Supplemental Material: Klähn et al.

Supplemental Figure S1

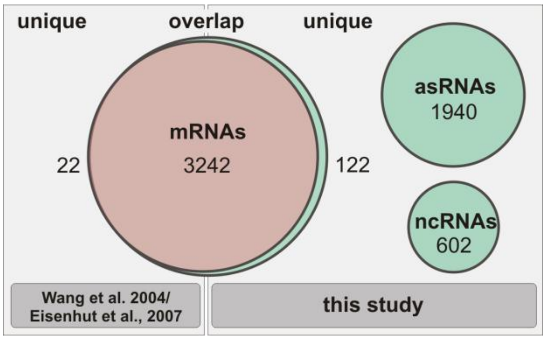

Figure S1: Overlap and additional features of the array design used here Mitschke et al. (2011) with arrays from Wang et al. (2004) and Eisenhut et al. (2007).

Supplemental Figure S2

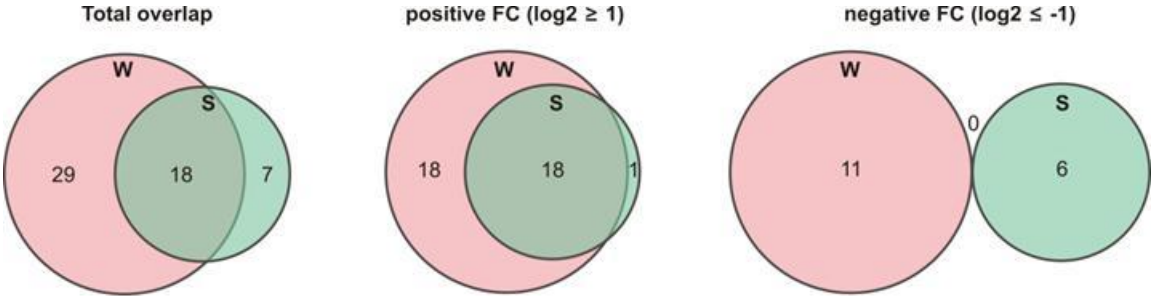

Figure S2: Overlap and differences in expression levels for protein-coding genes in our study (S – green circles) to Wang et al. (2004) (W-red circles) under HC conditions.

Supplemental Figure S3

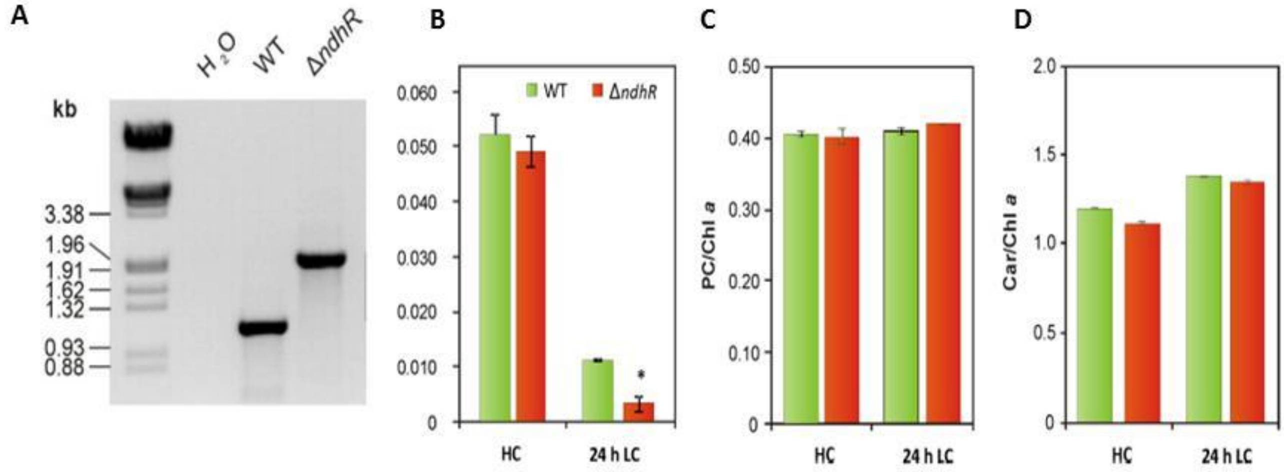

Figure S3: Genotypic and phenotypic characterization of the *Synechocystis* 6803 mutant Δ*ndhR*.

A: Verification of the mutant genotype by PCR.

B: Growth rate of Δ*ndhR* when cultivated under HC (5% CO_2) and LC (0.038% CO_2). C, D: Pigment ratios of phycocyanin (PC) and carotenoids (Car) relative to chlorophyll a (Chla) - content. (* - statistical significance determination using t-test at $p \leq 0.05$)

Supplemental Table S3 – Antisense:mRNA pairs for an expression change was observed for the asRNA but not for the corresponding mRNA.

Values are given as log2 fold changes and were regarded as significant (marked with *) if the log2 value was ≤ -1 or ≥ 1 and the according p-value ≤ 0.05.

asRNA			**mRNA**			**Annotation**	
asRNA	**3h LC**	**24h LC**	**Gene**	**3h LC**	**24h LC**	**Gene symbol**	**Protein names**
sll0922-as1	1.70*	2.25*	*sll0922*	0.05	-0.02		unknown protein
sll0723-as4	0.97	1.99*	*sll0723*	0.15	-0.48		unknown protein
sll0027-as1	2.34*	1.93*	*sll0027*	0.83	-0.20	*ndhD4*	NADH dehydrogenase subunit 4 (involved in constitutive, low affinity CO_2 uptake)
slr1534-as1	0.97	1.86*	*slr1534*	0.09	-0.20		Putative carboxy peptidase
sll1540-as1	0.35	1.70*	*sll1540*	0.16	-0.19	*dpm1*	dolichyl-phosphate-mannose synthase
slr0479-as1	-0.14	1.51*	*slr0479*	-0.03	-0.01		hypothetical protein
sll1161-as1	0.27	1.50*	*sll1161*	-0.05	0.12	*cya3*	probable adenylate cyclase
sll0898-as1	1.11	1.48*	*sll0898*	-0.73	-0.43	*rsgA (engC)*	putative ribosome biogenesis GTPase
slr1596-as2	0.98	1.38*	*slr1596*	0.16	0.13	*pcxA (cotA)*	Proton extrusion protein
slr0517-as1	0.39	1.38*	*slr0517*	-0.05	0.13		hypothetical protein
sll1319-as1	0.27	1.35*	*sll1319*	-0.12	-0.17		hypothetical protein
sll1939-as1	1.73*	1.34*	*sll1939*	0.20	0.18		unknown protein
slr0919-as1	1.98*	1.27*	*slr0919*	-0.40	-0.37		hypothetical protein
slr1744-as2	0.14	1.23*	*slr1744*	0.58	-0.35	*amiA (amiC)*	N-acetylmuramoyl-L-alanine amidase, periplasmic protein
sll1174-as2	0.78	1.20*	*sll1174*	-0.19	-0.28		unknown protein
slr1254-as1	0.45	1.17*	*slr1254*	-0.41	-0.57	*pds (crtD)*	phytoene dehydrogenase (phytoene desaturase)
sll0095-as1	0.57	1.16*	*sll0095*	0.37	-0.08		hypothetical protein
sll0247-as2	0.32	1.16*	*sll0247*	0.01	0.00	*isiA*	ironstress-induced chlorophyll-binding protein (CP43')
sll1174-as1	0.81	1.15*	*sll1174*	-0.19	-0.28		unknown protein
sll1665-as1	0.27	1.14*	*sll1665*	0.40	-0.07		unknown protein
ssl2982-as1	0.71	1.12*	*ssl2982*	-0.29	-0.67	*rpoZ, ycf61*	probable RNA polymerase omega subunit
sll1191-as2	0.06	1.11*	*sll1191*	-0.20	-0.05		hypothetical protein
slr0244-as1	0.78	1.09*	*slr0244*	-0.34	-0.33		hypothetical protein
slr1053-as4	0.43	1.09*	*slr1053*	0.45	-0.09		unknown protein
slr1053-as3	0.39	1.09*	*slr1053*	0.45	-0.09		unknown protein
slr1847-as1	-0.01	1.06*	*slr1847*	-0.32	-0.78		hypothetical protein
sll1934-as1	1.57	1.06*	*sll1934*	0.64	0.38		hypothetical protein
sll1127-as1	1.00*	1.05*	*sll1127*	0.11	-0.16	*menB*	1,4-dihydroxy-2-naphthoate synthase
slr1491-as1	0.23	1.04*	*slr1491*	0.29	0.11	*fecB*	iron(III) dicitrate transport system substrate-binding protein
slr1028-as2	0.29	1.02*	*slr1028*	0.06	0.31		unknown protein
sll1723-as1	-0.53	-1.02*	*sll1723*	0.11	0.01		probable glycosyltransferase
sll0986-as1	-0.82	-1.04*	*sll0986*	-0.02	-0.08		putative transposase ISY120f
slr1334-as1	-0.71	-1.06*	*slr1334*	0.09	-0.21	*Pgm*	phosphoglucomutase/phosphomannomutase
slr0354-as4	-1.12*	-1.08*	*slr0354*	0.20	0.23		ATP-binding protein of ABC transporter
slr1476-as1	-1.09*	-1.09*	*slr1476*	-0.04	-0.28	*pyrB*	aspartate carbamoyltransferase
slr0015-as1	0.11	-1.13*	*slr0015*	0.15	0.17	*lpxB*	lipid A disaccharide synthase
slr1237-as1	-0.31	-1.24*	*slr1237*	0.03	0.03	*codA*	cytosine deaminase
slr1876-as1	-1.05*	-1.31*	*slr1876*	0.14	0.11		hypothetical protein
sll0494-as1	-1.35*	-1.47*	*sll0494*	0.24	0.09		unknown protein
slr0776-as5	-1.79*	-1.57*	*slr0776*	-0.32	-0.42	*lpxD*	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase

Supplemental Table S4 – LC-induced features that are independent from NdhR but whose expression induction appeared delayed.

Values are given as log2 fold changes and were regarded as significant (marked with *) if the log2 value was ≤ -1 or ≥ 1 and the according p-value ≤ 0.05. The expression values for HC were used as reference. Fold changes between WT and Δ*ndhR* were calculated for each time point by subtracting the corresponding WT-value.

				WT		**Δ*ndhR***		**Δ*ndhR*-WT**		
Systematic	**Gene name**	**Protein name**	**Feature**	**3h LC**	**24h LC**	**3h LC**	**24h LC**	**HC**	**3h LC**	**24h LC**
sll0217	NA	flavoprotein	mRNA	5.58*	4.95*	2.06	5.04*	-0.02	**-3.54***	0.08
sll0218	NA	hypothetical protein	mRNA	5.33*	5.08*	1.88	4.83*	-0.01	**-3.46***	-0.25
sll0219	NA	flavoprotein	mRNA	5.23*	5.05*	1.88	4.78*	0.03	**-3.33***	-0.25
sll0519	*ndhA*	NADH dehydrogenase subunit 1	mRNA	2.16*	2.07*	1.00	2.00*	0.03	**-1.13***	-0.03
sll0520	*ndhI*	NADH dehydrogenase subunit NdhI	mRNA	1.76*	2.01*	0.70	1.89*	0.03	**-1.03***	-0.09
slr0006	NA	unknown protein	mRNA	3.68*	3.26*	1.68	3.69*	0.09	**-1.91***	0.53
slr0007	NA	probable sugar-phosphate nucleotidyltransferase	mRNA	2.53*	2.00*	1.06	2.42*	0.08	**-1.38***	0.49
slr0040	*cmpA*	bicarbonate transport system substrate-binding protein	mRNA	5.28*	4.73*	1.95	4.90*	0.00	**-3.33***	0.16
slr0041	*cmpB*	bicarbonate transport system permease protein	mRNA	5.14*	4.66*	2.00	4.75*	-0.02	**-3.16***	0.07
slr0042	NA	probable porin	mRNA	4.54*	4.21*	1.79	4.34*	-0.03	**-2.78***	0.10
slr0043	*cmpC*	bicarbonate transport system ATP-binding protei n	mRNA	4.24*	3.64*	1.65	3.79*	-0.01	**-2.60***	0.13
slr0044	*cmpD*	bicarbonate transport system ATP-binding protei n	mRNA	3.99*	3.75*	1.52	3.72*	-0.01	**-2.48***	-0.04
slr0373	NA	hypothetical protein	mRNA	2.70*	3.57*	1.34*	3.89*	-0.10	**-1.46***	0.21
slr0374	NA	hypothetical protein	mRNA	2.65*	3.64*	1.27*	3.90*	-0.10	**-1.48***	0.17
slr0376	NA	hypothetical protein	mRNA	2.25*	4.01*	0.98	4.16*	-0.05	**-1.32***	0.10
slr0616	NA	unknown protein	mRNA	2.00*	2.06*	0.68	2.02*	0.00	**-1.32***	-0.04
slr0789	NA	hypothetical protein	mRNA	1.81*	1.92*	0.51	1.87*	0.23	**-1.08***	0.18
slr1279	*ndhC*	NADH dehydrogenase subunit 3	mRNA	2.28*	1.88*	0.85	1.69*	0.08	**-1.35***	-0.12
slr1280	*ndhK*	NADH dehydrogenase subunit NdhK	mRNA	1.89*	1.73*	0.69	1.42*	0.07	**-1.12***	-0.24
slr1281	*ndhJ*	NADH dehydrogenase subunit I	mRNA	1.88*	1.88*	0.78	1.67*	-0.01	**-1.11***	-0.23
ssl1911	*gifA*	glutamine synthetase inactivating factor IF7	mRNA	1.91	2.11*	0.71	3.69*	-0.88	**-2.08***	0.69
ssr1038	NA	unknown protein	mRNA	1.46*	2.23*	0.37	2.11*	0.03	**-1.05***	-0.09
NC-101	ncr1200	NA	ncRNA	1.94*	3.85*	0.80	4.22*	-0.16	**-1.30***	0.22
NC-392	ncr0840	NA	ncRNA	2.60*	2.71*	1.09	2.82*	0.12	**-1.40***	0.22
NC-425	CsiR1, SyR14, ncr0380	NA	ncRNA	3.03*	5.69*	0.59	5.64*	0.07	**-2.37***	0.02