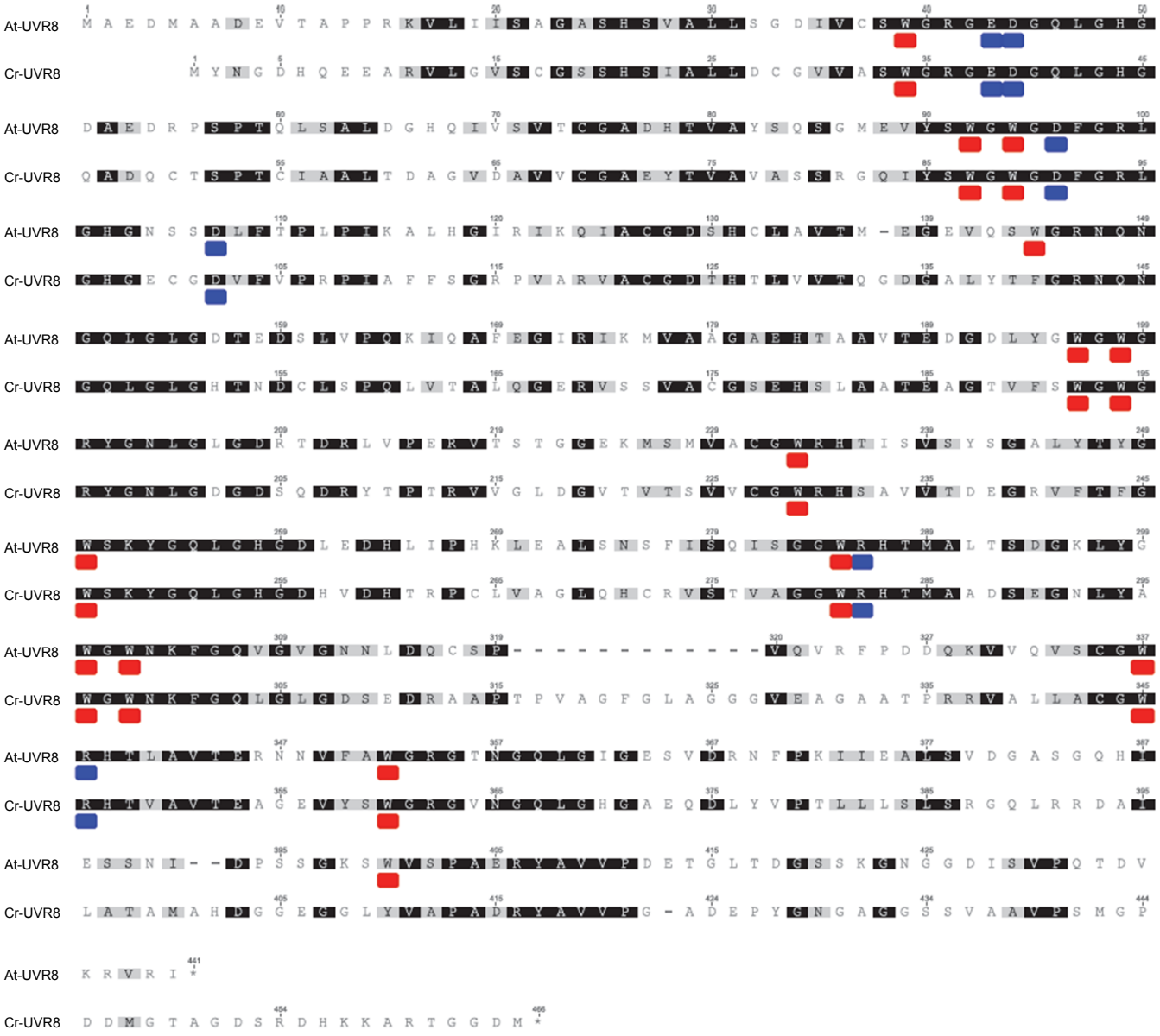
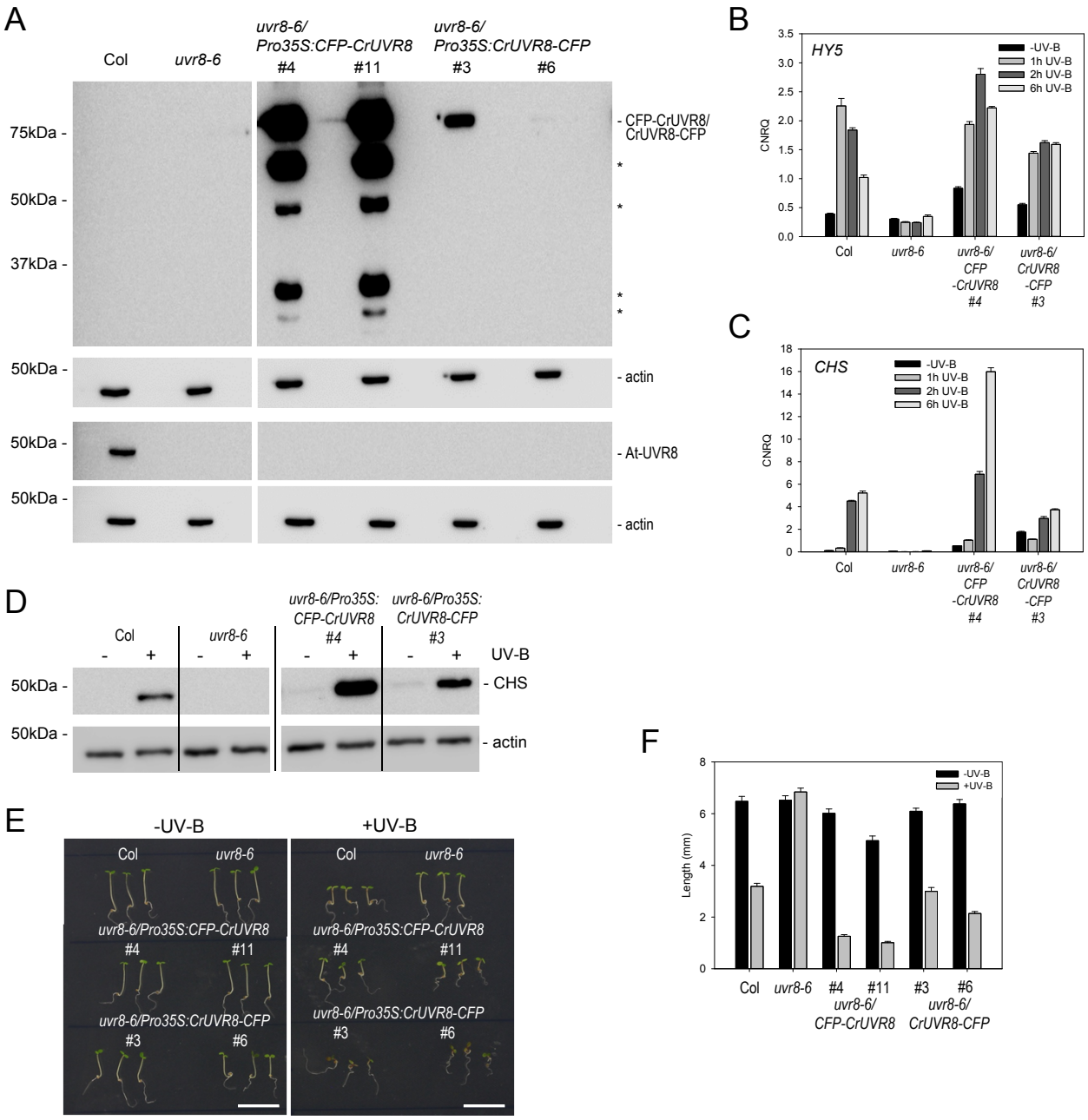



**Supplemental Figure 1.** Protein alignment of At-UVR8 with Cr-UVR8.
Identical aligned residues highlighted in black and similar and non-similar residues highlighted in grey and white, respectively. Position of Trp residues are indicated with red markers and positions of residues involved in interactions that maintain the homodimer are indicated with blue markers (only main residues specifically mentioned in the text are shown).



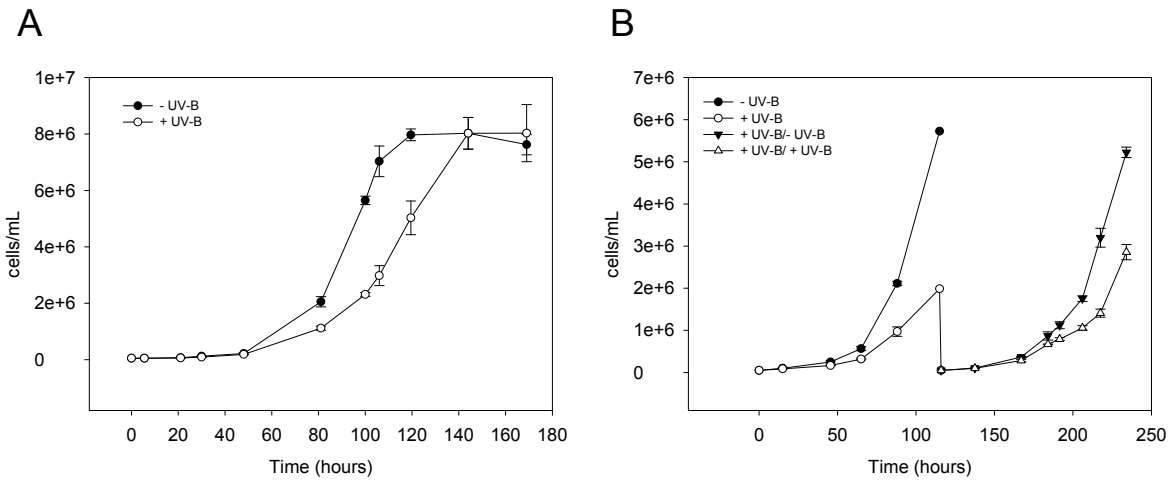

**Supplemental Figure 2.** Transgenic expression of *CrUVR8-CFP* and *CFP-CrUVR8* in Arabidopsis complements the *uvr8* mutant UV-B phenotype.

**(A)** Presence of CFP-CrUVR8 or CrUVR8-CFP fusion proteins or At-UVR8 in wild-type (Col), *uvr8-6* mutant and complemented (*uvr8-6*/*Pro35S:CFP-CrUVR8* and *uvr8-6/Pro35S:CrUVR8-CFP*) Arabidopsis lines. *Upper panel*: anti-CrUVR8 immunoblot, *lower panel*: anti-AtUVR8 immunoblot. Actin is shown as protein loading control. Asterisks (*) indicate degradation products. Note that Col wild-type and *uvr8-6* mutant samples are identical to the data shown in Figure 3A (extension of same original blot with the lines *uvr8-6*/*Pro35S:CrUVR8* #1 and #14 cut out here).

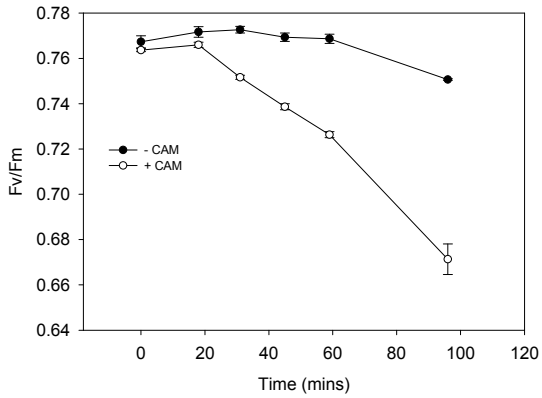
**(B)** and **(C)** UV-B-dependent induction of **(B)** *HY5* and **(C)** *CHS* UV-B marker genes. CNRQ: Calibrated Normalized Relative Quantities. Means and SE are shown (n = 3).

**(D)** UV-B-dependent CHS protein accumulation. Actin is shown as protein loading control.

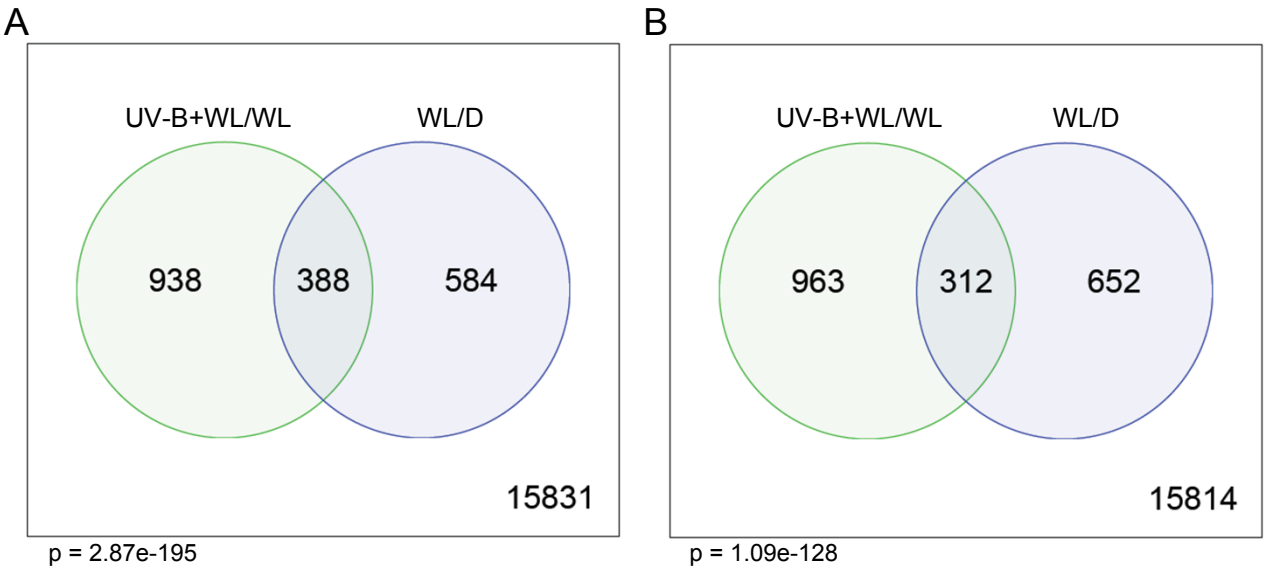
**(E)** and **(F)** UV-B-induced hypocotyl growth inhibition. Images of representative individuals (bar: 1cm) **(E)** and quantification of hypocotyl lengths **(F)** of 4-d-old seedlings grown under white light with (+UV-B) or without (-UV-B) supplementary UV-B light. Means and SE are shown (n = 15).

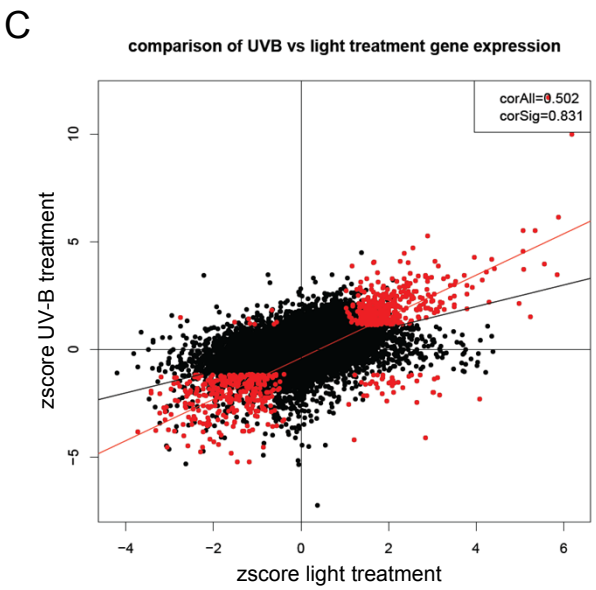



**Supplemental Figure 3.** Low-level UV-B delays Chlamydomonas culture growth.
**(A)** Growth curves of Chlamydomonas cultures grown with (+UV-B) or without supplemental narrowband UV-B (-UV-B).
**(B)** Growth curves of sequential Chlamydomonas cultures grown with (+UV-B) or without supplemental narrowband UV-B (-UV-B). Initial +UV-B cultures were diluted to initiate subsequent cultures which were then grown again either with (+UV-B/+UV-B) or without (+UV-B/-UV-B) supplemental narrowband UV-B. Means and SE are shown (n = 3).




**Supplemental Figure 4.** Chloramphenicol usage to block chloroplast translation.
Photosynthetic efficiency (Fv/Fm) in 4-day-old Chlamydomonas plate cultures over a narrowband UV-B exposure time course. -CAM: Plate cultures were mock treated with the addition of water prior to UV-B exposure. +CAM: Plate cultures were treated with chloramphenicol (CAM) at a final concentration of 100ug/mL prior to UV-B exposure. Means and SE are shown (n = 3).




**Supplemental Figure 5.** Comparative RNA-Seq analysis.
Comparative RNA-Seq analysis reveals a common set of UV-B (UV-B+WL/WL) and white light (WL/D; Duanmu et al., 2013) regulated genes in Chlamydomonas. WL/D: transfer from dark to light (30 min); UV-B+WL/WL: transfer from white light to white light supplemented with UV-B. The diagrams show the number of non-overlapping and shared differentially regulated transcripts with ≥two-fold change and false discovery rate < 5%; **(A)** shows number of up-regulated genes, **(B)** shows repressed genes. Genes of each subgroup are listed in Supplemental Tables 2 and 3. **(C)** Scatter plot of zscore transformed expression values between the two experiments. In red highlighted are genes which are significantly differently regulated in both subgroups. The black and red line represent the linear regression respectively.

**Supplemental Table 1.** Primer sequences used in this study.
Complementary sequence to target genes is indicated in uppercase.

| Name | Sequence (5'-3') | Purpose |
|---|---|---|
| CrUVR8attB1 Fd | ggggacaagtttgtacaaaaaagcaggcttcATGTACAATGGAGACCATCAGGAGG | Cr-*UVR8* cloning |
| CrUVR8attB2 Rv | ggggaccactttgtacaagaaagctgggtcTTACATGTCACCGCCGGTGCGGGCC | |
| CrUVR8(-stop)attB2 Rv | ggggaccactttgtacaagaaagctgggtcCATGTCACCGCCGGTGCGGGCC | |
| CrCOP1 Fd | ATGTCAGTCACCACTCGTGTTACTG | Cr-*COP1* cloning |
| CrCOP1 Rv | CTACAGCTGCAGCCCTAGCAGCCAC | |
| CrCOP1attB1 Fd | ggggacaagtttgtacaaaaaagcaggcttcATGTCAGTCACCACTCGTGTTACTG | |
| CrCOP1attB2 Rv | ggggaccactttgtacaagaaagctgggtcCTACAGCTGCAGCCCTAGCAGCCAC | |
| At18S-Fd | TGGAGGGCAAGTCTGGTGCC | Arabidopsis RT-qPCR normalisation. |
| At18S-Rv | CGGCCGACCCATCCCAAGG | |
| AtUPL7-Fd | AGGTGCCAGCAGTGGGGAGA | |
| AtUPL7-Rv | GTGATGCAGCATTAGCGCGTC | |
| AtHY5-Fd | GCTCTTTTCCTCTTTATCCTTTTCAC | Arabidopsis RT-qPCR target. |
| AtHY5-Rv | TGTTCCTGCATTTTTCTTACTCTTTG | |
| AtCHS-Fd | AGTACCGCCGGCGAAGCAAC | |
| AtCHS-Rv | GCGTTTAGCGGTCCAGCACCC | |
| RACK1-Fd | CTTCTCGCCCATGACCAC | Chlamydomonas RT-qPCR normalisation. |
| RACK1-Rv | CCCACCAGGTTGTTCTTCAG | |
| CrUPL7-Fd | GCGGCTACAGGCACGACTCC | |
| CrUPL7-Rv | GCGGCTGCAGGAAGTCACGA | |
| Cre01.g016600-Fd | CCGCCATCAACGGCAAGCAG | Chlamydomonas RT-qPCR target. |
| Cre01.g016600-Rv | CCACCATGGCCAGGCGACC | |
| Cre06.g280150-Fd | TGTCCGGCACCAGCAAGACG | |
| Cre06.g280150-Rv | TGCAGGCCGTGAACGAGTGG | |
| Cre01.g053850-Fd | TGCGTGACAGCCACGACGAC | |
| Cre01.g053850-Rv | CTCATCCGACGCCGCCTTCC | |
| Cre06.g310500-Fd | TCCGAGAGCAGCAGAGCCACA | |
| Cre06.g310500-Rv | AAGCCACGCATGGTGCGGAT | |
| Cre06.g278251-Fd | ATGTGGCTGTCCGCCTCTGC | |
| Cre06.g278251-Rv | AGCACCGGCAGGAACTTGCG | |
| Cre12.g537000-Fd | CCGCCACCTGGACTTCAGCG | |
| Cre12.g537000-Rv | ACACTGGAACCGGCCTTGATGG | |
| Cre03.g164600-Fd | ACTGCGCGCTGCATCTTCCA | |
| Cre03.g164600-Rv | AGCGCGAACACGGCGATGAA | |
| Cre03.g207550-Fd | TGCGAATTCCGGACAGCCTGC | |
| Cre03.g207550-Rv | TTGTCCAGGCCGAAGTGCCG | |
| Cre09.g391650-Fd | AAGATTGACTTCGCGGCGTTCC | |
| Cre09.g391650-Rv | ACAGGCCGGTCTCGTTGATGG | |

**Supplemental Table 2.** Coverage of RNA-Seq data.

| Sample | # raw reads | # tophat2 mapped reads | % aligned reads |
|---|---|---|---|
| -UVB1 | 33,307,948 | 26,832,746 | 80.6 |
| -UVB2 | 30,443,168 | 24,448,915 | 80.3 |
| -UVB3 | 34,435,914 | 28,821,165 | 83.7 |
| 1h+UVB1 | 33,273,956 | 27,805,121 | 83.6 |
| 1h+UVB2 | 32,799,638 | 26,761,755 | 81.6 |
| 1h+UVB3 | 33,338,698 | 28,111,660 | 84.3 |