	Q8L838	At4g01395	0	3	0	6	Golgi apparatus
P-type ATPase of Arabidopsis 2 OS=Arabidopsis thaliana OX=3702 GN=PPA2 PE=3 SV=1	A0A1P8BE56 (+1)	At5g22190	0	3	0	6	Chloroplast, chloroplast thylakoid membrane
Putative septum site-determining protein minD homolog, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=MIND1 PE=1 SV=1	Q9MBA2	At5g24020	0	2	0	6	Chloroplast, chloroplast envelope, chloroplast stroma
Cytochrome P450 705A5 OS=Arabidopsis thaliana OX=3702 GN=CYP705A5 PE=2 SV=1	Q9F139	At5g47990	0	2	0	5	Endoplasmic reticulum, mitochondrion
Mitochondrial import inner membrane translocase subunit TIM17-2 OS=Arabidopsis thaliana OX=3702 GN=TIM17-2 PE=1 SV=2	Q9SP35	At2g37410	0	4	0	5	Endoplasmic reticulum, mitochondrial inner/outer membrane, mitochondrion
UPF0051 protein ABC18, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ABC18 PE=2 SV=1	Q9Z597	At4g04770	0	3	0	5	Chloroplast, chloroplast stroma
Uncharacterized methyltransferase At2g41040, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=At2g41040 PE=1 SV=1	Q9WP77	At2g41040	0	4	0	5	Chloroplast, plastoglobule
AT3g23700/MYM9_3 OS=Arabidopsis thaliana OX=3702 GN=At3g23700 PE=2 SV=1	Q9LK47	At3g23700	0	3	0	5	Chloroplast, chloroplast stroma, nucleus
AnimeMemeoIdSam system protein B OS=Arabidopsis thaliana OX=3702 GN=AD2g25280 PE=2 SV=1	Q9SR95	At2g25280	0	3	0	5	Nucleus
Lycopene beta cyclase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=LCY1 PE=1 SV=1	Q38933	At3g10230	0	2	0	5	Chloroplast
Ycf3-interacting protein 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=Y3P1 PE=1 SV=1	Q9LU01	At5g44650	0	5	0	4	Chloroplast, chloroplast thylakoid membrane
Sulfoquinovosyl transferase SQD2 OS=Arabidopsis thaliana OX=3702 GN=SQD2 PE=1 SV=1	Q854F6	At5g01220	0	5	0	3	Chloroplast, chloroplast envelope, plasma membrane, plastid
NAD(P)H-quinone oxidoreductase subunit L, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ndhL PE=2 SV=1	Q9CAC5	At1g70760	0	5	0	3	Chloroplast, chloroplast thylakoid membrane
NAD(P)H-quinone oxidoreductase subunit N, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ndhN PE=2 SV=1	Q9LVM2	At5g58260	0	9	0	0	Chloroplast, chloroplast envelope, chloroplast thylakoid membrane
Found in the eluate of ABC1K1 only in red light							
LETM1-like protein OS=Arabidopsis thaliana OX=3702 GN=MBL20.10 PE=4 SV=1	F4KZ07	At5g06220	0	0	0	11	Chloroplast, chloroplast envelope, mitochondrial inner membrane
Aspartokinase 2, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=AK2 PE=1 SV=2	O23853	At5g14060	0	0	0	11	Chloroplast, chloroplast stroma
Serine/threonine-protein kinase SRK2B OS=Arabidopsis thaliana OX=3702 GN=SRK2B PE=1 SV=1	Q9C958	At1g60940	0	0	0	8	nucleus
P-loop containing nucleoside triphosphate hydrolases superfamily protein OS=Arabidopsis thaliana OX=3702 GN=SPD1 PE=4 SV=1	F4J3K7	At3g10420	0	0	0	7	Chloroplast, chloroplast envelope, chloroplast intermembrane space
Isopentenyltransferase 9 OS=Arabidopsis thaliana OX=3702 GN=IPT9 PE=3 SV=1	F4KZQ7 (+1)	At5g20040	0	0	0	7	Nucleus
Probable galactinol-sucrose galactosyltransferase 2 OS=Arabidopsis thaliana OX=3702 GN=RF52 PE=2 SV=2	Q94A08	At3g57520	0	0	0	7	Cytoplasm, plasmodesma
Protein EXECUTER 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=EX1 PE=1 SV=1	Q93W0	At4g33630	0	0	0	6	Chloroplast, thylakoid membrane
Thermosome subunit gamma OS=Arabidopsis thaliana OX=3702 GN=DY1 PE=2 SV=1	Q949W7	At5g19540	0	0	0	6	Chloroplast, chloroplast stroma
Cytochrome P450 71B5 OS=Arabidopsis thaliana OX=3702 GN=CYP71B5 PE=2 SV=1	O65784	At3g53280	0	0	0	6	Chloroplast
Argonate dehydratase/prephenate dehydratase 6, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ADT6 PE=1 SV=1	Q9SGD6	At1g08250	0	0	0	6	Chloroplast
Insulinase (Peptidase family M16) protein OS=Arabidopsis thaliana OX=3702 GN=MIK19.18 PE=1 SV=1	A0A2H1ZE93	At5g56730	0	0	0	6	Chloroplast, mitochondrion, plastid

Table S1: List of ABC1K1 interaction candidates. The proteins identified by mass spectrometry in the co-immunoprecipitation eluate with ABC1K1::HA are shown in the table (spectral count >4). The protein identification was based on TAIR database, from which the protein description and the corresponding accession number were taken. The corresponding gene locus was also obtained from TAIR. The peptide counts are shown in the column for the negative control and the ABC1K1::HA samples (CTL and K1 respectively) prepared from plants grown under constant white light (NL) or red light (RL). Protein localization , as annotated in TAIR, is reported in the last column. The top part of the table shows proteins identified in both growth conditions, while the bottom part shows the proteins identified in the protein samples obtained only from plants grown under red light.

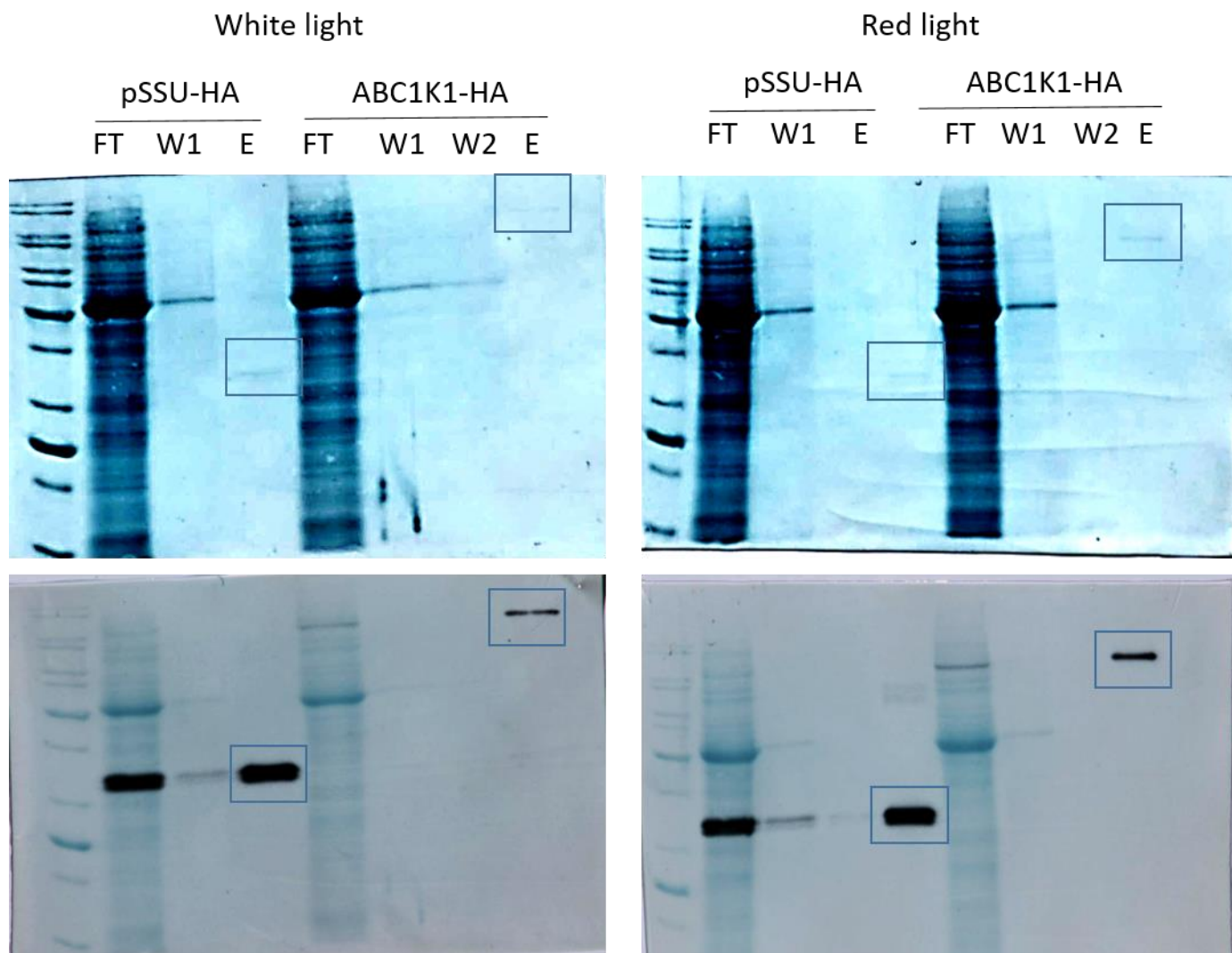


Figure S2: Co-immuno purification of ABC1K1-HA with putative interaction partners. Total protein extracts were prepared from 5 days old seedling of pSSU-HA control line and ABC1K1-HA complemented line, grown under white light (80 μ E) or pure red light (60 μ E). The extracts were loaded on affinity chromatography, the picture shows the protein staining (top membrane) of the flow through (FT), the first washing (W1), the second washing (W2) and the eluate (E), of the isolation process for the two lines and the two light condition. On the bottom membrane is shown the chemiluminescent signal obtained by the decoration of the membrane with an antibody anti-HA. The bands corresponding to pSSU-HA and ABC1K1-HA in the respective eluates, are framed in blue.

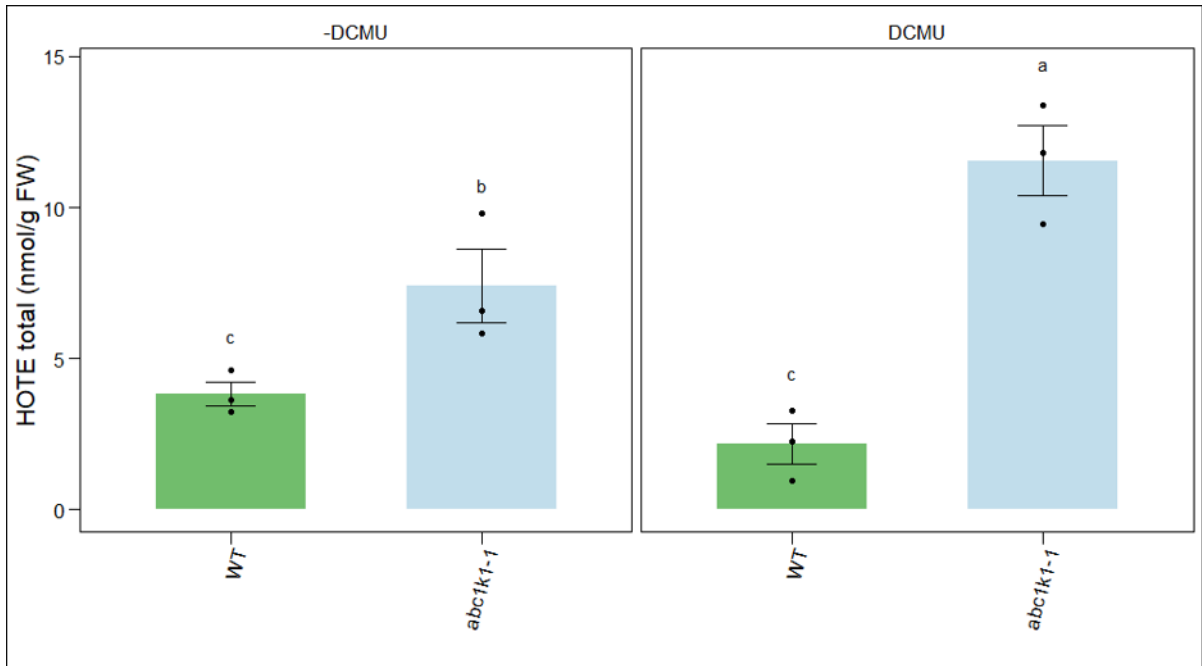


Figure S3: DCMU treatment increases lipid peroxidation in *abc1k1-1*. The lipid peroxidation was measured by the hydroxy-octodecatrienoic acid levels (HOTEs), in 5 days old WT and *abc1k1* seedlings grown under white light (80 μ E) in the presence or absence of 12.5nM DCMU (n=3). The different letters represent statistically different groups ($\alpha=0.05$) as identified by a Tukey HSD test.

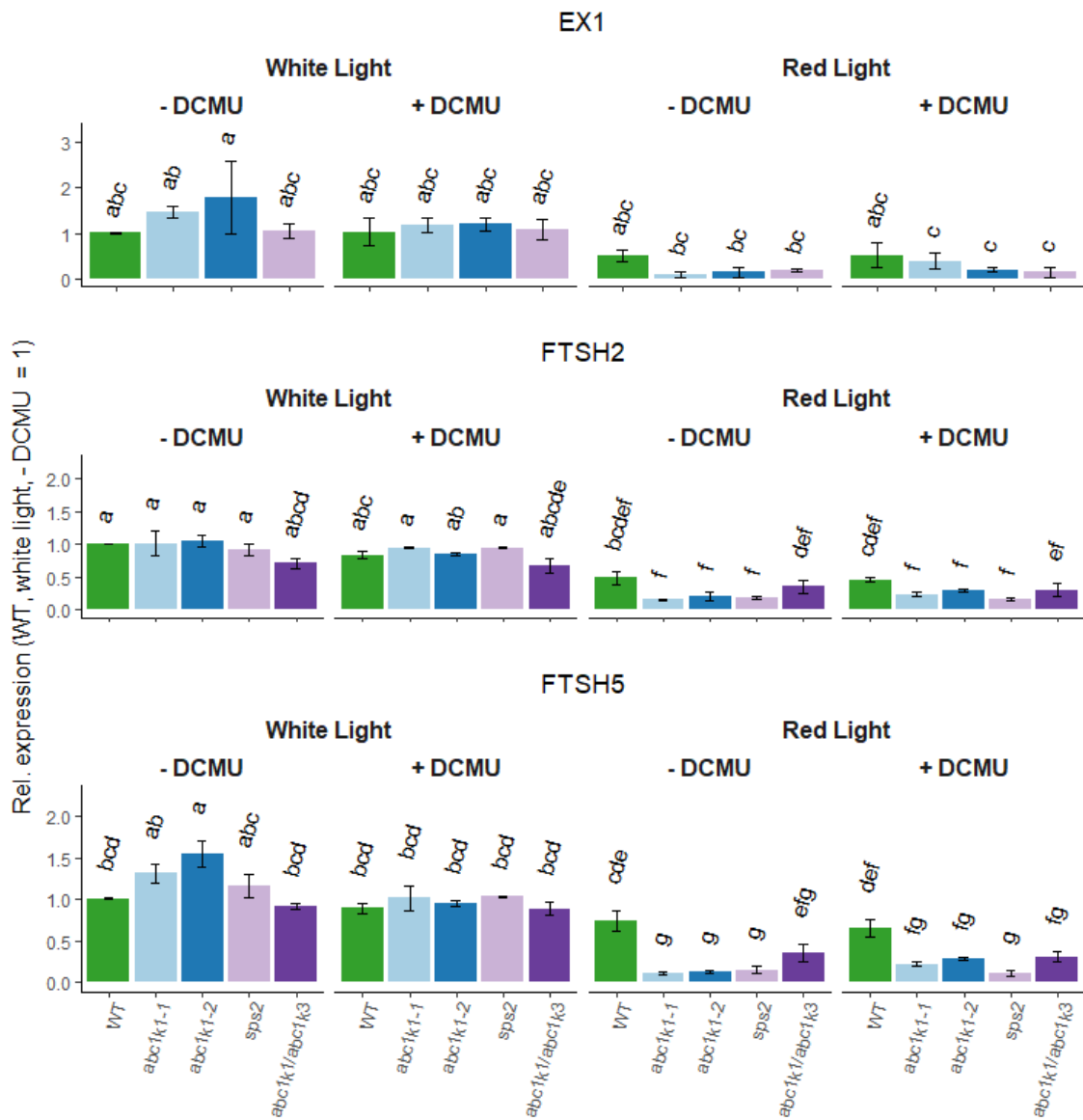


Figure S4: Gene expression of EX1 and FTSH proteases in various genotypes and light conditions. Transcript levels of Ex1 (At4g33630), ftsh2 (At2g30950) and ftsh5 (At5g42270) analyzed by quantitative PCR (qRT-PCR) of 5 days old WT, *abc1k1-1*, *abc1k1-2*, and *sps2* seedlings grown under white light (80 μ E) or red light (60 μ E) with or without 12.5 nM of DCMU. Error bars indicate the standard error (n= 2). The different letters represent statistically different groups (alpha=0.05) as identified by a Tukey HSD test.

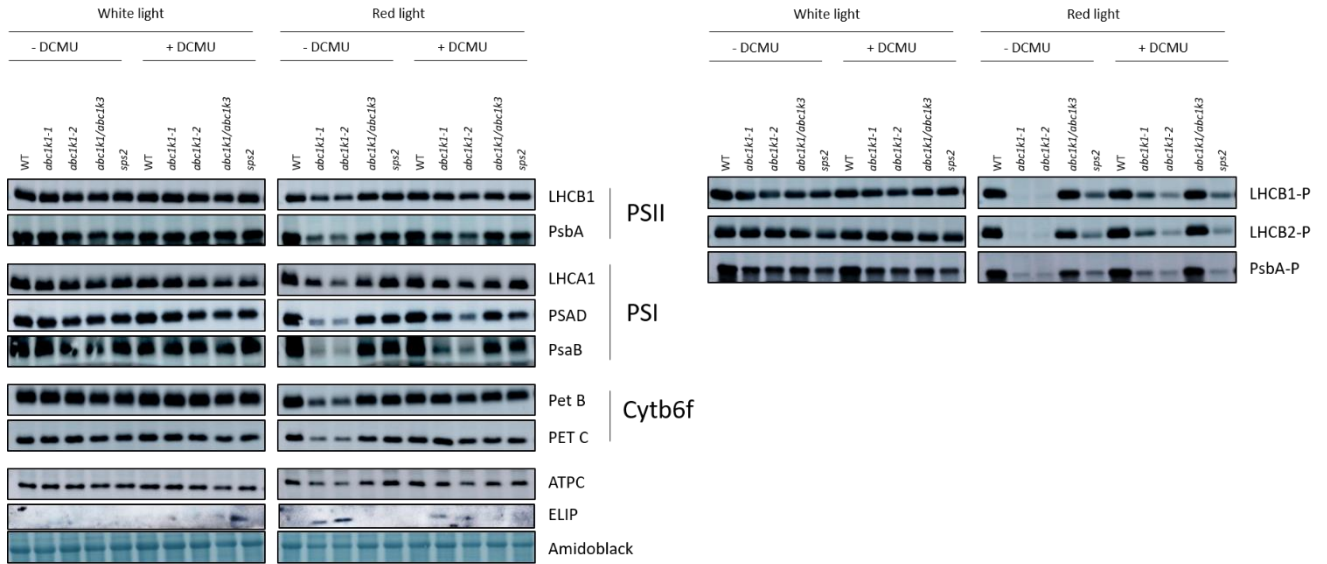
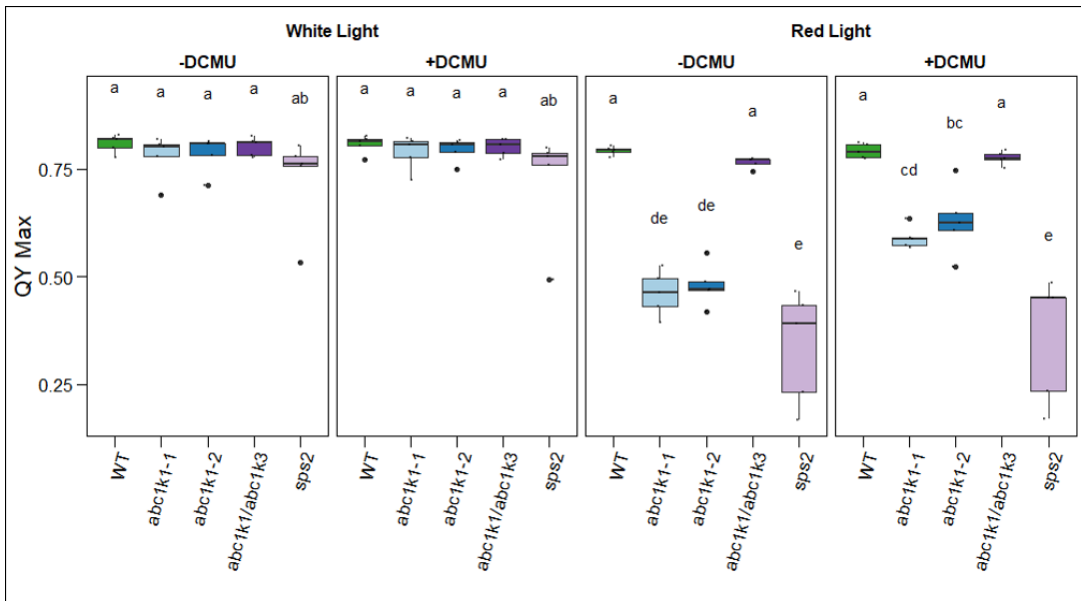
a**b**

Figure S5: DCMU treatment partially restored the level of photosynthesis-associated proteins and the maximum quantum yield in *abc1k1* under red light.

a) Representative immunoblot image showing the accumulation of photosynthetic proteins representative of the electron transport chain complexes in 5 days old seedling grown under four tested conditions: White light, red light, with and without DCMU. The phosphorylation level of LHCII and PSII was assessed with antibodies recognizing the main phosphorylated peptide of these proteins. Amidoblack staining of the membrane is showed as the loading control. b) PSII maximum quantum yield (QY MAX = FV/FM) measured in 5 days old seedlings, whiskers and box plot shows the minimum, first quartile, median, average, third quartile and maximum of each dataset, outlier measures are plotted as separated points. (n=4).

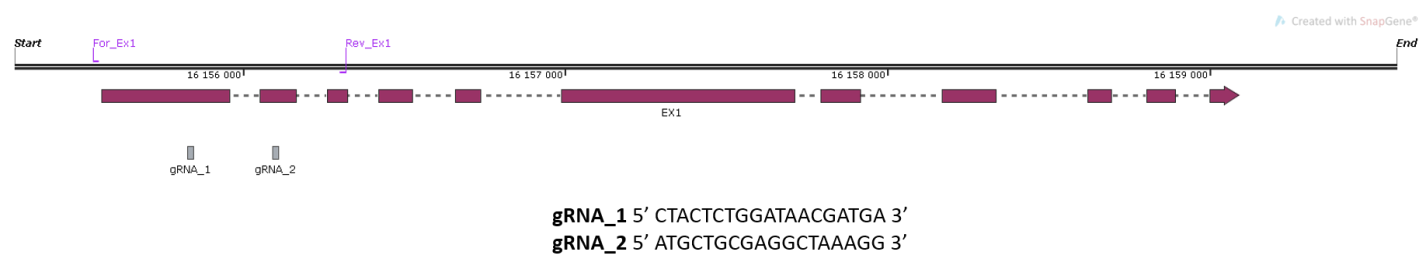
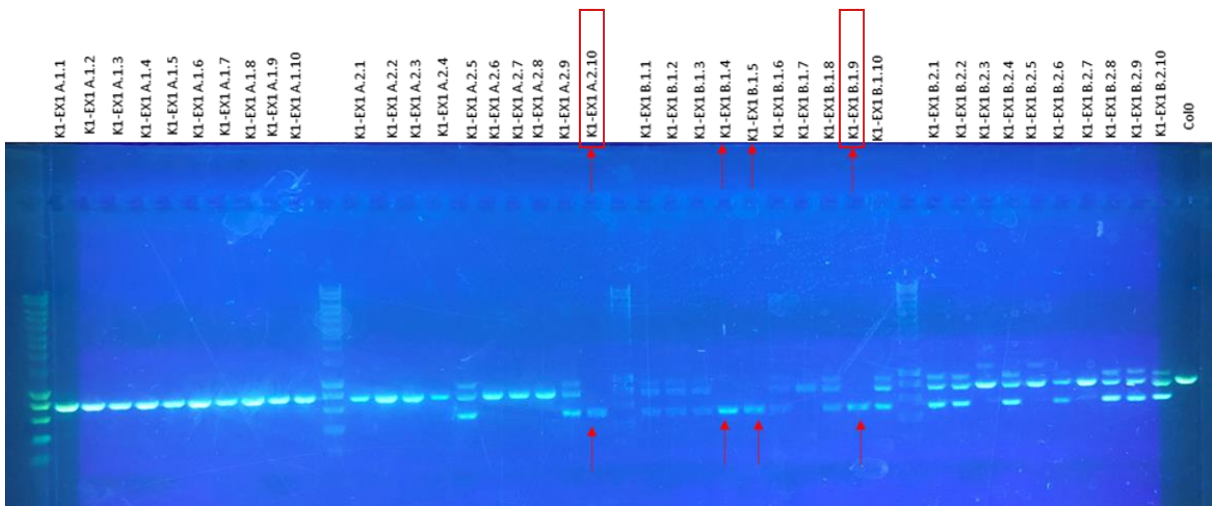


Figure S6: Schematic representation of the *ex1* gene showing the position of the two guide RNAs and primers used for CRISPR/Cas 9 mutation and validation. The sequences of the two gRNAs used for the targeted mutation are reported below the scheme.

a



b

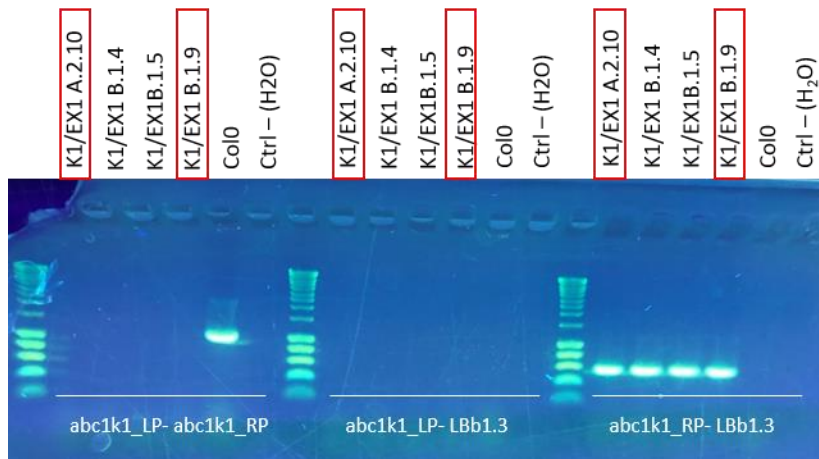


Figure S7: Screening by genomic PCR of the double *abc1k1/ex1* CRISPR/Cas9 mutants.

Total genomic DNA was extracted from WT (Col-0) and multiple *abc1k1/ex1* CRISPR/Cas9 lines originated from two transformed plants and tested by PCR a) using primers listed in table S3 and represented in figure S6. The *abc1k1/ex1* A2 10, *abc1k1/ex1* B1 4, 5 and 9 (red arrow) show only one band at about 400 bp which confirms the homozygous mutation of the *EX1* gene. b) The presence of the T-DNA insert in the *ABC1K1* gene mutation was confirmed by PCR using primers *abc1k1_LP*, *abc1k1_RP* and *LBb1.3* listed in table s3. In red squares, the *abc1k1/ex1* lines used for experiments.

Gene name	Primer ID	Nucleotide sequences 5' -> 3'	References
<i>qRT-PCR</i>			
EX1	At4g33630-For	CTACTGCTACTAATGATGCTGTTG	Page et al., 2016
	At4g33630-Rev	GACATCTTCCGAAATACCAGAC	
FTSH2	At2g30950-For	GTGTGTGGAACATTGACTCCAG	
	At2g30950-Rev	GGTGATCTGTTGTAAGTCACC	
FTSH5	At5g42270-For	GCTTACCATGAGGCTGGG	
	At5g42270-Rev	GCAACAGCCATTTGGTTCTC	
ACT2	At3g18780-For	CTTGCACCAAGCAGCATGAA	Yang et al., 2016
	At3g18780-Rev	CCGATCCAGACACTGTACTTCCTT	
<i>Genotyping</i>			
ABC1K1	abc1k1-1_LP	AGCTGATTCATCATCTGTCGG	
	abc1k1-1_RP	TCCCTTCCCACACTAAAAGTG	
EX1	Ex1-For	CCACACGCTCTCACATCTCT	
	Ex1-Rev	ACCAGCTTTGTCTCGCAAGT	
<i>Cloning</i>			
EX1	Ex1g1-BsF	ATATATGGTCTCGATTGCTACTCTGGATAACGATGAGTT	
	Ex1g1-F0	TGCTACTCTGGATAACGATGAGTTTTAGAGCTAGAAATAGC	
	Ex1g2-R0	AACCCTTTAGCCTCGCAGCATCCAATCTCTTAGTCGACTCTAC	
	Ex1g2-BsR	ATTATTGGTCTCGAAACCCTTTAGCCTCGCAGCATCCAA	
pSSU, At5g38430	RBCS1B-For	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGGCTTCCTCTATGCTCTCC	
	RBCS1B-Rev	GGGGACCACTTTGTACAAGAAAGCTGGGTGCTTCTTTCCGATTGGTGGCCA	

Table S2: List of the oligonucleotides used in this report