Supporting Information

Hemschemeier et al. 10.1073/pnas.1302592110

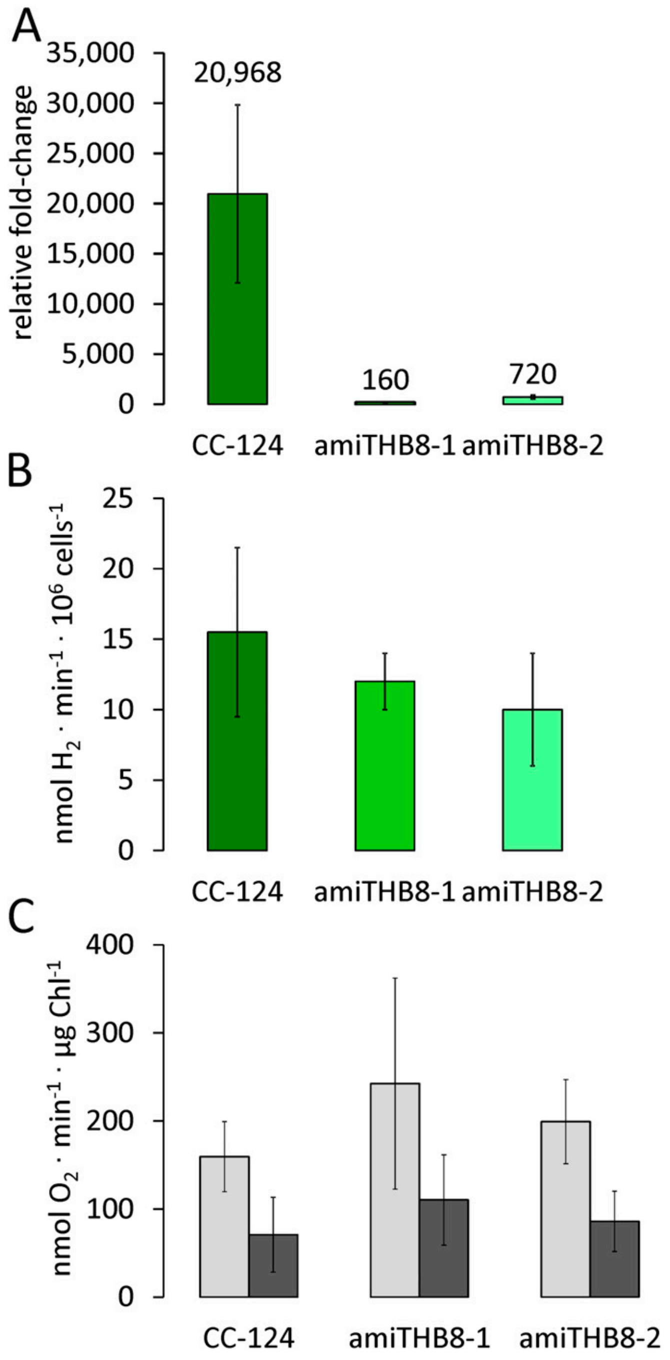

Fig. S1. Additional characteristics of the transformants in which *THB8* transcript amounts were reduced by applying the artificial microRNA (amiRNA) technology, ami*THB8*-1 and -2. (*A*) *Chlamydomonas reinhardtii* wild-type CC-124 and transformants ami*THB8*-1 and -2 were grown aerated in the light and then incubated anaerobically in the dark for 7 h. RNA was extracted from the precultures and after dark–anoxic incubation. Quantitative real-time PCR (qPCR) analyses of relative *THB8* transcript amounts were done as described before (1). Fold-changes were calculated using the $^{\Delta\Delta}$C(t) method. (*B*) In vitro hydrogenase activity of transformants ami*THB8*-1 and ami*THB8*-2 in comparison with strain CC-124 determined after 7 h of anaerobiosis. (*C*) O_2 evolution upon illumination (light gray bars) and O_2 uptake in the dark (dark gray bars) of the indicated strains grown aerobically in the light. (*B* and *C*) Hydrogenase activity and O_2 exchange rates were determined as described previously (2). (*A*–*C*) Bars show the average of two independent experiments. Error bars indicate the SD.

1. Pape M, Lambertz C, Happe T, Hemschemeier A (2012) Differential expression of the *Chlamydomonas* [FeFe]-hydrogenase-encoding *HYDA1* gene is regulated by the copper response regulator1. *Plant Physiol* 159(4):1700–1712.
2. Philipps G, Happe T, Hemschemeier A (2012) Nitrogen deprivation results in photosynthetic hydrogen production in *Chlamydomonas reinhardtii*. *Planta* 235(4):729–745.

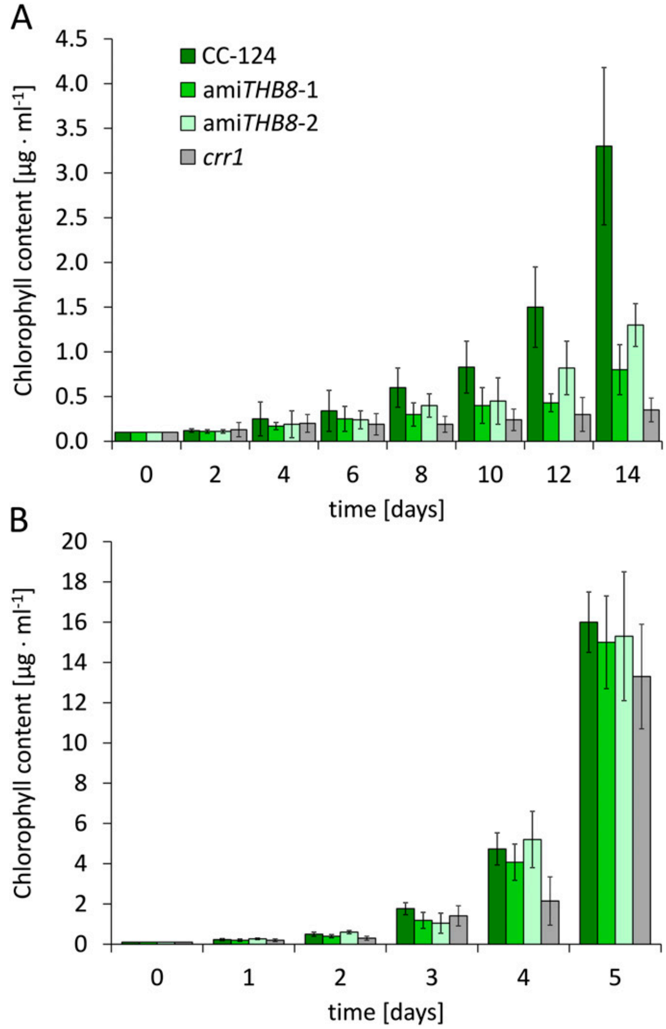

Fig. S2. Growth of the *C. reinhardtii* wild type and transformants ami*THB8*-1 and -2, as well as of the COPPER RESPONSE REGULATOR 1 (*crr1*) mutant under hypoxic conditions in dim light. (*A*) Algal cultures were inoculated at a chlorophyll concentration of 0.1 µg of Chl·mL^{-1} in 100 mL of Tris Acetate Phosphate (TAP) medium in squared glass bottles. These bottles were sealed with Suba Seals and incubated on a magnetic stirrer in dim light (15 µmol of photons·s^{-1}·m^{-2}). The medium was continuously purged with 0.1% CO_2 in N_2. After the indicated time points, samples were withdrawn for determining the chlorophyll content. The *crr1* mutant was used as a control for hypoxia as it grows poorly under hypoxic conditions (1). Cellular chlorophyll content in units of µg of chlorophyll per 1 million cells was similar in all strains analyzed: 3.2 ± 0.2 (CC-124), 2.9 ± 0.3 (strain ami*THB8*-1), 3.0 ± 0.5 (strain ami*THB8*-2), and 2.6 ± 0.4 (*crr1* mutant). (*B*) Cells were equally inoculated and incubated under the same conditions, but purged with 0.1% CO_2 in air.

1. Eriksson M, et al. (2004) Genetic dissection of nutritional copper signaling in *Chlamydomonas* distinguishes regulatory and target genes. *Genetics* 168(2):795–807.

Table S1. List of Hb sequences used as queries to detect Hb encoding genes

Query	Hb type	Hits *C. reinhardtii**	Hits *Volvox carteri**
>gi|44955888|ref|NP_976312.1| myoglobin [Homo sapiens]	3/3Hb (Mb)	None	None
>gi|56749856|sp|P68871.2|HBB_HUMAN RecName: Full = Hemoglobin subunit beta; AltName: Full = Beta-globin; AltName: Full = Hemoglobin beta chain; Contains: RecName: Full = LVV-hemorphin-7	3/3Hb (Gb)	None	None
>gi|57013850|sp|P69905.2|HBA_HUMAN RecName: Full = Hemoglobin subunit alpha; AltName: Full = Alpha-globin; AltName: Full = Hemoglobin alpha chain	3/3Hb (Gb)	None	None
>gi|19549331|ref|NP_599030.1| cytoglobin [Homo sapiens]	3/3Hb (Cb)	None	None
>gi|10864065|ref|NP_067080.1| neuroglobin [Homo sapiens]	3/3Hb (Nb)	None	None
>gi|168823435|ref|NP_078970.3| androglobin [Homo sapiens]	3/3Hb (Ab)	None[†]	None
>gi|58332516|ref|NP_001011196.1| x globin [*Xenopus* (Silurana) tropicalis]	3/3Hb (GbX)	None	None
>gi|14600601|ref|NP_147118.1| protogloblin ApPgb [Aeropyrum pernix K1]	3/3Hb (PGb)	None	None
>gi|73670387|ref|YP_306402.1| hypothetical protein Mbar_A2927 [Methanosarcina barkeri str. Fusaro]	3/3Hb (PGb)	None	None
>gi|154351341|gb|ABS73420.1| HemAT [*Bacillus* amyloliquefaciens FZB42]	3/3Hb (GCS)	None	None
>gi|300817675|ref|ZP_07097890.1| flavohemoprotein [*Escherichia coli* MS 107–1]	3/3Hb (FHb)	None	None[‡]
gi|3980177|emb|CAA38024.1| leghemoglobin [Medicago sativa]	3/3Hb (sHb)	None	None
>gi|1518444|emb|CAA90868.1| leghemoglobin B [Vicia faba]	3/3Hb (sHb)	None	None
>gi|441461|emb|CAA54331.1| leghemoglobulin II [Lupinus luteus]	3/3Hb (sHb)	None	None
>gi|313503|emb|CAA23731.1| leghemoglobin [Glycine max]	3/3Hb (sHb)	None	None
>gi|18015|emb|CAA37898.1| hemoglobin [Casuarina glauca]	3/3Hb (nsHb-1)	None	None
>gi|1707907|sp|Q08753.1|TRHN1_CHLMO RecName: Full = Group 1 truncated hemoglobin LI637; Short = CtrHb; Short = Truncated Hb; AltName: Full = Globin LI637; Flags: Precursor	2/2Hb-I	12 hits[§]	10 hits[¶]
>gi|1707909|sp|P52334.1|TRHN2_CHLMO RecName: Full = Group 1 truncated hemoglobin LI410; Short = Truncated Hb; AltName: Full = Globin LI410; Flags: Precursor	2/2Hb-I	10 hits[‖]	9 hits**
>gi|307107379|gb|EFN55622.1| hypothetical protein CHLNCDRAFT_35393 [Chlorella variabilis]	2/2Hb-I	None	None
>gi|18418064|ref|NP_567901.1| hemoglobin 3 [*Arabidopsis* thaliana]	2/2Hb-I	None	Vocar20005548m.g, E-value 1.62e−2
>gi|75318578|sp|O65532|O65532_ARATH Hypothetical protein F4D11.110 (Hypothetical protein AT4g32690)	2/2Hb-II	None	None
>gi|55379358|ref|YP_137208.1| cyanoglobin [Haloarcula marismortui ATCC 43049]	2/2Hb-I	10 hits[‖]	9 hits**
>gi|170078229|ref|YP_001734867.1| cyanoglobin [Synechococcus sp. PCC 7002]	2/2Hb-I	11 hits[‖]	10 hits**
>gi|16330583|ref|NP_441311.1| cyanoglobin [Synechocystis sp. PCC 6803]	2/2Hb-I	12 hits[§]	10 hits**
>gi|15608680|ref|NP_216058.1| glbN gene product [*Mycobacterium tuberculosis* H37Rv]	2/2Hb-I	11 hits[‖]	10 hits**

Protein sequences used for BlastP analyses on Phytozome v8.0 *Chlamydomonas reinhardtii v4.3* and *Volvox carteri*. Ab, androglobin; Cb, cytoglobin; Gb, animal α- or β-globin; GbX, globin X; FHb, flavohemoglobin; 2/2Hb, 2-on-2 helices ("truncated") Hbs; 2/2Hb-I, -II, -II, 2/2Hbs group I, II, III; 3/3Hbs, 3-on-3 helices Hbs (myoglobin-fold); Mb, myoglobin; Nb, neuroglobin; nsHb, nonsymbiotic hemoglobin (nsHb-1, -2, nsHb class1, 2); PGb, protoglobin; sHb, symbiotic hemoglobin.

*Phytozome v8.0, *Chlamydomonas reinhardtii v.4.3*, and *Volvox carteri*, BlastP using default settings.

[†] Two none-Hb domain containing proteins were detected, Cre12.g519950 (Flagellar Associated Protein, adenylate/guanylate kinase-like, E-value: 1.4e–8, and Cre10.g448850, Calpain cystein protease and Flagellar Associated Protein, E-value: 1.48e–3).

[‡] One hit Vocar20012052m.g, oxidoreductase, no hit using only the globin domain (1–148).

[§] All 12 (putative) 2/2Hbs identified as shown in Fig. 1 in the main article.

[¶] Vocar20011139m, Vocar20010321m, Vocar20010250m, Vocar20010617m, Vocar20010444m, Vocar20001214m, Vocar20005615m, Vocar20005548m, Vocar20002059m, Vocar20001900m.

[‖] Included in the list shown in Fig. 1.

**Included in ¶.

Table S2. List of 2/2Hb sequences used for the phylogenetic analysis

Organism	Abbreviation	Accession no.	Database	Total protein length (aa)/position 2/2Hb-domain* [length 2/2Hb domain (aa)]
Prokaryota				
Acetobacter pasteurianus IFO 3283–01	*A. past.*	YP_003189286	GenBank	193 /60–193(134)
Bacillus cereus ATCC 10987	*B. cereus*	NP_977638	GenBank	132 /7–132(126)
Bordetella pertussis Tohama I	*B. pertussis*	NP_880766	GenBank	134/1–124 (124)
Brachyspira murdochii DSM 12563	*B. murdochii*	YP_003632527	GenBank	124/(124)
Bradyrhizobium japonicum USDA 110	*B. japonicum*	NP_772862	GenBank	154/23–154 (132)
Burkholderia graminis C4D1M	*B. graminis* C4D1M	ZP_02883481	GenBank	180/11–130 (120)
Burkholderia multivorans ATCC 17616	*B. multivorans*	YP_001579609	GenBank	184/14–134 (121)
Campylobacter coli RM2228	*C. coli* RM2228	ZP_00367734	GenBank	150 /22–150(129)
Campylobacter fetus	*C. fetus*	YP_892161	GenBank	124 /(124)
Campylobacter jejuni subsp. *jejuni* 1336	*C. jejuni*	ZP_06373377	GenBank	127 /(127)
Campylobacter lari RM2100	*C. lari* RM2100	YP_002574763	GenBank	127 /(127)
Campylobacter upsaliensis RM3195	*C. upsaliensis*	ZP_00370192	GenBank	129 /(129)
Chloroflexus aggregans DSM 9485	*C. aggregans*	YP_002462570	GenBank	125 /(125)
Corynebacterium diphtheriae NCTC 13129	*C. diphtheriae*	NP_940138	GenBank	130 /6–130(125)
Flavobacteria bacterium BAL38	*Flavob. bact.*. BAL38	ZP_01733305	GenBank	123 /(123)
Flavobacteria bacterium BBFL7	*Flavob bact.* BBFL7	ZP_01200962	GenBank	131 /(131)
Flavobacteriaceae bacterium 3519–10	*F. bacterium*	YP_003094561	GenBank	125 /(125)
Frankia alni ACN14a	*Frankia* GlbN	YP_712694	GenBank	118 /2–118(117)
Frankia alni ACN14a	*Frankia* HbO	YP_712079	GenBank	135 /14–135(122)
Frankia sp. EuI1c	*Frankia sp.* EuI1c	YP_004014801	GenBank	150/8–150 (143)
Helicobacter bilis ATCC 43879	*H. bilis*	ZP_04580628	GenBank	132 /3–132(130)
Helicobacter canadensis MIT 98–5491	*H. canadensis*	ZP_04869854	GenBank	127 /(127)
Kordia algicida OT-1	*K. algicida*	ZP_02163608	GenBank	129 /(129)
Legionella longbeachae D-4968	*L. longbeachae*	ZP_06187916	GenBank	128 /(128)
Methylobacterium chloromethanicum CM4	*M. chloromethanicum*	YP_002423259	GenBank	130 /(130)
Mycobacterium avium 104	*M. avium*	YP_883162	GenBank	154 /5–127(123)
Mycobacterium leprae TN	*M. leprae* GlbO	NP_301903	GenBank	128 /4–128(125)
Mycobacterium sp. MCS	*Myc. sp.* MCS	YP_642448	GenBank	162 /19–162 (144)
Mycobacterium tuberculosis H37Ra	*M. tub. H37Ra*	ZP_02552072	GenBank	131 /7–131(125)
Mycobacterium tuberculosis H37Rv	*M. tub. H37Rv*	NP_216058	GenBank	136 /14–136(123)
Nitrobacter sp. Nb-311A	*N. sp.* Nb 311A	ZP_01045872	GenBank	140 /5–140(136)
Nostoc punctiforme PCC 73102	*N. punctif.*	YP_001864679	GenBank	174 /58–174(122)
Oceanobacter sp. RED65	*Oceanobacter*	ZP_01305408	GenBank	121 /(121)
Ochrobactrum anthropi ATCC 49188	*O. anthropi*	YP_001370024	GenBank	139 /6–139(134)
Paracoccus denitrificans PD1222	*P. denitrificans*	YP_917377	GenBank	140 /9–140(132)
Pedobacter heparinus DSM 2366	*P. heparinus*	YP_003092108	GenBank	129 /(129)
Pseudomonas syringae pv. syringae B728a	*P. syringae*	YP_237008	GenBank	142 /27–142 (116)
Rhizobium leguminosarum bv. viciae 3841	*R leg. viciae*	YP_765868	GenBank	155 /22–155(134)
Ralstonia eutropha H16	*R. eutropha* H16	YP_725533	GenBank	138 /15–138(124)
Rhodococcus equi 103S	*R. equi*	YP_004008063	GenBank	128 /6–128(123)
Roseobacter sp. MED193	*Ros. sp.* MED193	ZP_01057748	GenBank	144 /11–144(134)
Roseiflexus castenholzii DSM 13941	*R. castenholzii*	YP_001431358	GenBank	133 /(133)
Ruegeria pomeroyi DSS-3	*R. pomeroyi* DSS-3	YP_165021	GenBank	139 /8–139(132)
Sacharophagus degradans	*S. degradans*	ABD80803	GenBank	141 /15–141(127)
Sagittula stellata E-37	*S. stellata*	ZP_01747349	GenBank	134 /3–134(132)
Silicibacter sp. TrichCH4B	*Sil. sp. TrichCH4B*	ZP_05741205	GenBank	137 /6–137(132)
Sinorhizobium meliloti 1021	*S. meliloti*	NP_386684	GenBank	155 /22–155(134)
Sphingomonas sp. SKA58	*Sph. sp.* SKA58	ZP_01304894	GenBank	145 /1–121(121)
Synechocystis sp. PCC 6803	*S. CyGLB*	NP_441311	GenBank	124 /(124)
Tetrahymena pyriformis	*T. pyr HbN*	P17724	GenBank	121/6–121 (116)
Thiomonas intermedia K12	*T. intermedia*	YP_003643170	GenBank	162 /43–162(120)
Xanthomonas axonopodis pv. punicae str. LMG 859	*X. axonopodis*	ZP_10260820	GenBank	142 /27–142(116)
Eukaryota				
Paramecium caudatum	*P. caudatum*	P15160	GenBank	117/2–116 (116)
Chlorophyta				
Chlamydomonas meowusii	*Cm*HBN	Q08753	GenBank	164 /44–164(121)
Chlamydomonas reinhardtii	*Cr*THB1	Cre14.g615400	Phytozome	136/10–129 (120)
Chlamydomonas reinhardtii	*Cr*THB2	Cre14.g615350	Phytozome	147/ 27–147 (121)
Chlamydomonas reinhardtii	*Cr*THB3	Cre04.g218800	Phytozome	297/105–225(121)
Chlamydomonas reinhardtii	*Cr*THB4	Cre04.g218750	Phytozome	214/ 59–178 (120)

Table S2. Cont.

Organism	Abbreviation	Accession no.	Database	Total protein length (aa)/position 2/2Hb-domain* [length 2/2Hb domain (aa)]
Chlamydomonas reinhardtii	*Cr*THB5D1	Cre07.g351100	Phytozome	959 /62–182 (121)
Chlamydomonas reinhardtii	*Cr*THB5D2	Cre07.g351100	Phytozome	959/203–326(124)
Chlamydomonas reinhardtii	*Cr*THB6	Cre16.g654250	Phytozome	347 /99–224 (126)
Chlamydomonas reinhardtii	*Cr*THB7	Cre16.g661000	Phytozome	292 /54–182 (129)
Chlamydomonas reinhardtii	*Cr*THB8	Cre16.g661200	Phytozome	519 /46–166 (121)
Chlamydomonas reinhardtii	*Cr*THB9	Cre16.g661250	Phytozome	712 /53–176 (124)
Chlamydomonas reinhardtii	*Cr*THB10	Cre16.g661300	Phytozome	483 /53–175 (123)
Chlamydomonas reinhardtii	*Cr*THB11	Cre16.g662750	Phytozome	395 /51–163 (113)
Chlamydomonas reinhardtii	*Cr*THB12	Cre16.g663000	Phytozome	432 /46–166 (121)
Chlorella sp. NC64A	*C64*THB1	EFN57932	GenBank	107/(107)
Chlorella sp. NC64A	*C64*THB2	EFN56894.1	GenBank	151 /28–151 (124)
Chlorella sp. NC64A	*C64*THB3	EFN59290.1	GenBank	217 /15–141 (127)
Chlorella sp. NC64A	*C64*THB4	EFN55622.1	GenBank	244 /59–180 (122)
Chlorella sp. NC64A	*C64*THB5	EFN59229	GenBank	124 /7–124 (118)
Micromonas pusilla CCMP1545	*Mp*THB1	XP_003064586	GenBank	111 /2–111 (110)
Volvox carteri .f. nagariensis	*Vc*THB1	Vocar20001214m	Phytozome	142 /22–142(121)
Volvox carteri .f. nagariensis	*Vc*THB2	Vocar20001900m	Phytozome	290/142–270(129)
Volvox carteri .f. nagariensis	*Vc*THB3	Vocar20002059m	Phytozome	161 /6–127 (122)
Volvox carteri .f. nagariensis	*Vc*THB4	Vocar20005548m	Phytozome	462 /69–184 (116)
Volvox carteri .f. nagariensis	*Vc*THB5	Vocar20005615m	Phytozome	319 /64–184 (121)
Volvox carteri .f. nagariensis	*Vc*THB6	Vocar20010250m	Phytozome	399/146–280(135)
Volvox carteri .f. nagariensis	*Vc*THB7	Vocar20010321m	Phytozome	521 /51–171 (121)
Volvox carteri .f. nagariensis	*Vc*THB8	Vocar20010444m	Phytozome	729 /25–145 (121)
Volvox carteri .f. nagariensis	*Vc*THB9	Vocar20010617m	Phytozome	528 /54–174 (121)
Volvox carteri .f. nagariensis	*Vc*THB10	Vocar20011139m	Phytozome	244 /85–208 (124)
Planta				
Arabidopsis thaliana	*A.thal.*	NP_567901	GenBank	175/26–147 (122)
Glycine max	*G.max*	NP_001237344	GenBank	172/26–147 (122)
Vitis vinifera	*V.vinifera*	XP_002284484	GenBank	169/26–147 (122)

From left to right, columns indicate sequence origin, sequence abbreviation used in Fig. 2 in the main article, accession number of the polypeptide sequence, and data bank source, as well as total protein length, position, and length of compared 2/2Hb domains.

*No numbers are indicated when the whole protein was used.

Table S3. Relative transcript abundances of the indicated genes in anaerobic *C. reinhardtii* wild-type CC-124 and transformants ami*THB8*-1 and -2

	Relative transcript abundance				
Gene	CC-124	ami*THB8*-1	ami*THB8*-2	ami*THB8*-1 vs. CC-124	ami*THB8*-2 vs. CC-124
HYDA1	53	67	47	1.3	0.9
HYDA2	6	1	3	0.2	0.5
HYDEF	4	3	6	0.8	1.4
HYDG	13	5	10	0.4	0.8
PFR1	3.9	2.5	1.9	0.6	0.5
PFL1	65	29	45	0.4	0.7
CRR1	40	31	48	0.8	1.2
CPX1	483	429	525	0.9	1.1
CYC6	16	79	65	4.8	4.0
FDX5	646	443	497	0.7	0.8
CAT1	11	19	19	1.8	1.8
MSD3	0.4	0.6	1.5	1.5	3.5
HCP4	14	3	9	0.2	0.6
CYG12	0.6	0.1	0.2	0.2	0.3
THB8	6	0.03	0.1	0.01	0.02
RBOL2	0.1	0.06	0.08	0.5	0.7
HSP22A	474	770	1043	1.6	2.2
DES6	0.1	0.4	0.4	2.9	2.4
NAR1.3	1.6	0.6	1.0	0.4	0.6
Cre12.g512400	5	4	5	0.7	1.0
Cre01.g013450	0.01	0.01	0.007	1.0	0.6
Cre16.g668550	3	5	2	1.4	0.7
Cre03.g209200	2.4	4.3	4.2	1.8	1.7

C. reinhardtii wild-type CC-124 and transformants ami*THB8*-1 and -2 were incubated in the absence of O_2 in the dark for 7 h. Relative transcript abundances were determined by qPCR as described by Pape et al. (1). The calculated values were multiplied by 1,000. Indicated genes encode the following proteins: *CAT1*, catalase; *CPX1*, coproporphyrinogen III oxidase; *Cre01.g013450*, hemerythrin HHE cation binding domain containing protein; *Cre03.g209200*, RRM (RNA recognition motif) containing protein; *Cre12.g512400*, protein containing Sigma-54 interaction domain; *Cre16.g668550*, RING- and FYVE-type zinc finger containing protein; *CRR1*, Copper Response Regulator 1; *CYC6*, cytochrome c_6; *CYG12*, heme/nitric oxide-binding guanylate cyclase; *DES6*, omega-6-fatty acid desaturase, chloroplast isoform; *FDX5*, ferredoxin 5; *HCP4*, hybrid cluster protein 4; *HSP22A*, small heat-shock protein 22A; *HYDA1* and *HYDA2*, [FeFe]-hydrogenase isoforms HYDA1 and HYDA2; *HYDEF* and *HYDG*, [FeFe]-hydrogenase assembly proteins HYDEF and HYDG; *MSD3*, Mn superoxide dismutase; *NAR1.3*, formate nitrite transporter; *PFL1*, pyruvate:formate lyase 1; *PFR1*, pyruvate:ferredoxin oxidoreductase 1; *RBOL2*, respiratory burst oxidase 2; *THB8*, truncated hemoglobin 8.

1. Pape M, Lambertz C, Happe T, Hemschemeier A (2012) Differential expression of the *Chlamydomonas* [FeFe]-hydrogenase-encoding *HYDA1* gene is regulated by the copper response regulator1. *Plant Physiol* 159(4):1700–1712.

Table S4. Oligonucleotides used for qPCR analyses

Locus	Name	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)
Cre13.g599400	*RCK1*	GCCACACCGAGTGGGTGTCGTGCG	CCTTGCCGCCCGAGGCGCACAGCG
Cre03.g199800	*HYDA1*	GCGATTGACGTTGGTGTAGG	GTGCTTACAAGCGGCTGATG
Cre09.g396600	*HYDA2*	CGCTCCACCGACAAGCAGAT	AGCTGGTTGACCGCCTCGTT
Cre06.g296750	*HYDEF*	CTGCATGATTGACGCCCAGA	AGGCGGCCCAAGAGAAGAAC
Cre06.g296700	*HYDG*	CCGGTCAATGACGCTGACTT	ATCTGGCTCATGCCGCACTT
Cre11.g473950	*PFR1*	CGATGTGGAGGAGTGGCTGA	CAGCTCGTGGTGCAGCTTGT
Cre01.g044800	*PFL1*	CAAGTACGGCAACGACGATG	ACGTTGGAGGTGATGGTCAG
Cre02.g125250	*CRR1*	TGCGTGTTTGTTGTTTCAGG	GCCAGGTGTGATGGAGAGAC
Cre02.g085450	*CPX1*	CCAGACCTCCAAGCGTGTGT	GCGTTGCGGATCACCTTCTC
Cre16.g651050	*CYC6*	GCGGCTGCCAAGCGCGGTGCGGATG	CTGCTCAAGGGCGGCCTTGTCCAG
Cre17.g700950	*FDX5*	CGGCTTCATCCTCATGTGCT	ACGCTGACACGAATGGTACG
Cre09.g417150	*CAT1*	GATGGTATGGCCTGGTGCTG	CAATCGGATGGGCTCCCTAA
Cre16.g676150	*MSD3*	CAGCCCCAACCAGGATAAC	ACCAGACCCACCCAGGAG
Cre09.g391650	*HCP4*	AGTGGAAGTGGTGCGTGTCATTG	AGAGTACACCTAGCGCATTGCA
Cre07.g320750	*CYG12*	CGAAGGCTGCTTGCTTGAGA	GGTGGCATTGCGTGTGGTAA
Cre16.g661200	*THB8*	CGGGAGTCAGCAAGCTGTCAAC	CCGCCCGTACACAAACAAGCAC
Cre03.g188400	*RBOL2*	GGAGAGCGTGTGATACATTCG	CTGCACCCTACCATTGTCTTG
Cre07.g318800	*HSP22A*	TGCCGGCTGTGTTCGTTGAC	GGCGGGCCACAATTTGATAG
Cre13.g590500	*DES6*	TTGCGCGGGCGGCTTTGTTC	CACCGCTGCTCCACAGACAC
Cre03.g210900	*NAR1.3*	GCGTGCTGGCGGGTTTCTACA	ACAGATCCGCGCCAACCACC
Cre12.g512400	n.a.	ACACTAGCGCACTACCTACC	CCGCAGTCAGCAATGAGATG
Cre01.g013450	n.a.	CCTTCAGTGCCAAGGAGCTGAC	ATGCCGTGCTGCTGCATCATGG
Cre16.g668550	n.a.	TGAGGGCCGTCTTGACTGAG	GAACTGACGCCGTGAGAAGC
Cre03.g209200	n.a.	GAGGCGCTGATGCAGACCTT	TGTCTTCCGCGTGCTCGAA

Locus ID on Phytozome (www.phytozome.net/chlamy), gene name (n.a., not applicable), and forward and reverse oligonucleotide sequences are shown. Except for RCK1 (receptor of activated protein kinase C), gene names are the same as indicated in the legend of Table S3.