

1 **Short title:** Regulation of PSII function by light signaling

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10 **Light Signaling-Dependent Regulation of Photosystem II Biogenesis and**  
11 **Functional Maintenance**

12

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24 **One sentence summary:** The photoreceptors phytochrome and cryptochrome  
25 regulate photosystem II biogenesis, assembly, and repair mediated by  
26 regulation of gene expression by ELONGATED HYPOCOTYL5 (HY5).

27

28 **Footnotes:**

29 H. -L. J. and H.-B. W. designed the research project; X. L. and H.-L. J.  
30 performed the experiments; X. L. and H.-L. J. wrote the article. H.-L. J. and  
31 H.-B. W. revised the article.

32

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38

39 **ABSTRACT**

40 Light is a key environmental cue regulating photomorphogenesis and  
41 photosynthesis in plants. However, the molecular mechanisms underlying the  
42 interaction between light signaling pathways and photosystem function are  
43 unknown. Here, we show that various monochromatic wavelengths of light  
44 cooperate to regulate photosystem II (PSII) function in *Arabidopsis thaliana*.  
45 The photoreceptors cryptochromes and phytochromes modulate the  
46 expression of HIGH CHLOROPHYLL FLUORESCENCE173 (HCF173), which  
47 is required for PSII biogenesis by regulating PSII core protein D1 synthesis  
48 mediated by the transcription factor ELONGATED HYPOCOTYL5 (HY5). HY5  
49 directly binds to the ACGT-containing element ACE motif and *G-box*  
50 *cis*-element present in the *HCF173* promoter and regulates its activity. PSII  
51 activity was decreased significantly in *hy5* mutants under various  
52 monochromatic wavelengths of light. Interestingly, we demonstrate that HY5  
53 also directly regulates the expression of the genes associated with PSII  
54 assembly and repair, including *ALBINO3*, *HCF136*, *HYPERSENSITIVE TO*  
55 *HIGH LIGHT1*, *etc.*, which is required for the functional maintenance of PSII  
56 under photodamaging conditions. Moreover, deficiency of *HY5* broadly  
57 decreases the accumulation of other photosystem proteins besides PSII  
58 proteins. Thus, our study reveals an important role of light signaling in both  
59 biogenesis and functional regulation of the photosystem and provides insight  
60 into the link between light signaling and photosynthesis in land plants.

61

## 62 INTRODUCTION

63 Chloroplasts and non-photosynthetic plastid organelles are derived from  
64 cyanobacterial endosymbionts and many of the endosymbiont's genes have  
65 migrated to the plant cell nucleus by gene transfer (Timmis et al., 2004).  
66 Therefore, the chloroplast proteome of several thousand proteins is dominated  
67 by nuclear-encoded proteins (Barkan, 2011). The thylakoid membrane system,  
68 a major structural component of chloroplasts, functions in photosynthetic  
69 electron transport and ATP synthesis and consists of four major multimeric  
70 complexes: photosystem II (PSII), cytochrome *b<sub>6</sub>/f*, PSI, and ATP synthase.  
71 PSII structure has been resolved to near-atomic resolution, and the protein  
72 subunits, cofactors, and coordinates for different ligands are largely known  
73 (Zouni et al., 2001; Loll et al., 2005). PSII biogenesis involves the collaborative  
74 assembly of over 30 different polypeptides and a multitude of nuclear-encoded  
75 regulatory proteins (Nickelsen and Rengstl, 2013). While plants depend on light  
76 for growth, they are sensitive to the damaging effects of radiation. PSII is the  
77 major component of the photosystem that is damaged by light (Liere and  
78 Börner, 2007). Therefore, PSII repair is required for its functional maintenance.  
79 PSII repair is a complex process, including protein phosphorylation,  
80 disassembly, and reassembly, which are regulated by numerous regulatory  
81 factors (Nickelsen and Rengstl, 2013; Lu, 2016).

82 The PSII reaction center protein, D1 (encoded by the chloroplast gene  
83 *psbA*), is damaged by light and must be rapidly turned over and replaced with  
84 newly synthesized D1 for PSII reassembly and repair. Therefore, the efficient  
85 synthesis of D1 is important for PSII biogenesis, assembly, and repair. In land  
86 plants, D1 protein synthesis increased up to 100-fold when induced by light, but  
87 without an equivalent increase in *psbA* mRNA levels, indicating that translation  
88 is the pivotal regulation step (Fromm et al., 1985; Klein et al., 1988; Malnoe et  
89 al., 1988; Krupinska and Apel, 1989). Previous studies have revealed that

90 HIGH CHLOROPHYLL FLUORESCENCE173 (HCF173) and HCF244, two  
91 regulators of *psbA* mRNA translation, promote D1 biosynthesis (Schult et al.,  
92 2007). LOW PHOTOSYNTHETIC EFFICIENCY 1 (LPE1), a nuclear-encoded  
93 chloroplast-targeted pentatricopeptide repeat (PPR) protein, plays a vital role in  
94 D1 translation by promoting the association of HCF173 and *psbA* mRNA (Jin et  
95 al., 2018). The expression of *HCF173*, but not *LPE1*, was drastically induced by  
96 light (Jin et al., 2018), but the mechanism of regulation remains unclear.

97 In addition to being the primary energy source for plant growth, light is a  
98 key environmental factor affecting plant development. More than 32% of genes  
99 respond to changing light conditions in *Arabidopsis thaliana* (Ma et al., 2001).  
100 At least four types of photoreceptors perceive different wavelengths of light,  
101 including phytochromes (PHY), the red (R) and far-red (FR) light receptors;  
102 cryptochromes (CRY) and phototropins, the blue (B) and ultraviolet-A (UV-A)  
103 light receptors, respectively; and the ultraviolet-B (UV-B) light receptor UV  
104 RESISTANCE LOCUS 8 (UVR8) (Cashmore et al., 1999; Briggs and Christie,  
105 2002; Quail, 2002; Rizzini et al., 2011). Photoreceptors transmit light signals to  
106 downstream transcription factors, such as the basic helix-loop-helix (bHLH)  
107 proteins phytochrome-interacting factors (PIFs) (Leivar and Quail, 2011) and  
108 the bZIP protein ELONGATED HYPOCOTYL5 (HY5) (Osterlund et al., 2000),  
109 and thereby affect plant growth and development. HY5 regulates diverse  
110 signaling pathways by directly binding to the *cis*-regulatory elements of  
111 promoters in a sequence-specific manner (Gangappa and Botto, 2016). In  
112 darkness (D) condition, the E3 ubiquitin ligase CONSTITUTIVELY  
113 PHOTOMORPHOGENIC1 (COP1) is enriched in the nucleus in darkness and  
114 specifically targets positive photomorphogenic factors such as HY5 for  
115 ubiquitination and degradation (Lau and Deng, 2012; Huang et al., 2014).  
116 Although the mechanisms by which light signals regulate chloroplast gene

117 expression are well understood, the relationship between light signaling  
118 pathways and PSII function remains largely unknown.

119       In this study, we demonstrate that the light signaling pathway is required  
120 for regulation of PSII biogenesis and functional maintenance. We found that  
121 various monochromatic wavelengths of light cooperate to regulate PSII  
122 function in Arabidopsis. Photoreceptor-mediated light signaling regulates PSII  
123 function, including PSII biogenesis, assembly, and repair, through the  
124 transcription factor HY5. HY5 directly binds to the promoter of genes related to  
125 PSII assembly and repair, which is required for the functional maintenance of  
126 PSII.

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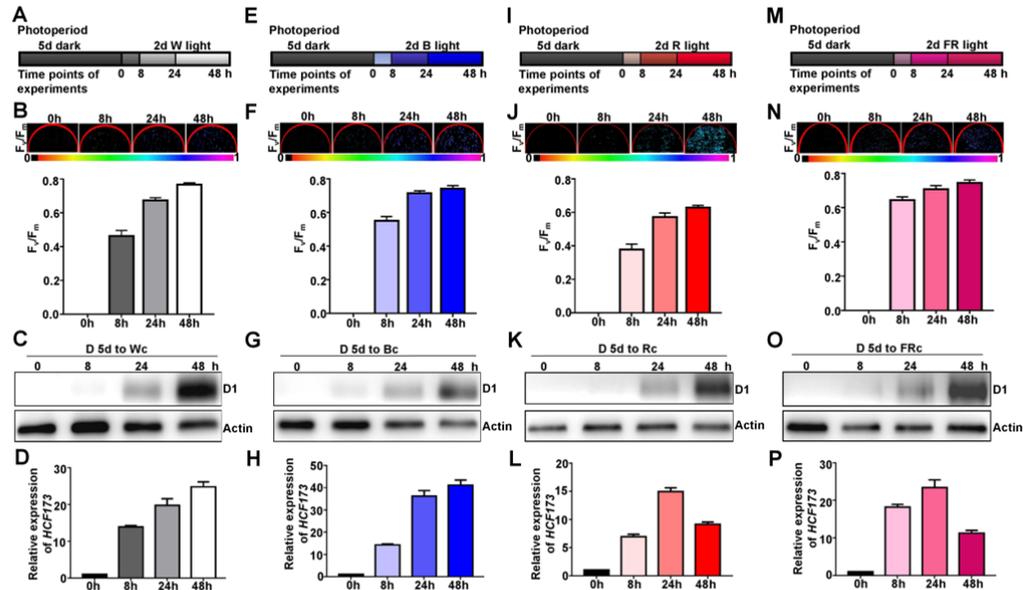
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129 **RESULTS**

130 **Various Monochromatic Wavelengths of Light Cooperatively Contribute**  
131 **to PSII activity, D1 Protein Accumulation, and *HCF173* Expression**

132 Prompted by our previous observation that PSII activity and accumulation  
133 of the PSII core protein D1 are induced by white (W) light (Jin et al., 2018), we  
134 examined whether PSII activity and D1 accumulation are regulated by specific  
135 wavelengths of light. Arabidopsis wild-type (WT) Columbia-0 (Col-0) seedlings  
136 were grown in darkness (D) for five days, transferred to W light (100  $\mu\text{mol}$   
137 photons  $\text{m}^{-2} \text{s}^{-1}$ ), blue (B) light (58  $\mu\text{mol}$  photons  $\text{m}^{-2} \text{s}^{-1}$ ), red (R) light (44  $\mu\text{mol}$   
138 photons  $\text{m}^{-2} \text{s}^{-1}$ ), or far-red (FR) light (10  $\mu\text{mol}$  photons  $\text{m}^{-2} \text{s}^{-1}$ ) for 0 to 48 h  
139 (Fig. 1A, E, I and M), and then harvested and subjected to immunoblot and  
140 chlorophyll fluorescence analysis. As previously observed for W light (Jin et al.,  
141 2018; Fig. 1B and C), both PSII activity and D1 protein levels increased  
142 substantially following exposure to all of the specific wavelengths of light (Fig.  
143 1F, J, N, G, K and O), indicating that B, R, and FR light induce PSII activity and  
144 D1 protein accumulation.

145 We previously demonstrated that LPE1 and HCF173 cooperatively  
146 regulate D1 synthesis and PSII biogenesis. Light induces the association of  
147 LPE1 and *psbA* mRNA, which promotes PSII biogenesis (Jin et al., 2018). We  
148 showed that light induces the expression of *HCF173* but not *LPE1* in etiolated  
149 Arabidopsis Col-0 seedlings (Jin et al., 2018). However, the mechanism by  
150 which light regulates HCF173 in PSII biogenesis is unclear. To provide insight  
151 into the mechanism by which light induces *HCF173* expression, we  
152 investigated whether *HCF173* expression is also regulated by specific  
153 wavelengths of light. Reverse transcription quantitative PCR (RT-qPCR)  
154 analysis showed that *HCF173* transcript levels were significantly elevated over  
155 a two-day period under the various light conditions compared with the D  
156 condition, with at least a 7-fold induction under W, B, R, and FR light (Fig. 1D,



**Figure 1. Single wavelengths of light regulate PSII activity, as well as D1 and HCF173 protein accumulation during greening.**

(A, E, I, M) Schematic representation of the experimental set-up used with white (W), blue (B), red (R), and far-red (FR) light during greening. Five-day-old *Arabidopsis* Col-0 seedlings were maintained under darkness and were then transferred to different light conditions and harvested at 0, 8, 24, and 48 h for analysis.

(B, F, J, N) False-color images representing the maximal photochemical efficiency of PSII ( $F_v/F_m$ ) during W, B, R, and FR light-induced greening of etiolated wild-type *Arabidopsis* seedlings. After growth in darkness for 5 days, etiolated seedlings were illuminated for 0, 8, 24, or 48 h, and false-color images representing  $F_v/F_m$  were captured.

(C, G, K, O) Western blot analysis of D1 proteins isolated from 5 d etiolated *Arabidopsis* Col-0 seedlings during W, B, R, or FR light-induced greening for the indicated periods. Anti-Actin was used as a sample loading control.

(D, H, L, P) RT-qPCR analysis showing the relative expression of *HCF173* after five-day-old etiolated *Arabidopsis* Col-0 seedlings were transferred to W, B, R, or FR light conditions for the indicated periods. Data are represented as mean  $\pm$  SEM. All experiments were repeated at least three times with similar results.

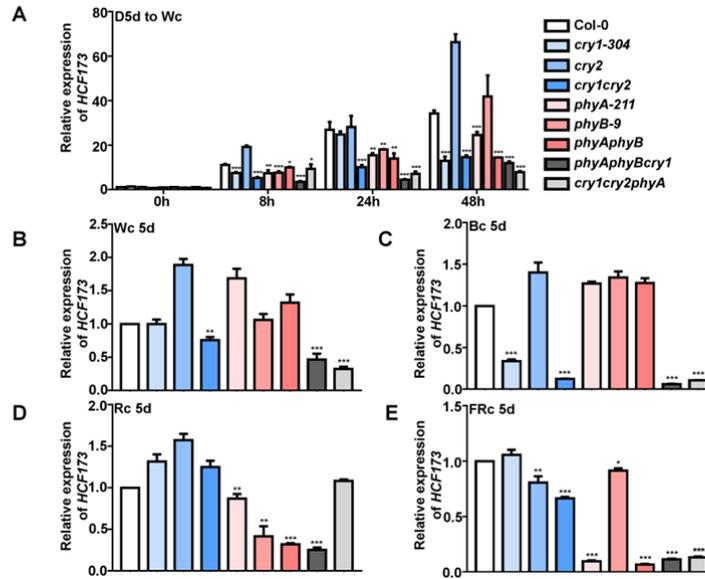
157 H, L and P). Transcript levels peaked at 24 h under FR and R light conditions in  
 158 contrast with peaks under W and B light at 48 h. After five days of continuous  
 159 treatment under D, W, B, R, and FR light conditions, *HCF173* transcript levels  
 160 were significantly up-regulated in each of the light conditions compared with the  
 161 D condition, with at least a 20-fold induction (Supplemental Fig. S1). These  
 162 results indicate that specific wavelengths of light, including B, R, and FR,  
 163 induce *HCF173* expression.

164

165 **Both Cryptochromes and Phytochrome Influence *HCF173* Expression**

166 To examine whether photoreceptors regulate *HCF173* expression, we  
167 quantified *HCF173* transcript levels in Col-0 and the phytochrome and  
168 cryptochrome single, double, and triple mutants. The seedlings were grown in  
169 the D condition for five days, and then transferred to W light for 0 to 48 h. After  
170 8 h of exposure to W light, *HCF173* expression was significantly lower in the  
171 *cry1-304*, *phyA-211*, and *phyB-9* single mutants, the *cry1 cry2* and *phyA phyB*  
172 double mutants, and the *phyA phyB cry1* and *cry1 cry2 phyA* triple mutants  
173 than in Col-0. However, *HCF173* expression was higher in the *cry2* single  
174 mutant than in Col-0 (Fig. 2A). After 24 h of exposure to W light, *HCF173*  
175 expression was significantly lower in the *phyA-211* and *phyB-9* single mutants,  
176 the *cry1 cry2* and *phyA phyB* double mutants, and the *phyA phyB cry1* and *cry1*  
177 *cry2 phyA* triple mutants than in Col-0. However, *HCF173* expression was  
178 similar in the *cry1* and *cry2* single mutants and in Col-0 (Fig. 2A). After 48 h of  
179 exposure to W light, *HCF173* expression was significantly lower in the *cry1-304*  
180 and *phyA-211* single mutants, the *cry1 cry2* and *phyA phyB* double mutants,  
181 and the *phyA phyB cry1* and *cry1 cry2 phyA* triple mutants compared to Col-0.  
182 However, *HCF173* expression was much higher in the *cry2* single mutant than  
183 in Col-0 (Fig. 2A). These data demonstrate that *HCF173* expression is  
184 redundantly regulated by phytochrome and cryptochrome during light  
185 induction, and that CRY2 has a minor role in this process.

186 To confirm this, we quantified *HCF173* transcript levels in WT Col-0,  
187 cryptochrome mutants, and phytochrome mutants grown under continuous W  
188 light for five days. After induction by W light, *HCF173* expression in *phyA*, *phyB*,  
189 *cry1*, or *cry2* single mutants and a *phyA phyB* double mutant showed no  
190 obvious differences compared with Col-0. By contrast, *HCF173* expression in  
191 the *cry1 cry2* double mutant was slightly lower than in the wild type. *HCF173*



**Figure 2. Both cryptochromes and phytochrome influence *HCF173* expression.**

(A) RT-qPCR analysis of *HCF173* transcript levels after five-day-old etiolated Col-0 and different photoreceptor mutants were transferred to W light for the indicated periods.

(B–E) Analyses of *HCF173* expression under W, B, R, and FR light conditions in *phyA-211*, *phyB-9*, *cry1-304*, and *cry2* single and higher order mutants under five days of continuous light (Wc, Bc, Rc, and FRc) conditions as indicated. The expression levels were normalized to that of *ACTIN*. Data are represented as mean  $\pm$  SEM (Three biological repeats). Asterisks represent statistically significant differences (\* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; Student's t-test). All experiments were repeated at least three times with similar results. We did not perform statistical analyses on those mutants that showed up-regulation of *HCF173* transcripts.

192 expression was nearly abolished in the *cry1 cry2 phyA* and *phyA phyB cry1*  
 193 triple mutants (Fig. 2B), further supporting that both phytochrome and  
 194 cryptochrome mediate W-light-induced *HCF173* expression in a functionally  
 195 redundant manner.

196 To further explore the role of different photoreceptors in regulation of the  
 197 *HCF173* transcript levels in response to various monochromatic wavelengths  
 198 of light, we quantified *HCF173* transcript levels in WT Col-0, cryptochrome  
 199 mutants, and phytochrome mutants grown under continuous B, R, or FR light  
 200 for five days. After induction by B light, *HCF173* expression was lower in the  
 201 *cry1-304* single mutant and the *cry1 cry2* double mutant than in Col-0. The  
 202 decrease in *HCF173* expression in the *cry1 cry2 phyA* and *phyA phyB cry1*  
 203 triple mutants was more drastic (Fig. 2C), indicating that CRY1 is the major

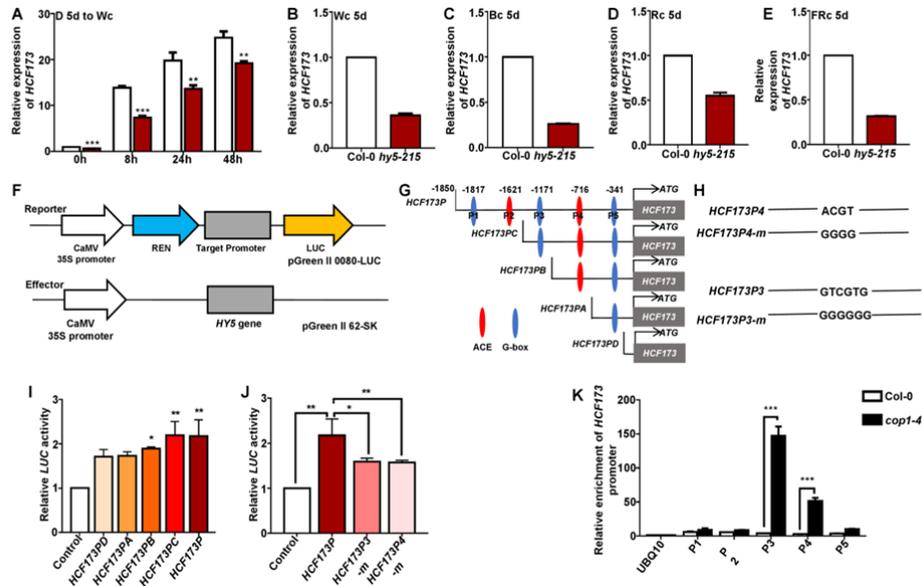
204 regulator of *HCF173* expression under B light conditions. After induction by R  
205 light, *HCF173* expression was lower in the *phyA-211* and *phyB-9* single  
206 mutants and in the *phyA phyB* double mutant than in Col-0. The decrease in  
207 *HCF173* expression in the *phyB-9* mutant was greater than that in the  
208 *phyA-211* mutant. The decrease of *HCF173* expression in the *phyA phyB cry1*  
209 triple mutant was more drastic than that in the *cry1 cry2 phyA* triple mutant (Fig.  
210 2D), indicating that PHYB is the major regulator of *HCF173* expression under R  
211 light conditions. After induction by FR light, the decrease in *HCF173* expression  
212 in the *phyA-211* mutant was greater than that in the *phyB-9* mutant (Fig. 2E),  
213 indicating that PHYA is the major regulator of *HCF173* expression under FR  
214 light conditions.

215 Collectively, these data indicate that *HCF173* expression is induced by  
216 various monochromatic wavelengths of light and is redundantly regulated by  
217 the phytochrome and cryptochrome photoreceptors.

218

## 219 **HY5 Directly Binds to the Promoter of *HCF173* and Regulates Its** 220 **Expression**

221 As HY5 is activated by light signals sensed by upstream photoreceptors  
222 (Oyama et al., 1997; Ang et al., 1998), we next examined whether HY5 affects  
223 the transcript level of *HCF173* during W light-induced greening, using  
224 RT-qPCR analysis. *HCF173* transcript levels were markedly elevated after  
225 etiolated Col-0 and *hy5-215* mutant seedlings were transferred to W light for up  
226 to 48 h (Fig. 3A); however, *HCF173* expression was lower in the *hy5-215*  
227 mutant than in Col-0 at all time points examined, indicating that HY5 specifically  
228 positively regulates *HCF173* expression in response to W light during early  
229 plant development. Next, we examined whether *HCF173* transcript levels are  
230 regulated by HY5 during continuous W, B, R, or FR light conditions. *HCF173*  
231 transcript levels were dramatically lower in the *hy5-215* mutant than in the WT



**Figure 3. HY5 regulates the transcript level of *HCF173* through directly associating with its promoter.**

**(A)** RT-qPCR analysis of the relative expression of *HCF173* after five-day-old etiolated Col-0 and *hy5-215* mutant seedlings were transferred to W light for the indicated time points. The expression levels were normalized to that of *ACTIN*.

**(B–E)** RT-qPCR analysis showing the expression levels of *HCF173* in five-day-old Col-0 and *hy5-215* mutant seedlings grown under continuous W, B, R, and FR light conditions.

**(F)** Schematic representation of various constructs used in the transient transfection assay in Arabidopsis protoplasts. Reporter, A schematic map of the transient expression vector pGreenII-0800-LUC. REN, Renilla luciferase; LUC, firefly luciferase. Effector, Diagram of the HY5 effector of the transient expression vector pGreenII 62-SK.

**(G)** Diagram representing different variants of the *HCF173* promoter. Part of the coding region of *HCF173* is shown. Positions of the putative G-boxes (blue) and ACE motifs (red) are numbered.

**(H)** DNA sequences of the wild-type *HCF173* promoter containing the ACE motifs (*HCF173P4*) or G-boxes (*HCF173P3*) and mutant *HCF173* promoters harboring a mutant ACE motif (*HCF173P4-m*) or G-box (*HCF173P3-m*).

**(I)** Effects of HY5 on *HCF173* transcriptional regulation using different *HCF173* promoter variants in Col-0 protoplasts.

**(J)** The roles of ACE motif or G-box for activity of *HCF173* promoter regulated by HY5. The protoplasts without the HY5 effector were used as a negative control. The relative LUC activities were normalized to REN activities.

**(K)** The analyses of association between HY5 and the *HCF173* promoter in vivo by ChIP-qPCR assays. Anti-HY5 antibody was used to immunoprecipitate the HY5-HCF173 complex. Col-0 and *UBQ10* were used as negative controls. Data are represented as mean  $\pm$  SEM. Asterisks represent statistically significant differences (\* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; Student's t-test). All experiments were repeated at least three times with similar results.

232 Col-0 when grown in continuous W, B, R, or FR light conditions for five days  
 233 (Fig. 3B–E), further demonstrating that HY5 indeed positively regulates the

234 transcript levels of *HCF173* in response to various wavelengths of light.

235 To establish whether HY5 affects *HCF173* accumulation during  
236 light-induced greening, the WT Col-0 and *hy5-215* mutant seedlings were  
237 grown in darkness for five days, transferred to W light for up to 48 h, and then  
238 harvested and subjected to immunoblot analysis. *HCF173* protein levels  
239 increased after illumination in both genotypes, consistent with the *HCF173*  
240 transcript levels, but were lower in the *hy5-215* mutant than in Col-0  
241 (Supplemental Fig. S2A and B). We further examined whether HY5 affects  
242 *HCF173* accumulation after induction by B, R, or FR light. The WT Col-0 and  
243 *hy5-215* mutant seedlings were grown under continuous B, R, or FR light for  
244 five days, harvested, and then subjected to immunoblot analysis. *HCF173*  
245 protein levels were lower in the *hy5-215* mutant than in Col-0 under continuous  
246 B, R, or FR light conditions (Supplemental Fig. S3A-C), demonstrating that  
247 *HCF173* accumulation is positively regulated by HY5 in response to various  
248 monochromatic wavelengths of light. Thus, *HCF173* accumulation is positively  
249 regulated by HY5 in response to W light-induced greening, and single  
250 wavelengths of light can also induce the expression of *HCF173* protein.

251 Previous studies revealed that HY5 can directly bind to the ACE motif or  
252 G-box *cis*-acting elements within the promoters of its target genes (Lee et al.,  
253 2007; Zhang et al., 2011). We therefore analyzed the 1850-bp *HCF173*  
254 promoter region directly upstream of the start codon (ATG) and identified two  
255 ACE motifs and three atypical G-box *cis*-elements. The basic domain/Leu  
256 zipper transcription factor HY5 acts downstream of COP1 and is degraded by  
257 COP1 in darkness (Osterlund et al., 2000). We thus analyzed the effect of HY5  
258 on the activity of the *HCF173* promoter using the dual-luciferase (LUC) reporter  
259 system in *Arabidopsis* Col-0 protoplasts (Fig. 3F and G). The truncated  
260 promoter fragments (*HCF173PA-LUC*, *HCF173PB-LUC*, *HCF173PC-LUC*,  
261 and *HCF173PD-LUC*) and full-length promoter (*HCF173P-LUC*) were

262 transiently expressed in protoplasts with or without the HY5 effector. HY5  
263 increased the activity of *HCF173PA/PB/PC/PD/P-LUC* approximately 1.5- to  
264 2.2-fold, and the activity of the *HCF173* promoter fragments containing the ACE  
265 (*HCF173PB*) motif and G-box (*HCF173PC*) element were more significantly  
266 increased by HY5 (Fig. 3I). An analysis using point mutations that specifically  
267 disrupted the *P3* G-box or the *P4* ACE motif (Fig. 3J) revealed that the *P4* ACE  
268 motif and *P3* G-box in the *HCF173* promoter are required for HY5 binding.

269 Next, we performed a chromatin immunoprecipitation (ChIP)-qPCR  
270 analysis to determine whether HY5 binds to the *HCF173* promoter *in vivo*.  
271 Considering that HY5 accumulation is limited in etiolated WT seedlings  
272 illuminated for two days and that the *cop1-4* mutant accumulates more HY5  
273 protein than the wild type (Supplemental Fig. S4B), we used etiolated *cop1-4*  
274 seedlings grown under continuous D for five days in this analysis. *HCF173*  
275 protein accumulation and *HCF173* transcript levels were markedly higher in the  
276 *cop1-4* mutant than in Col-0 (Supplemental Fig. S4A and C). Under the D  
277 condition, HY5 levels increased to a greater extent in the *cop1-4* mutant than in  
278 Col-0 (Supplemental Fig. S4B), consistent with a previous report (Osterlund et  
279 al., 2000). ChIP-qPCR assays using etiolated Col-0 and *cop1-4* seedlings and  
280 an anti-HY5 antibody were employed to confirm the binding of HY5 to the  
281 *HCF173* promoters *in vivo*. HY5 could immunoprecipitate the *HCF173*  
282 promoter region containing the *P4* ACE motif and *P3* G-box (Fig. 3K),  
283 suggesting that HY5 associates with the *HCF173* promoter *in vivo*. To further  
284 examine the interaction between HY5 and the *HCF173* promoter, we  
285 conducted a ChIP-qPCR analysis using transgenic Arabidopsis protoplasts  
286 (Saleh et al., 2008) expressing *35S:HY5-HA*, and protoplasts without  
287 transfection and a *UBIQUITIN10* (*UBQ10*) promoter fragment were used as a  
288 negative control. DNA was immunoprecipitated using an anti-HA affinity gel.  
289 ChIP-qPCR results showed that HY5 could also recognize the chromatin region

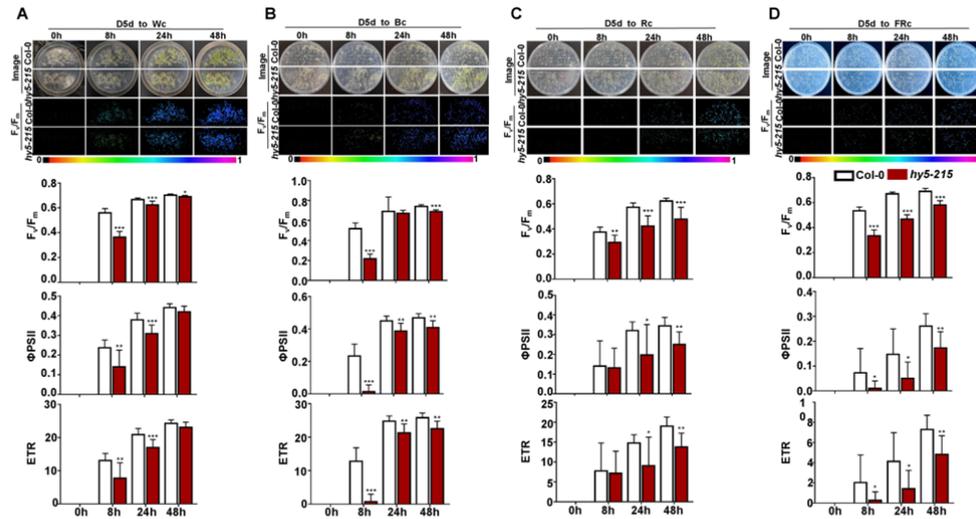
290 containing the ACE motif (*P4*) and G-box (*P3*) of the *HCF173* promoter  
291 (Supplemental Fig. S4D and E).

292 To determine whether HY5 directly binds to the promoter of *HCF173*, we  
293 performed electrophoretic mobility shift assays (EMSA). CHIP assays indicated  
294 that HY5 preferably binds to the *P3* region of the *HCF173* promoter (Figure 3K).  
295 Thus, we chose the *P3* region of the *HCF173* promoter containing the G-box  
296 *cis*-element as the DNA probe. We purified the HY5 proteins from Arabidopsis  
297 plants by immunoprecipitation using HY5 antibody. The purified HY5 proteins  
298 were incubated with the *HCF173* promoter DNA probe. The results showed that  
299 the HY5–DNA complex was detected as a band that migrated more slowly than  
300 the free probe in the gel; increasing retardation of the band was detected as the  
301 amount of HY5 proteins was increased (Supplemental Fig. S5). The  
302 association of HY5 with the *HCF173* promoter DNA probe was also confirmed  
303 by competition experiments with an unlabeled *HCF173* promoter DNA probe  
304 (Supplemental Fig. S5), indicating that HY5 directly binds to the *HCF173*  
305 promoter. Together, these data suggest that HY5 directly binds to the promoter  
306 of *HCF173* and regulates its expression.

307

### 308 **HY5 Deficiency Results in Decreased PSII Activity under Various** 309 **Monochromatic Wavelengths of Light**

310 Analyses of chlorophyll fluorescence parameters indicated that single  
311 wavelengths of light can induce PSII activity. To determine whether HY5 is  
312 involved in the functional maintenance of PSII during induction with various  
313 monochromatic wavelengths of light, we established an induction system using  
314 various monochromatic wavelengths of light to control PSII biogenesis in  
315 Arabidopsis. After 5 d of growth in the D condition, etiolated seedlings were  
316 exposed to W, B, R, and FR light for 0, 8, 24, or 48 h. The leaves of WT  
317 seedlings gradually turned green when exposed to increasing periods of W and



**Figure 4. HY5 promotes PSII activity during light-induced greening with various monochromatic light.** Photographs and false-color images representing  $F_v/F_m$  during W (A), B (B), R (C), and FR (D) light-induced greening of etiolated wild-type and *hy5-215* Arabidopsis seedlings. After growth in darkness for 5 days, etiolated seedlings were illuminated for 0, 8, 24, or 48 h, and photographs and false-color images representing  $F_v/F_m$  were captured.

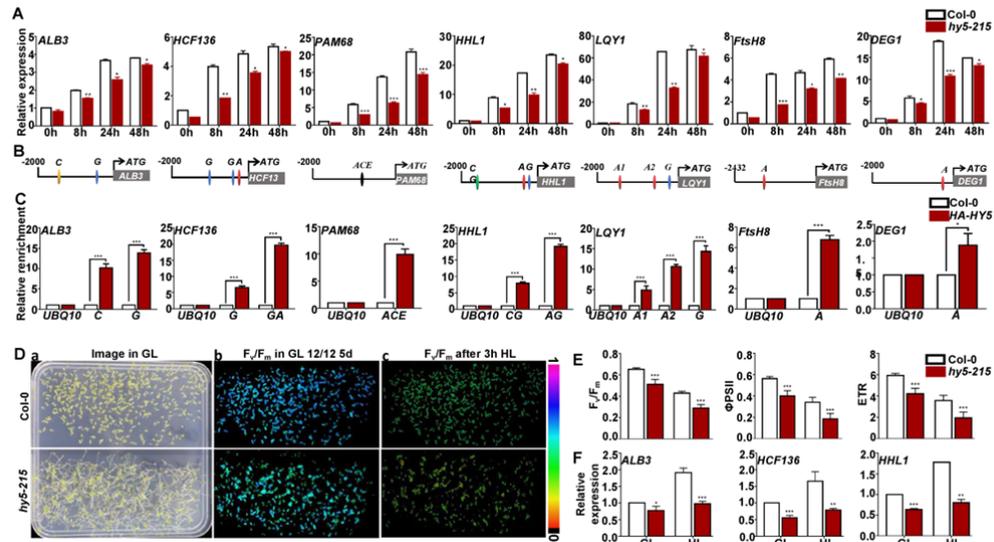
The maximal photochemical efficiency of PSII ( $F_v/F_m$ ), PSII quantum yield ( $\Phi$ PSII), and electron transport rate (ETR) of etiolated seedlings during W (A), B (B), R (C), and FR (D) light-induced greening are shown below the images. After growth in darkness for 5 days, etiolated seedlings of the wild type and *hy5-215* mutant were illuminated for 0, 8, 24, or 48 h, and  $F_v/F_m$ ,  $\Phi$ PSII, and ETR were measured. Data are represented as mean  $\pm$  SEM. Asterisks represent statistically significant differences (\* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; Student's *t*-test). All experiments were repeated at least three times with similar results.

318 other specific wavelengths of light (Fig. 4A–D), and chlorophyll fluorescence  
 319 parameters, including the maximum photochemical efficiency of PSII ( $F_v/F_m$ ),  
 320 the kinetics curves of PSII quantum yield ( $\Phi$ PSII), and the electron transport  
 321 rate (ETR), increased simultaneously (Fig. 4A–D). However, HY5-deficient  
 322 *hy5-215* seedlings showed reduced  $F_v/F_m$ ,  $\Phi$ PSII, and ETR values when  
 323 exposed to W and other various monochromatic wavelengths of light (Fig. 4A–  
 324 D). In conclusion, these data suggest that HY5-mediated PSII biogenesis  
 325 contributes to the increase in PSII activity during W, B, R, and FR-induced  
 326 de-etiolation.

327 **HY5 Regulates the Expression of PSII Assembly- and Repair-Associated**  
 328 **Genes and the Functional Maintenance of PSII**

329 As our results indicated that HY5 functions in PSII biogenesis under  
330 various wavelengths of light, we next investigated whether PSII assembly and  
331 repair are regulated by HY5. The expression of several types of PSII assembly-  
332 and repair-associated genes, including *HCF136*, *ALBINO 3 (ALB3)*, and  
333 *PHOTOSYNTHESIS AFFECTED MUTANT 68 (PAM68)*, was lower in the  
334 *hy5-215* mutant than in the WT during W light-induced greening (Fig. 5A). The  
335 expression of *HYPERSENSITIVE TO HIGH LIGHT 1 (HHL1)*, encoding a  
336 thylakoid protein and an important regulator of PSII repair (Jin et al., 2014), was  
337 induced by light in both genotypes, but to a lesser extent in the *hy5-215* mutant,  
338 suggesting that *HHL1* is positively regulated by HY5 (Fig. 5A). In addition, the  
339 expression of a gene encoding a chloroplast protease,  
340 *FILAMENTATION-TEMPERATURE-SENSITIVE PROTEIN H 8 (FtsH8)*,  
341 involved in the degradation of photodamaged D1, was lower in the *hy5-215*  
342 mutant than in the WT during de-etiolation (Fig. 5A). Collectively, these data  
343 indicate that HY5 positively regulates the expression of several light-responsive  
344 genes involved in PSII assembly and repair.

345 Next, we conducted a ChIP-qPCR assay to examine whether HY5 directly  
346 binds to the promoters of light-responsive genes and accelerates their  
347 transcription. HY5 immunoprecipitated the promoter region of *HCF136*  
348 containing a G-box and an A-box, the *ALB3* promoter region containing a C-box  
349 and a G-box, the *HHL1* promoter region containing a CG-box, A-box, and  
350 G-box (Fig. 5B and C), the *PAM68* promoter region containing an ACE-box, the  
351 *LOW QUANTUM YIELD OF PHOTOSYSTEM II 1 (LQY1)* promoter region  
352 containing two A-boxes and a G-box, the *FtsH8* promoter region containing an  
353 A-box, and the *DEGRADATION OF PERIPLASMIC PROTEINS 1 (DEG1)*  
354 promoter region containing an A-box (Fig. 5B and C), suggesting that HY5  
355 associates with the promoters of genes encoding PSII assembly and repair  
356 factors *in vivo*. To verify these results, we then performed a LUC reporter



**Figure 5. HY5 accelerates the expression of PSII assembly- and repair-associated genes and PSII activity.**

(A) RT-qPCR analysis showing the relative expression of *ALB3*, *HCF136*, *PAM68*, *HHL1*, *LQY1*, *FtsH8*, and *DEG1* after five-day-old etiolated Col-0 and *hy5-215* mutant seedlings were transferred to W light for the indicated periods.

(B) Diagram of the promoter structure of *ALB3*, *HCF136*, *PAM68*, *HHL1*, *LQY1*, *FtsH8*, and *DEG1*. Part of the coding region of each gene is shown. Positions of the putative G-box (G, blue), C-box (C, yellow), CG-box (green), ACE-box (black), or A-boxes (A1, A2, red) fragments amplified in the ChIP-qPCR assay are shown.

(C) ChIP-qPCR results showing that HY5 binds to the promoters of *ALB3*, *HCF136*, *PAM68*, *HHL1*, *LQY1*, *FtsH8*, and *DEG1* in vivo. Anti-HA antibody was used to immunoprecipitate the above-mentioned genes. Col-0 and *UBQ10* were used as negative controls.

(D) Photographs in (a) are of five-day-old Col-0 and *hy5-215* plants under growth light (12 h light /12h dark) conditions. (b) False-color images representing  $F_v/F_m$  under growth light conditions in five-day-old Col-0 and *hy5-215* seedlings. (c) False-color images representing  $F_v/F_m$  after a 3-h high light treatment in five-day-old Col-0 and *hy5-215* plants. GL, growth light ( $\sim 100 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ ); HL, high light ( $\sim 1200 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ ).

(E) The maximal photochemical efficiency of PSII ( $F_v/F_m$ ), PSII quantum yield ( $\Phi_{\text{PSII}}$ ), and electron transport rate (ETR) were measured in Col-0 and *hy5-215* seedlings after 5 d of growth under light conditions and again after a 3-h high light treatment.

(F) RT-qPCR analysis showing the relative expression of *ALB3*, *HCF136*, and *HHL1*. After growth for 5 d in growth light conditions (GL), Col-0 and *hy5-215* mutant seedlings were transferred to a 3-h high light (HL) treatment. The gene expression levels were normalized to that of *ACTIN*. Data are represented as mean  $\pm$  SEM. Asterisks represent statistically significant differences (\* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; Student's t-test). All experiments were repeated at least three times with similar results.

357 plasmid assay. Indeed, HY5 activates *proALB3:LUC*, *proHCF136:LUC*, and  
 358 *proHHL1:LUC* when transiently expressed in Arabidopsis protoplasts  
 359 (Supplemental Fig. S6). Together, these results suggest that HY5 accelerates

360 the transcriptional activation activity of genes encoding PSII assembly and  
361 repair factors through direct binding to their promoters and thereby maintains  
362 efficient photosynthesis.

363 PSII performs the energy-demanding chemical reaction of water oxidation  
364 and thereby renders its own protein components at risk of photodamage. PSII  
365 repair is required to maintain efficient photosynthesis (Mulo et al., 2008). Our  
366 data showed that five-day-old Col-0 seedlings had a higher  $F_v/F_m$  in growth light  
367 conditions ( $\sim 100 \mu\text{mol photons m}^{-2} \text{ s}^{-1}$ ) than the *hy5-215* mutant, suggesting  
368 that PSII activity was disturbed in the *hy5-215* mutants. High intensity light  
369 energy can induce greater photodamage of PSII (Takahashi and Badger, 2011).  
370 We further examined whether HY5 is involved in the high light-induced PSII  
371 damage repair process. High light treatment (3 h) ( $\sim 1200 \mu\text{mol photons m}^{-2} \text{ s}^{-1}$ )  
372 caused substantially greater photodamage via reducing  $F_v/F_m$  values in the  
373 *hy5-215* mutant than in Col-0 (Fig. 5D and E), suggesting that HY5 participates  
374 in the functional maintenance of PSII under both growth light and high light  
375 conditions.

376 To further characterize the photosynthetic apparatus, we analyzed the light  
377 intensity dependence of two chlorophyll fluorescence parameters,  $\Phi\text{PSII}$  and  
378 the ETR, before and after a 3-h high light treatment. After a short-term high light  
379 treatment (3 h), Col-0 and *hy5-215* seedlings had a much lower  $\Phi\text{PSII}$  and ETR  
380 than after a 3-h treatment under growth light conditions. Furthermore, *hy5-215*  
381 seedlings had significantly reduced  $F_v/F_m$ ,  $\Phi\text{PSII}$ , and ETR values compared  
382 with those in Col-0 before and after the high light treatment (Fig. 5D and E),  
383 indicating that HY5 might regulate PSII repair after exposure to high light.

384 It was previously reported that high light-induced damage of the PSII core  
385 protein D1 can be rapidly repaired and reassembled to maintain photosynthetic  
386 electron transport (Nickelsen and Rengstl, 2013). The defects in PSII activity  
387 displayed by the *hy5-215* mutants were possibly caused by a decreasing level

388 or malfunction of thylakoid protein supercomplexes in the electron transport  
389 chain. To further investigate the effects of a lack of functional HY5 on PSII  
390 structure and function, we analyzed the accumulation of various thylakoid  
391 complexes in WT and *hy5-215* plants. Thylakoid membranes were solubilized  
392 in 2% dodecylmaltoside (DM), membrane protein complexes were separated  
393 by blue native polyacrylamide gel electrophoresis (BN-PAGE) (Supplemental  
394 Fig. S7A), and the complexes were analyzed by immunoblotting with antibodies  
395 specific for PSII core proteins. Analysis with antisera against PSII core antenna  
396 proteins, anti-CP47, showed that *hy5-215* mutants contain lower levels of the  
397 PSII-light harvesting complex II (LHCII) supercomplex, PSII dimer, and PSII  
398 core monomer than WT thylakoid membranes, especially after high light  
399 treatment (Supplemental Fig. S7C), suggesting that the absence of HY5 may  
400 affect the formation and stability of the PSII supercomplex after high light  
401 treatment. Moreover, the reduction in PSI monomer in the *hy5-215* mutants  
402 was confirmed by immunoblot analysis with anti-PsaD antisera before and after  
403 the high light treatment, suggesting that the absence of HY5 may affect PSI  
404 monomer formation before and after the high light treatment (Supplemental Fig.  
405 S7D).

406 Next, we determined whether high light-induced damage induced the  
407 transcription of PSII assembly- and repair-associated genes. Col-0 and  
408 *hy5-215* mutant seedlings were grown for 5 d in growth light conditions and  
409 transcript levels were measured by RT-qPCR analysis. The seedlings were  
410 transferred to high light conditions for 3 h and gene expression was measured  
411 again. The expression levels of *PAM68*, *ALB3*, *HCF136*, *HHL1*, *LQY1*, *FtsH8*,  
412 and *DEG1* were dramatically increased in the WT after a 3-h high light  
413 treatment in wild type plants, but the increase of their expression levels was  
414 also suppressed in the *hy5-215* mutant. The difference in gene expression  
415 between the WT and the *hy5-215* mutant was greater under the high light

416 treatment compared to growth light conditions (Fig. 5F; Supplemental Fig.  
417 S8A–D). These results suggest that HY5 is required for the functional  
418 maintenance of PSII under photodamaging conditions.

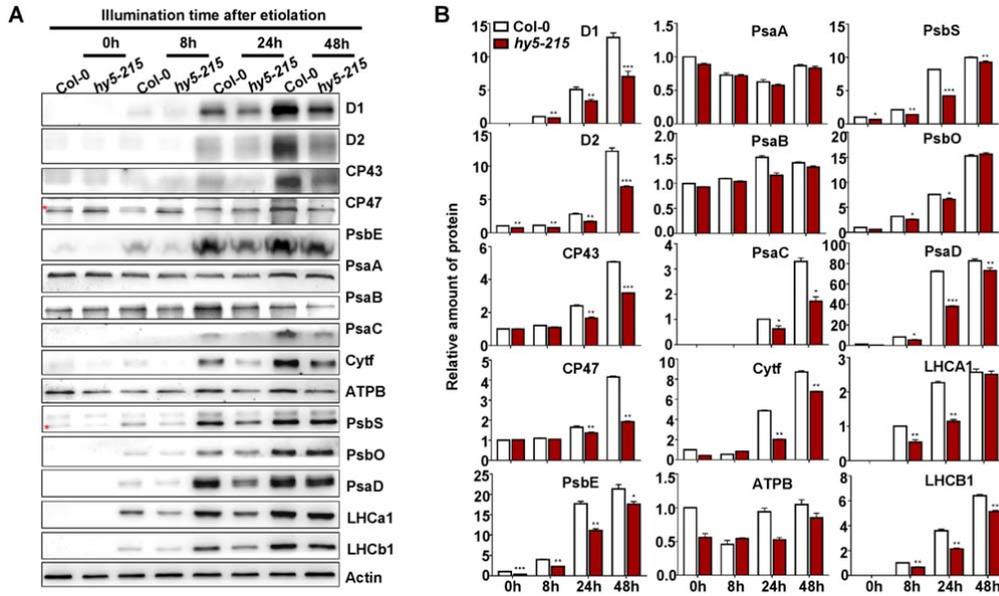
419

## 420 **HY5 Broadly Regulates the Protein Accumulation of Photosystem** 421 **Subunits**

422 D1 protein accumulation was induced after etiolated Arabidopsis seedlings  
423 perceived light (Fig. 1C), which prompted us to question whether the D1 protein  
424 level was also regulated by HY5 during de-etiolation. Etiolated Col-0 and  
425 *hy5-215* mutant seedlings were grown in darkness for five days followed by  
426 exposure to W light for 0, 8, 24, and 48 h, and then harvested. Immunoblot  
427 analysis showed that D1 also accumulated after light perception in the *hy5-215*  
428 mutant, but the D1 protein level was lower in the *hy5-215* mutant than in Col-0  
429 (Fig. 6A and B), indicating that D1 accumulation was positively regulated by  
430 HY5 during de-etiolation.

431 We also examined if specific wavelengths of light (B, R, and FR) mediated  
432 the regulation of D1 protein levels by HY5. Col-0 and the *hy5-215* mutant were  
433 grown in continuous B, R, or FR light conditions for five days and then  
434 harvested. Immunoblot analysis showed that the D1 protein level was lower in  
435 the *hy5-215* mutant than in Col-0 under all specific wavelengths of light tested,  
436 indicating that HY5 positively regulates D1 accumulation in response to B, R,  
437 and FR light (Supplemental Fig. S3A-C).

438 Next, we examined whether the protein levels of other plastid-encoded and  
439 nuclear-encoded photosystem subunits were regulated by HY5 during  
440 light-induced greening. Immunoblot analysis indicated that the levels of the  
441 PSII proteins D2, CP43, CP47, PsbO, PsbE, and PsbS were dramatically lower  
442 in the *hy5-215* mutant than in Col-0 following exposure to light. In addition, the  
443 levels of the PSI proteins PsaC and Cyf were also dramatically lower in the



**Figure 6. HY5 promotes the synthesis of thylakoid subunits.**

(A) Immunoblots showing D1 protein and other photosystem proteins isolated from etiolated WT Col-0 and *hy5-215* mutant seedlings during light-induced greening. The asterisk represent PsbS protein. Anti-Actin was used as a sample loading control.

(B) The relative abundance of PSII proteins was analyzed with Phoretix 1D Software (Phoretix International, UK). Data are represented as mean  $\pm$  SEM. Asterisks represent statistically significant differences (\* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; Student's t-test). All experiments were repeated at least three times with similar results.

444 *hy5-215* mutant than in Col-0 (Fig. 6A and B). These observations indicate that  
 445 HY5 systematically and broadly regulates the protein accumulation of  
 446 photosystem subunits in response to W light-induced greening.

447

448

449 **DISCUSSION**

450 Light is required for photosynthesis and is a key environmental signal  
451 regulating the biosynthesis, assembly, and repair of the photosystem  
452 (Nickelsen and Rengstl, 2013; Lu, 2016). Photoreceptors, including  
453 cryptochromes and phytochrome, sense light and regulate plant growth and  
454 development. However, the crosstalk of light signaling and photosystem  
455 function remains largely unknown. In this study, we confirmed that  
456 cryptochromes and phytochrome cooperatively regulate PSII biogenesis and  
457 maintenance of its function through HY5 in Arabidopsis.

458 PSII plays a critical role in water splitting, oxygen evolution, and  
459 plastoquinone reduction. PSII biogenesis refers to the synthesis of its protein  
460 subunits and the concerted assembly as well as the incorporation of various  
461 auxiliary proteins (Nickelsen and Rengstl, 2013; Lu, 2016). Plastid-encoded  
462 PSII proteins are synthesized on thylakoid-bound ribosomes and inserted into  
463 the thylakoid membrane, and the core protein D1 is co-translationally  
464 incorporated into PSII, not only for D1 assembly but also for photodamage  
465 repair (Klein et al. 1988; Keegstra and Cline 1999; Zhang et al. 1999). HCF173,  
466 a short-chain dehydrogenases/reductase-like protein, plays critical roles in PSII  
467 biogenesis. *HCF173* deficiency results in impaired *psbA* mRNA stability as well  
468 as decreased synthesis of the PSII reaction center protein D1 (Schult et al.,  
469 2007). We recently revealed that a newly identified regulator of *psbA* mRNA  
470 translation, LPE1, could interact with HCF173 to regulate D1 synthesis (Jin et  
471 al., 2018). Furthermore, we showed that *HCF173* but not *LPE1* expression was  
472 greatly induced by light during de-etiolation (Jin et al., 2018), an observation  
473 confirmed in our present study (Fig. 1D). In addition, our data indicated that  
474 various monochromatic wavelengths of light, including B, R, and FR light,  
475 cooperatively regulate *HCF173* expression, D1 accumulation, and PSII activity  
476 (Fig. 1H, L and P, Supplemental Fig. S1; Fig. 1G, K and O; Fig. 1F, J and N).

477 Moreover, *HCF173* expression, D1 accumulation, and PSII activity are  
478 positively regulated by HY5 in response to specific wavelengths of light (B, R,  
479 and FR light) (Supplemental Fig. S3; Fig. 4B–D), and this redundancy probably  
480 ensures the functional maintenance of the photosystem in plants under various  
481 light-quality conditions. Partial PSII activity still occurs in mutant plants lacking  
482 HY5 (Fig. 4), suggesting that other transcription factors may also regulate PSII  
483 function.

484 Light signal transduction pathways refer to a series of specific  
485 photoreceptors that regulate critical developmental processes such as  
486 skotomorphogenesis and photomorphogenesis (Chen et al., 2004; Kami et al.,  
487 2010; Von Arnim and Deng, 1996). Our results indicated that both  
488 cryptochromes and phytochrome influence *HCF173* expression (Fig. 2),  
489 suggesting that cryptochromes and phytochrome cooperate to regulate the  
490 expression of *HCF173*. As partial PSII activity still occurs in mutants lacking  
491 cryptochromes and/or phytochromes (Fig. 2), other wavelengths of light  
492 besides R, FR, and B light may also contribute to PSII function. A previous  
493 study reported that CRY2 is more quickly degraded in blue light and its role is a  
494 bit more complicated than that of CRY1 (Zuo et al., 2012). Our results show  
495 that many PSII-related regulatory genes including *HCF173*, *HCF136*, *ALB3*,  
496 *DEG1*, *HHL1* and *PAM68* also show higher expression levels in the *cry2*  
497 monogenic mutant compared to the wild type after 48 h white light exposure  
498 (Fig. 2A, Supplemental Fig. S9A–E), and most of these genes show increased  
499 expression after five days of continuous W, B, and R light conditions but  
500 decreased expression after five days of continuous FR light conditions (Fig.  
501 2B–E, Supplemental Fig. S9H–L). However, the expression level of *FtsH8* and  
502 *LQY1* was much lower in the *cry2* monogenic mutant than in the wild type after  
503 48 h of W light exposure (Supplemental Fig. S9F and G), or five days of  
504 continuous W, B, R, and FR light conditions (Supplemental Fig. S9M and N).

505 These results suggest that CRY2 can act as a positive or negative regulator to  
506 regulate different gene expression under different light conditions or during  
507 different developmental stages, implying a bit more complicated roles in the  
508 regulation of light signaling.

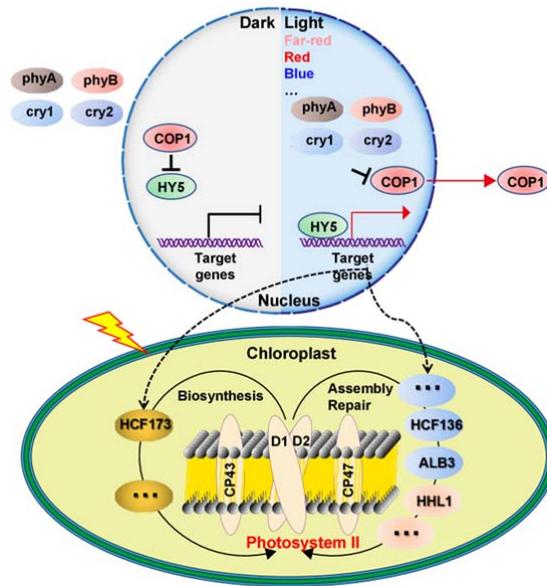
509 A previous study reported that HY5 constitutively binds to its target sites in  
510 both darkness and light and affects the expression of its target genes (Lee et  
511 al., 2007; Zhang et al., 2011). COP1 is inactivated upon light irradiation and  
512 acts in the dark as an E3 ubiquitin ligase as well as the central repressor of light  
513 signaling through ubiquitinating and degrading downstream substrates  
514 including HY5 (Lau and Deng, 2012; Huang et al., 2014). Hence, the COP1–  
515 HY5 regulatory module plays a central role in the light signal transduction  
516 pathway between transcriptional and posttranslational network hubs. However,  
517 the role of the COP1-HY5 regulatory module in the functional maintenance of  
518 the photosystem was largely unknown. Here, we verified that a variety of  
519 wavelengths of light induce *HCF173* expression, but also function through the  
520 COP1–HY5 regulatory module (Fig. 2, 3A–E, Supplemental Fig. S2;  
521 Supplemental Fig. S4A and C). When grown in darkness, *cop1* mutant  
522 seedlings had increased *HCF173* transcript and protein levels, due to the  
523 accumulation of HY5, and HY5 directly bound to the ACE motif and G-box  
524 *cis*-element present in the promoter of *HCF173*, activating its transcription (Fig.  
525 3K). Light triggered the accumulation of HY5 due to the light-controlled  
526 inactivation of COP1 (Supplemental Fig. S4B), and HY5 associated directly  
527 with the *HCF173* promoter (Supplemental Fig. S4E). These findings suggest  
528 that HY5, a positive regulator of light signaling, affects *HCF173* expression by  
529 binding to the *HCF173* promoter *in vivo* both in dark and light conditions, thus  
530 providing a transcriptional regulatory mechanism that fine-tunes translational  
531 regulator-based PSII biogenesis in response to changing light conditions.

532 In addition, the induction of *HCF173* expression by light may also be  
533 associated with the enrichment of histone H2B ubiquitination in its promotor  
534 region (Bourbousse et al., 2012). However, *LPE1*, encoding another regulator  
535 of D1 translation, is not obviously regulated by light (Supplemental Fig. S10),  
536 which is consistent with the results of a previous study (Jin et al., 2018).  
537 Furthermore, we found that the expression of *LPE1* is not affected obviously in  
538 the *hy5* mutant compared to the wild type during the light induction process  
539 overall, and is only decreased slightly at 8 h (Supplemental Fig. S10),  
540 suggesting that *LPE1* is not HY5-dependent. A previous study reported that  
541 light triggers D1 synthesis to contribute to PSII biogenesis through inducing  
542 *LPE1* and *psbA* mRNA association based on a redox mechanism (Jin et al.,  
543 2018), suggesting that PSII biogenesis is controlled by dual strategies of  
544 transcriptional regulation in the nucleus and translational regulation in the  
545 chloroplasts.

546 Although light energy powers photosynthesis, excessive light causes  
547 photoinhibition and damage to the photosynthetic apparatus, especially to PSII  
548 (Takahashi and Badger, 2011). D1 is the main target of photodamage and has  
549 an unusually high turnover rate. Photodamaged D1 is rapidly removed and  
550 replaced by newly synthesized D1 (Mulo et al., 2012). Given that HY5 functions  
551 in D1 synthesis, this transcription factor may also function in PSII repair. The  
552 decreased photosynthetic efficiency during light-induced greening by various  
553 monochromatic wavelengths of light and increased high light-sensitive  
554 phenotype in the *hy5-215* mutant support this hypothesis (Fig. 4; Fig. 5D and  
555 E). The PSII repair cycle involves the phosphorylation, disassembly, and  
556 reassembly of the PSII-LHCII supercomplex from grana stacks to the stroma  
557 lamellae. Several assembly and repair factors important for the biogenesis of  
558 the PSII core complex have been identified, including HCF136 (Mabbitt et al.,  
559 2014), ALB3 (Walter et al., 2015), and PAM68 (Armbruster et al., 2010). Deg

560 proteases (Schuhmann and Adamska, 2012) and FtsH proteases (Silva et al.,  
561 2003; Nixon et al., 2005; Nixon et al., 2010; Huesgen et al., 2009; Kato et al.,  
562 2012; Komenda et al., 2012) are involved in the degradation of photodamaged  
563 D1. LQY1 (Lu et al., 2011) and HHL1 (Jin et al., 2014) are involved in the repair  
564 cycle and reassembly of PSII. We demonstrated that HY5 directly associates  
565 with the promoters of assembly- and repair-related genes to regulate their  
566 expression (Fig. 5A–C, Supplemental Fig. S6A–C). Furthermore, a deficiency  
567 of HY5 results in reduced expression of these genes, particularly after  
568 exposure to high light (Fig. 5F; Supplemental Fig. S8), suggesting that HY5 is  
569 involved in the functional maintenance of PSII through regulating the  
570 expression of PSII assembly- and repair-associated genes. Although HY5 can  
571 associate with numerous PSII-related genes, the associated *cis*-acting element  
572 varies for different genes. More interestingly, our results showed that HY5 also  
573 affects the protein accumulation of other photosynthetic complexes besides  
574 PSII (Fig. 6), suggesting that HY5 may act as a hub to control the expression of  
575 regulators of other photosynthetic complex-related genes besides PSII.

576 In summary, our data indicate that various monochromatic wavelengths of  
577 light cooperate to regulate the biogenesis and functional maintenance of PSII.  
578 The photoreceptors cryptochromes and phytochromes and the transcription  
579 factor HY5 are key regulators of PSII function. During de-etiolation,  
580 light-induced HY5 directly binds to the promoter of *HCF173* or of other  
581 PSII-associated translation factor genes, thereby promoting their expression,  
582 the synthesis of PSII subunits, and the biogenesis of the PSII complex. Under  
583 high light conditions, light-induced HY5 directly binds to the promoters of PSII  
584 repair factor genes, thereby promoting their expression and PSII repair and  
585 maintaining efficient photosynthesis (Fig. 7). This study establishes a  
586 relationship between PSII function and light signaling mediated by



**Figure 7. Proposed working model depicting how photoreceptor–HY5 regulatory modules mediate PSII biogenesis and functional maintenance.**

During de-etiolation, light-induced HY5 directly binds to the promoter of *HCF173* or of other PSII-associated translation factor genes, thereby accelerating their expression and promoting the synthesis of PSII subunits and the biogenesis of the PSII complex. Under photodamaging conditions, light-induced HY5 directly binds to the promoters of PSII assembly and repair factor-related genes, including *HCF136*, *ALB3*, and *HHL1*, thereby accelerating their expression and promoting PSII assembly and repair and maintaining efficient photosynthesis.

587 photoreceptors and HY5, providing insight into the light-mediated regulation of

588 PSII function in land plants.

589

590

## 591 **METHODS**

### 592 **Plant Materials and Growth Conditions**

593 The *Arabidopsis thaliana* mutants *phyA-211*, *phyB-9* (Zhang et al., 2017),  
594 *cry1-304*, *cry2* (Liu et al., 2013), *phyA phyB* (Chen et al., 2013), *cry1 cry2* (Liu et  
595 al., 2013), *phyA phyB cry1* (Kang et al., 2009), *cry1 cry2 phyA* (Liu et al., 2013),  
596 *hy5-215*, and *cop1-4* (Zhang et al., 2017), as well as the *HA-HY5 hy5-215*  
597 transgenic line (Heng et al., 2019), are all in the Columbia-0 (Col-0)  
598 background. All seeds were surface sterilized with 20% (v/v) bleach for 20 min  
599 and sown on ½ Murashige and Skoog (MS) media with 1% (w/v) sucrose and  
600 0.8% (w/v) agar. After vernalization in darkness at 4°C for 2 d, the plates were  
601 placed in white (W) light with an irradiance of 100  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ , red (R)  
602 light with an irradiance of 44  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ , blue (B) light with an  
603 irradiance of 58  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ , or far-red (FR) light with an irradiance of  
604 10  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  at 22°C.

605

### 606 **Plasmid Construction**

607 The full-length *HY5* open reading frame was cloned into the BamHI/EcoRI sites  
608 of the pGreen II-62-SK vector under the 35S promoter. Then, 297-bp, 664-bp,  
609 1107-bp, 1611-bp, and 1850-bp fragments of the *HCF173* promoter upstream  
610 of the ATG start site were amplified by PCR using primer pairs listed in  
611 Supplemental Table S1 and then cloned into the HindIII/BamHI sites of the  
612 pGreen II 0800-LUC vector.

613

### 614 **Chlorophyll Fluorescence Analysis**

615 Chlorophyll fluorescence parameters were measured with the MAXI version of  
616 the Imaging-PAM M-Series chlorophyll fluorescence system (Heinz-Walz  
617 Instruments). The maximal photochemical efficiency of PSII ( $F_v/F_m$ ), the  
618 kinetics curves of PSII quantum yield ( $\Phi\text{PSII}$ ), and the electron transport rate

619 (ETR) were measured in five-day-old Col-0 and *hy5-215* plants after irradiation  
620 with 100  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  under a growth light and a 3-h high light  
621 treatment ( $\sim 1200 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ ).

622

### 623 **RNA Isolation and RT-qPCR Assays**

624 Total RNA was extracted from Arabidopsis seedlings using an RNAeasy Plant  
625 Mini Kit (MAGEN). The RNA samples were reverse transcribed into first strand  
626 cDNA using the PrimeScript RT Reagent Kit (TaKaRa). Quantitative PCR was  
627 carried out using gene-specific primers, SYBR Premix ExTaq reagent (Takara),  
628 and a real-time PCR system (RoChe-LC480). *UBQ4* and *ACTIN2* were used as  
629 internal controls. Primer sequences of genes tested in RT-qPCR are listed in  
630 Supplemental Table S1.

631

### 632 **Thylakoid Membrane Isolation**

633 Thylakoid membranes were prepared as previously described (Robinson and  
634 Yocum, 1980). Isolated thylakoid membranes were quantified based on total  
635 chlorophyll as previously described (Porra et al., 1989). Total proteins extracted  
636 from leaf thylakoid membrane preparations were prepared as described (Liu et  
637 al., 2012). Protein concentrations were determined using the Bio-Rad  
638 detergent-compatible colorimetric protein assay according to the  
639 manufacturer's protocol (Bio-Rad).

640

### 641 **BN-PAGE and Immunoblot Analyses**

642 BN-PAGE and immunodetection of proteins on a polyvinylidene difluoride  
643 (PVDF) membrane were performed as previously described (Schägger et al.,  
644 1994) with the modifications described (Peng et al., 2006). For quantification of  
645 thylakoid proteins, gels were loaded on an equivalent chlorophyll basis, in  
646 amounts ensuring that immunodetection was in the linear range. All primary

647 antibodies and antisera were raised in rabbits. Antisera against photosynthetic  
648 proteins were purchased from Agrisera.

649

### 650 **Immunoblot Assay**

651 Total proteins were extracted with protein extraction buffer containing 50 mM  
652 Tris-HCl at pH 7.5, 150 mM NaCl, 5 mM EDTA, 0.1% (v/v) Triton X-100, and  
653 protease inhibitor cocktail (Roche). The extracts were subsequently centrifuged  
654 at 18,000 x g for 10 min at 4°C to collect the supernatants for immunoblot  
655 analyses. Total proteins were separated by sodium dodecyl sulfate  
656 polyacrylamide gel electrophoresis (SDS-PAGE). After electrophoresis, the  
657 proteins were transferred to PVDF membranes (Millipore) and probed using  
658 specific antibodies. Primary antibodies used in this study were anti-Actin (which  
659 were raised in mice), anti-HY5 (which were raised in rabbits), and antisera  
660 against photosynthetic proteins (which were raised in rabbits). Antisera against  
661 HY5 and photosynthetic proteins were purchased from Agrisera. D1, AS05084;  
662 D2, AS06146; CP43, AS111787; CP47, AS10939; PsbE, AS06112; PsbF,  
663 AS06113; PsbO, AS05092; PsbS, AS09533; CytF, AS08306; PsaA, AS06172;  
664 PsaB, AS10695; PsaC, AS10939; PsaD, AS09461; LHCA1, AS01005; LHCB1,  
665 AS01004; ATPB, AS05085; HY5, AS121867.

666

### 667 **LUC Assay**

668 To explore the transcriptional activation of the *HCF173* promoter by HY5,  
669 truncated and site-specific mutant sequences of the *HCF173* promoter were  
670 each cloned into the pGreen II 0800-LUC vector to generate reporter  
671 constructs. Each reporter construct was then co-transformed with the HY5  
672 effector into Col-0 protoplasts for the transcriptional activity assay. The LUC  
673 activity was normalized to Renilla luciferase (REN). Firefly and Renilla

674 luciferase signals were assayed using the dual-luciferase assay reagents,  
675 according to the manufacturer's instructions (Promega).

676

### 677 **ChIP Assay**

678 Chromatin was isolated from Col-0 and the *cop1-4* mutant grown under  
679 constant dark conditions for five days. Col-0 and *HA-HY5 hy5-215* transgenic  
680 plants grown under constant W light for five days and an anti-HA antibody were  
681 used to confirm the binding of HY5 to the targeted-gene promoters *in vivo*. The  
682 chromatin was sonicated to 250- to 500-bp fragments in an ice-water bath.  
683 About 10% of the sonicated chromatin was used as an input DNA control. The  
684 sheared chromatin was immunoprecipitated by anti-HY5 (Cat# AS121867,  
685 Agrisera) antibody and anti-HA (Cat# H3663, Sigma). Both immunoprecipitated  
686 DNA and input DNA were analyzed by RT-qPCR. All primers used for this  
687 assay are listed in Supplemental Table S1.

688

### 689 **EMSA Assays**

690 The HY5 protein was purified from soluble extracts of *cop1-4* mutant plants by  
691 immunoprecipitation of anti-HY5 antibody. For labeling of the synthetic  
692 nucleotides of the *P3* promoter of *HCF173* DNA from -1225 bp upstream to  
693 -1076 bp upstream containing the G-box *cis*-element, the DIG DNA Labeling  
694 and Detection Kit (Roche) was employed. The purified HY5 was incubated  
695 with DNA probes in binding buffer at room temperature for 30 min. The DNA–  
696 protein complexes were separated on 10% native polyacrylamide gels. After  
697 electrophoresis, the DNA was transferred onto a nylon membrane. The signals  
698 from the labeled DNA were detected using DIG DNA Labeling and Detection  
699 Kit (Roche).

700

### 701 **Statistical Analyses**

702 For RT-qPCR, CHIP-qPCR, and LUC/REN, Student's *t*-test was used to  
703 determine significant differences. \*  $P < 0.05$ , was considered to indicate  
704 statistical significance, \*\*  $P < 0.01$ , was considered highly significant, and \*\*\*  $P$   
705  $< 0.001$ , was considered extremely significant.

706

#### 707 **ACCESSION NUMBERS**

708 Sequence data from this article can be found in the Arabidopsis Genome  
709 Initiative data library under the following accession numbers: *HY5*  
710 (AT5G11260), *HCF173* (AT1G16720), *ALB3* (AT2G28800), *HCF136*  
711 (AT5G23120), *HHL1* (AT1G67700), *LQY1* (AT1G75690), *FtsH8* (AT1G06430),  
712 *DEG1* (AT3G27925), *PAM68* (AT4G19100), *LPE1* (AT3G46610), *ACTIN*  
713 (AT3G18780), and *UBQ10* (AT4G05320).

714

#### 715 **SUPPLEMENTAL INFORMATION**

716 The following supplemental information is available.

717 **Supplemental Figure S1.** The expression of *HCF173* is induced by single  
718 wavelengths of light.

719 **Supplemental Figure S2.** *HY5* regulates the expression of *HCF173* under  
720 light-induced greening.

721 **Supplemental Figure S3.** *HY5* regulates the protein abundance of D1 and  
722 *HCF173* in continuous B, R, and FR light.

723 **Supplemental Figure S4.** *HY5* associates with the *HCF173* promoter.

724 **Supplemental Figure S5.** Electrophoretic mobility shift assays (EMSAs)  
725 containing *HY5* protein and *HCF173* promoter probe.

726 **Supplemental Figure S6.** *HY5* regulates the promoter activity of the genes  
727 related to PSII assembly and repair.

728 **Supplemental Figure S7.** Immunological analysis of PSII complexes  
729 separated by BN-PAGE.

730 **Supplemental Figure S8.** Transcript levels of the assembly- and repair  
731 factor-related genes in the wild type and the *hy5-215* mutants.  
732 **Supplemental Figure S9.** Transcript levels of PSII assembly- and repair  
733 factor-related genes in the wild type and *cry2* mutant.  
734 **Supplemental Figure S10.** Transcript levels of *HCF173* and *LPE1* during  
735 white light-induced greening in the wild type and *hy5-215* mutant.  
736 **Supplemental Table S1.** Sequence of Primers Used in this Study.

737

### 738 **ACKNOWLEDGMENTS**

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740 providing Arabidopsis *HA-HY5 hy5-215* seeds, Prof. Rongcheng Lin from the  
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742 *phyB-9*, *phyA phyB*, *hy5-215*, and *cop1-4* seeds, Prof. Hongtao Liu from  
743 Institute of Plant Physiology and Ecology of CAS for kindly providing *cry1-304*,  
744 *cry2*, *cry1 cry2*, and *cry1 cry2 phyA* seeds, and Prof. Hongquan Yang from  
745 Shanghai Normal University for kindly providing *phyA phyB cry1* seeds.

### 746 **FIGURE LEGENDS**

747 **Figure 1. Single wavelengths of light regulate PSII activity, as well as D1**  
748 **and HCF173 protein accumulation during greening.**

749 **(A, E, I, M)** Schematic representation of the experimental set-up used with  
750 white (W), blue (B), red (R), and far-red (FR) light during greening.  
751 Five-day-old Arabidopsis Col-0 seedlings were maintained under darkness  
752 and were then transferred to different light conditions and harvested at 0, 8, 24,  
753 and 48 h for analysis.

754 **(B, F, J, N)** False-color images representing the maximal photochemical  
755 efficiency of PSII ( $F_v/F_m$ ) during W, B, R, and FR light-induced greening of  
756 etiolated wild-type Arabidopsis seedlings. After growth in darkness for 5 days,

757 etiolated seedlings were illuminated for 0, 8, 24, or 48 h, and false-color  
758 images representing  $F_v/F_m$  were captured.

759 **(C, G, K, O)** Western blot analysis of D1 proteins isolated from 5-d-old  
760 etiolated *Arabidopsis* Col-0 seedlings during W, B, R, or FR light-induced  
761 greening for the indicated periods. Anti-Actin was used as a sample loading  
762 control.

763 **(D, H, L, P)** RT-qPCR analysis showing the relative expression of *HCF173*  
764 after five-day-old etiolated *Arabidopsis* Col-0 seedlings were transferred to W,  
765 B, R, or FR light conditions for the indicated periods.

766 Data are represented as mean  $\pm$  SEM. All experiments were repeated at  
767 least three times with similar results.

768

769 **Figure 2. Both cryptochromes and phytochrome influence *HCF173***  
770 **expression.**

771 **(A)** RT-qPCR analysis of *HCF173* transcript levels after five-day-old etiolated  
772 Col-0 and different photoreceptor mutants were transferred to W light for the  
773 indicated periods.

774 **(B–E)** Analyses of *HCF173* expression under W, B, R, and FR light conditions  
775 in *phyA-211*, *phyB-9*, *cry1-304*, and *cry2* single and higher order mutants  
776 under five days of continuous light (Wc, Bc, Rc, and FRc) conditions as  
777 indicated. The expression levels were normalized to that of *ACTIN*. Data are  
778 represented as mean  $\pm$  SEM (three biological repeats). Asterisks represent  
779 statistically significant differences ( $*P < 0.05$ ;  $**P < 0.01$ ;  $***P < 0.001$ ;  
780 Student's *t*-test). All experiments were repeated at least three times with  
781 similar results. We did not perform statistical analyses on those mutants that  
782 showed up-regulation of *HCF173* transcripts.

783

784 **Figure 3. HY5 regulates the transcript level of *HCF173* through directly**  
785 **associating with its promoter.**

786 **(A)** RT-qPCR analysis of the relative expression of *HCF173* after five-day-old  
787 etiolated Col-0 and *hy5-215* mutant seedlings were transferred to W light for the  
788 indicated time points. The expression levels were normalized to that of *ACTIN*.

789 **(B–E)** RT-qPCR analysis showing the expression levels of *HCF173* in  
790 five-day-old Col-0 and *hy5-215* mutant seedlings grown under continuous W,  
791 B, R, and FR light conditions.

792 **(F)** Schematic representation of various constructs used in the transient  
793 transfection assay in Arabidopsis protoplasts. Reporter, A schematic map of  
794 the transient expression vector pGreenII-0800-LUC. REN, Renilla luciferase;  
795 LUC, firefly luciferase. Effector, Diagram of the HY5 effector of the transient  
796 expression vector pGreenII 62-SK.

797 **(G)** Diagram representing different variants of the *HCF173* promoter. Part of  
798 the coding region of *HCF173* is shown. Positions of the putative G-boxes (blue)  
799 and ACE motifs (red) are numbered.

800 **(H)** DNA sequences of the wild-type *HCF173* promoter containing the ACE  
801 motifs (*HCF173P4*) or G-boxes (*HCF173P3*) and mutant *HCF173* promoters  
802 harboring a mutant ACE motif (*HCF173P4-m*) or G-box (*HCF173P3-m*).

803 **(I)** Effects of HY5 on *HCF173* transcriptional regulation using different *HCF173*  
804 promoter variants in Col-0 protoplasts.

805 **(J)** The roles of the ACE motif or G-box for activity of the *HCF173* promoter  
806 regulated by HY5. The protoplasts without the HY5 effector were used as a  
807 negative control. The relative LUC activities were normalized to REN activities.

808 **(K)** The analyses of association between HY5 and the *HCF173* promoter *in*  
809 *vivo* by ChIP-qPCR assays. Anti-HY5 antibody was used to immunoprecipitate  
810 the HY5-*HCF173* complex. Col-0 and *UBQ10* were used as negative controls.

811 Data are represented as mean  $\pm$  SEM. Asterisks represent statistically

812 significant differences ( $*P < 0.05$ ;  $**P < 0.01$ ;  $***P < 0.001$ ; Student's *t*-test). All  
813 experiments were repeated at least three times with similar results.

814

815 **Figure 4. HY5 promotes PSII activity during light-induced greening with**  
816 **various monochromatic wavelengths of light.**

817 Photographs and false-color images representing  $F_v/F_m$  during W (**A**), B (**B**), R  
818 (**C**), and FR (**D**) light-induced greening of etiolated wild-type and *hy5-215*  
819 *Arabidopsis* seedlings. After growth in darkness for 5 days, etiolated seedlings  
820 were illuminated for 0, 8, 24, or 48 h, and photographs and false-color images  
821 representing  $F_v/F_m$  were captured.

822 The maximal photochemical efficiency of PSII ( $F_v/F_m$ ), PSII quantum yield  
823 ( $\Phi_{PSII}$ ), and electron transport rate (ETR) of etiolated seedlings during W (**A**),  
824 B (**B**), R (**C**), and FR (**D**) light-induced greening are shown below the images.  
825 After growth in darkness for 5 days, etiolated seedlings of the wild type and  
826 *hy5-215* mutant were illuminated for 0, 8, 24, or 48 h, and  $F_v/F_m$ ,  $\Phi_{PSII}$ , and  
827 ETR were measured. Data are represented as mean  $\pm$  SEM. Asterisks  
828 represent statistically significant differences ( $*P < 0.05$ ;  $**P < 0.01$ ;  $***P <$   
829  $0.001$ ; Student's *t*-test). All experiments were repeated at least three times with  
830 similar results.

831

832 **Figure 5. HY5 accelerates the expression of PSII assembly- and**  
833 **repair-associated genes and PSII activity.**

834 **(A)** RT-qPCR analysis showing the relative expression of *ALB3*, *HCF136*,  
835 *PAM68*, *HHL1*, *LQY1*, *FtsH8*, and *DEG1* after five-day-old etiolated Col-0 and  
836 *hy5-215* mutant seedlings were transferred to W light for the indicated periods.

837 **(B)** Diagram of the promoter structure of *ALB3*, *HCF136*, *PAM68*, *HHL1*, *LQY1*,  
838 *FtsH8*, and *DEG1*. Part of the coding region of each gene is shown. Positions of  
839 the putative G-box (G, blue), C-box (C, yellow), CG-box (green), ACE-box

840 (black), or A-boxes (A1, A2, red) fragments amplified in the ChIP-qPCR assay  
841 are shown.

842 **(C)** ChIP-qPCR results showing that HY5 binds to the promoters of *ALB3*,  
843 *HCF136*, *PAM68*, *HHL1*, *LQY1*, *FtsH8*, and *DEG1* *in vivo*. Anti-HA antibody  
844 was used to immunoprecipitate the above-mentioned genes. Col-0 and *UBQ10*  
845 were used as negative controls.

846 **(D)** Photographs in (a) are of five-day-old Col-0 and *hy5-215* plants under  
847 growth light (12 h light /12h dark) conditions. (b) False-color images  
848 representing  $F_v/F_m$  under growth light conditions in five-day-old Col-0 and  
849 *hy5-215* seedlings. (c) False-color images representing  $F_v/F_m$  after a 3-h high  
850 light treatment in five-day-old Col-0 and *hy5-215* plants. GL, growth light ( $\sim 100$   
851  $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$ ); HL, high light ( $\sim 1200 \mu\text{mol photons m}^{-2} \text{ s}^{-1}$ ).

852 **(E)** The maximal photochemical efficiency of PSII ( $F_v/F_m$ ), PSII quantum yield  
853 ( $\Phi\text{PSII}$ ), and electron transport rate (ETR) were measured in Col-0 and  
854 *hy5-215* seedlings after 5 d of growth under light conditions and again after a  
855 3-h high light treatment.

856 **(F)** RT-qPCR analysis showing the relative expression of *ALB3*, *HCF136*, and  
857 *HHL1*. After growth for 5 d in growth light conditions (GL), Col-0 and *hy5-215*  
858 mutant seedlings were transferred to a 3-h high light (HL) treatment. The gene  
859 expression levels were normalized to that of ACTIN. Data are represented as  
860 mean  $\pm$  SEM. Asterisks represent statistically significant differences ( $*P <$   
861  $0.05$ ;  $**P < 0.01$ ;  $***P < 0.001$ ; Student's *t*-test). All experiments were repeated  
862 at least three times with similar results.

863

#### 864 **Figure 6. HY5 promotes the synthesis of thylakoid subunits.**

865 **(A)** Immunoblots showing D1 protein and other photosystem proteins isolated  
866 from etiolated WT Col-0 and *hy5-215* mutant seedlings during light-induced  
867 greening. Anti-Actin was used as a sample loading control.

868 **(B)** The relative abundance of PSII proteins was analyzed with Phoretix 1D  
869 Software (Phoretix International, UK). Data are represented as mean  $\pm$  SEM.  
870 Asterisks represent statistically significant differences ( $*P < 0.05$ ;  $**P < 0.01$ ;  
871  $***P < 0.001$ ; Student's *t*-test). All experiments were repeated at least three  
872 times with similar results.

873

874 **Figure 7. Proposed working model depicting how photoreceptor–HY5**  
875 **regulatory modules mediate PSII biogenesis and functional maintenance.**

876 During de-etiolation, light-induced HY5 directly binds to the promoter of  
877 *HCF173* or of other PSII-associated translation factor genes, thereby  
878 accelerating their expression and promoting the synthesis of PSII subunits and  
879 the biogenesis of the PSII complex. Under photodamaging conditions,  
880 light-induced HY5 directly binds to the promoters of PSII assembly and repair  
881 factor-related genes, including *HCF136*, *ALB3*, and *HHL1*, thereby accelerating  
882 their expression and promoting PSII assembly and repair and maintaining  
883 efficient photosynthesis.

884

885

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