Tables S1 and S2 [dataset]

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Description
Table S1. Genes encoding subunits of Photosystem I (PS I), Photosystem II (PS II), and phycobilisomes (PBS) and related proteins in strain JSC-1. The table shows transcript ratios for the listed genes for cells grown in far-red light for 24 hours compared to transcript levels for cells grown in white light. The table also shows those proteins that were identified by tryptic peptide LC-MS/MS analysis in gradient fractions containing PS I, PS II, and PBS from cells grown in red light and far-red light. An “unused peptide” score of 1.3 indicates at least 95% confidence for a positive identification, and a score greater than 2.0 indicates a 99% confidence for a positive identification. The pink (PS I), green (PS II) and blue (PBS) shading identifies the genes (proteins) for core components that are encoded in the 21-gene photosynthesis cluster shown in Fig. S2. Phycobiliproteins were low-abundance contaminants of fractions #1 and #2 containing PS I and PS II or PS I trimers (see Fig. 4). The composition data for PBS are more accurately reflected from the data for isolated PBS from cells grown in 645-nm light or 710-nm light. Table S2. Complete transcription profiling data for transcripts for strain JSC-1 cells grown in white light and far-red light. Cells were grown in white light to an OD750 nm = 0.3 and were then transferred to far-red light for 24 hours prior to isolation of RNA from each condition. For additional details, see SOM, Materials and Methods.

Citation
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Related publication
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