Electronic Supplementary Material (ESI) for Photochemical & Photobiological Sciences.
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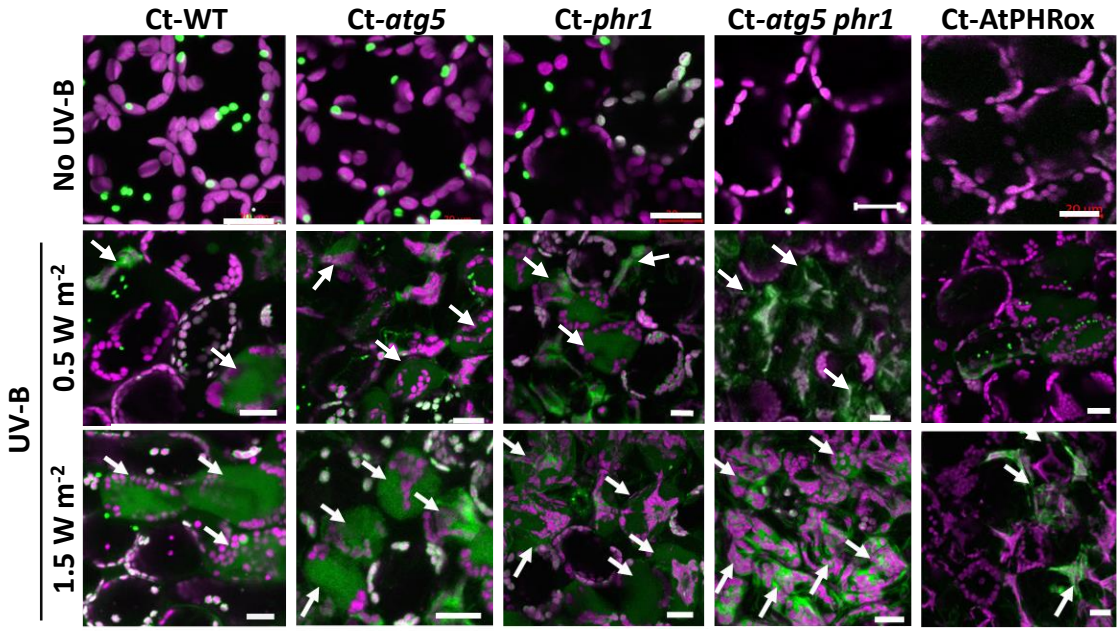
Supplementary Table 1

Supplemental Table 1. Primers used for real-time RT-PCR.

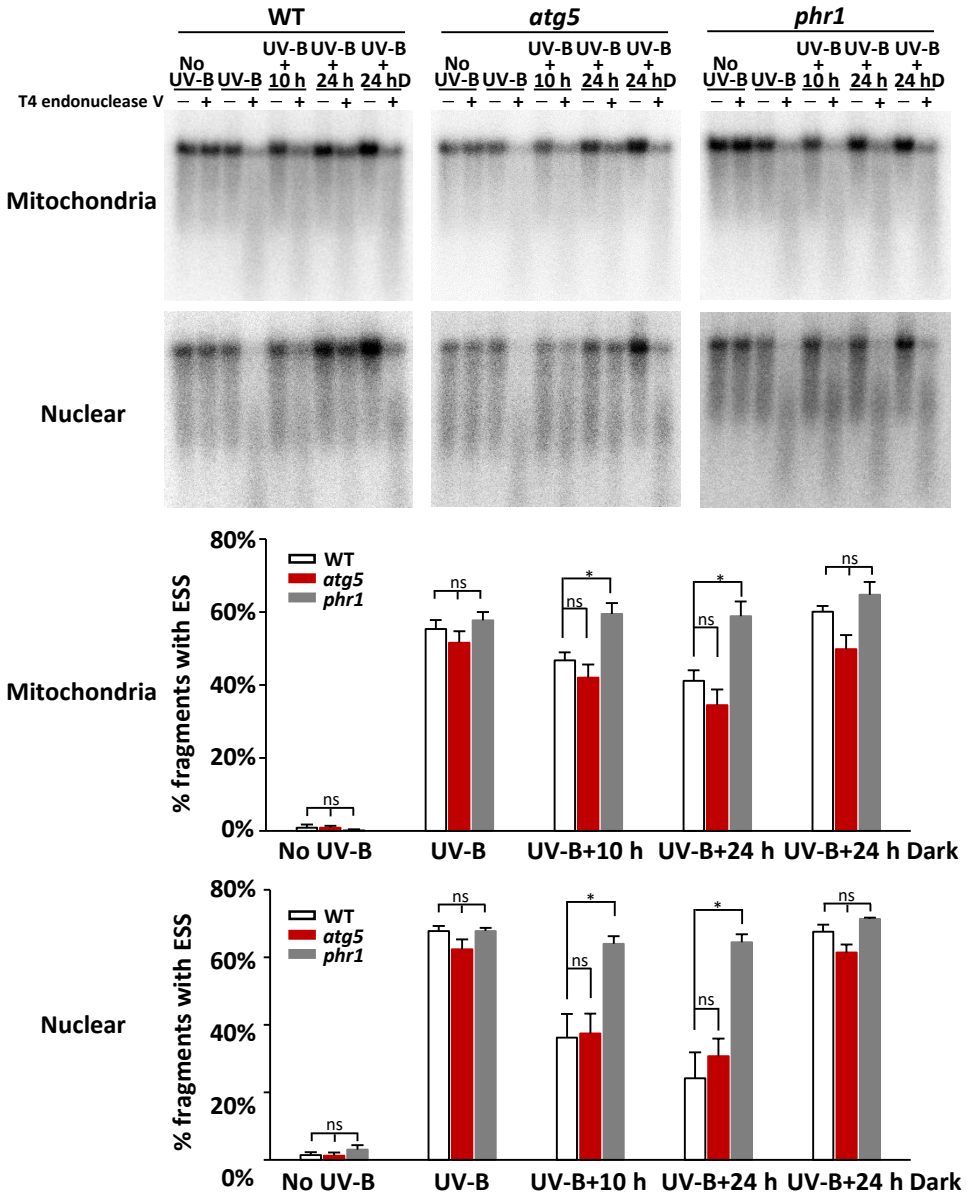
Primer name	Sequences (5′ - 3′)
TUB-F	CCAGCTTTGGTGATTTGAAC
TUB-R	CAAGCTTTCGGAGGTCAGAG
ATG2-F	AATGGATAGCAAGTGGAAGC
ATG2-R	AGATAGACCTACCGTTAGCC
ATG5-F	ACTGATACCATGTGAAGGAG
ATG5-R	GTATAGGCATCAAGATCACC
ATG7-F	GAAGATTGTCTAGGTCGTGG
ATG7-R	CCTGCTTTCTCTTGTATCGG
ATG8A-F	CAATTTGTATACGTGGTTCGT
ATG8A-R	AGCAACGGTAAGAGATCCAA
ATG8B-F	TTGGCCAATTTGTGTACGTT
ATG8B-R	TCCACCAAATGTGTTCTCTCC
ATG8C-F	TGAGTGCCGAAAAGGCTATC
ATG8C-R	ACCAAACCAAAGGTGTTCTCT
ATG8D-F	TTTGACTGTTGGCCAGTTTG
ATG8D-R	AACCCGTCTTCGTCTTTGTG
ATG8E-F	TCAAGCGTTTACGAGGATAAGAAA
ATG8E-R	TGTTCTCGCCACTGTAAGTGATG
ATG8F-F	TGGGGCAGTTTGTGTATG
ATG8F-R	GGAACCCATCATCATCCTTTT
ATG8G-F	TGTGATTCGTAAGAGAATCCAAC
ATG8G-R	CCAAAAGTGTTTTCCCCACT
ATG8H-F	CCAAAGCTCTCTTTGTTTTCG
ATG8H-R	AAGAACCCGTCTTCTTCCTTG
ATG8I-F	TGTCAACAACACTCTCCCTCA
ATG8I-R	AACCAAAGGTTTTCTCACTGC
ATG10-F	ATCATACAAGGTTCCTGTGC
ATG10-R	GATGTAGCTTGAACCATGGC
ATG18A-F	AGATCATGCTTGCTTCGCTG
ATG18A-R	AGAGTTCTCCGATACATCGG

Supplemental Table 2. Primers used for generation of Southern blot probes.

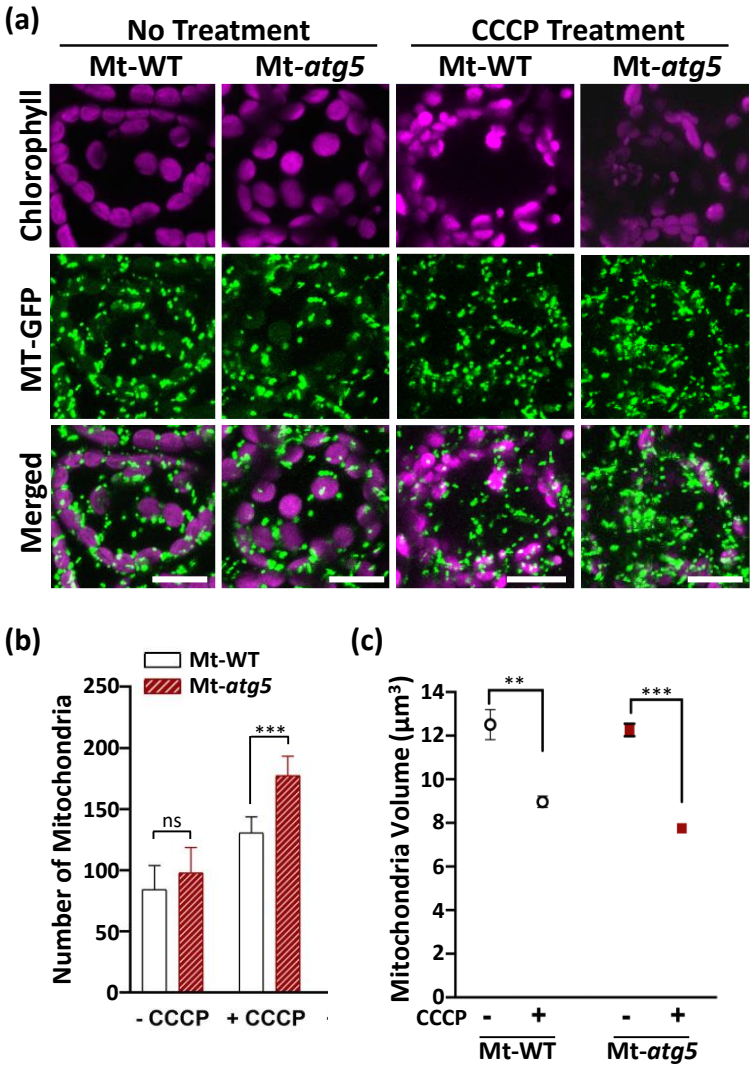
Primer name	Sequences (5’ - 3’)
COX1-F	TTCTATGGGAGCCGTTTTG
COX1-R	TAGTAGCAGTCGGCGACCTT
PHT2;1-F	ACCGATACAGAACCCTCACG
PHT2;1-R	GGAGACCAGCAAAGAGCAAC



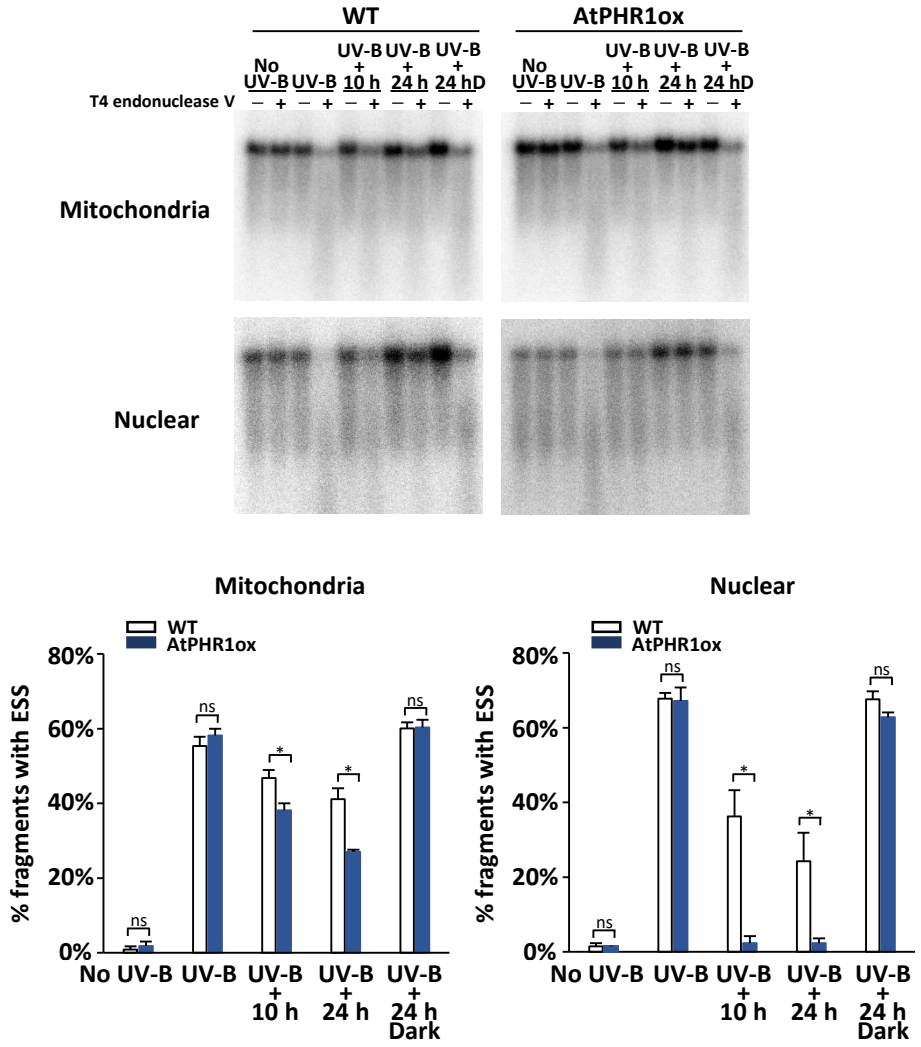
Supplementary Figure 1. UV-B-induced cell death in leaf mesophyll of *Arabidopsis* lines. UV-B-induced cell death in chloroplast stroma–targeted (CT)-GFP-expressing transgenic lines of wild-type Colombia (WT), *atg5* and *phr1* mutants, *atg5 phr1* double mutant, and AtPHR1-overexpressing transgenic (AtPHR1ox) seedlings as observed by LSCM at 2 d after UV-B exposure (280 nm, 0.5 or 1.5 W m^{-2} for 1 h). Green, GFP; magenta, chlorophyll. Arrows indicate dead cells (entirely green due to distribution of GFP throughout cells after vacuolar degradation). Scale bars, 20 µm. Proportion of dead cells out of total cells per fixed area (see Materials and Methods) is shown in Fig. 1c.



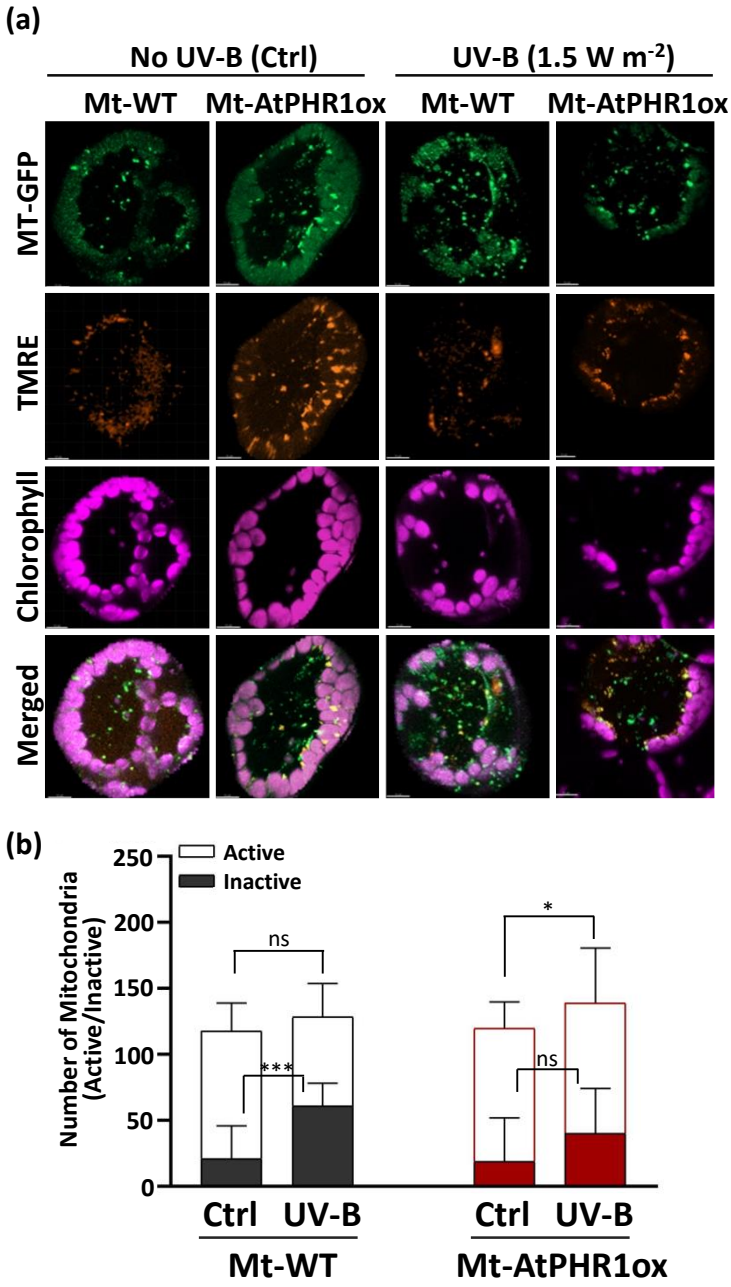
Supplementary Figure 2. Repair of CPDs in mitochondrial DNA induced by UV-B exposure by CPD photolyase, PHR1. Fourteen-day-seedlings of WT, *atg5*, and *phr1* were non-irradiated (No UV-B) or exposed to UV-B (1.5 W m^{-2} for 1 h) (UV-B). UV-B-irradiated seedlings were returned to the growth chamber with white light for repair of CPDs (UV-B + 10 h and UV-B + 24 h). To measure the level of CPD photolyase-independent repair, UV-B-irradiated seedlings were placed in a light-tight box and returned to the growth chamber (UV-B + 24 h Dark). Genomic DNA was isolated and digested with restriction enzymes, then digested DNA was incubated with (+) or without (−) T4 endonuclease V. The membrane was incubated with ^{32}P-labeled probes for mitochondrial-encoded *COX1* and nuclear-encoded *PHT2;1*. Percentage (%) fragments with enzyme-sensitive sites were calculated as the ratio of intensity of T4 endonuclease V-treated to the intensity of untreated DNA. Data are means ± SE. Asterisks indicate significant difference (*$p < 0.05$). ns., not significant.



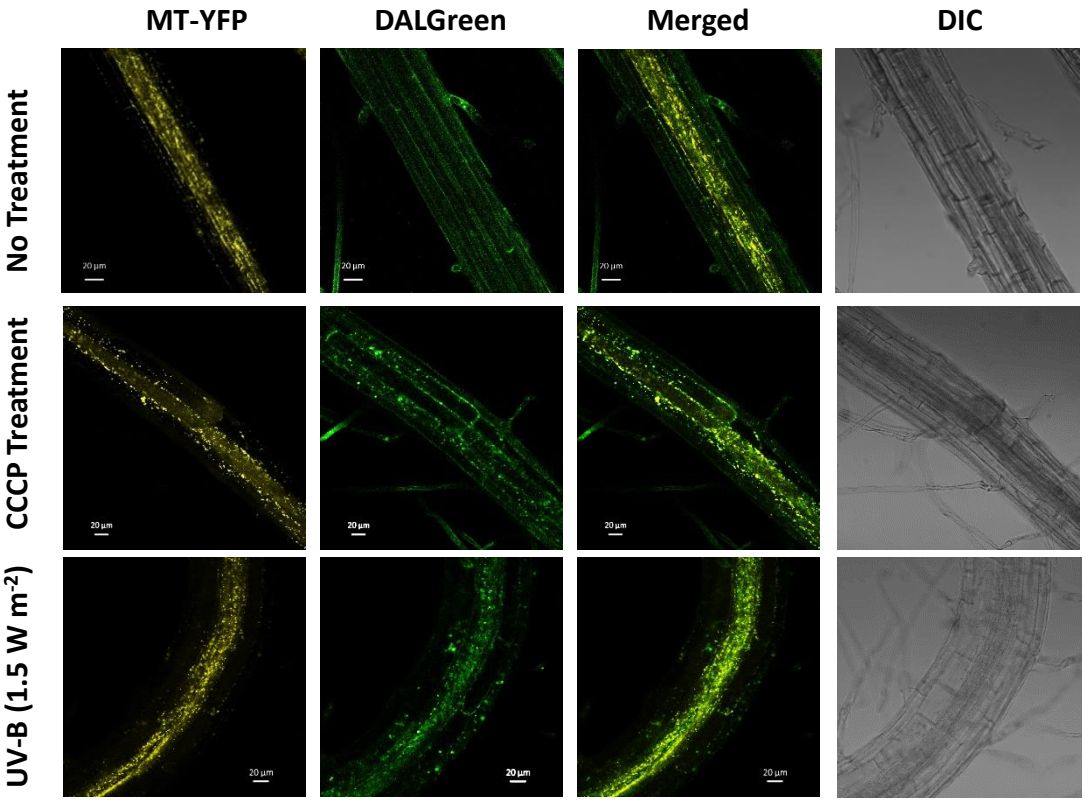
Supplementary Figure 3. Induction of mitochondrial fragmentation by carbonyl cyanide m-chlorophenyl hydrazone. (a) Mt-WT and Mt-*atg5* were non-treated (control) or treated with 10 μM carbonyl cyanide m-chlorophenyl hydrazone (CCCP), a mitochondrial uncoupler that results in rapid and dramatic fragmentation of mitochondria. Laser scanning confocal microscopy images were taken at 6 h after treatment. Magenta, chlorophyll; green, mitochondria. Images are representative of three independent plants. Scale bars, 20 μm. (b) At 6 h after treatment, the number of mitochondria per cell was determined by Imaris software (number of MT-GFP dots within each cell in a fixed area; see Materials and Methods) (n = 6 leaves). (c) The volume of each mitochondrion was estimated by 3D conversion of MT-GFP dots by Imaris software (n = 6 leaves). Data are means ± SE. Asterisks indicate a significant difference based on one-way ANOVA (**p < 0.01, ***p < 0.001). ns., not significant.



Supplementary Figure 4. More effective removal of CPDs from mitochondrial DNA in AtPHR1-overexpressing line (AtPHR1ox). Transgenic plant stably over-expressing *AtPHR1*was non-irradiated (No UV-B) or exposed to UV-B (1.5 W m^{-2} for 1 h) (UV-B). UV-B-irradiated seedlings were returned to the growth chamber with white light for repairing CPD (UV-B + 10 h and UV-B + 24 h). To measure the level of CPD photolyase-independent repair, UV-B-irradiated seedlings were placed in a light-tight box and returned to the growth chamber (UV-B + 24 h Dark). Genomic DNA was isolated and digested with restriction enzymes, then digested DNA was incubated with (+) or without (−) T4 endonuclease V. The membrane was incubated with ^{32}P-labeled probes for mitochondrial-encoded *COX1* and nuclear-encoded *PHT2;1*. Percentage (%) fragments with enzyme-sensitive sites was calculated as the ratio of intensity of T4 endonuclease V-treated to the intensity of untreated DNA. Data are means ± SE. Asterisks indicate significant difference (*$p < 0.05$). ns., not significant. Data for WT are same as in Supplementary Figure 2.



Supplementary Figure 5. Comparison of UV-B-induced mitochondrial deactivation between WT and CPD photolyase-overexpressing AtPHR*ox* plants. (a) Transgenic plants stably over-expressing mitochondrial matrix MT-GFP (Mt-WT and Mt-AtPHR1ox) were non-irradiated or exposed to UV-B (1.5 W m^{-2} for 1 h), then co-stained 24 h later with mitochondrial membrane potential indicator TMRE. Laser-scanning confocal microscope images of leaf mesophyll cells are shown. Images are representative of three independent experiments. Green, mitochondria; magenta, chlorophyll; orange, active mitochondria. Scale bars, 10 µm. (b) Numbers of mitochondria (GFP dots) or active mitochondria (TMRE-signal dots) per cell as counted with Imaris software (number of inactive mitochondria = total number of mitochondria – number of active mitochondria). Images from three replicates were used for calculations. Data represent means ± SE ($n \geq 20$ cells). Asterisks denote significant differences based on two-way ANOVA (*$p < 0.05$, ***$p < 0.001$). ns, not significant.



Supplementary Figure 6. Autophagosome activity in *Arabidopsis* plants treated with CCCP or exposed to UV-B radiation. Transgenic plants stably over-expressing mitochondria-targeted YFP (MtY-WT) were non-treated (No Treatment) or treated with CCCP (10 µM for 6 h) (CCCP Treatment) in the growth chamber, then stained with DALGreen 4 h later. MtY-WT were exposed to UV-B (1.5 W m^{-2} for 1 h). After UV-B irradiation, the irradiated seedlings were incubated in the growth chamber for 5 h, and then stained with DALGreen 4 h later (UV-B). Laser-scanning confocal microscope images of root cells. Fluorescence images of DALGreen (excitation 405 nm, emission 500–550 nm), and of YFP (excitation 488 nm, emission 500–550 nm) were obtained. Images are representative of three independent experiments. Yellow, mitochondria; Green, active autophagosome. Scale bars, 20 µm.