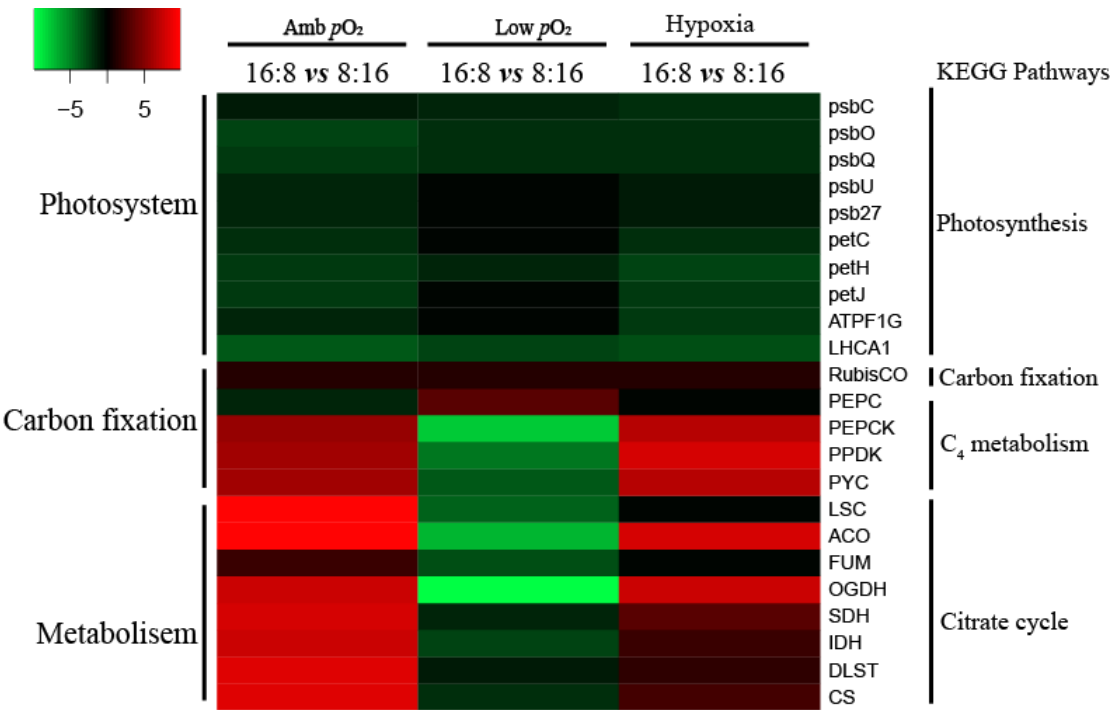


Supplemental materials

**Figure S1:** Heatmap of the photoperiod-caused changes ( $|\log_2(\text{Fold Change})| > 2$ ) in the differential expressed genes (DEGs) related to metabolism, photosystem, oxidation and carbon fixation of *T. pseudonana* under ambient  $pO_2$  (Amb  $pO_2$ ), low  $pO_2$  (Low  $pO_2$ ) and hypoxia (Hypoxia). Red and green colors indicate the up- and down-regulations of the DEGs, respectively. The complete gene names are shown in Table S2.



**Table S1:** The log-2-fold value of DEGs of *T. pseudonana* regulated by lowered  $pO_2$  under 8:16 and 16:8 L:D cycles, that are relevant to respiration, photosynthesis, carbon fixation and metabolism.

Name	L:D 8:16		L:D 16:8		Complete name	KEGG pathway
	Low $pO_2$ vs Amb $pO_2$	Hypoxia vs Amb $pO_2$	Low $pO_2$ vs Amb $pO_2$	Hypoxia vs Amb $pO_2$		
TKT	6.41	4.56	0.00	-4.72	transketolase	
ALDO	-1.38	0.00	0.00	7.08	fructose-bisphosphate aldolase	
SEBP	0.00	0.00	0.00	0.00	sedoheptulose-1,7-bisphosphatase	
XFP	0.00	0.00	0.00	0.00	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase	
RPI	-1.06	0.00	0.00	0.00	ribose 5-phosphate isomerase	
GAP	0.00	1.67	0.00	0.00	glyceraldehyde-3-phosphate dehydrogenase (NADP+)	Calvin cycle
TPI	-4.54	-2.36	0.00	0.00	triosephosphate isomerase	
GPI	0.00	0.00	0.00	0.00	glucose-6-phosphate isomerase	
PRK	-1.38	0.00	1.20	0.00	phosphoribulokinase	
FBP	0.00	0.00	0.00	0.00	fructose-1,6-bisphosphatase	
G6PC	0.00	0.00	0.00	0.00	glucose-6-phosphatase	
Rubisco	0.00	0.00	0.00	0.00	ribulose-1,5-bisphosphate carboxylase/oxygenase	
PGK	0.00	0.00	-7.20	-7.86	phosphoglycerate kinase	
PPDK	1.22	-2.74		-7.12	pyruvate, orthophosphate dikinase	C <sub>4</sub> metabolism
PEPC	-4.60	-1.52	1.16	-8.63	phosphoenolpyruvate carboxylase	

PYC	-3.73	1.19	-8.69	-8.18	pyruvate carboxylase	
PYK	2.42	4.48	1.29		pyruvate kinase	
PEPC					phosphoenolpyruvate	
K	-4.45	0.00	-5.96	-8.47	carboxykinase (ATP)	
					2,3-bisphosphoglycerate-	
PGAM	6.70	1.68	0.00	0.00	dependent phosphoglycerate	
					mutase	
ENO	-5.89	1.85	0.00	0.00	enolase	
PGP	0.00	0.00	0.00	0.00	phosphoglycolate phosphatase	
GLC	0.00	2.08	-7.34	-7.46	glycolate oxidase	
CAT	0.00	0.00	0.00	0.00	catalase	
					glycine	
GLY	1.79	3.04	-3.94	-9.10	hydroxymethyltransferase	glyoxylate and
					glycine dehydrogenase	dicarboxylate
GDC	7.21	1.36	0.00	-8.09	glutamate--glyoxylate	metabolism
					aminotransferase	
GGAT	1.34	1.60	0.00	0.00	alanine-glyoxylate transaminase	
AGXT	0.00	0.00	0.00	0.00	glyoxylate/hydroxypyruvate	
GHR	0.00	0.00	0.00	-7.62	reductase	
GLYK	0.00	0.00	0.00	0.00	D-glycerate 3-kinase	
GLU	0.00	1.61	-2.62	-7.80	glutamate synthase (ferredoxin)	
GLN	6.85	2.50	-2.46	-5.56	glutamine synthetase	
					glucose-6-phosphate	1-
G6PD	0.00	-1.43	-2.84	-7.42	dehydrogenase	Pentose
PGL	0.00	0.00	0.00	0.00	6-phosphogluconolactonase	phosphate
6PGD	0.00	0.00	0.00	0.00	6-phosphogluconate	pathway

RPE	0.00	0.00	0.00	0.00	dehydrogenase	
CS	-4.87	0.00	0.00	-8.83	ribulose-phosphate 3-epimerase	
ACO	-5.99	-6.69	-11.06	-7.06	citrate synthase	
IDH	-9.48	-4.83	-9.27	-4.94	aconitate hydratase	
DLST	-6.37	-5.15	-7.12	-8.82	isocitrate dehydrogenase	
LSC	-6.81	-6.88	0.00	-8.63	2-oxoglutarate dehydrogenase	
SDH	-7.97	-6.33	-9.13	-9.25	succinyl-CoA synthetase	
FUM	-6.11	-4.92	-4.28	-5.40	succinate dehydrogenase	Citrate cycle
NAD-ME	-5.21	0.00	0.00	0.00	(ubiquinone) fumarate hydratase	
OGDH	-6.39	-7.65	-8.31	-9.23	malate dehydrogenase	
PSB27	-1.19	0.00	0.00	0.00	(oxaloacetate-decarboxylating) (NADP+)	
PETC	-1.19	0.00	0.00	0.00	2-oxoglutarate dehydrogenase E1 component	
PETJ	-1.59	0.00	0.00	0.00	photosystem II Psb27 protein	
petH	0.00	0.00	0.00	-8.85	cytochrome b6-f complex iron-sulfur subunit	
ATPF1 B	-3.78	-1.90	0.00	0.00	cytochrome c6	
ATPF1 A	-1.33	0.00	0.00	0.00	ferredoxin--NADP+ reductase	
LHCA 1	-3.48	-2.64	0.00	-1.01	F-type H+/Na+-transporting ATPase subunit beta	Photosynthesis
					F-type H+/Na+-transporting ATPase subunit alpha	
					light-harvesting complex I	
					chlorophyll a/b binding protein 1	

ACAC	-7.57	-7.36	7.98	-7.55	acetyl-CoA carboxylase	
FabF	9.15	-2.53	-7.25	-9.51	3-oxoacyl-[acyl-carrier-protein] synthase II	
FabG	-3.36	-3.02	-5.04	-9.61	3-oxoacyl-[acyl-carrier protein] reductase	
FabI	-4.15	-2.08	-7.34	7.47	enoyl-[acyl-carrier protein] reductase I	Fatty acid biosynthesis
FabZ	-1.21	0.00	0.00	0.00	3-hydroxyacyl-[acyl-carrier- protein] dehydratase	
ACSL	-1.55	-1.06	0.00	-9.02	long-chain acyl-CoA synthetase	
FabH	6.77	0.00	3.78	-4.33	3-oxoacyl-[acyl-carrier-protein] synthase III	
FabD	0.00	0.00	0.00	-6.96	[acyl-carrier-protein] S- malonyltransferase	
SOD	-5.53	0.00	-8.99	-9.11	superoxide dismutase	Peroxisome
ACSL	-1.55	-1.06	0.00	-9.02	long-chain acyl-CoA synthetase	
ACOX	0.00	0.00	0.00	-4.60	acyl-CoA oxidase	
GCDH	0.00	0.00	3.26	-7.55	glutaryl-CoA dehydrogenase	
ACAT	-6.72	-3.55	-5.35	-5.77	acetyl-CoA C-acetyltransferase	Fatty acid degradation
ALDH	-6.37	-2.34	0.00	-5.60	aldehyde dehydrogenase (NAD+)	
HADH	-4.89	-2.43	0.00	0.00	3-hydroxyacyl-CoA dehydrogenase	
FadA	-8.49	-4.22	0.00	0.00	acetyl-CoA acyltransferase	
ND1	-4.37	-3.19	0.00	0.00	NADH-ubiquinone oxidoreductase chain 1	Oxidative phosphorylation

ND4	-6.51	-7.76	0.00	0.00	NADH-ubiquinone oxidoreductase chain 4
ND5	-3.80	0.00	0.00	0.00	NADH-ubiquinone oxidoreductase chain 5
ND6	0.00	0.00	-7.57	-7.71	NADH-ubiquinone oxidoreductase chain 6
NDUF S2	-8.03	-4.41	-7.96	-8.09	NADH dehydrogenase (ubiquinone) Fe-S protein 2
NDUF S7	-2.59	-3.76	-4.20	-5.23	NADH dehydrogenase (ubiquinone) Fe-S protein 7
NDUF S8	0.00	0.00	0.00	-6.71	NADH dehydrogenase (ubiquinone) Fe-S protein 8
NDUF V1	-4.03	-3.83	-7.63	-7.76	NADH dehydrogenase (ubiquinone) flavoprotein 1
NDUF V2	-1.06	0.00	0.00	-7.65	NADH dehydrogenase (ubiquinone) flavoprotein 2
NDUF A9	-1.53	-1.11	0.00	0.00	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 9
NDUF A12	-4.14	1.68	0.00	7.79	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 12
SDHA	-7.97	-6.33	-4.65	-5.98	succinate dehydrogenase (ubiquinone) flavoprotein subunit
SDHB	-4.74	-3.96	-9.13	-9.25	succinate dehydrogenase

					(ubiquinone) iron-sulfur subunit
ISP	-5.03	-2.70	0.00	0.00	ubiquinol-cytochrome c
					reductase iron-sulfur subunit
Cyt b	-4.42	-3.56	7.52	8.43	ubiquinol-cytochrome c
					reductase cytochrome b/c1
					subunit
COX1 0	-7.46	0.00	0.00	-3.84	heme o synthase
COX1	-4.48	-3.81	-5.76	-6.69	cytochrome c oxidase subunit 1
COX2	-6.85	-6.64	-4.62	-10.0	cytochrome c oxidase subunit 2
COX3	0.00	0.00	-9.40	-9.53	cytochrome c oxidase subunit 3
COX1 1	0.00	-4.88	-6.67	0.00	cytochrome c oxidase assembly
					protein subunit 11
COX1 5	-1.07	0.00	0.00	-6.93	heme a synthase
ATP1	9.63	8.10	0.00	-4.87	F-type H <sup>+</sup> -transporting ATPase
					subunit alpha
ATP2	7.61	-6.88	-7.90	-10.65	F-type H <sup>+</sup> -transporting ATPase
					subunit beta
ATP3	0.00	0.00	-3.06	-5.78	F-type H <sup>+</sup> -transporting ATPase
					subunit gamma
ATP6	-4.46	-4.21	-4.51	-5.95	F-type H <sup>+</sup> -transporting ATPase
					subunit a

---

**Table S2:** The log-2-fold value (n=2) of DEGs of *T. pseudonana* regulated by photoperiod under ambient  $pO_2$  (Amb  $pO_2$ ), low  $pO_2$  (Low  $pO_2$ ) and hypoxia (Hypoxia), that are relevant to respiration, photosynthesis, carbon fixation and metabolism.

Name	16:8 L:D vs 8:16 L:D			Complete name	KEGG pathway
	Amb $pO_2$	Low $pO_2$	Hypoxia		
RubisCO	1.47	1.51	1.45	ribulose-1,5-bisphosphate carboxylase/oxygenase	Calvin cycle
psbC	-1.12	-1.2	-1.67	photosystem II CP43 chlorophyll apoprotein	
psbO	-2.38	-1.92	-1.85	photosystem II oxygen-evolving enhancer protein 1	Photosynthesis
psbQ	-2.21	-1.69	-1.86	photosystem II oxygen-evolving enhancer protein 3	
psbU	-1.31	0	-1.11	photosystem II PsbU protein	
psb27	-1.5	0	-1.12	photosystem II Psb27 protein	
petC	-1.69	0	-1.62	cytochrome b6-f complex iron-sulfur subunit	
petH	-2.06	-1.42	-2.74	ferredoxin--NADP+ reductase	
petJ	-2.3	0	-2.26	cytochrome c6	
ATPFI	-1.46	0	-2.01	F-type H <sup>+</sup> -transporting ATPase subunit gamma	
LHC A1	-3.5	-2.61	-2.95	light-harvesting complex I chlorophyll a/b binding protein 1	
PEPC	-1.54	3.17	0	phosphoenolpyruvate carboxylase	
PEPC K	5.69	-7.48	6.79	phosphoenolpyruvate carboxykinase (ATP)	C4 metabolism
PPDK	5.88	-4.56	7.92	pyruvate, orthophosphate dikinase	
PYC	5.88	-3.25	6.75	pyruvate carboxylase	
LSC	9.45	-3.76	0	succinyl-CoA synthetase	
ACO	9.49	-6.97	8.16	aconitate hydratase	Citrate cycle
FUM	2.22	-2.81	0	fumarate hydratase	
OGDH	7.61	-9.78	7.68	2-oxoglutarate dehydrogenase E1 component	
SDH	7.93	-1.26	3.24	succinate dehydrogenase (ubiquinone)	
IDH	7.61	-2.66	1.98	isocitrate dehydrogenase	
DLST	8.3	-1.02	1.96	2-oxoglutarate dehydrogenase	
CS	8.31	-1.95	2.37	citrate synthase	



**Table S3:** Sequencing results of the transcriptome data of *T. pseudonana* under 8:16 and 16:8 Light:Dark (L:D) cycles, under ambient  $pO_2$  (Amb  $pO_2$ ), low  $pO_2$  (Low  $pO_2$ ) and hypoxia (Hypoxia) conditions.

Light cycle	Sample	Clean Reads	Clean Bases	Error (%)	Q20 (%)	Q30 (%)	GC Content (%)
L:D 8:16	Amb $pO_2$ 1	20982710	6.29G	0.03	97.3	92.68	48.32
	Amb $pO_2$ 2	21031757	6.31G	0.03	97.23	92.61	48.19
	Low $pO_2$ 1	22018345	6.61G	0.03	97.26	92.53	48.42
	Low $pO_2$ 2	21253450	6.38G	0.03	97.27	92.58	48.13
	Hypoxia 1	21215167	6.36G	0.03	97.38	92.72	49.06
	Hypoxia 2	22068261	6.62G	0.03	97.39	92.88	48.73
L:D 16:8	Amb $pO_2$ 1	22034592	6.61G	0.03	96.57	91.56	46.51
	Amb $pO_2$ 2	21943845	6.58G	0.03	96.32	91.14	45.48
	Low $pO_2$ 1	21462414	6.44G	0.03	97.01	91.95	47.28
	Low $pO_2$ 2	21426806	6.43G	0.03	96.91	91.99	46.3
	Hypoxia 1	21673292	6.50G	0.03	97.55	93.1	48.06
	Hypoxia 2	21424291	6.43G	0.03	97.37	92.7	47.89

**Table S4:** Numbers of unigenes annotated in seven databases of *T. pseudonana* grown under 8:16 and 16:8 Light:Dark (L:D) cycles, under ambient  $pO_2$  (Amb  $pO_2$ ), low  $pO_2$  (Low  $pO_2$ ) and hypoxia (Hypoxia) conditions.

	Number of Unigenes	Percentage (%)
Annotated in NR	19249	62.24
Annotated in NT	8672	28.04
Annotated in KO	7181	23.22
Annotated in SwissProt	17397	56.25
Annotated in PFAM	19390	62.7
Annotated in GO	19389	62.7
Annotated in KOG	6845	22.13
Annotated in all Databases	2267	7.33
Annotated in at least one Database	24945	80.66
Total Unigenes	30923	100

**Table S5:** Statistical results of DEGs of *T. pseudonana* grown under 8:16 and 16:8 Light:Dark (L:D) cycles, under ambient  $pO_2$  (Amb  $pO_2$ ), low  $pO_2$  (Low  $pO_2$ ) and hypoxia (Hypoxia) conditions.

Light cycle	O <sub>2</sub> concentration	All	Up	Down
L:D 8:16	Low $pO_2$ vs Amb $pO_2$	3048	1397	1651
	Hypoxia vs Amb $pO_2$	2333	1160	1173
	Low $pO_2$ vs Hypoxia	2343	1216	1127
L:D 16:8	Low $pO_2$ vs Amb $pO_2$	992	236	756
	Hypoxia vs Amb $pO_2$	2043	395	1648
	Low $pO_2$ vs Hyp	414	65	349
16:8 vs 8:16	Amb $pO_2$	3983	1428	2555
	Low $pO_2$	2378	963	1415
	Hypoxia	2659	939	1720