SUPPORTING INFORMATION

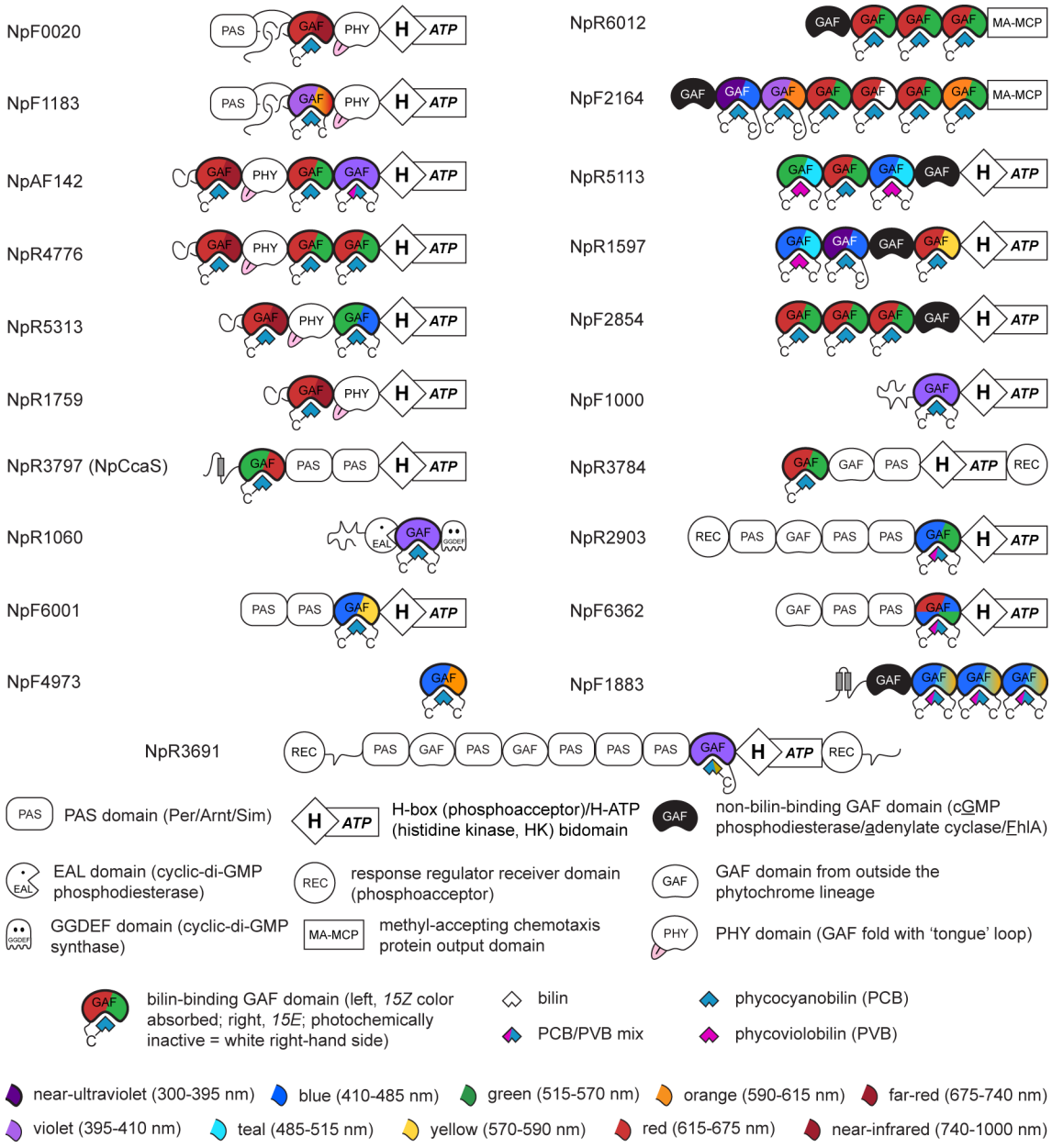

Figure S1. The phytochrome superfamily in Nostoc punctiforme. Jellybean domain architecture diagrams are shown for phytochromes and CBCRs of *N. punctiforme*. CBCR photocycles are color-coded as described in Note A and ref. [68].

Figure S2. Multiple sequence alignment of representative CBCRs. Representative DXCF (blue; teal-DXCF underlined) and red/green (red) CBCRs are aligned with known members of the NpR3784 group (brick red). The alignment spans the GAF β sheet, and the Asp-motif is highlighted in green. Key residues in the red/green CBCRs and NpR3784 group are highlighted (yellow and cyan, respectively). Accession details on members of the NpR3784 group are presented in Fig. 7.

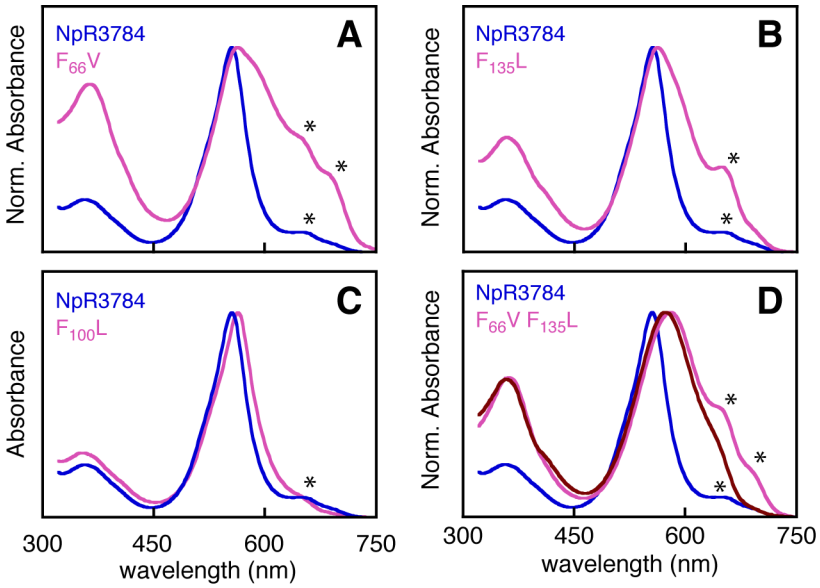

Figure S3. Comparison of 15E photoproducts formed by NpR3784 variants. (A) Normalized absorption spectra are shown for the *15E* photostates of wild-type (dark blue) and $F_{66}V$ (pink) NpR3784. (B) Normalized absorption spectra are shown for the *15E* photostates of wild-type (dark blue) and $F_{135}L$ (pink) NpR3784. (C) Normalized absorption spectra are shown for the *15E* photostates of wild-type (dark blue) and $F_{100}L$ (pink) NpR3784. (D) Normalized absorption spectra are shown for the *15E* photostates of wild-type (dark blue), $F_{66}V$ $F_{135}L$ (pink), and $F_{66}V$ $F_{100}L$ $F_{135}L$ (brick red) NpR3784. Asterisks indicate noncovalently bound and/or incompletely converted covalently bound *15Z* species.

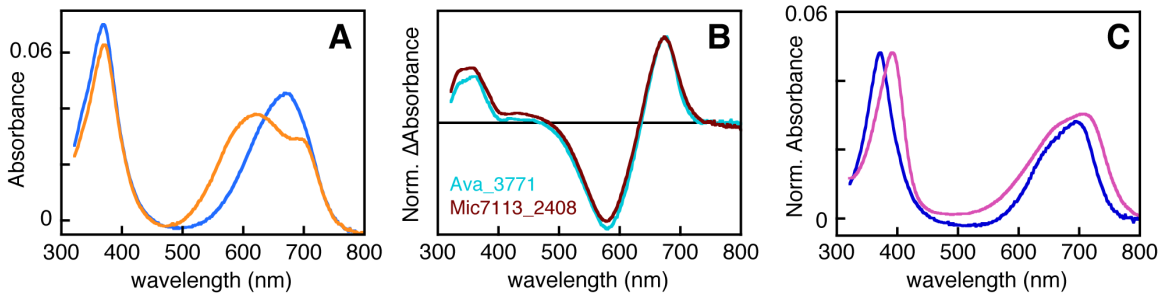

Figure S4. Denaturation analysis of Ava_3771. (A) Absorption spectra are shown for denatured Ava_3771 in the color scheme of Fig. 2. (B) Normalized photochemical difference spectra for denatured Ava_3771 (teal) and Mic7113_2408 (brick red) are shown. (C) To generate a denatured spectrum for the long-wavelength population of Ava_3771, the denatured difference spectra for Ava_3771 and Mic7113_2408 were used without normalization to calculate a scaling factor for the relative amounts of photochemically active PCB present in the two protein preparations. The absorption spectrum of denatured *15Z* Mic7113_2408 was scaled using this factor and subtracted from the absorption spectrum of Ava_3771 to generate a denatured spectrum for the long-wavelength population (dark blue; peaks at 372, 694 nm). The absorption spectrum for denatured *15Z* DrBphP (pink; peaks at 392, 708 nm) is shown for comparison.

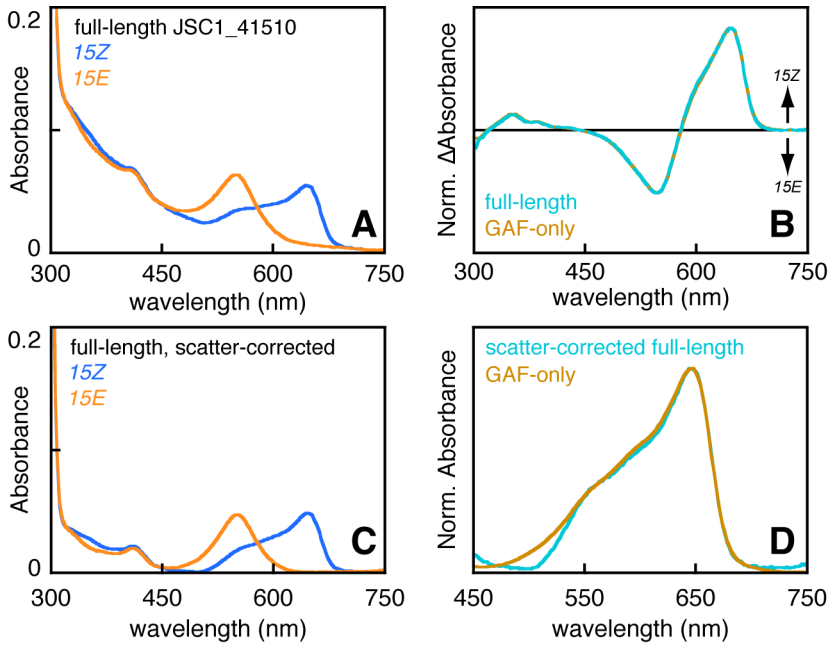

Figure S5. Characterization of full-length JSC1-41510. (A) Absorption spectra are shown for full-length JSC1_41510 in the color scheme of Fig. 2. (B) Normalized photochemical difference spectra are shown for GAF-only (brown) and full-length (teal) JSC1_41510. (C) Absorption spectra are shown for full-length JSC1_41510 after scatter correction. (D) Normalized absorption spectra are shown for GAF-only (brown) and scatter-corrected full-length (sea foam green) JSC1_41510 in the *15Z* photostate.

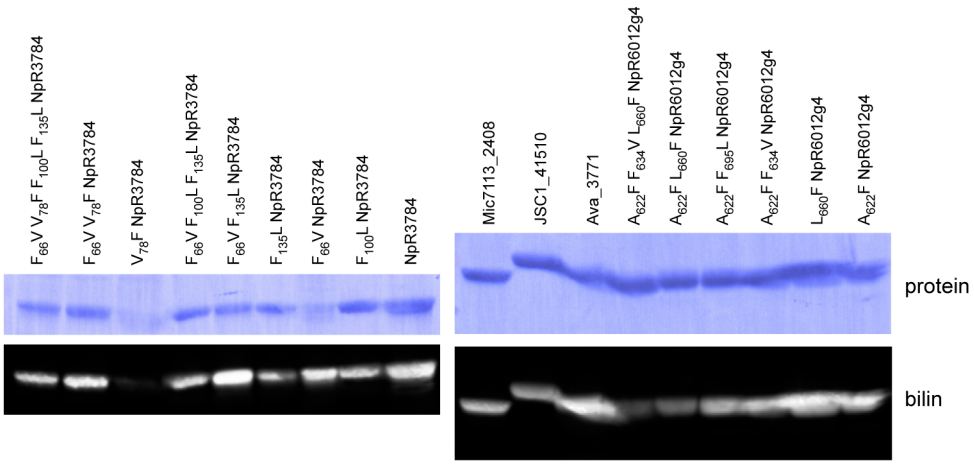

Figure S6. Characterization of purified CBCRs. The indicated proteins were characterized by SDS-PAGE and transfer to PVDF membranes, followed by amido black staining (top) and zinc blotting (bottom).

Table S1: Known cyanobacterial genomes containing members of the NpR3784 group.

Organism	GenBank Assembly ID
Nostoc punctiforme ATCC 29133 (= PCC 73102)	GCA_000020025.1
Nostoc sp. strain PCC 7524	GCA_000316645.1
Nostoc sp. 152 (= sp. strain PCC 9237/1)[1]	KC699835
Anabaena variabilis ATCC 29413	GCA_000204075.1
Cyanothece sp. strain PCC 7424	GCA_000021825.1
Cyanothece sp. strain PCC 7425	GCA_000022045.1
Cyanothece sp. strain PCC 7822	GCA_000147335.1
Chroococcidiopsis thermalis PCC 7203	GCA_000317125.1
Leptolyngbya sp. strain JSC-1	GCA_000733415.1
Gloeocapsa sp. strain PCC 7428	GCA_000317555.1
Coleofasciculus chthonoplastes PCC 7420	GCA_000155555.1
Microcoleus sp. strain PCC 7113	GCA_000317515.1
Scytonema hofmanni PCC 7110	GCA_000346485.1
Calothrix sp. strain PCC 7103	GCA_000331305.1
Oscillatoria sp. strain PCC 10802	GCA_000332335.1

1. Accession for nucleotide fragment, not genome assembly.