Supplementary information

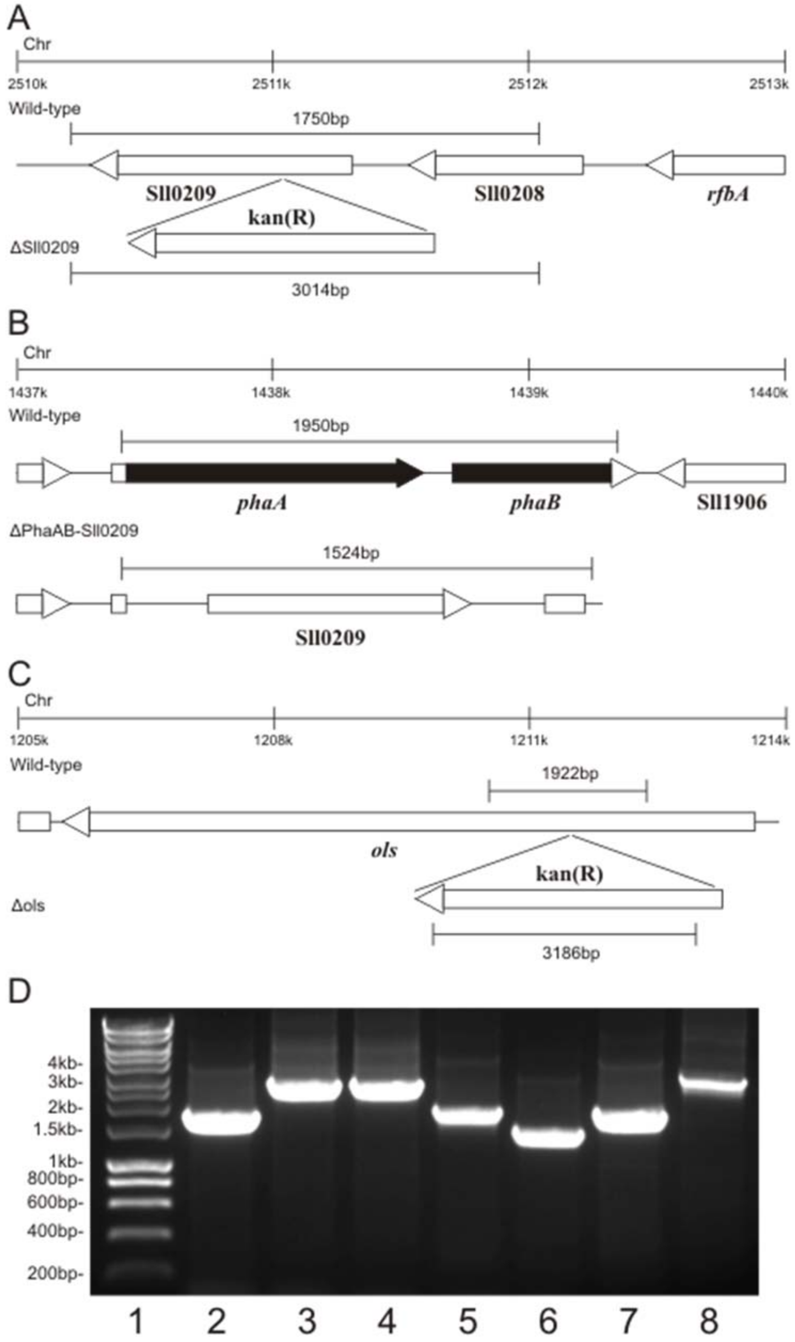

Figure S1: Generation of mutant strains in *Synechocystis* and *Synechococcus*. Schematic representations of locus location in the genome (top), and the wild-type and mutant strain (bottom) profiles expected in (A) ΔFAR (ΔSll0209), (B) Complemented (ΔFAR:comp) and (C)

ΔOls strains following amplification with primers flanking the deleted/inserted sequence. Regions deleted in ΔFAR:comp are shaded in black. (D) Amplification of genomic DNA in wild-type *Synechocystis* (Lane 2) and ΔFAR (Lane 3) and ΔFAR:comp (Lane 4) using Sll0209for/Sll0209rev primers; in wild-type *Synechocystis* (Lane 5) and ΔFAR:comp (Lane 6) using Phafor/Pharev primers; in wild-type *Synechococcus* (Lane 7) and ΔOls (Lane 8) using Olsfor/Olsrev primers. Markers are in lane 1.

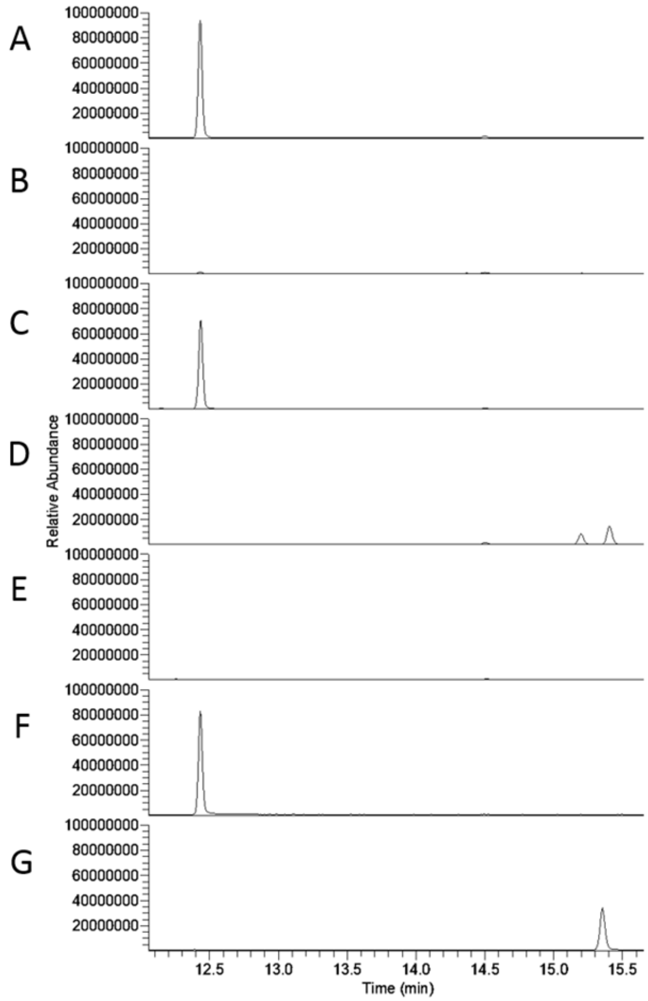

Figure S2: Chromatograms showing separation of hydrocarbons from whole cells. Hydrocarbons were extracted from (A) *Synechocystis* wild-type; (B) ΔFAR; (C) ΔFAR:comp; (D) *Synechococcus* wild-type; (E) ΔOls; (F) heptadecane standard 0.0039 mg/mL; (G) nonadecene standard 0.0038 mg/mL by GC-MS (Thermo Scientific Trace GC 1310 – ISQ LT Single Quadruple EI MS, A1-1310 Autosampler) using a Thermo TG-SQC GC column (15 m × 0.25 mm, 0.25-μm film thickness). Peaks were identified as (12.43 min) heptadecane and (15.41 min) nonadecene. 8-heptadecene was detected at 12.15 min but is not visible due to scaling. The peak at 15.2 minutes in (D) *Synechococcus* wild-type was identified (by nist library) as a hexadecan-1-ol.

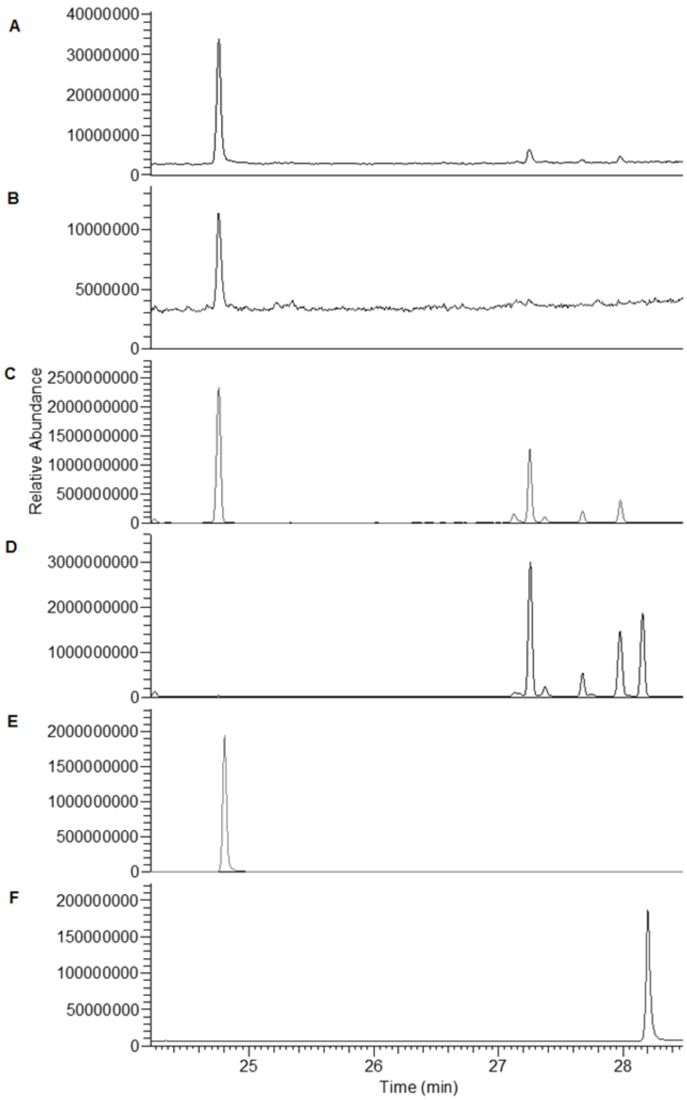

Figure S3: Chromatograms showing separation of hydrocarbons from membrane fractions. Hydrocarbons were extracted from *Synechocystis* wild-type (A) thylakoid membrane; (B) cytoplasmic membrane; (C) total membrane and (D) *Synechococcus* wild-type total membrane fractions; (E) heptadecane standard; (F) nonadecene standard GC-MS (Thermo Scientific Trace GC 1310 – ISQ LT Single Quadruple EI MS, A1-1310 Autosampler) using a Phenomenex Zebron ZB-5MSi Capillary GC Column (30m x 0.25mm x 0.25 µm). Peaks were identified as (24.76 min) heptadecane and (28.27 min) nonadecene. 8-heptadecene was detected at 24.34 min but is not visible due to scaling.

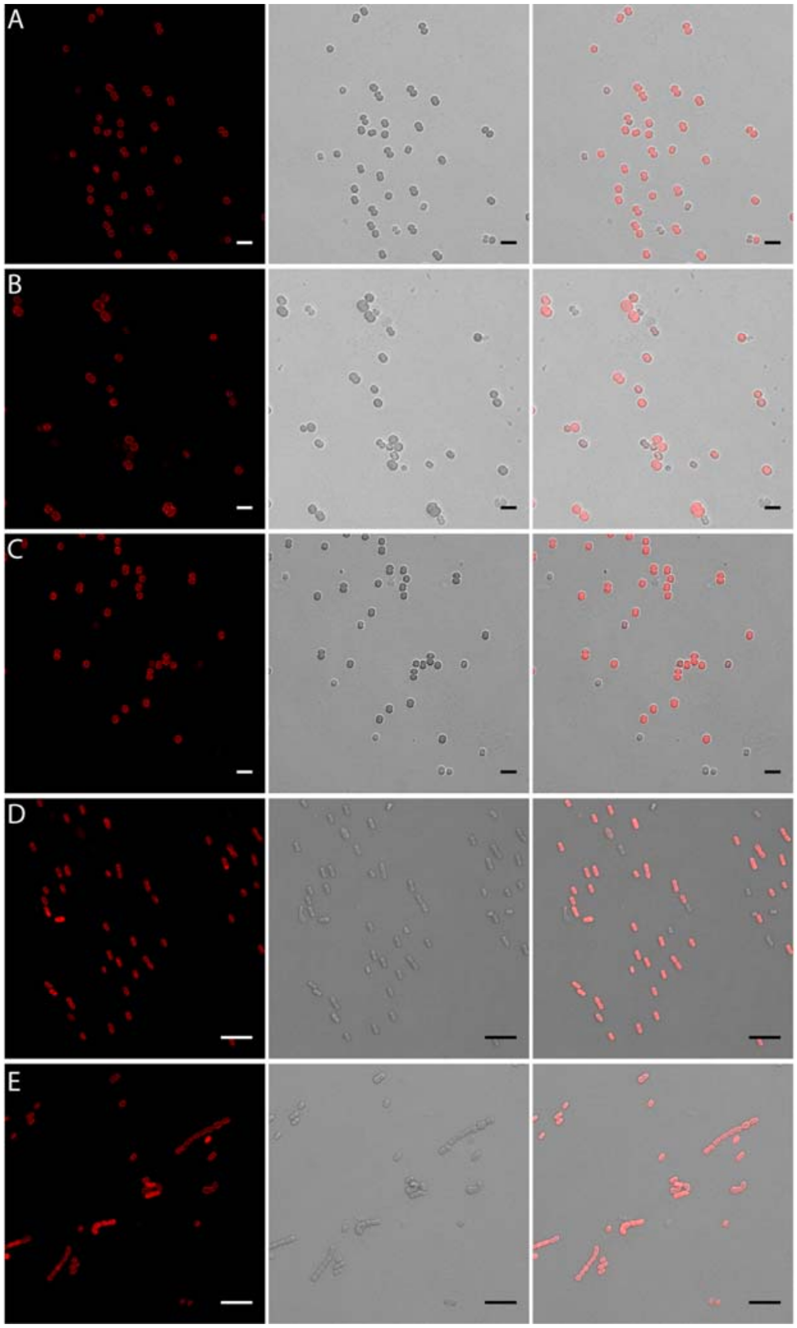

Figure S4: Brightfield confocal images of *Synechocystis* and *Synechococcus* strains. Cell morphology of strains used in this study. (A) wild-type *Synechocystis*, (B) ΔFAR and (C) ΔFAR:comp. Scale bars, 5 µm. (D) wild-type *Synechococcus* and (E) ΔOls. Scale bars, 10 µm. Images show autofluorescence (red, left), bright-field (grey, middle) and an overlay of both (right).

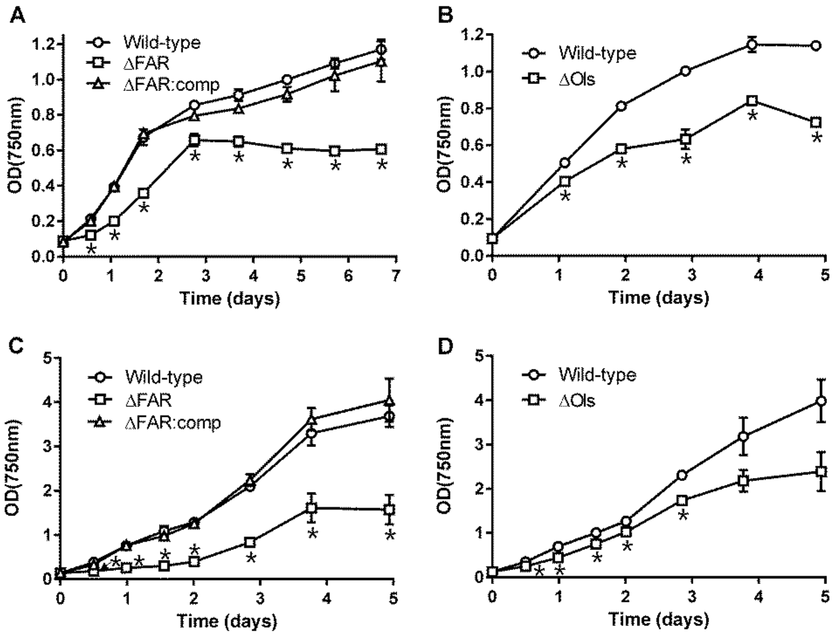

Figure S5: **Growth of *Synechocystis* and *Synechococcus* under moderate and high light.** Growth of (A, C) *Synechocystis* and (B, D) *Synechococcus* strains was measured at an OD_{750nm} under (A, B) moderate (40 µmol photons m^{-2} s^{-1}) and (C, D) high (120 µmol photons m^{-2} s^{-1}) light. Cultures were inoculated with a similar amount of cyanobacteria as measured by optical density. Samples grown under high light were bubbled with air. From strains cultured under moderate light the growth rate constants (µ) of wild-type *Synechocystis*, ΔFAR and ΔFAR:comp were 0.015±0.002, 0.007±0.0003 and 0.015±0.001 hr^{-1}, respectively, and in wild-type *Synechococcus* and ΔOls were 0.027±0.001 and 0.019±0.001 hr^{-1}, respectively. From strains cultured under high light the growth rate constants (µ) of wild-type *Synechocystis*, ΔFAR and ΔFAR:comp were 0.035±0.005, 0.016±0.005 and 0.038±0.005 hr^{-1}, respectively, and in wild-type *Synechococcus* and ΔOls were 0.034±0.008 and 0.023±0.005 hr^{-1}, respectively. Results are from three biological replicates. Errors bars indicate S.D. Asterisks indicate significant differences between wild-type and hydrocarbon deficient samples (Student's paired *t* test: $P < 0.05$).

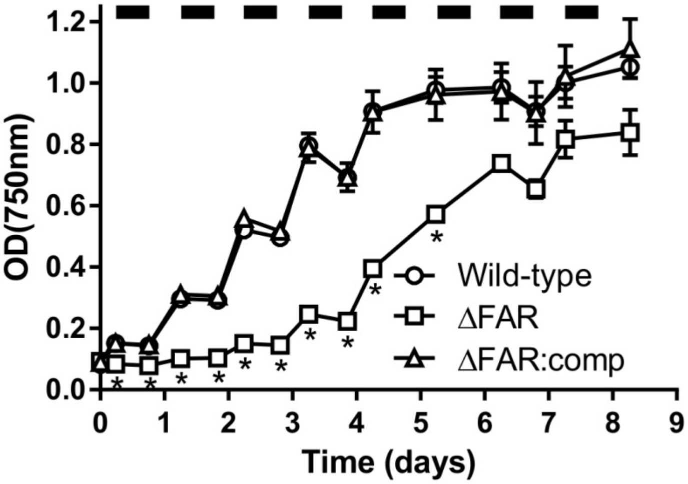

Figure S6: **Growth of *Synechocystis* under moderate light/dark cycles.** Growth of *Synechocystis* was measured at an OD_{750nm} under 12 hour light (40 μmol photons m^{-2} s^{-1})/12 hour dark cycles. The growth rate constants (μ) of wild-type *Synechocystis*, ΔFAR and ΔFAR:comp were 0.011±0.0003, 0.003±0.0001 and 0.011±0.0001 hr^{-1}. Dark periods are indicated by black bars. Results are from three biological replicates. Errors bars indicate S.D. Asterisks indicate significant differences between wild-type and hydrocarbon deficient samples (Student's paired *t* test: $P < 0.05$).

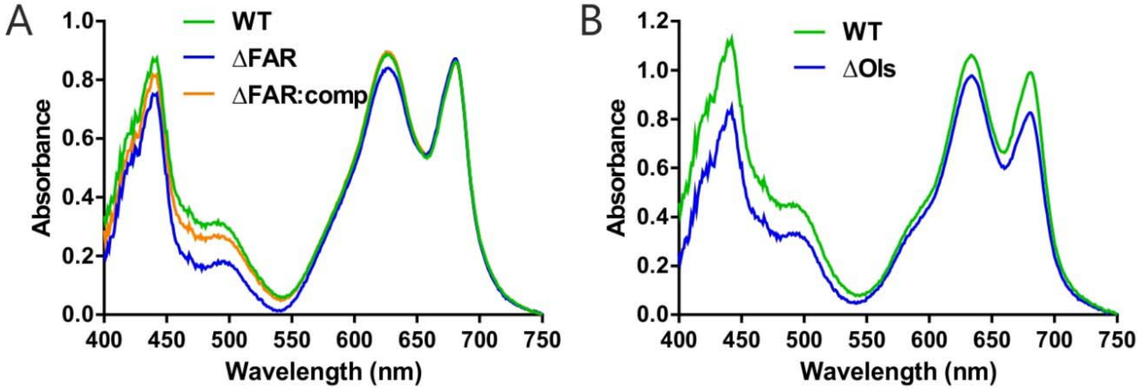

Figure S7: **Absorbance profiles of *Synechocystis* and *Synechococcus* strains.** Spectrum showing the absorbance profile of (A) *Synechocystis* and (B) *Synechococcus* cells. Values are averages from four biological replicates and are standardized to 750 nm.

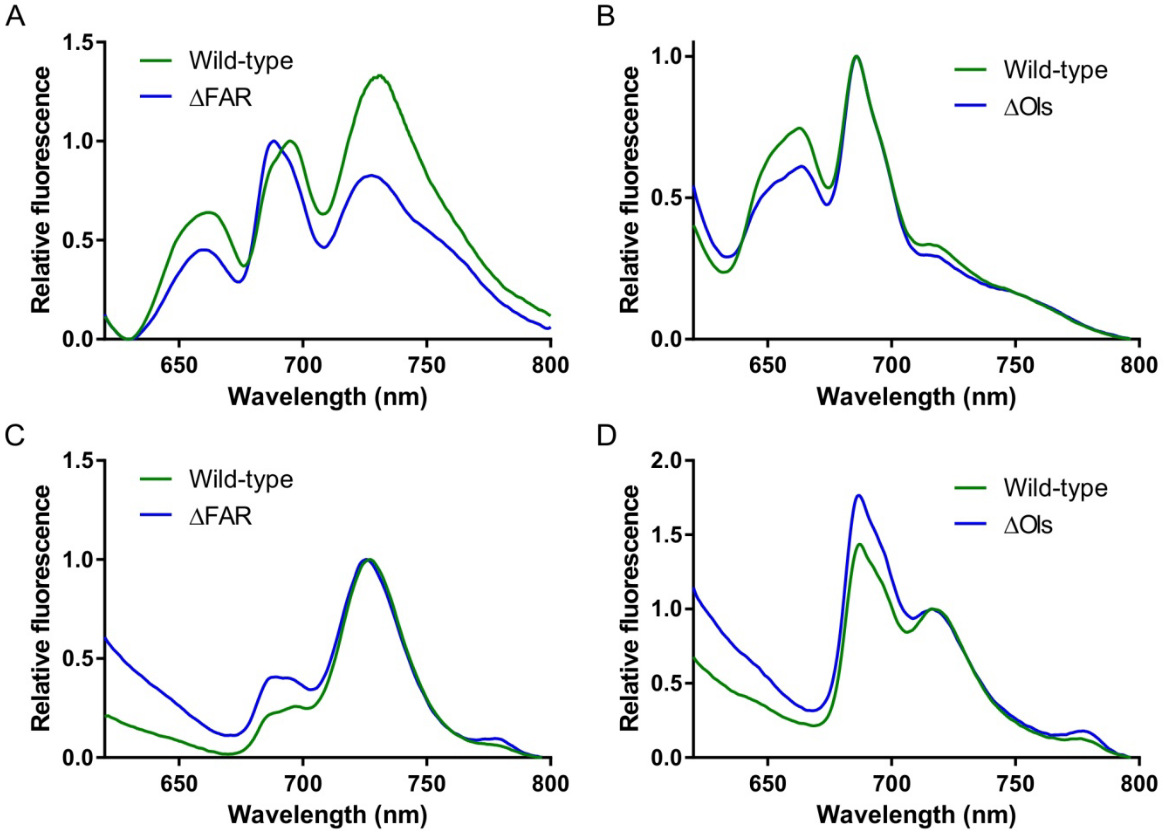

Figure S8: **77K fluorescence of *Synechocystis* and *Synechococcus* strains.** The fluorescence emission spectra of (A) *Synechocystis* and (B) *Synechococcus* cells were recorded with an excitation wavelength at 600 nm at 77K. The spectra were normalized to the highest peak between 625 and 710 nm. The fluorescence emission spectra of (C) *Synechocystis* and (D) *Synechococcus* cells were recorded with an excitation wavelength at 435 nm at 77K. The spectra were normalized to the highest peak between 710 and 750 nm. Results are representative of three biological replicates.

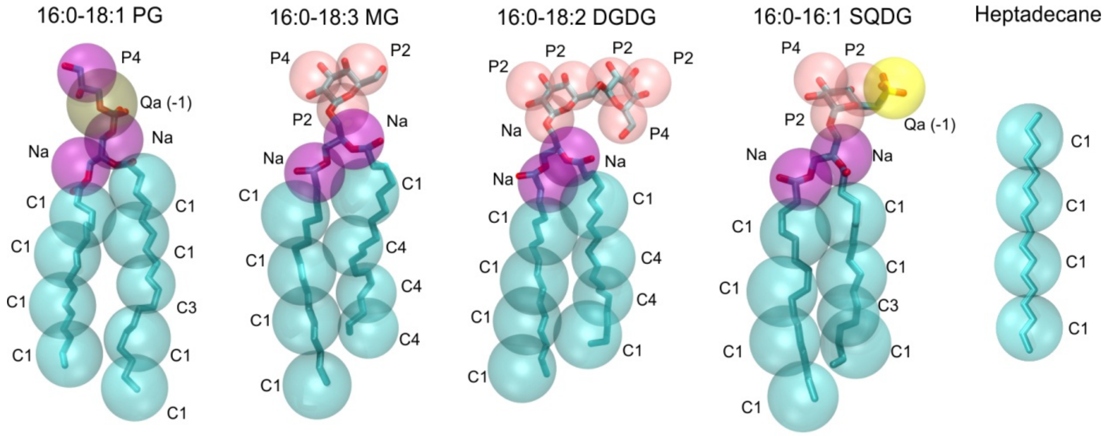

Figure S9: CG topologies of representative lipids of the membrane. These are overlaid on atomistic topologies of the same lipids. Labels refer to Martini bead type used to describe relevant interactions.

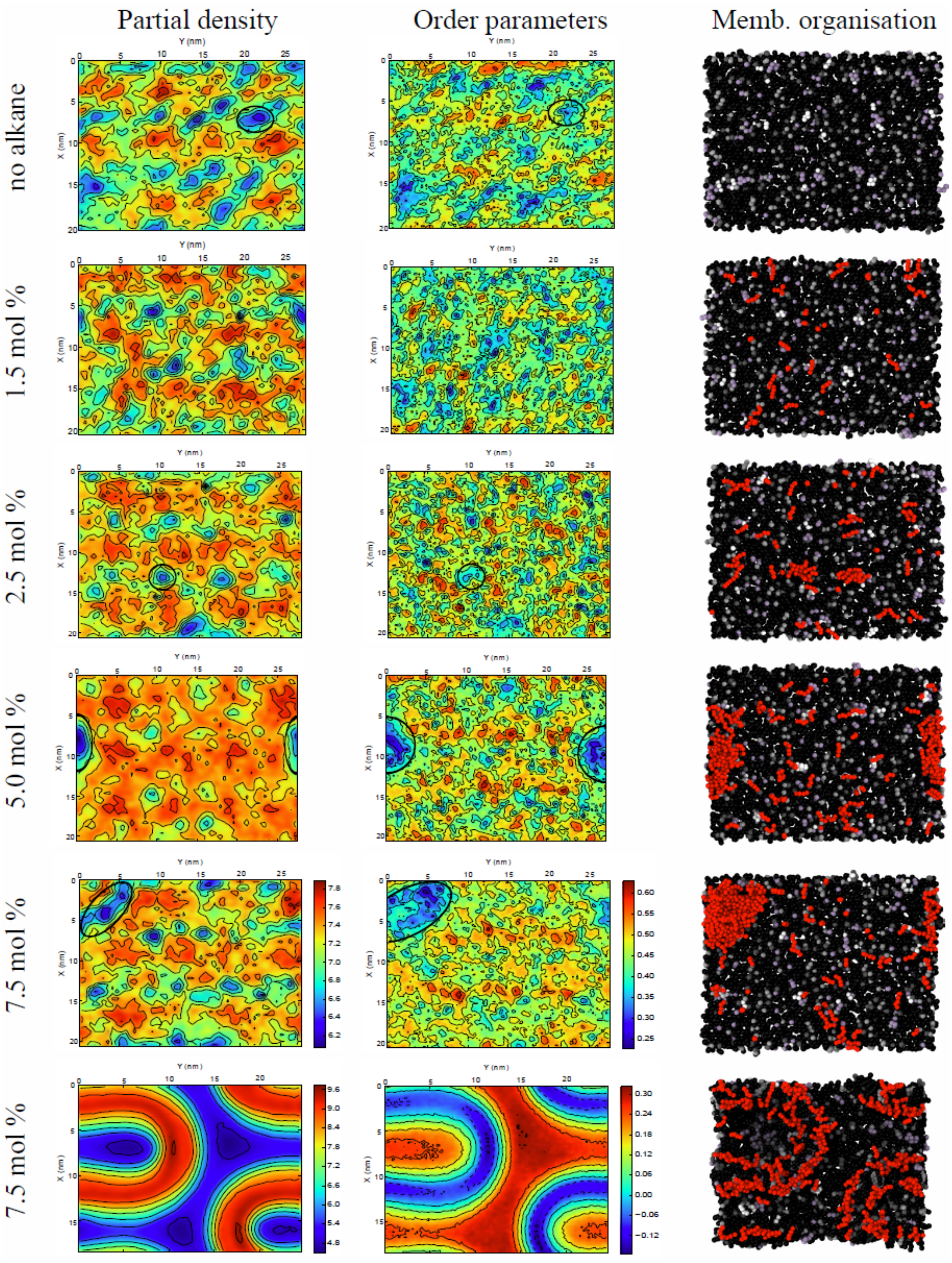
Partial density
Order parameters
Memb. organisation
no alkane
1.5 mol %
2.5 mol %
5.0 mol %
7.5 mol %
7.5 mol %
Y (nm)
X (nm)
0
5
10
15
20
25
7.8
7.6
7.4
7.2
7.0
6.8
6.6
6.4
6.2
0.60
0.55
0.50
0.45
0.40
0.35
0.30
0.25
9.6
9.0
8.4
7.8
7.2
6.6
6.0
5.4
4.8
0.30
0.24
0.18
0.12
0.06
0.00
−0.06
−0.12

Figure S10: Membrane partial density (left panels), lipid acyl chain order parameter (central panel), and organization (right panel) in differing hydrocarbon contents averaged over the last 2 µs of simulation, seen as a bilayer landscape. In the 7.5 mol % lamellar system, these properties are shown for the first 1.2 µs of simulation, before phase transition. Regions of accumulated alkane molecules are highlighted as circles. In membrane snapshots only the tail beads are visualized, and colored according to degree of saturation. 16:0 tails are black, 16:1 grey, 18:1 white, 18:2 ice blue and 18:3 pale blue. Hydrocarbons are shown in red van der Waals representation and overlaid on the membranes for clarity.

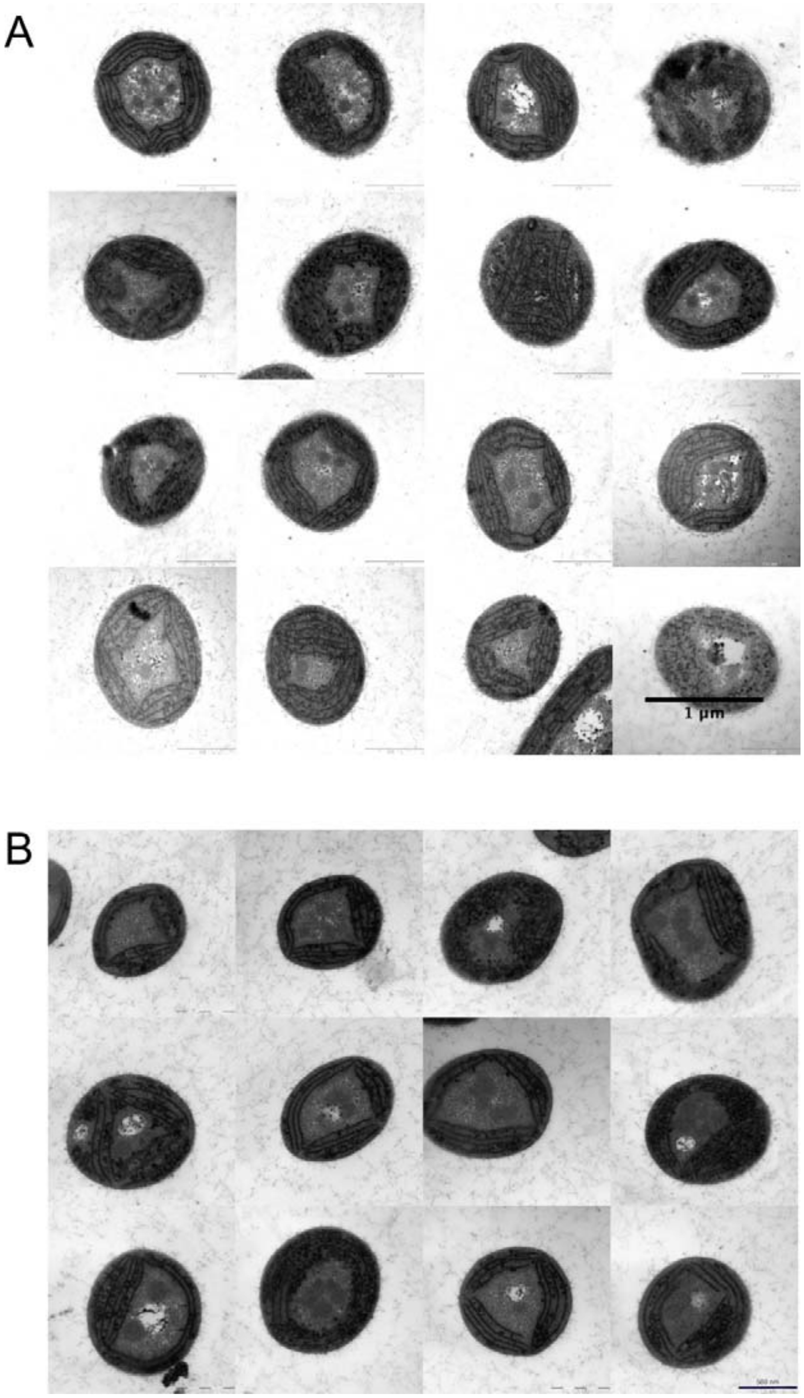

Figure S11: Electron microscopy images of *Synechococcus* cells. Transverse sections of (A) wild-type *Synechococcus* and (B) ΔOls cells used for measuring curvature.

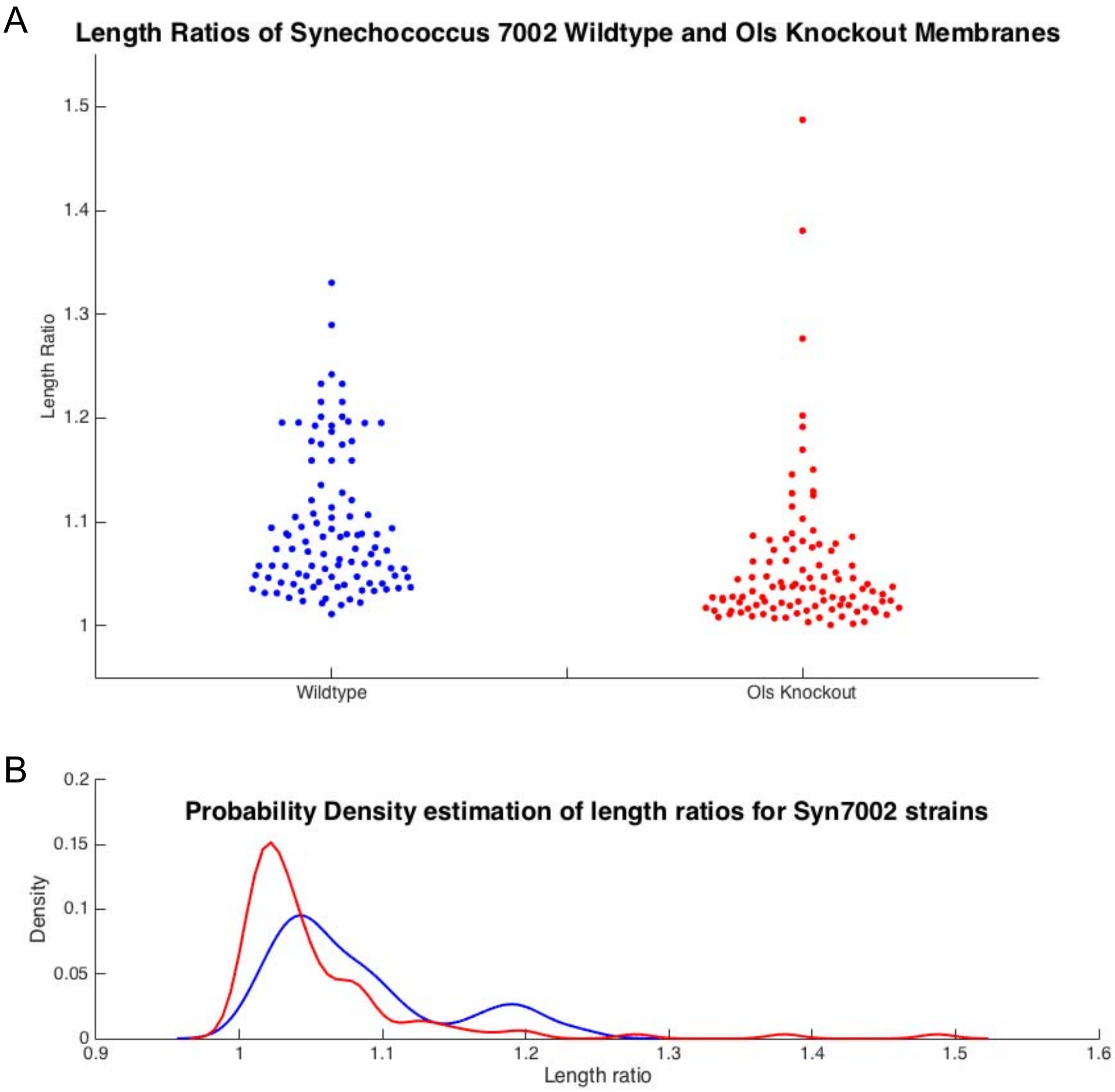

Figure S12: Length ratios (curvatures) of membranes from Synechococcus 7002 strains. **(**A) Categorical scatter plot of length ratios of all membranes sampled. (B) Kernel Density Plots of Length ratios from wild-type (blue) and ΔOls (red) membranes.

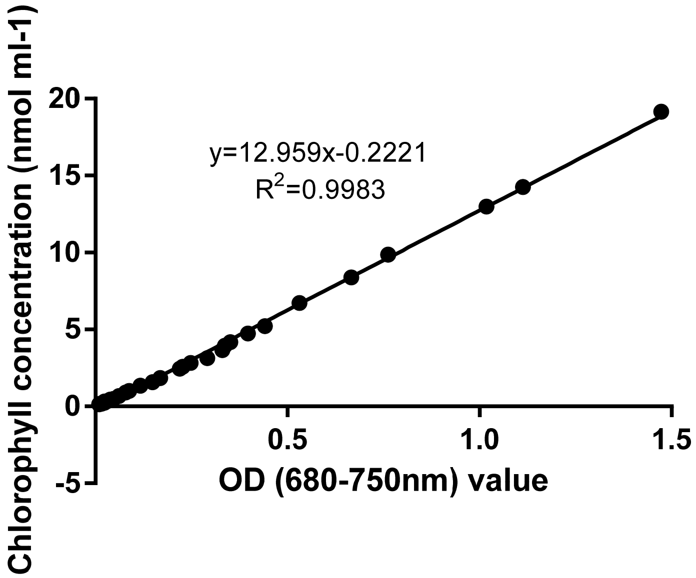

Figure S13: **Correlation between the absorbance at 680 nm and 750 nm, and amounts of chlorophyll measured following methanol extraction.** Twenty-nine samples were measured at an absorbance of 750 nm and 680 nm, followed by extraction with methanol to measure chlorophyll concentration. The amount of chlorophyll was correlated with absorbance (A_{680nm}-A_{750nm}). The regression line is shown. The slope of the regression line (R^2=0.9983), equivalent to 12.959, was calculated.

Table S1. Conservation of hydrocarbon biosynthetic pathway proteins and CurT in sequenced cyanobacteria strains. The *Synechocystis* FAD/FAR/CurT and *Synechococcus* Ols amino acid sequences were subjected to BLAST analysis against sequenced cyanobacterial genomes in the NCBI database. The positive values of these BLAST results are listed. Due to similarities between Ols and other polyketide synthase proteins only matches greater than 50% identity over the length of the query sequence are shown.

Strain	Fad	Far	Ols	CurT
Acaryochloris marina MBIC11017	292/337(86%)	191/230(83%)		55/92(60%)
Anabaena cylindrica PCC7122	301/338(89%)	197/223(88%)		82/124(66%)
Anabaena sp. 90	297/338(87%)	196/223(87%)		90/137(66%)
Anabaena sp. PCC7108	302/338(89%)	197/223(88%)		91/138(66%)
Anabaena variabilis ATCC29413	305/338(90%)	204/230(88%)		90/138(65%)
Arthrospira maxima CS-328	295/338(87%)	206/231(89%)		90/134(67%)
Arthrospira platensis NIES-39	295/338(87%)	206/231(89%)		87/134(65%)
Calothrix sp. PCC6303	298/338(88%)	202/228(88%)		81/123(66%)
Calothrix sp. PCC7103	295/338(87%)	198/219(90%)		87/135(64%)
Calothrix sp. PCC7507	299/338(88%)	202/228(88%)		82/123(67%)
Candidatus atelocyanobacterium thalassa	296/338(87%)	198/228(86%)		81/105(77%)
Chamaesiphon minutus PCC6605	299/340(87%)	193/230(83%)		69/100(69%)
Chlorogloeopsis fritschii	297/338(87%)	202/231(87%)		79/123(64%)
Chroococcales CENA595	300/338(88%)	199/230(86%)		81/119(68%)
Chroococcidiopsis thermalis PCC7203	301/339(88%)	200/228(87%)		69/95(73%)
Coleofasciculus chthonoplastes PCC7420	298/338(88%)	199/230(86%)		83/111(75%)
Crinalium epipsammum PCC9333	299/339(88%)	190/225(84%)		89/126(71%)
Crocosphaera watsonii WH8501	291/339(85%)	206/231(89%)		98/134(73%)
Cyanobacterium aponinum PCC10605	290/340(85%)	193/225(85%)		88/133(66%)
Cyanobium gracile PCC6307	256/337(75%)	181/220(82%)		36/65(55%)
Cyanobium sp. PCC7001	261/334(78%)	182/220(82%)		
Cyanothece sp. ATCC51142	294/339(86%)	206/228(90%)		99/134(74%)
Cyanothece sp. CCY0110	301/338(89%)	207/230(90%)		94/134(70%)
Cyanothece sp. PCC7424			1871/2798(66%)	98/136(72%)
Cyanothece sp. PCC7425	290/338(85%)	196/230(85%)		74/121(61%)
Cyanothece sp. PCC7822			1873/2800(66%)	88/113(78%)
Cyanothece sp. PCC8801	306/339(90%)	205/230(89%)		95/131(73%)
Cylindrospermopsis raciborskii CS-505	301/338(89%)	191/222(86%)		88/136(65%)
Cylindrospermum stagnale PCC7417	299/338(88%)	199/231(86%)		92/137(67%)

Dactylococcopsis salina PCC8305	282/338(83%)	199/231(86%)		77/105(73%)
Dolichospermum circinale	298/338(88%)	197/221(89%)		78/115(68%)
Fischerella sp. PCC9339	296/338(87%)	200/228(87%)		68/117(58%)
Fischerella sp. PCC9431	296/338(87%)	200/228(87%)		69/117(59%)
Fischerella sp. PCC9605	299/338(88%)	203/228(89%)		81/123(66%)
Geitlerinema sp. PCC7407	292/339(86%)	204/231(88%)		75/104(72%)
Geminocystis herdmanii			1791/2846(62%)	76/105(72%)
Geminocystis sp. NIES-3708	292/340(85%)	199/230(86%)		92/137(67%)
Geminocystis sp. NIES-3709			1785/2865(62%)	87/136(64%)
Gloeobacter kilaueensis JS1	264/340(78%)	179/221(81%)		
Gloeobacter violaceus PCC7421	266/338(79%)	183/221(82%)		
Gloeocapsa sp. PCC7428	299/338(88%)	193/226(85%)		88/130(68%)
Halothece sp. PCC7418	287/338(84%)	202/228(88%)		66/95(69%)
Hassallia byssoidea VB512170	297/338(87%)	200/228(87%)		84/124(68%)
Leptolyngbya boryana	295/338(87%)	200/230(86%)		76/111(68%)
Leptolyngbya sp. JSC-1	294/338(86%)	201/230(87%)		89/136(65%)
Leptolyngbya sp. PCC7376			2161/2726(79%)	87/134(65%)
Limnorpahis robusta	297/338(87%)	204/231(88%)		71/94(76%)
Lyngbya aestuarii	298/338(88%)	201/230(87%)		91/153(59%)
Lyngbya sp. PCC8106	296/338(87%)	196/229(85%)		88/143(62%)
Mastigocoleus repens	294/338(86%)	201/230(87%)		82/123(67%)
Mastigocoleus testarum	296/338(87%)	202/228(88%)		
Microchaete sp. PCC7126	298/338(88%)	206/230(89%)		86/138(62%)
Microcoleus sp. PCC7113	301/340(88%)	201/230(87%)		95/142(67%)
Microcoleus vaginatus FGP-2	297/338(87%)	194/230(84%)		73/101(72%)
Microcystis aeruginosa NIES-843	299/338(88%)	207/231(89%)		77/110(70%)
Moorea producens 3L			1558/2851(55%)	91/137(66%)
Myxosarcina sp. GI1			1820/2823(64%)	73/111(66%)
Nodularia spumigena CCY9414	302/338(89%)	199/230(86%)		91/137(66%)
Nostoc azollae' 0708	299/338(88%)	197/223(88%)		91/140(65%)
Nostoc punctiforme PCC73102	298/338(88%)	196/222(88%)		91/141(65%)
Nostoc sp. KNUA003	307/338(90%)	197/230(85%)		
Nostoc sp. PCC6720	307/338(90%)	197/230(85%)		
Nostoc sp. PCC7107	305/338(90%)	195/230(84%)		91/137(66%)
Nostoc sp. PCC7120	305/338(90%)	204/230(88%)		90/138(65%)
Nostoc sp. PCC7524	303/338(89%)	202/230(87%)		88/137(64%)
Oscillatoria acuminata PCC6304	294/338(86%)	202/231(87%)		77/110(70%)
Oscillatoria cyanobacterium JSC-12	297/339(87%)	201/230(87%)		85/123(69%)
Oscillatoria nigro-viridis PCC7112	297/338(87%)	194/230(84%)		73/101(72%)
Oscillatoria sp. PCC6506	301/338(89%)	196/230(85%)		87/134(65%)
Oscillatoria sp. PCC10802	295/341(86%)	202/231(87%)		89/134(66%)
Pleurocapsa sp. PCC7319			1862/2843(65%)	83/135(61%)

Pleurocapsa sp. PCC7327			1890/2861(66%)	91/110(83%)
Prochlorococcus marinus str. AS9601	262/337(77%)	173/214(80%)		37/68(54%)
Prochlorococcus marinus str. CCMP1375	263/337(78%)	169/218(77%)		60/114(53%)
Prochlorococcus marinus str. CCMP1986	261/337(77%)	173/214(80%)		32/63(51%)
Prochlorococcus EQPAC1	261/337(77%)	173/214(81%)		32/63(51%)
Prochlorococcus GP2	262/337(78%)	173/214(81%)		53/114(46%)
Prochlorococcus LG	263/337(78%)	169/218(78%)		60/114(53%)
Prochlorococcus marinus str. MIT9107	258/337(77%)	171/214(80%)		53/114(46%)
Prochlorococcus marinus str. MIT9116	258/337(77%)	171/214(80%)		53/114(46%)
Prochlorococcus marinus str. MIT9123	258/337(77%)	171/214(80%)		53/114(46%)
Prochlorococcus marinus str. MIT9201	261/337(77%)	172/214(80%)		37/68(54%)
Prochlorococcus marinus str. MIT9202	262/337(77%)	148/186(80%)		37/68(54%)
Prochlorococcus marinus str. MIT9211	257/334(76%)	171/219(78%)		49/93(53%)
Prochlorococcus marinus str. MIT9215	262/337(77%)	171/214(79%)		37/68(54%)
Prochlorococcus marinus str. MIT9301	262/337(77%)	173/214(80%)		37/68(54%)
Prochlorococcus marinus str. MIT9302	262/337(78%)	173/214(81%)		38/79(48%)
Prochlorococcus marinus str. MIT9303	237/303(78%)	183/236(77%)		35/64(55%)
Prochlorococcus marinus str. MIT9311	260/337(77%)	174/214(81%)		37/67(55%)
Prochlorococcus marinus str. MIT9312	260/337(77%)	174/214(81%)		37/67(55%)
Prochlorococcus marinus str. MIT9313	265/337(78%)	178/218(81%)		37/67(55%)
Prochlorococcus marinus str. MIT9314	261/337(77%)	172/214(80%)		37/68(54%)
Prochlorococcus marinus str. MIT9322	262/337(78%)	173/214(81%)		37/68(54%)
Prochlorococcus marinus str. MIT9401	262/337(78%)	173/214(81%)		37/68(54%)
Prochlorococcus marinus str. MIT9515	263/337(78%)	169/214(79%)		32/59(54%)
Prochlorococcus marinus str. MIT0601	260/337(77%)	172/214(80%)		60/118(51%)
Prochlorococcus marinus str. MIT0604	262/337(78%)	172/214(80%)		37/68(54%)
Prochlorococcus marinus str. MIT0701	267/337(80%)	177/220(80%)		37/67(55%)
Prochlorococcus marinus str. MIT0702	268/337(80%)	177/220(80%)		37/67(55%)
Prochlorococcus marinus str. MIT0703	268/337(80%)	177/220(80%)		37/67(55%)
Prochlorococcus marinus str. MIT0801	259/334(78%)	174/222(78%)		38/68(56%)
Prochlorococcus marinus str. NATL1A	258/334(77%)	174/222(78%)		38/68(56%)
Prochlorococcus marinus str. NATL2A	257/334(76%)	174/222(78%)		38/68(56%)
Prochlorococcus marinus str. PAC1	257/334(77%)	174/222(78%)		38/68(56%)
Prochlorococcus marinus str. SB	260/337(77%)	173/214(81%)		37/68(54%)
Prochlorococcus marinus str. SS2	263/337(78%)	169/218(78%)		60/114(53%)
Prochlorococcus marinus str. SS35	263/337(78%)	169/218(78%)		60/114(53%)
Prochlorococcus marinus str. SS51	263/337(78%)	169/218(78%)		60/114(53%)
Prochlorococcus marinus str. SS52	263/337(78%)	169/218(78%)		60/114(53%)
Prochloron didemni			1831/2988(61%)	
Prochlorothrix hollandica	293/338(86%)	193/229(84%)		66/100(66%)
Pseudanabaena sp. PCC 7367	285/339(84%)	201/226(88%)		37/53(70%)
Raphidiopsis brookii D9	299/338(88%)	194/221(87%)		89/136(65%)
Rivularia sp. PCC 7116	294/338(86%)	194/228(85%)		73/110(66%)

Scytonema hofmanni UTEX B 1581	299/338(88%)	200/228(87%)		83/123(67%)
Scytonema millei	302/339(89%)	200/231(86%)		70/95(74%)
Scytonema tolypothrichoides	299/338(88%)	200/228(87%)		82/128(64%)
Stanieria cyanosphaera PCC7437			1899/2788(68%)	86/126(68%)
Synechococcus elongatus	279/337(82%)	195/231(84%)		78/118(66%)
Synechococcus sp. BL107	259/337(76%)	172/210(81%)		60/129(47%)
Synechococcus sp. CC9311	265/339(78%)	181/219(82%)		43/75(57%)
Synechococcus sp. CC9605	266/337(78%)	171/210(81%)		57/128(45%)
Synechococcus sp. CC9902	259/337(76%)	172/210(81%)		60/129(47%)
Synechococcus sp. NKBG15041c			2327/2724(85%)	93/135(69%)
Synechococcus sp. JA-2-3B'a(2-13)	268/338(79%)	179/221(80%)		33/64(52%)
Synechococcus sp. JA-3-3Ab	268/338(79%)	180/221(81%)		
Synechococcus sp. PCC6312	294/338(86%)	188/221(85%)		79/132(60%)
Synechococcus sp. PCC7002			2720/2720	90/133(68%)
Synechococcus sp. PCC7335	285/339(84%)	196/231(84%)		76/115(66%)
Synechococcus sp. PCC7502	283/339(83%)	188/222(84%)		80/139(58%)
Synechococcus sp. RCC307	265/337(78%)	182/220(82%)		59/130(45%)
Synechococcus sp. RS9916	263/337(78%)	173/210(82%)		38/69(55%)
Synechococcus sp. RS9917	262/337(77%)	176/210(83%)		53/116(46%)
Synechococcus sp. WH5701	264/334(79%)	182/220(82%)		42/67(63%)
Synechococcus sp. WH7803	264/337(78%)	180/219(82%)		42/75(56%)
Synechococcus sp. WH7805	265/337(78%)	175/210(83%)		51/103(50%)
Synechococcus sp. WH8102	263/337(78%)	174/210(82%)		60/128(47%)
Synechococcus sp. WH8109	265/337(78%)	174/210(82%)		44/94(47%)
Synechocystis sp. PCC6714	338/340(99%)	227/231(98%)		131/134(98%)
Synechocystis sp. PCC6803	340/340	231/231		149/149
Synechocystis sp. PCC7509	299/340(87%)	199/230(86%)		85/134(63%)
Thermosynechococcus elongatus BP-1	290/338(85%)	186/221(84%)		69/124(56%)
Tolypothrix campylonemoides	299/338(88%)	203/231(87%)		82/124(66%)
Tolypothrix sp. PCC7601	302/338(89%)	203/230(88%)		89/137(68%)
Trichodesmium erythraeum IMS101	297/338(87%)	192/220(87%)		66/93(71%)
Trichormus azollae	299/338(88%)	197/223(88%)		73/105(70%)
Xenococcus sp. PCC7305			1857/2848(65%)	87/137(64%)

Table S2: Cell size as determined via fluorescence microscopy. Values represent the cell diameter of *Synechocystis* cells and width/length of *Synechococcus* cells in µm. The cellular volume is measured in µm^3. Standard deviation (S.D.) is indicated. Asterisks indicate significant differences between samples (Student's t-test; $P < 0.0001$).

Strain	**Cells counted**	**Cell size (Mean)**	**cell size (S.D.)**	**Cell volume (±S.D.)**	**Minimum cell size**	**Median cell size**	**Maximum cell size**
Synechocystis							
Wild-type	171	2.06	0.13	4.63±0.83	1.60	2.08	2.38
ΔFAR	121	2.72*	0.34	11.02±4.23*	1.72	2.72*	3.85
ΔFAR:comp	186	2.09	0.15	4.83±0.99	1.60	2.08	2.40
Synechococcus							
Wild-type	102	1.61/2.30	0.13/0.50	3.08±0.72	1.36/1.60	1.58/2.21	2.13/4.36
Δols	128	1.76*/2.41	0.27/0.84	3.89±1.49*	1.36/1.40	1.7*/2.30	3.57/7.49

Table S3: Cell size as determined via particle counting measurements. Values represent the cell width/diameter of the cells in µm. The cellular volume is measured in µm^3. Standard deviation (S.D.) is indicated. Asterisks indicate significant differences between samples ($P < 0.0001$).

Strain	**Cells counted**	**Cell size (Mean)**	**Cell size (S.D.)**	**Cell volume**	**Minimum cell size**	**Median cell size**	**Maximum cell size**
Synechocystis							
Wild-type	1069396	2.06	0.31	4.58	1.60	2.08	2.38
ΔFAR	370156	2.80*	0.41	11.49*	1.72	2.72*	3.85
ΔFAR:comp	917114	2.00	0.23	4.19	1.60	2.08	2.40

Table S4: Cell counts of single and actively dividing *Synechocystis* cells. Asterisks indicate significant differences between samples ($P < 0.05$).

Strain	Single cells	Dividing cells	Total cells	% Single cells	% Dividing cells
Wild-type	257	172	429	59.9	40.1
ΔFAR	169	152	321	52.6*	47.4*
ΔFAR:comp	178	117	295	60.3	39.7

Table S5: Carotenoid/chlorophyll ratios in cyanobacterial strains. Results are from three biological replicates.

Strain	Mean	S.D.
Synechocystis		
Wild-type	0.31369	0.10439
ΔFAR	0.39693	0.10933
ΔFAR:comp	0.42608	0.10330
Synechococcus		
Wild-type	0.91792	0.01904
ΔOls	1.28426	0.15799

Table S6: **Lipid composition of cyanobacterial membranes.** The experimental lipid composition according to Sheng *et al* is shown in mM, and has been adjusted to account for lipids rather than fatty acids. The simplified composition used in a 2,400 lipid bilayer in the *in silico* models is given in brackets. ND = not detected.

	PG	**MGDG**	**SQDG**	**DGDG**
2x16:0	0.041 (96)	0.329 (840)	0.239 (600)	0.082 (192)
16:0-16:1$^{\Delta9}$	ND	0.044 (96)	0.040 (96)	0.006 (24)
16:0-18:1$^{\Delta9}$	0.014 (48)	0.018 (48)	0.032 (96)	0.012 (48)
16:0-18:2$^{\Delta9,12}$	0.006 (24)	0.030 (72)	0.017 (48)	0.010 (24)
16:0-α18:3$^{\Delta9,12,15}$	ND	0.024 (48)	ND	ND
Total	**0.061 (168)**	**0.445 (1104)**	**0.328 (840)**	**0.110 (288)**

Table S7: Sequence of primers used in this study. Restriction endonuclease sites introduced into the primer are underlined.

Primer	**Sequence**
Sll0209for	GTACGCATGCACCTTGTTCACCAGCTCCAC
Sll0209rev	GTACTCTAGACAAAATGGAAAACCGCCATA
olsfor	GATCGAATTCAGCAAACCGTTTTTGTGACC
olsrev	GTACGTCGACTGCAAGGTGGCGAACTGTAT
phaABleftfor	GTACTCTAGAGGGACCATCCTGACTACACG
phaABleftrev	GATCGGATCCGTTCGTTTAGCGGCAACAAT
phaABrightfor	GATCGAGCTCTTTTACTTTCCCCCGTAGCC
phaABrightrev	GACTGAATTCGCATTGTCTGGTCCATGTTG
Sll0209compfor	GATCGGATCCTTTGACCAGCAGCATTGAG
Sll0209comprev	GATCGAGCTCTTTCATGAGCCCACAAATCC
Phafor	ATTGTTGCCGCTAAACGAAC
Pharev	TACTGGCTACGGGGGAAAGT