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## SUPPLEMENTARY INFORMATION

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### **Combined pigment and metatranscriptomic analysis reveals highly synchronized diel patterns of phenotypic light response across domains in the open oligotrophic ocean**

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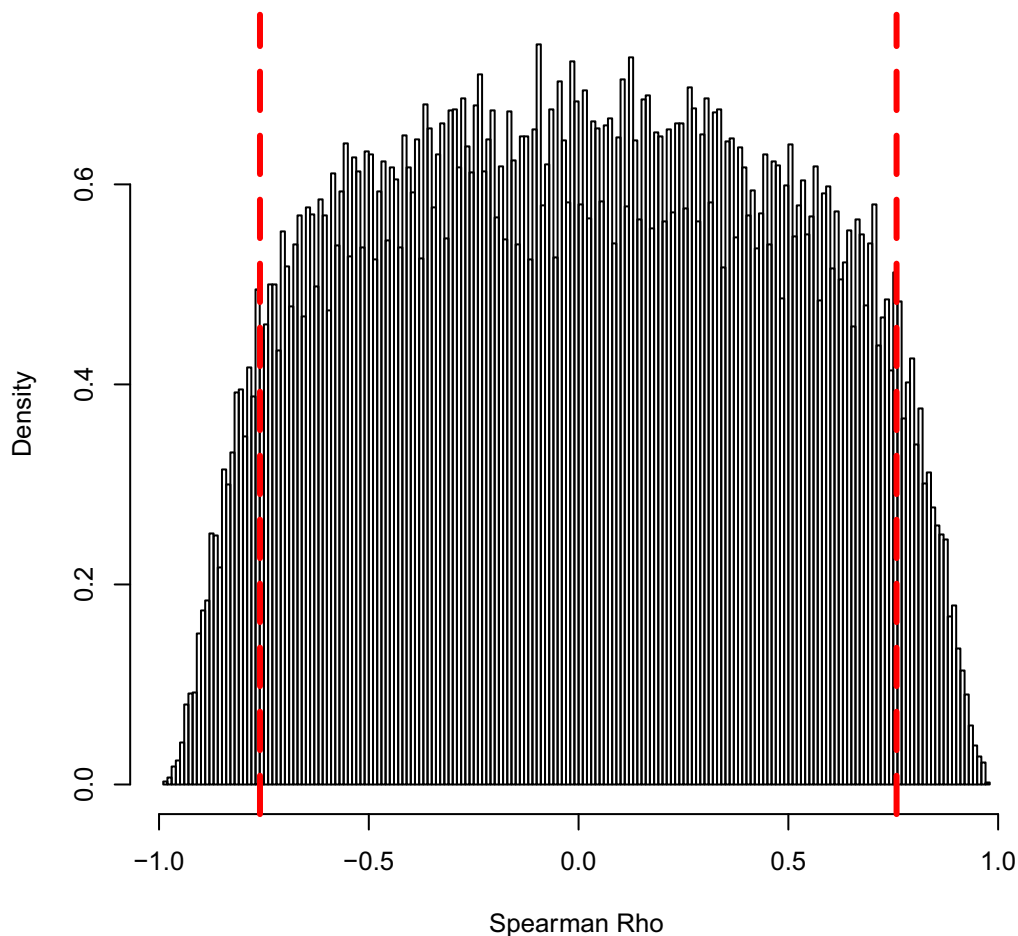
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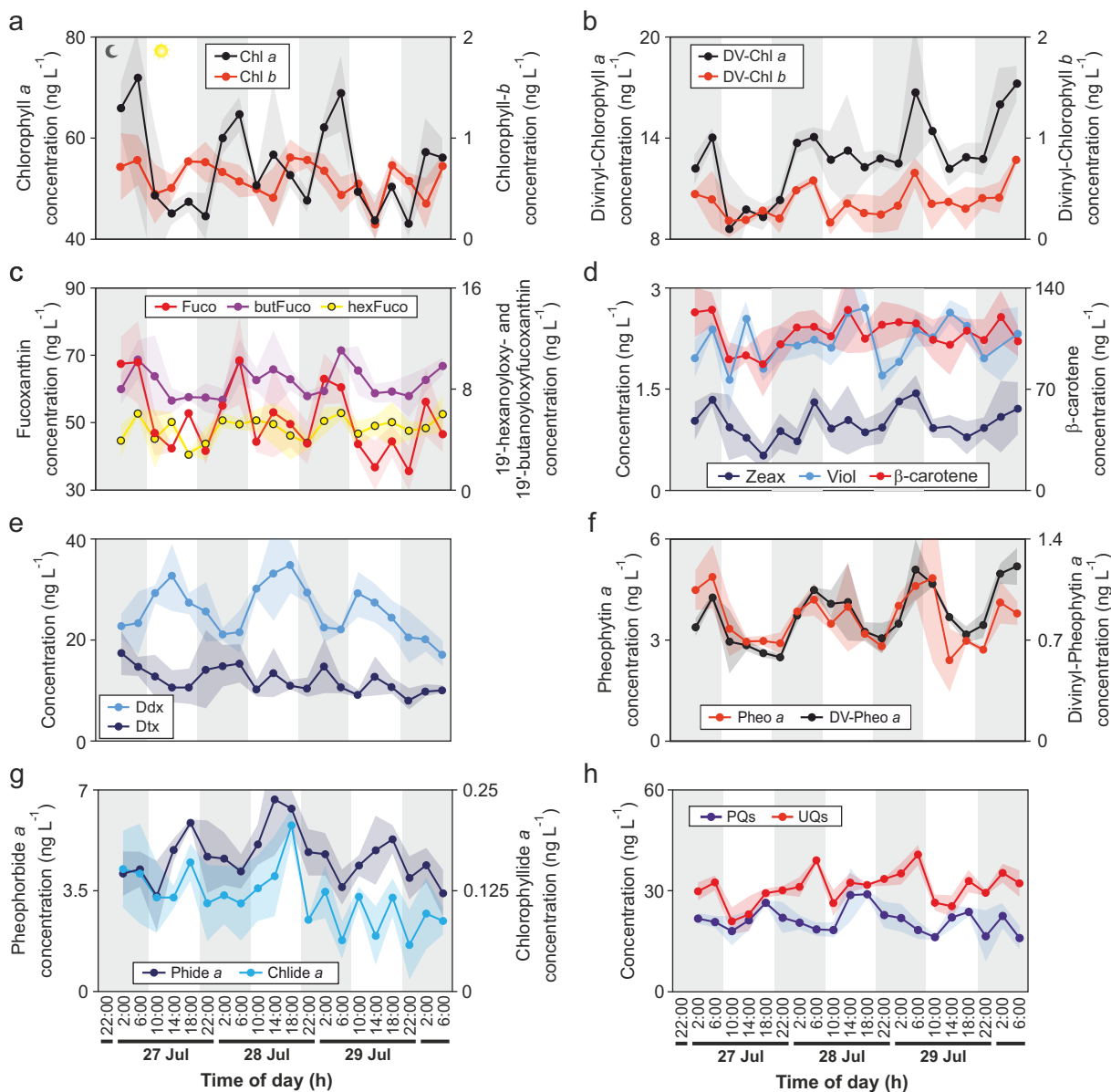
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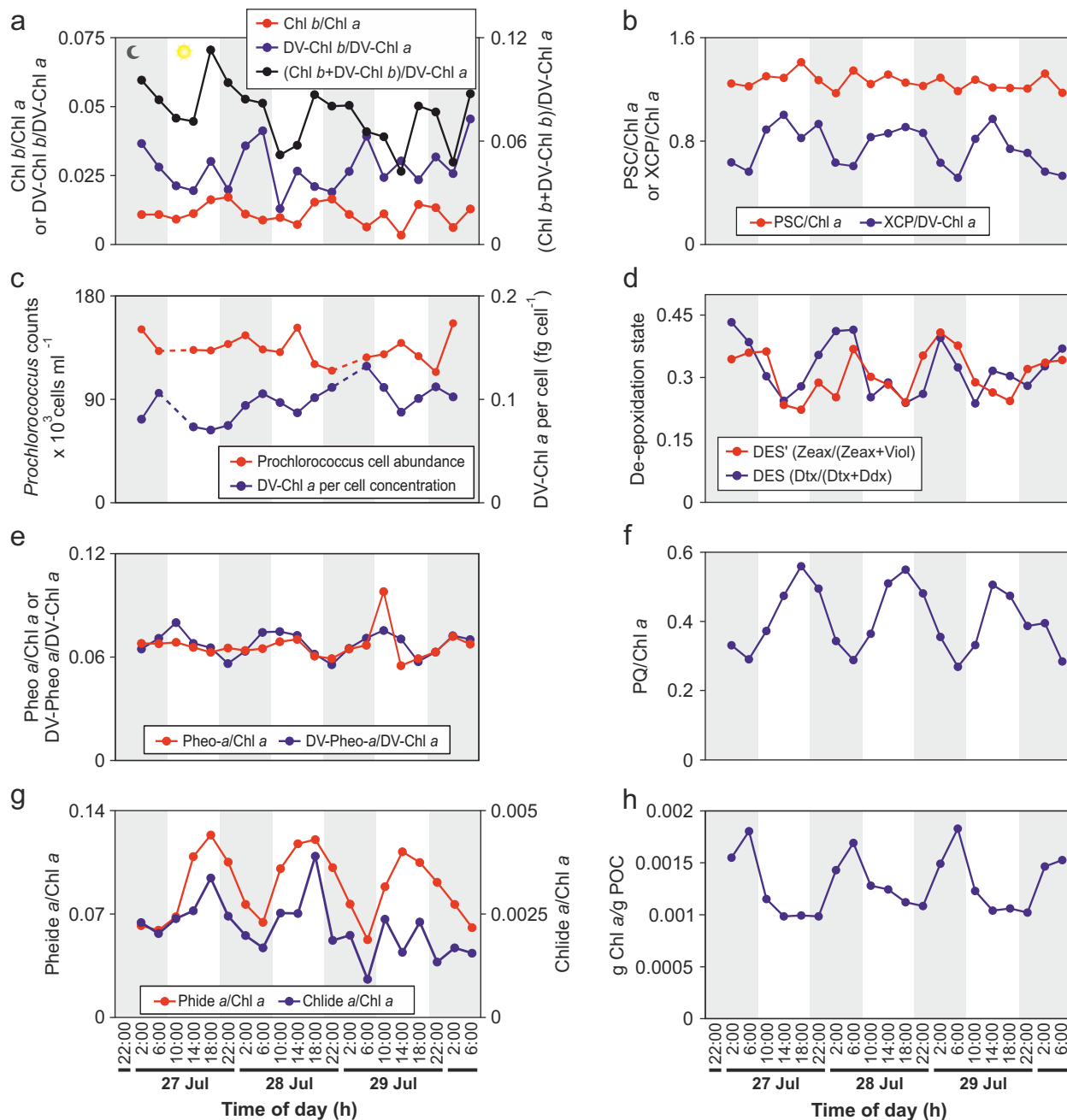
## Transcript and Lipid Synthetic Time Series Correlations



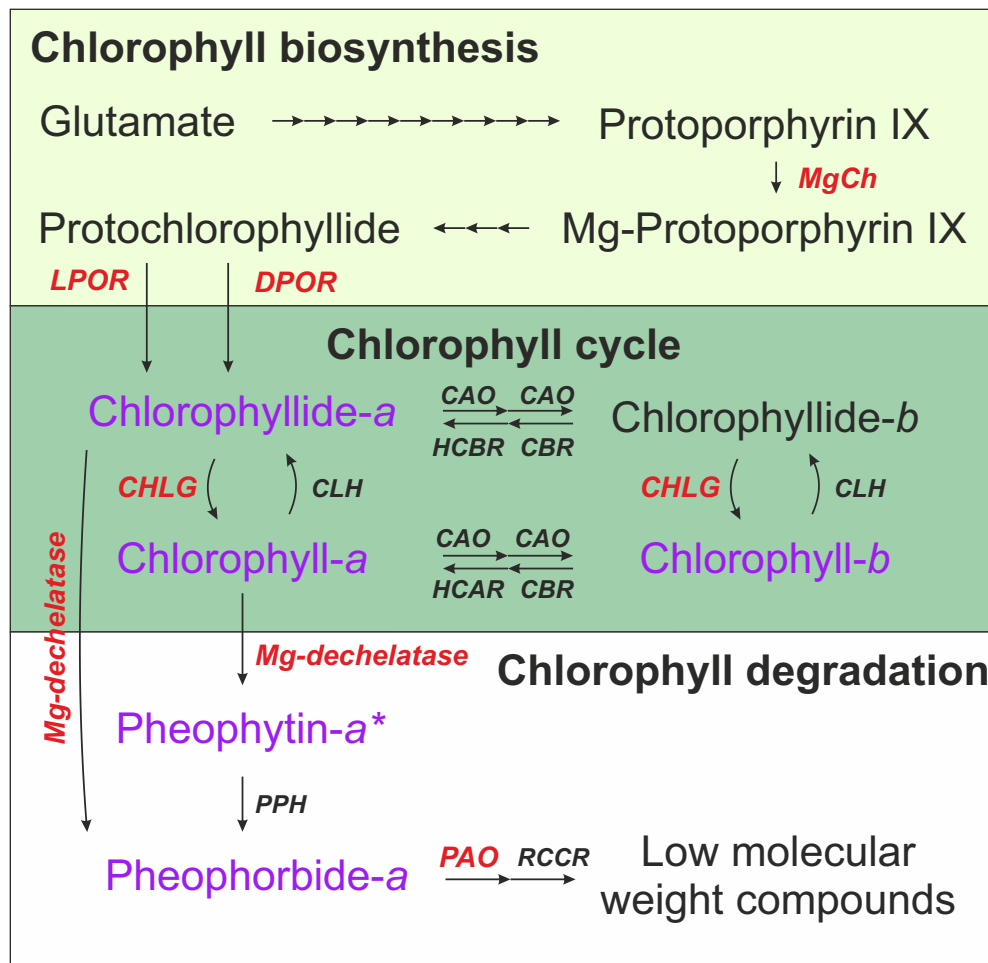
**Figure S1.** Histogram of simulated spearman's rho values for independently generated synthetic time series. 100,000 time series were simulated by bootstrap sampling from the distribution of observed lag 1 differences in transcript and lipid time series and cumulatively summing them. The spearman's rho was then calculated between 100,000 randomly chosen pairs from amongst these synthetic time series to simulate the probability density function of spearman's rho values between iid random walks (shown here) using the distribution of step sizes from the data. Red dashed lines indicate the 5th and 95<sup>th</sup> percentiles.



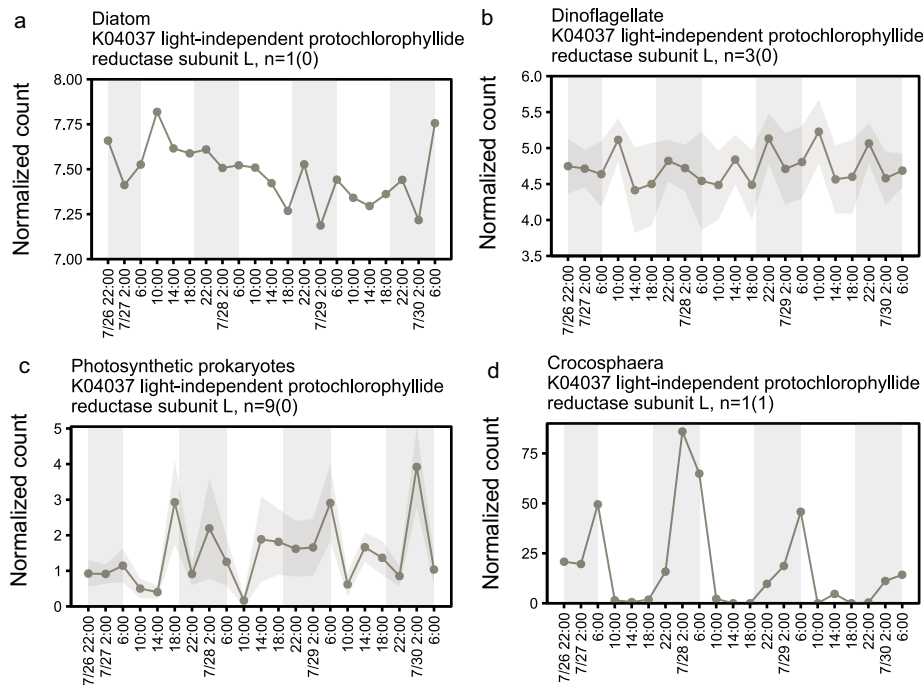
**Figure S2.** Diel variations of concentrations of **a** Chl *a* and *b*, **b** DV-Chl *a* and *b*, **c** Fuco, butFuco, and hexFuco, **d** Zeax, Viol, and  $\beta$ -carotene, **e** Ddx and Dtx, **f** Pheo *a* and DV-Pheo *a*, **g** Phide *a* and Chlide *a*, **h** PQs and UQs over 4 day/night cycles at 15m water depth in July and August 2015 at Station ALOHA. Values represent the average of environmental triplicates and shaded envelope the standard deviation ( $n=3$ ). Gray bars indicates night while white indicates day. Chl, chlorophyll; DV-Chl, divinyl chlorophyll; Fuco, fucoxanthin; butFuco, 19'-butanoyloxyfucoxanthin; hexFuco, 19'-hexanoyloxyfucoxanthin; Zeax, zeaxanthin; Viol, violaxanthin; Ddx, diadinoxanthin; Dtx, diatoxanthin; Pheo, pheophytin; DV-Pheo, divinyl pheophytin; Phide, pheophorbide; Chlide, chlorophyllide; PQs, plastoquinones; UQs, ubiquinones.



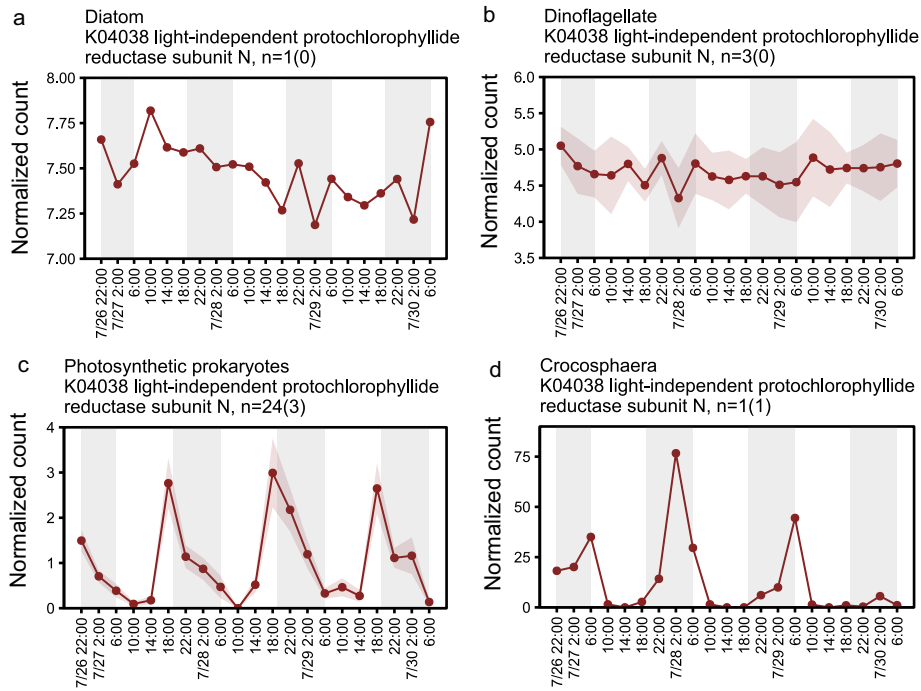
**Figure S3.** Diel variations of **a** Chl *b*/Chl *a*, DV-Chl *b*/DV-Chl *a* and (Chl *b*+DV-Chl *b*)/DV-Chl *a* **b** PSC/Chl *a* and XCP/Chl *a*, **c** *Prochlorococcus* cell abundance and DV-Chl *a* per cell concentrations, **d** De-epoxidation states of xanthophyll cycle pigments, **e** Pheo *a*/Chl *a* and DV-Pheo *a*/DV-Chl *a*, **f** PQ/Chl *a*, **g** Pheide *a*/Chl *a* and Chlide *a*/Chl *a*, and **h** g Chl *a*/g POC over 4 day/night cycles at 15m water depth in July and August 2015 at Station ALOHA. Chl, chlorophyll; DV-Chl, divinyl chlorophyll; PSC, photosynthetic pigments; XCP, xanthophyll cycle pigments; Zeax, zeaxanthin; Viol, violaxanthin; Ddx, diadinoxanthin; Dtx, diatoxanthin; DES, de-epoxidation state; Pheo, pheophytin; DV-Pheo, divinyl pheophytin; Phide, pheophorbide; Chlide, chlorophyllide; PQs, plastoquinones.



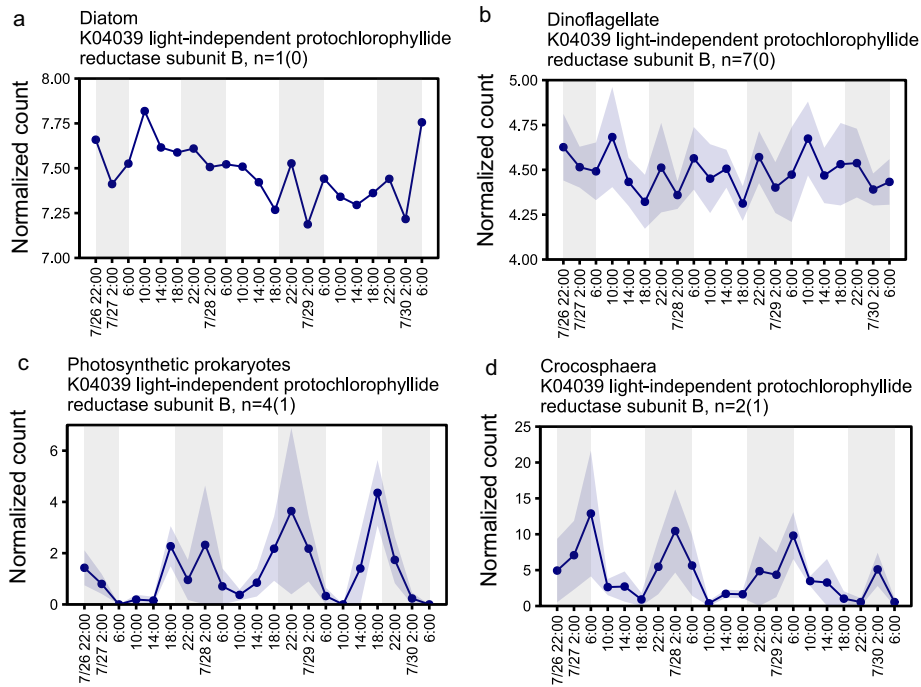
**Figure S4.** Schematic representation of chlorophyll metabolic pathways modified after [1], [2] and [3]. Only the main intermediates and enzyme names relevant for this study are shown. Pigment molecules detected in this study are highlighted in blue. Genes (italicized) shown or discussed in this study are highlighted in red. Abbreviations: MgCh, Mg-chelatase; LPOR, light-dependent protochlorophyllide oxidoreductase; DPOR, light-independent protochlorophyllide oxidoreductase; CHLG, chlorophyll synthase; CLH, chlorophyllase; CAO, chlorophyll(ide) a oxygenase; HCAR, hydroxymethyl chlorophyll a reductase; CBR, chlorophyll(ide) b reductase; PPH, Pheophytinase; PAO, pheophorbide a oxygenase; RCCR, red chlorophyll catabolite reductase. \*Pheophytin is not only an intermediate of chlorophyll breakdown, but also a metabolic endproduct, which is involved in the electron transport in PSII.



**Figure S5.** Averaged normalized expression patterns for genes involved in light-independent chlorophyll biosynthesis (*chlL*) across the sampling period for **a** diatoms, **b** dinoflagellates, **c** photosynthetic prokaryotes, and **d** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.

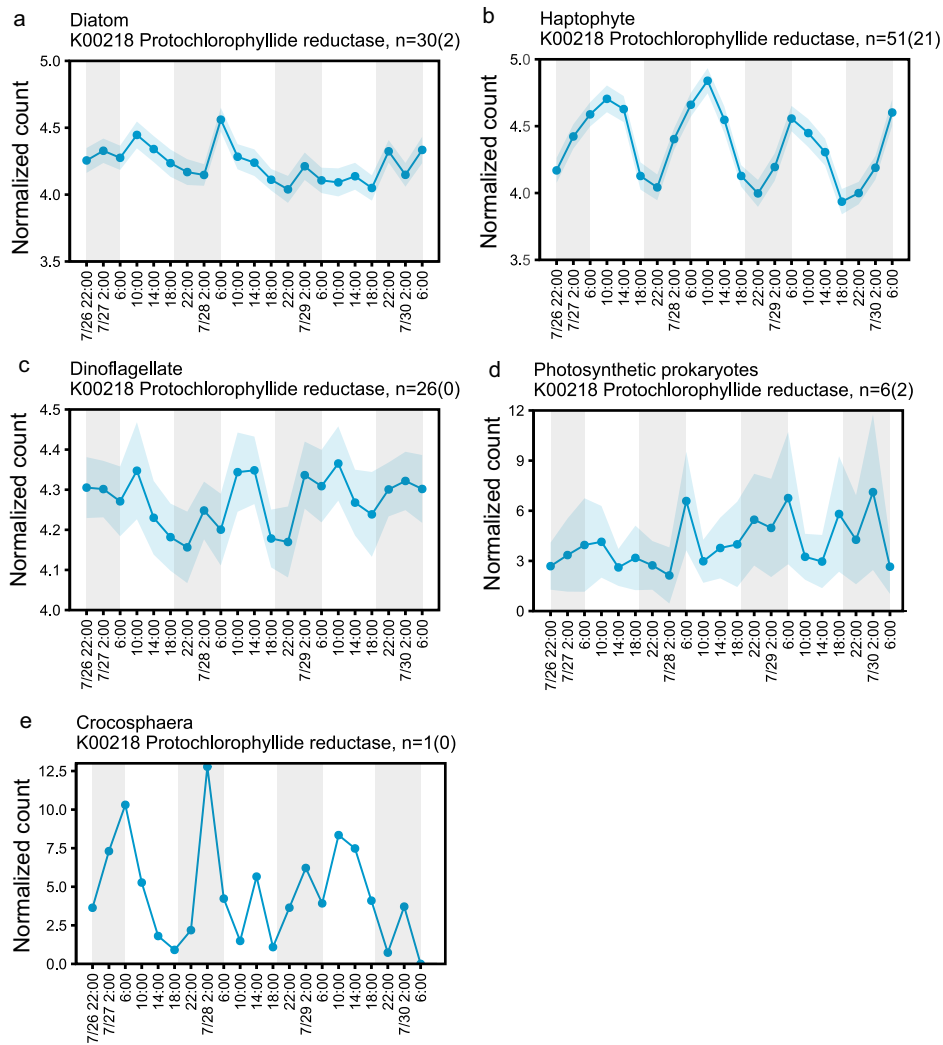


**Figure S6.** Averaged normalized expression patterns for genes involved in light-independent chlorophyll biosynthesis (*chlN*) across the sampling period for **a** diatoms, **b** dinoflagellates, **c** photosynthetic prokaryotes, and **d** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.

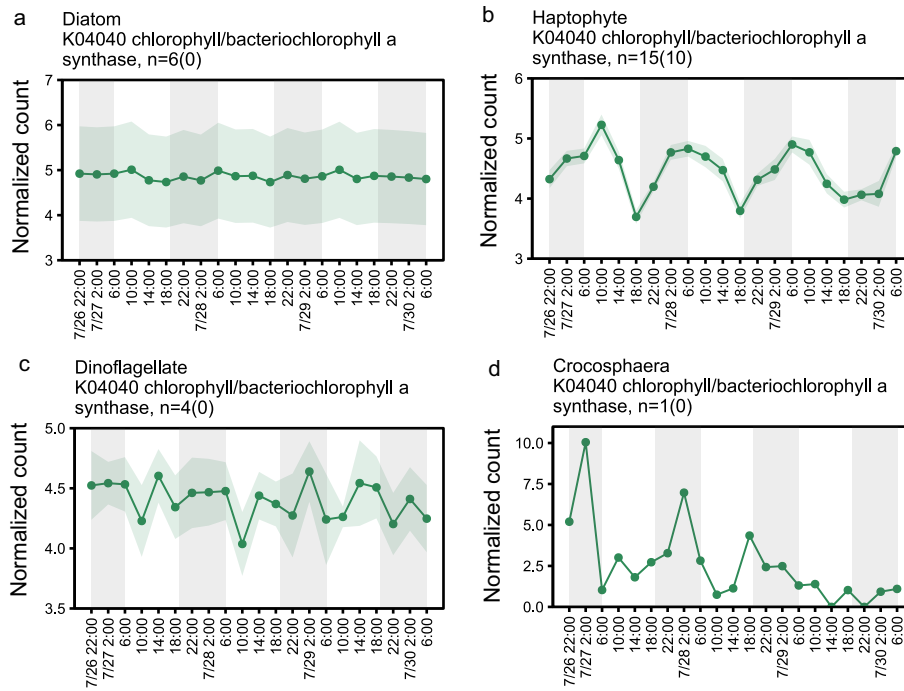


**Figure S7.** Averaged normalized expression patterns for genes involved in light-independent chlorophyll biosynthesis (*chlB*) across the sampling period for **a** diatoms, **b** dinoflagellates, **c** photosynthetic prokaryotes, and **d** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.

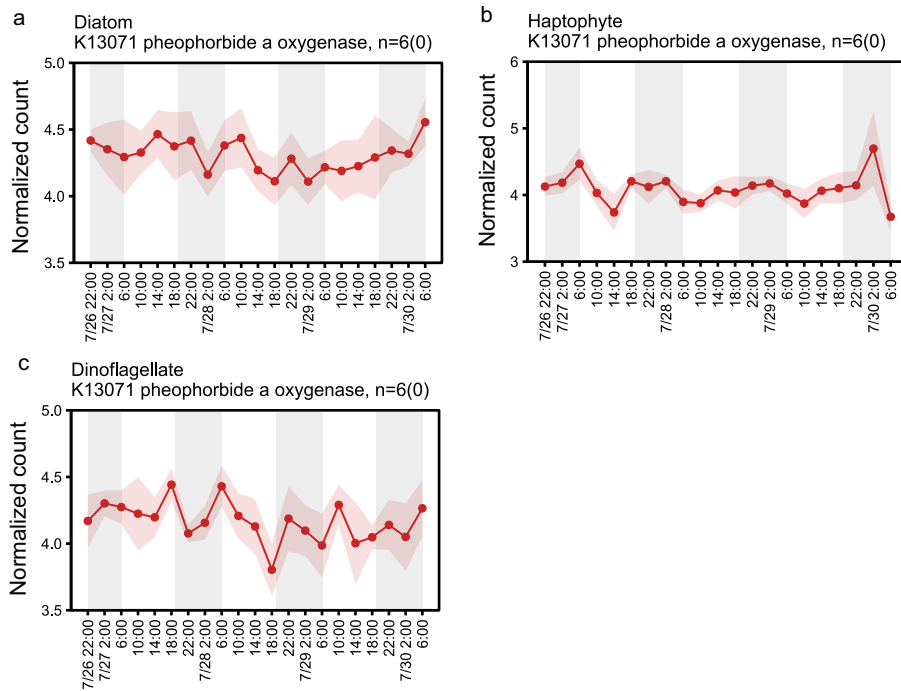




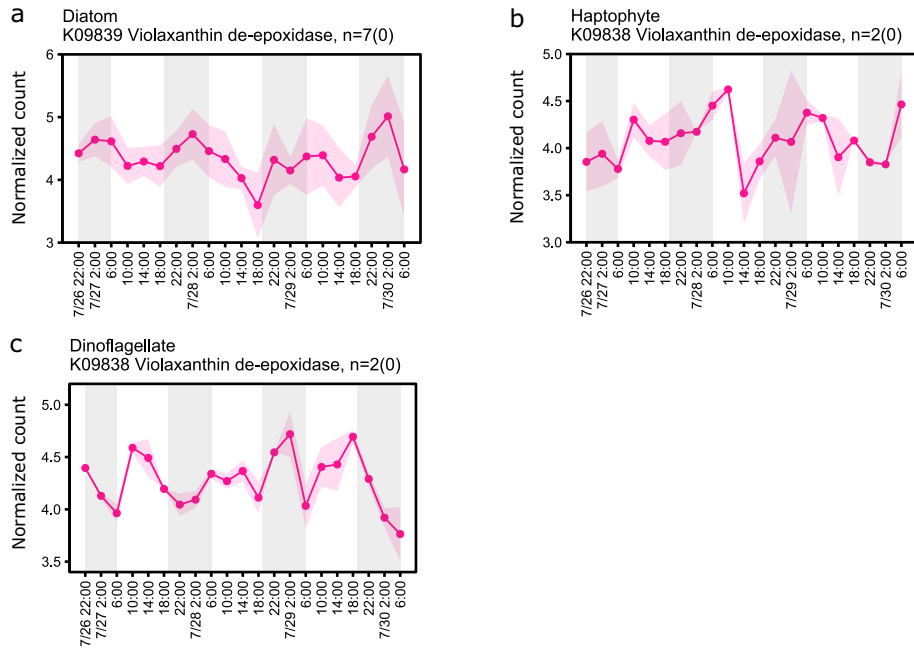
**Figure S8.** Averaged normalized expression patterns for genes involved in light-dependent chlorophyll biosynthesis across the sampling period for **a** diatoms, **b** haptophytes, **c** dinoflagellates, **d** photosynthetic prokaryotes, and **e** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.



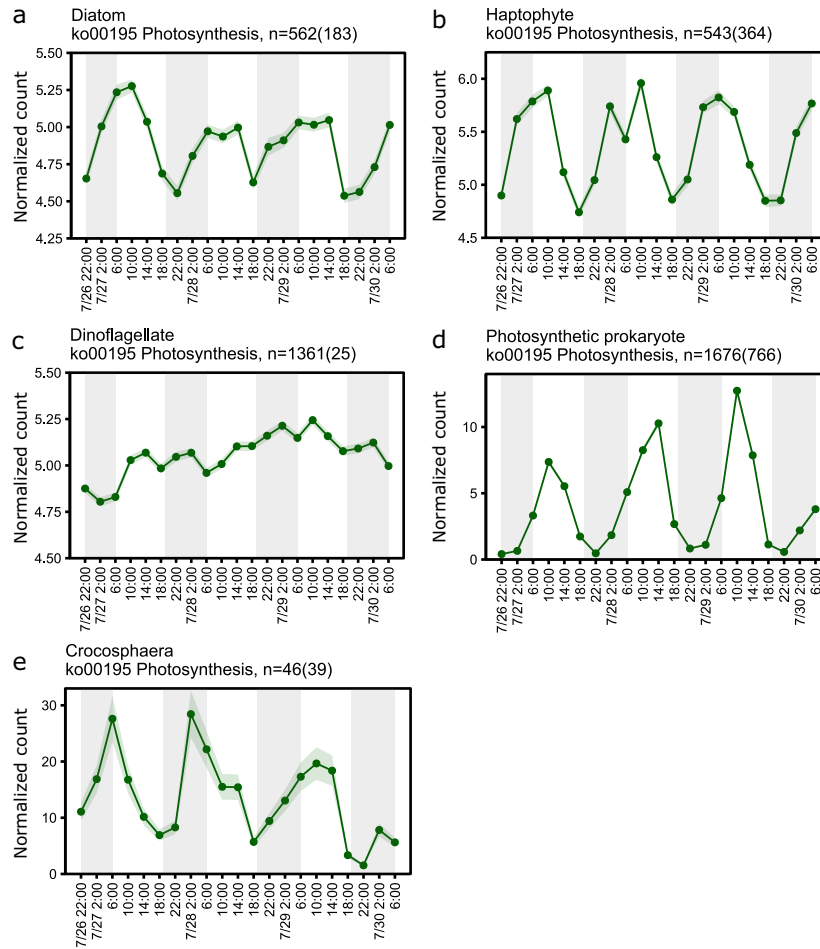
**Figure S9.** Averaged normalized expression patterns for genes involved in the final step of chlorophyll biosynthesis across the sampling period for **a** diatoms, **b** haptophytes, **c** dinoflagellates, and **d** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses



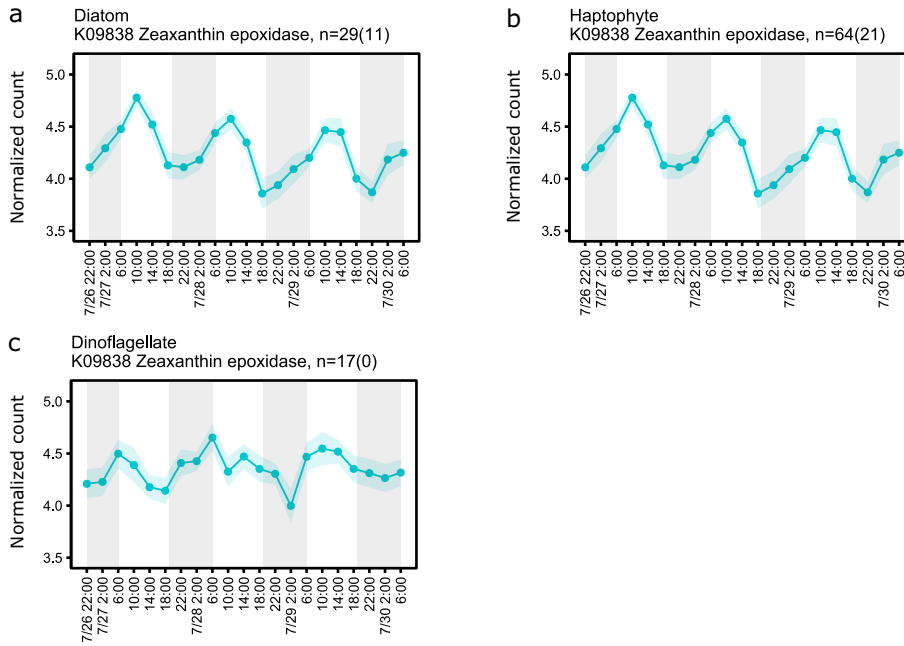
**Figure S10.** Averaged normalized expression patterns for genes involved in chlorophyll breakdown across the sampling period for **a** diatoms, **b** haptophytes, and **c** dinoflagellates. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.



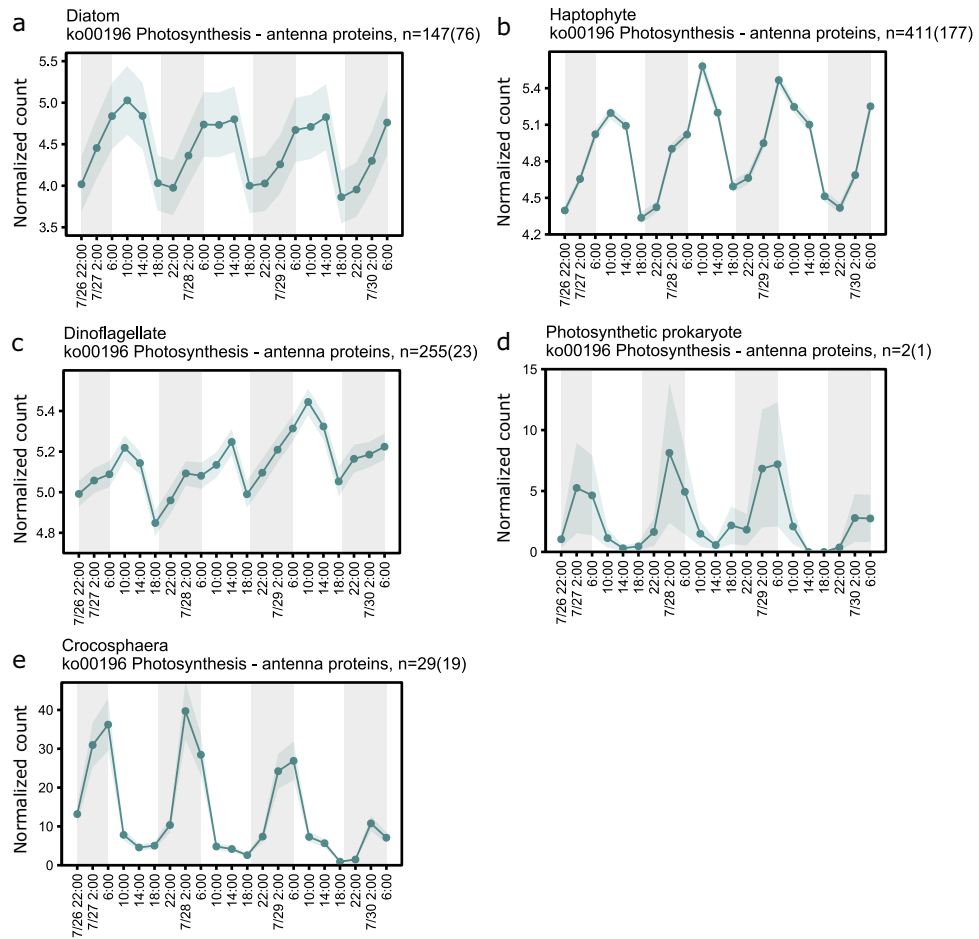
**Figure S11.** Averaged normalized expression patterns for genes involved in xanthophyll de-epoxidation across the sampling period for **a** diatoms, **b** haptophytes, and **c** dinoflagellates. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN,  $FDR \leq 0.05$ ) genes in parentheses.



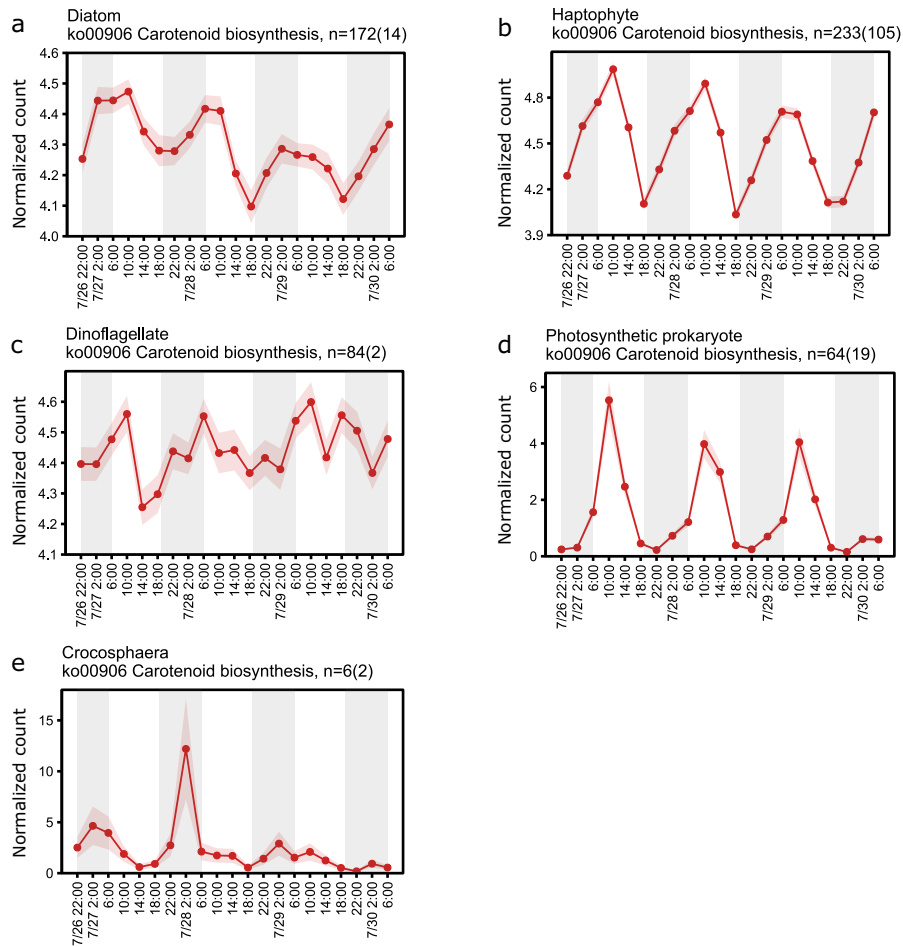
**Figure S12.** Averaged normalized expression patterns for genes within the KEGG Photosynthesis pathway (ko00195) across the sampling period for **a** diatoms, **b** haptophytes, **c** dinoflagellates, **d** photosynthetic prokaryotes, and **e** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.



**Figure S13.** Averaged normalized expression patterns for genes involved in xanthophyll epoxidation across the sampling period for **a** diatoms, **b** haptophytes, and **c** dinoflagellates. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.

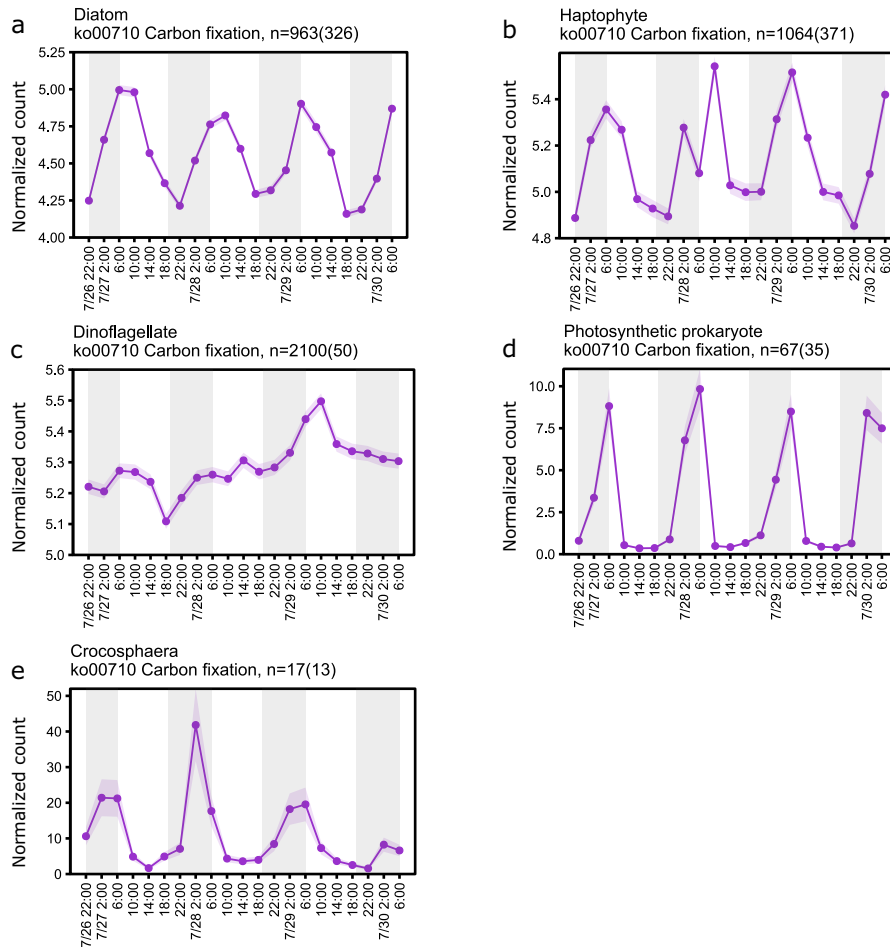


**Figure S14.** Averaged normalized expression patterns for genes within the KEGG Photosynthesis - antenna proteins pathway (ko00196) across the sampling period for **a** diatoms, **b** haptophytes, **c** dinoflagellates, **d** photosynthetic prokaryotes, and **e** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.

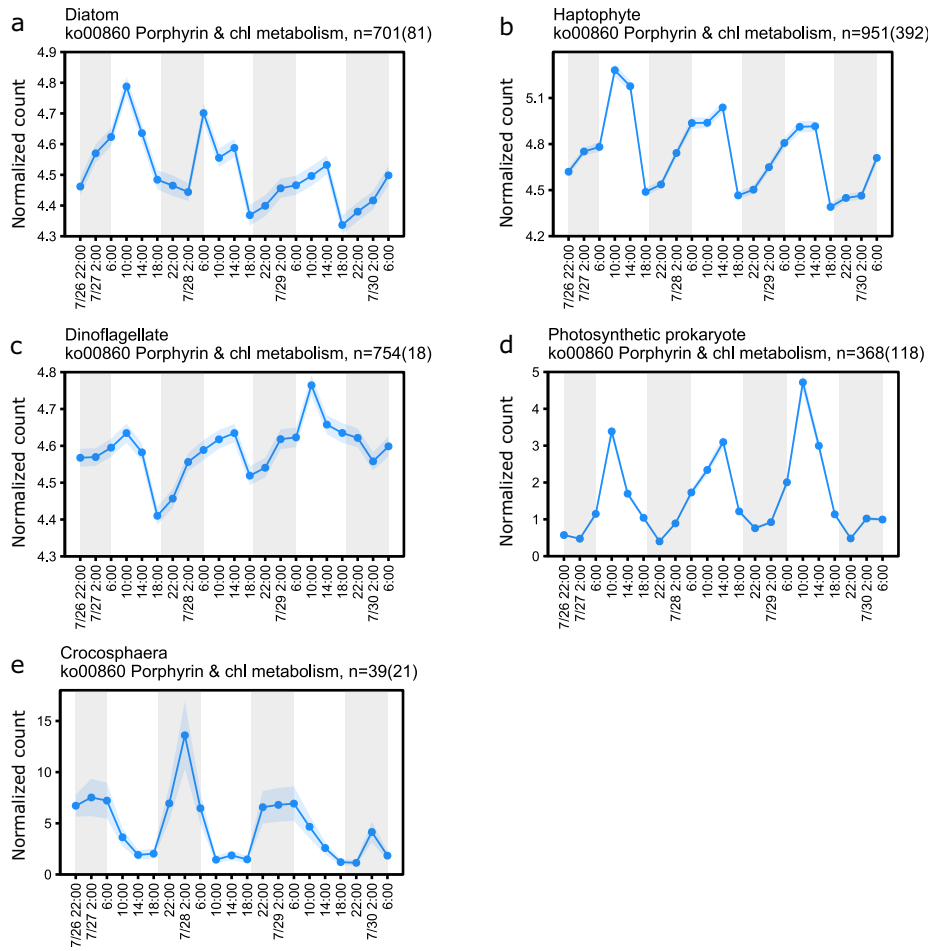


**Figure S15.** Averaged normalized expression patterns for genes within the KEGG Carotenoid biosynthesis pathway (ko00906) across the sampling period for **a** diatoms, **b** haptophytes, **c** dinoflagellates, **d** photosynthetic prokaryotes, and **e** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.



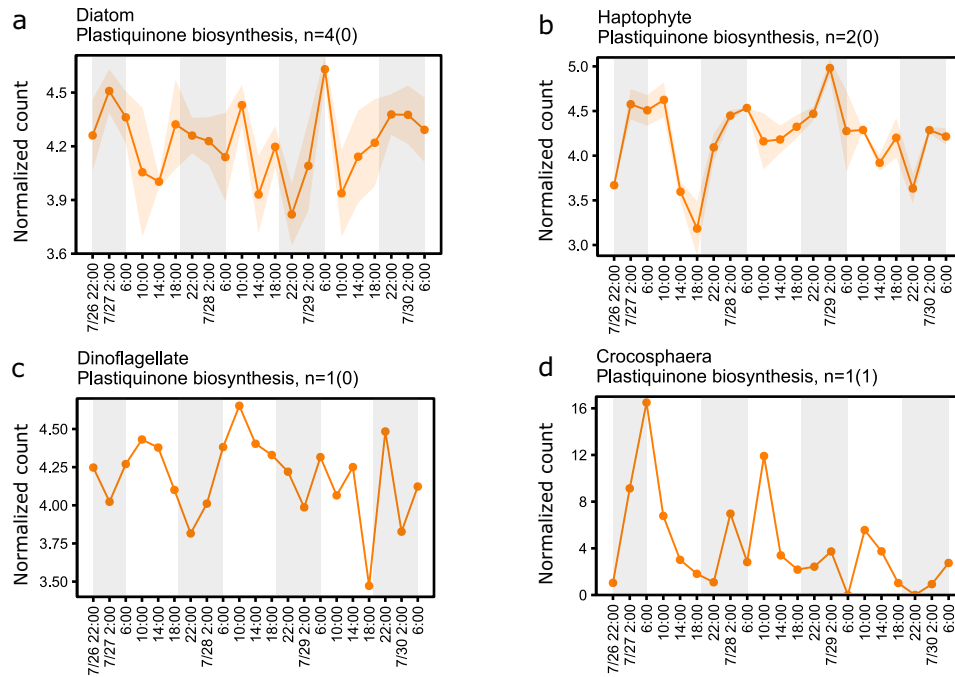


**Figure S16.** Averaged normalized expression patterns for genes within the KEGG Carbon fixation in photosynthetic organisms pathway (ko00710) across the sampling period for **a** diatoms, **b** haptophytes, **c** dinoflagellates, **d** photosynthetic prokaryotes, and **e** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.

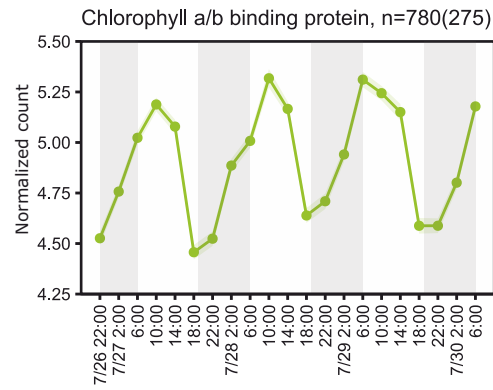


**Figure S17.** Averaged normalized expression patterns for genes within the KEGG Porphyrin and chlorophyll metabolism pathway (ko00860) across the sampling period for **a** diatoms, **b** haptophytes, **c** dinoflagellates, **d** photosynthetic prokaryotes, and **e** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.





**Figure S19.** Averaged normalized expression patterns for genes within the KEGG Ubiquinone and other terpenoid-quinone biosynthesis pathway (ko00130) which are involved in plastiquinone biosynthesis across the sampling period for **a** diatoms, **b** haptophytes, **c** dinoflagellates, **d** *Crocosphaera*. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes represented within each figure is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.



**Figure S20.** Averaged normalized expression patterns of chlorophyll a/b binding protein genes (ko08907-08917 and ko14172) in eukaryotes. Shaded envelope is the standard error of the mean. Gray bars indicates night while white indicates day. The number of genes is displayed in the heading with the number of significantly periodic (RAIN, FDR  $\leq 0.05$ ) genes in parentheses.

**References**

1. Vavilin D, Vermaas W. Continuous chlorophyll degradation accompanied by chlorophyllide and phytol reutilization for chlorophyll synthesis in *Synechocystis* sp. PCC 6803. *Biochim Biophys Acta* 2007; 1767: 920–929.
2. Ohmiya A, Hirashima M, Yagi M, Tanase K, Yamamizo C. Identification of Genes Associated with Chlorophyll Accumulation in Flower Petals. *PLoS One* 2014; 9: e113738.
3. Tanaka R, Tanaka A. Chlorophyll cycle regulates the construction and destruction of the light-harvesting complexes. *Biochim Biophys Acta* 2011; 1807: 968–976.