Supplemental Table and Figures

Table S1 Sequencing results detailing type of sequencing conducted, collection time, volume filtered per sample (liters), number of reads sequenced per sample, and the number of reads after trimming which were used for subsequent analysis.

Sample	SeqType	Date	Time	Volume Filtered [L]	Reads	Trimmed
SM001	Selected	26-Jul-15	22:00	18.5	82,804,818	80,868,600
SM002	Selected	27-Jul-15	2:00	20.0	104,412,586	102,065,024
SM003	Selected	27-Jul-15	6:00	19.0	95,321,226	93,338,226
SM004	Selected	27-Jul-15	10:00	19.0	101,136,891	98,987,416
SM005	Selected	27-Jul-15	14:00	19.0	91,209,079	89,152,418
SM006	Selected	27-Jul-15	14:00	19.5	84,332,817	82,459,267
SM007	Selected	27-Jul-15	14:00	20.0	84,649,327	82,770,017
SM008	Selected	27-Jul-15	18:00	19.0	77,185,948	76,157,781
SM009	Selected	27-Jul-15	22:00	19.0	71,403,462	70,265,212
SM010	Selected	28-Jul-15	2:00	20.0	90,686,522	89,385,823
SM011	Selected	28-Jul-15	6:00	19.0	71,052,838	70,077,820
SM012	Selected	28-Jul-15	10:00	19.5	85,443,334	83,990,646
SM013	Selected	28-Jul-15	14:00	19.0	91,287,548	90,174,268
SM014	Selected	28-Jul-15	14:00	19.0	82,959,687	81,784,036
SM015	Selected	28-Jul-15	14:00	20.0	77,105,700	75,833,575
SM016	Selected	28-Jul-15	18:00	19.0	100,054,397	98,675,685
SM017	Selected	28-Jul-15	22:00	19.5	80,015,073	78,875,883
SM018	Selected	29-Jul-15	2:00	20.0	80,508,121	79,402,387
SM019	Selected	29-Jul-15	6:00	19.5	97,723,236	96,416,134
SM020	Selected	29-Jul-15	10:00	19.5	99,883,736	97,936,288
SM021	Selected	29-Jul-15	14:00	15.0	96,373,025	94,638,953
SM022	Selected	29-Jul-15	14:00	18.5	103,302,918	100,929,460
SM023	Selected	29-Jul-15	14:00	17.5	99,055,311	97,500,687
SM024	Selected	29-Jul-15	18:00	18.5	82,011,783	80,787,557
SM025	Selected	29-Jul-15	22:00	19.0	92,091,844	90,638,583
SM026	Selected	30-Jul-15	2:00	19.5	90,895,258	89,302,208
SM027	Selected	30-Jul-15	6:00	20.5	75,012,386	73,971,764
SM058	Unselected	26-Jul-15	22:00	18.5	74,540,622	72,160,026
SM059	Unselected	27-Jul-15	2:00	20.0	86,358,595	83,636,076
SM060	Unselected	27-Jul-15	6:00	19.0	75,257,788	73,018,472
SM061	Unselected	27-Jul-15	10:00	19.0	72,991,024	70,971,759
SM062	Unselected	27-Jul-15	14:00	19.0	73,221,112	71,151,117
SM063	Unselected	27-Jul-15	14:00	19.5	79,961,867	77,677,292
SM064	Unselected	27-Jul-15	14:00	20.0	83,949,968	81,343,374
SM065	Unselected	27-Jul-15	18:00	19.0	72,412,581	70,526,818
SM066	Unselected	27-Jul-15	22:00	19.0	75,376,085	73,532,572
SM067	Unselected	28-Jul-15	2:00	20.0	78,755,369	76,252,256
SM068	Unselected	28-Jul-15	6:00	19.0	68,593,488	66,271,491
SM069	Unselected	28-Jul-15	10:00	19.5	68,000,244	65,942,879
SM070	Unselected	28-Jul-15	14:00	19.0	81,040,846	78,694,156
SM071	Unselected	28-Jul-15	14:00	19.0	68,243,422	65,993,473
SM072	Unselected	28-Jul-15	14:00	20.0	73,252,707	70,920,519
SM073	Unselected	28-Jul-15	18:00	19.0	67,006,815	64,845,754
SM074	Unselected	28-Jul-15	22:00	19.5	72,409,848	70,096,636
SM075	Unselected	29-Jul-15	2:00	20.0	64,544,561	62,300,869
SM076	Unselected	29-Jul-15	6:00	19.5	71,849,541	69,420,309
SM077	Unselected	29-Jul-15	10:00	19.5	68,078,147	65,471,742
SM078	Unselected	29-Jul-15	14:00	15.0	79,561,871	76,737,855
SM079	Unselected	29-Jul-15	14:00	18.5	72,277,327	69,748,299
SM080	Unselected	29-Jul-15	14:00	17.5	84,657,570	81,819,135
SM081	Unselected	29-Jul-15	18:00	18.5	62,659,289	60,038,409
SM082	Unselected	29-Jul-15	22:00	19.0	73,364,717	70,718,059
SM083	Unselected	30-Jul-15	2:00	19.5	71,056,308	68,421,257
SM084	Unselected	30-Jul-15	6:00	20.5	74,987,106	72,365,506

Figure S1 Scale independence and mean connectivity plots of variance stabilized count data for *Rhizosolenia* and *Richelia* transcript abundances. A soft-thresholding power of 7 was chosen for construction of gene networks and identifying modules for WGCNA.

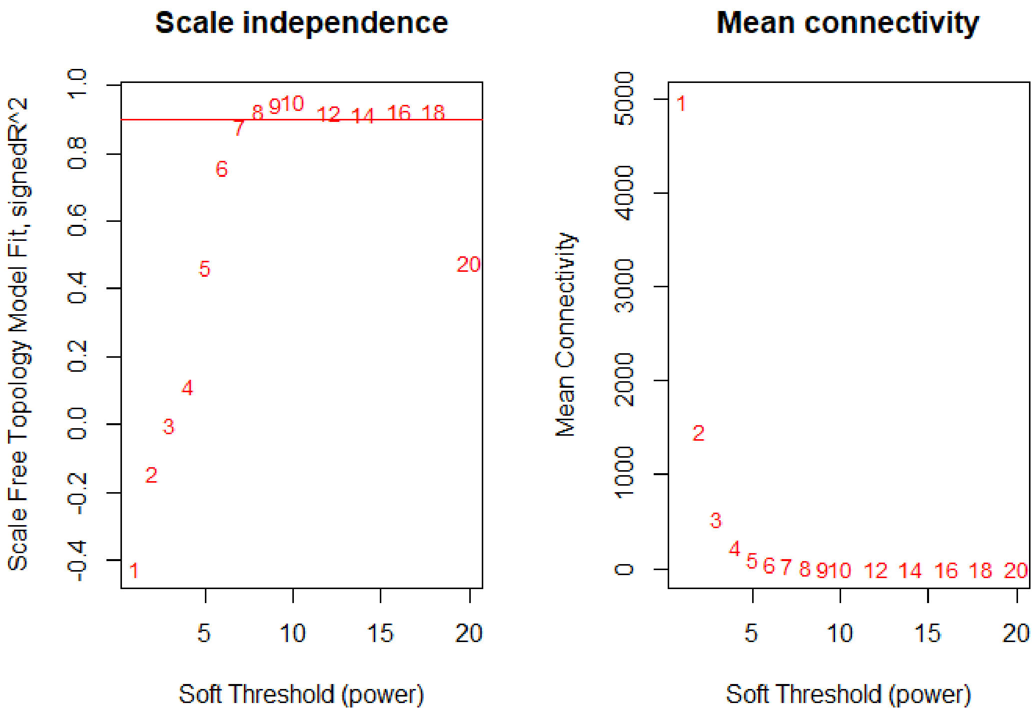


Figure S2 Surface abundance (15 m) of *nifH* gene copies per liter belonging to major groups of diazotrophic cyanobacteria. The het-1 group contains *Richelia* (*Rhizosolenia* associated). For methods and bulk trends see Wilson et al. (1). Here UCYN and het data were separated to highlight *Richelia* (*Rhizosolenia*-associated) presence.

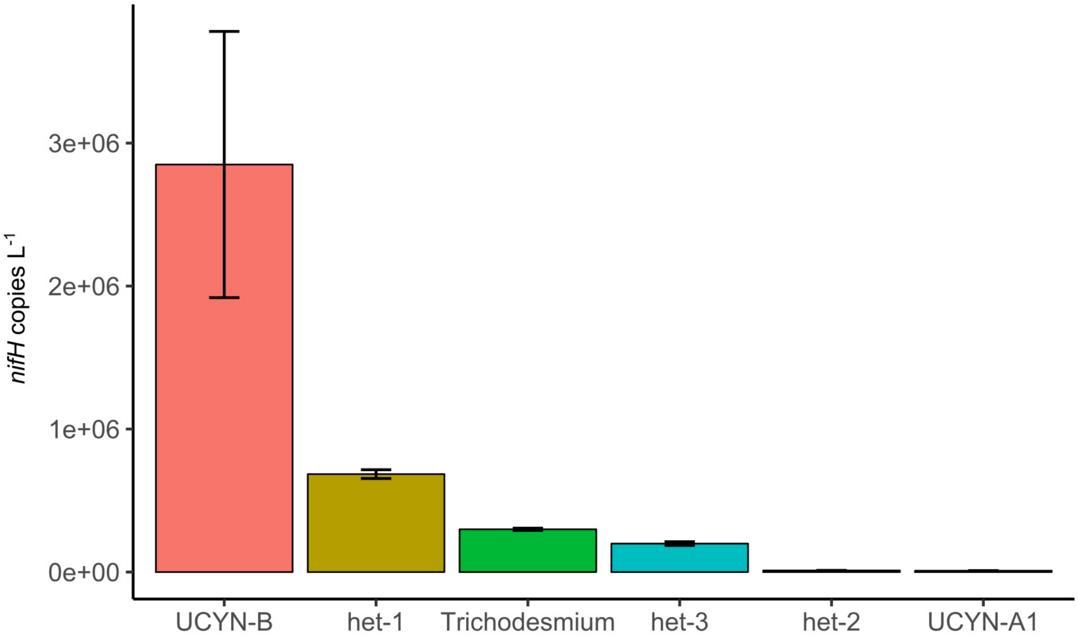


Figure S3 Hierarchically clustered heat map of *Rhizosolenia* genes that were significantly periodic (RAIN, FDR < 0.05) where red indicates the maximum normalized expression (row max) and blue indicates the minimum normalized expression (row min) for that row (contig). Grey bars below the figure indicate dark periods (7 pm to 6 am) while yellow indicates light periods (6 am to 7 pm).

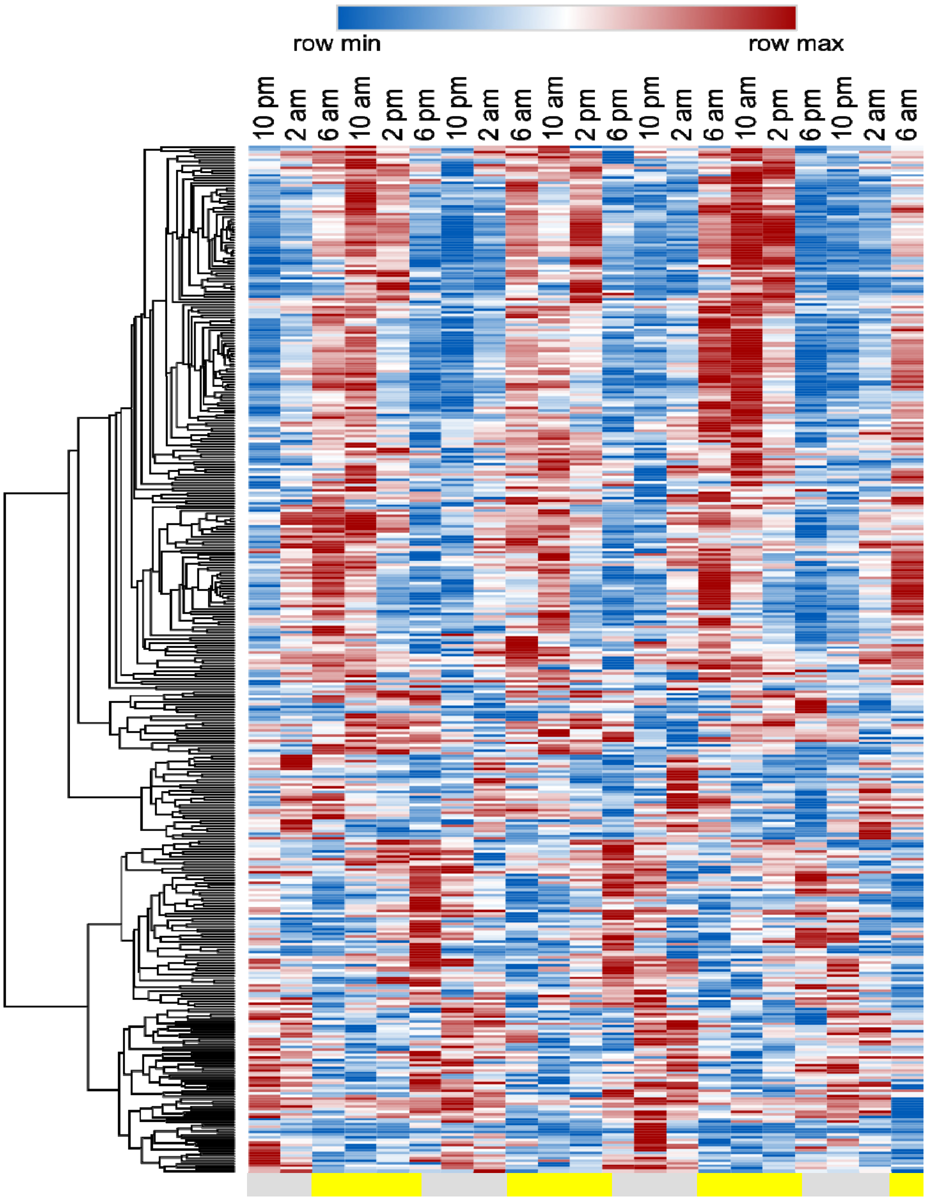


Figure S4 Normalized expression patterns of the significantly diel genes involved in photosynthesis and carbon fixation in *Rhizosolenia*. Forty-three chlorophyll *a*/*b* binding proteins are represented as an average in plot A (SE ± 0.13). Gray shading highlights dark hours (7 pm to 6 am) while light periods are white (6 am to 7 pm).

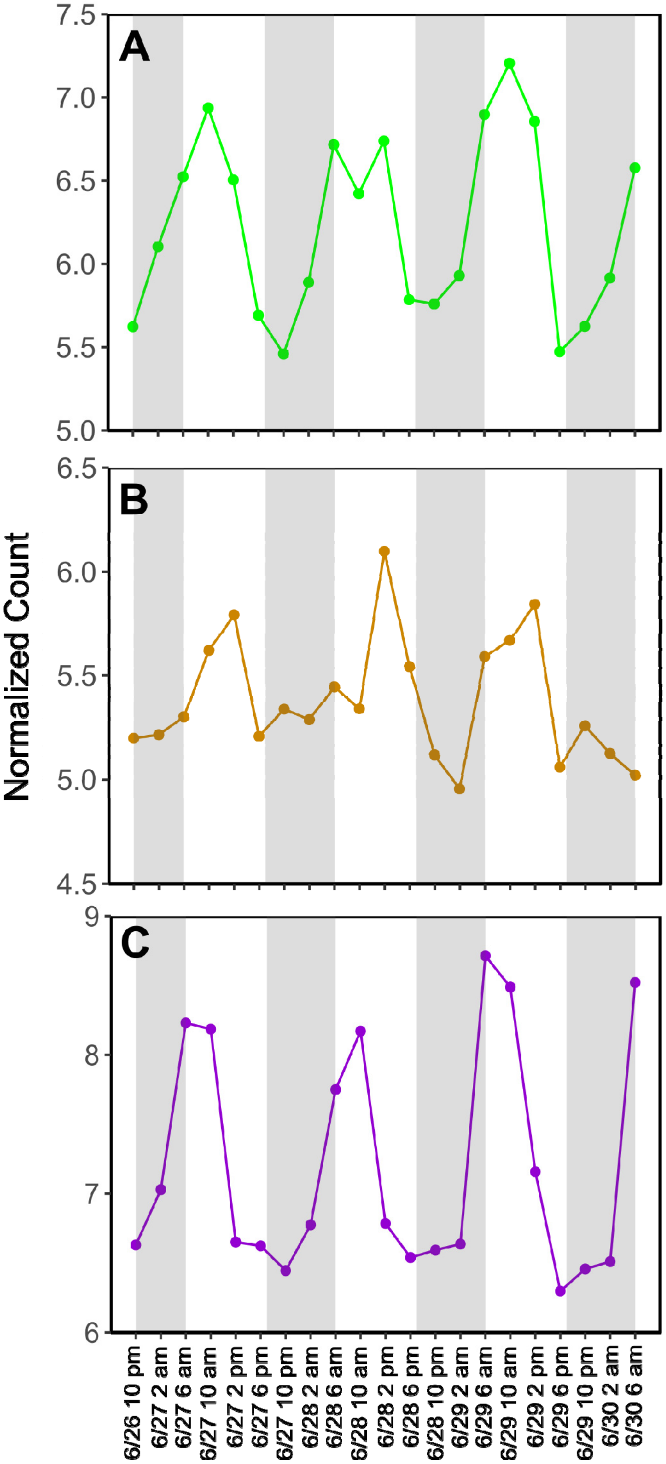


Figure S5 The distribution of features (gene or contig) for each species in each WGCNA module.

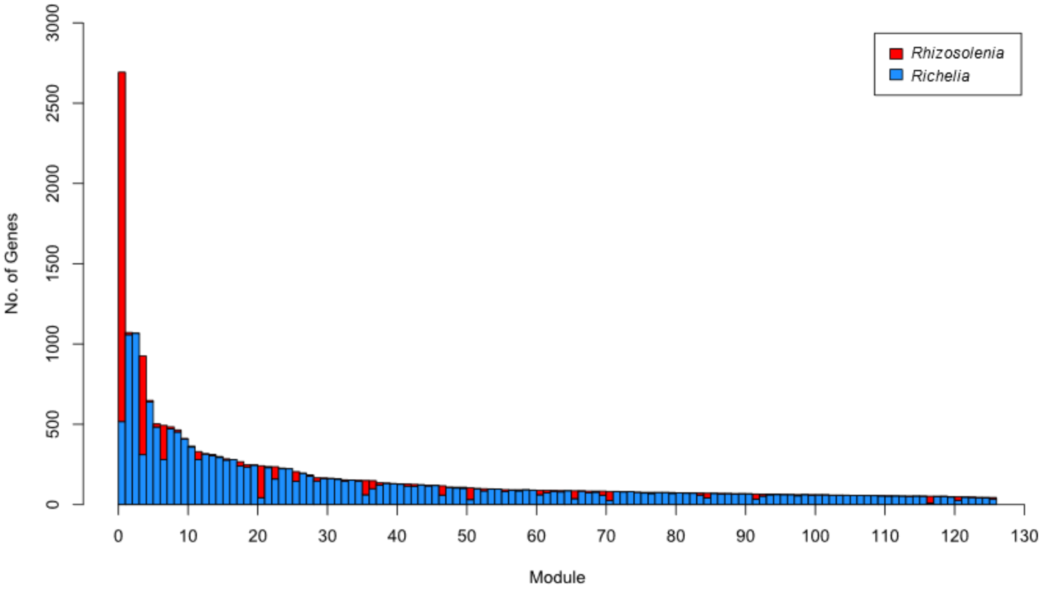


Figure S6 Average normalized expression patterns of features within the WGCNA module 6 for *Richelia* (63 genes, SE ± 0.28) and *Rhizosolenia* (680 contigs, SE ± 0.17). Gray shading highlights dark hours (7 pm to 6 am) while light periods are white (6 am to 7 pm).

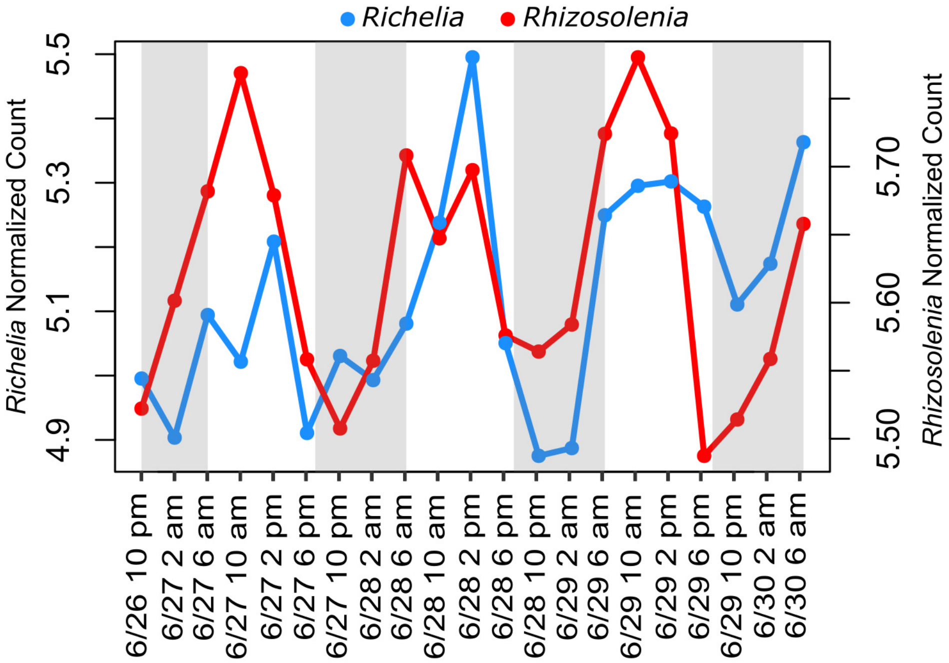


Figure S7 Normalized expression patterns of silicic acid transport genes in *Rhizosolenia* with significant periodic expression (RAIN, FDR < 0.05). Gray shading highlights dark hours (7 pm to 6 am) while light periods are white (6 am to 7 pm).

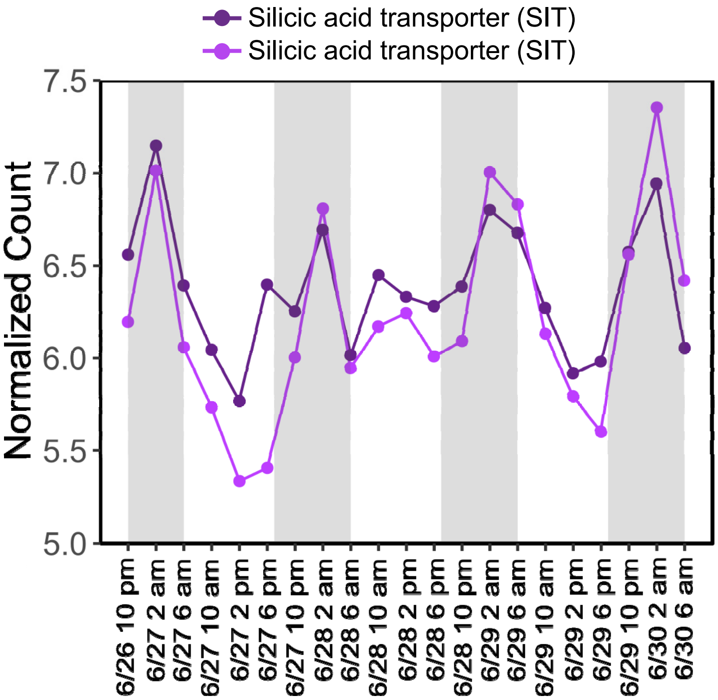
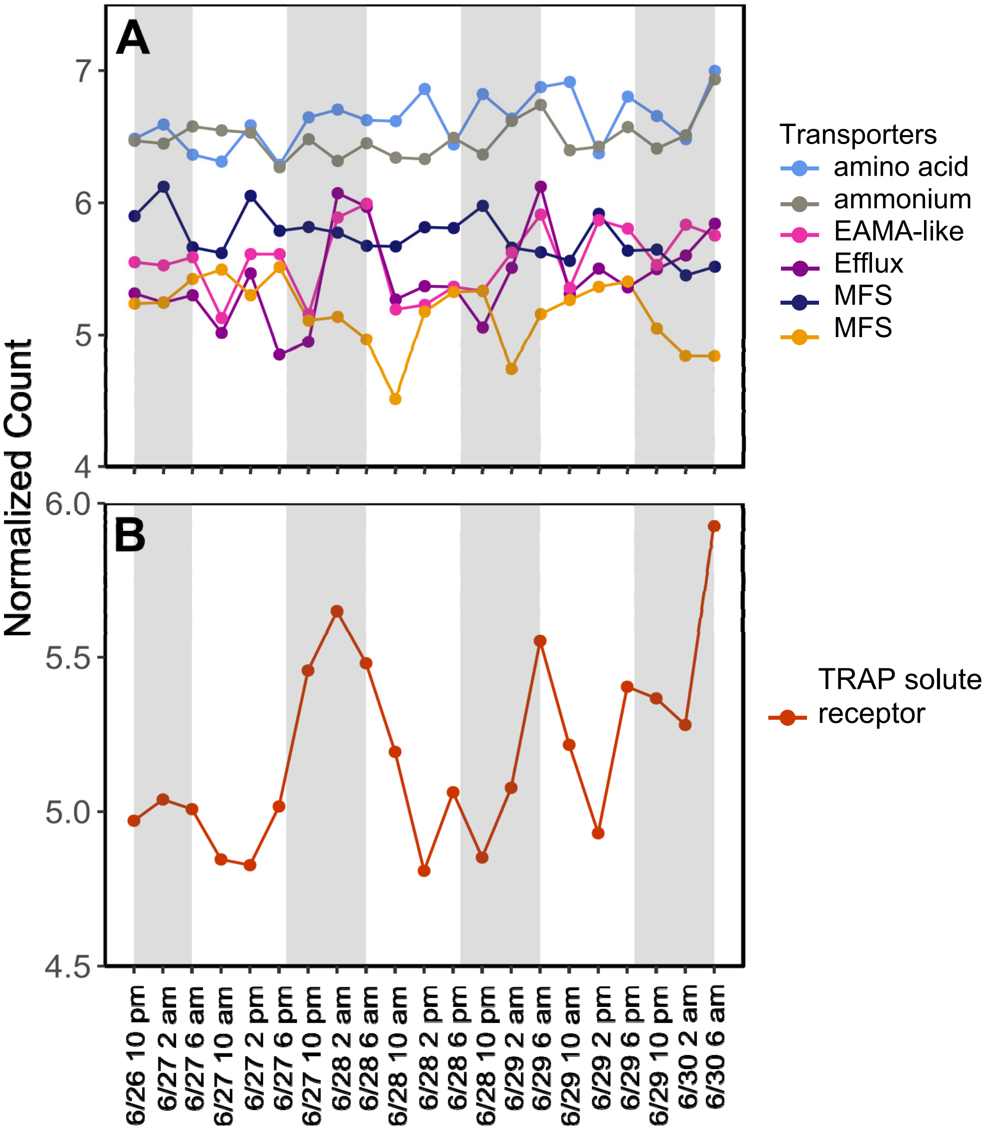


Figure S8 Normalized expression patterns of A) putative nitrogen and carbon transporters in *Rhizosolenia* and B) a TRAP solute receptor in *Richelia*. TRAP = tripartite ATP-independent periplasmic and MFS = major facilitator superfamily. Gray shading highlights dark hours (7 pm to 6 am) while light periods are white (6 am to 7 pm).



References

1. Wilson ST, Aylward FO, Ribalet F, Barone B, Casey JR, Connell PE, et al. Coordinated regulation of growth, activity and transcription in natural populations of the unicellular nitrogen-fixing cyanobacterium *Crocosphaera*. Nat Microbiol. 2017; **2**: 17118.