

**Table S1.** Genes, products, and primers.

Locus tag	Symbol	Product	Primers
CHLRE_10g424500v5	<i>CPK4</i>	ribokinase	GCTTCCCGACCTTCTTG CCGCCACAATGATGATG
CHLRE_01g026250v5	<i>AGA1</i>	alpha-galactosidase	GATGACTGCTGGATGGAGAA TACACGCCAACITGAGG
CHLRE_08g359350v5	<i>CARB1</i>	acetyl-CoA carboxylase, biotin carboxylase subunit	GCGGCAGAGATTGCTGTG GGGATGTTGAGGTAGGACT
CHLRE_04g216950v5	<i>KASIII</i>	3-oxoacyl-[acyl-carrier-protein] synthase III	GCCTCCTACGCCAACATCCACAT GCATCACCAAGCCAGTCCACAGA
CHLRE_17g709850v5	<i>ACK2</i>	acetate kinase	GCGTCTGGTCCTGAAC ACATTCTCCTTGATGAAATCC
CHLRE_09g396700v5	<i>ACK1</i>	acetate kinase	CCTGTCGGGTCGGCAGTG GTGGTCCTGGCGGGAAATCT
CHLRE_12g552200v5	<i>PHOB</i>	starch phosphorylase	GTGTTGGAGGGCGACGA TGTGGCAGCGGTGTTCT
CHLRE_01g055408v5	<i>ACS2</i>	acetyl CoA synthetase	GCAGGACAAGCAACAGTACCGAGG TCCAGGCAGTTGAGGCGATG
CHLRE_03g181500v5	<i>STA11</i>	4-alpha-glucanotransferase	GCTCATCAAGGACGGACTGC ACTGCCACCACGCCAACT
CHLRE_02g080200v5	<i>TRK1</i>	transketolase	CGACGCCATCAACAAGTCCAAGT TCGTAGCCAGTCAGGTGCATCAT
CHLRE_12g501000v5	<i>TPT</i>	triose phosphate/phosphate translocator	GTCAAGTCGTGGCAGCAGTT GAAGAAGGGCGTCGTGGAG
CHLRE_06g263850v5	<i>PPT2</i>	phosphate/phosphoenolpyruvate translocator	GCTCTGCAAAGGCACCAAGTC GCCCTTATCGGACTGCCATCT
CHLRE_06g307150v5	<i>AMYB1</i>	beta-amylase	AGCCAGTGCCTCTCAGA AAGCGGTCCCTCGTCTATCATT
CHLRE_12g519100v5	<i>ACX2</i>	acetyl-CoA carboxylase carboxyl transferase subunit alpha	CGGTATCGGCAGCATCAAT ACATCTCACGCCAGGTTCAC
CHLRE_17g715250v5	<i>BCC1</i>	acetyl-coa biotin carboxyl carrier	CCGAGGAGGTTGAGGCTGCTA CAGGCTGAAACGCTTGCTCTTC
CHLRE_17g713350v5	<i>OMT1</i>	oxoglutarate:malate antiporter	GGAGTGCCTGAACACAAC AGAAGTAGTGCAGTAGAAAGT
CHLRE_02g088600v5	<i>ACLB1</i>	ATP citrate lyase, subunit B	CGAGACTCCATCTGTCGCTGCT CTGCGGAAGGAGGCGTAGTTGAT
CHLRE_01g071662v5	<i>ACS1</i>	acetyl CoA synthetase	CTGACTCTATTGTTGCGAAGG CGTTGATGTTGGACTGGC
CHLRE_03g149100v5	<i>CIS2</i>	citrate synthase	AACACCACCGCCGTAC TCACATCAATCACCTCCGTG
CHLRE_02g075700v5*	<i>RPL19</i>	ribosomal protein L19	TCGGTTCTGAAC TGCGGTCTG CGGGCTGCTTACGGAAGATGA
CHLRE_03g195600v5	<i>TRE1</i>	alpha,alpha-trehalase	GACTCCTACTGGGTACCTGGG GCTGGCTGCGGTTGGTGT

CHLRE_03g206800v5	<i>HXT1</i>	hexose transporter	CTGATCGCGTGTGCTGTTC ACGGAGGATGAGAAGTAGACCAGG G
CHLRE_14g630847v5	<i>TAL2</i>	transaldolase	CCGCCTTCCACCATTGT GCTGTTGCTGTTCTGCC
CHLRE_05g241850v5	<i>ACLA1</i>	ATP citrate lyase, subunit A	TGCCTATCCAGGTGTTCAGTTCA CGGGCGGTGGCGAAATCAAT
CHLRE_02g141400v5	<i>PCK1</i>	phosphoenolpyruvate carboxykinase	TTATGAACAACGCCCGCATCC GCTCAGTCACGCCCATCTCAGT
CHLRE_01g045550v5	<i>APE2</i>	triose phosphate translocator	GCTCGTCCGTGCTGTTCTCA CCTTCTTGCTGTTGTGCTTGCT
CHLRE_12g486600v5	<i>MEX1</i>	maltose exporter-like protein	GATGGAAGGGCGACGGACAAC CATTCTGGACGACTTGCAGAAC
CHLRE_06g260450v5	<i>DIT</i>	2-oxoglutarate/malate translocator	GCGGCGACCACCAATGAGAT GCGACTTGATGATGGGCACAAAGA
CHLRE_02g117500v5	<i>HXK1</i>	hexokinase	CACTCGGCATCCTCATCCTA CGTCGGCAGCATCATCAT
CHLRE_05g234550v5	<i>FBA3</i>	fructose-1,6-bisphosphate aldolase	GCCCTGATGATGAAGTCGTCGG CAACGGTGCCAGCGGTCTT
CHLRE_01g029300v5	<i>TPIC1</i>	triose phosphate isomerase	ACGAGGTGGTGGCGAAGAAGACT GGCGTCCAGAACCTTGAACACAGA
CHLRE_02g120100v5	<i>RBCS1</i>	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit 1	CTGAAGCCCGCCGTCAAGG AGAGGAGGCAGGTAGGAGAAGGT
CHLRE_10g444700v5	<i>SBE3</i>	starch branching enzyme	CCAACTGCGTCACCATCG GCTTCATCACCTCAATCCACTT

**Table S2.** Cell density.

Days after inoculation	CD 10 <sup>6</sup> cells/mL	t-test
mixotrophic		
	MM	MA
		<i>p</i> -value
1	0.031±0.0033	0.012±0.004
2	1.1±0.13	0.43±0.14
3	4.2±1.2	2.0±0.19
4	8.6±1.3	6.7±0.54
5-7 *	9.41±0.95	8.46±0.94
autotrophic		
	C	
	AM	AA
		<i>p</i> -value
3	0.15±0.058	0.016±0.0054
6	0.8±0.21	0.35±0.14
9	1.9±0.34	1.4±0.21
12	3.1±0.24	2.9±0.39
17-23*	4.28±0.54	4.59±0.65

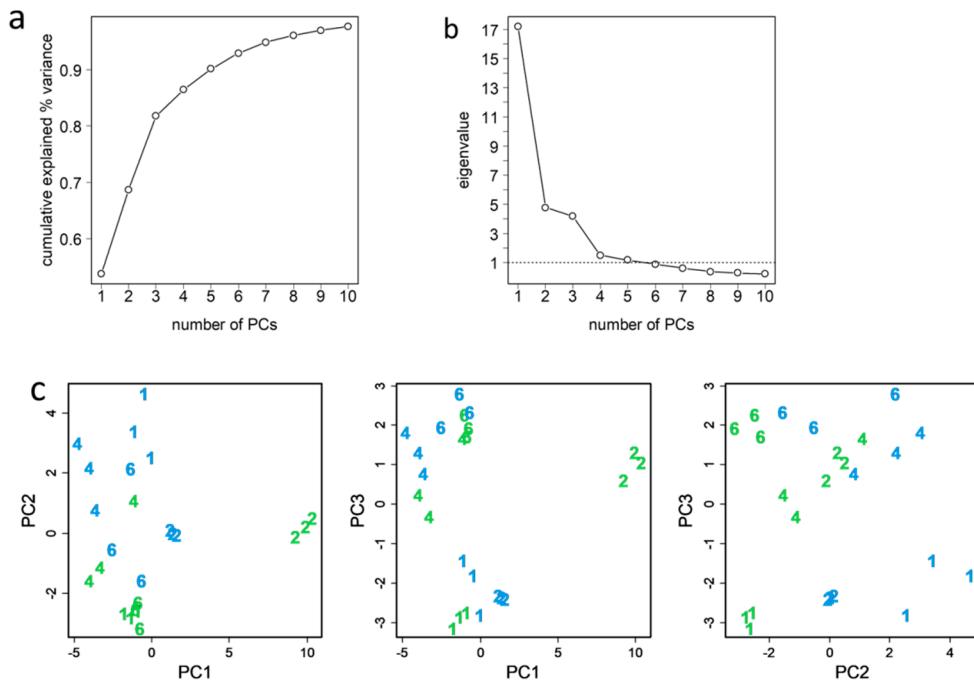
\*stationary phase

**Table S3.** Fold changes in relative gene expression and adjusted *p*-value from *t*-test for mixotrophic cultures.

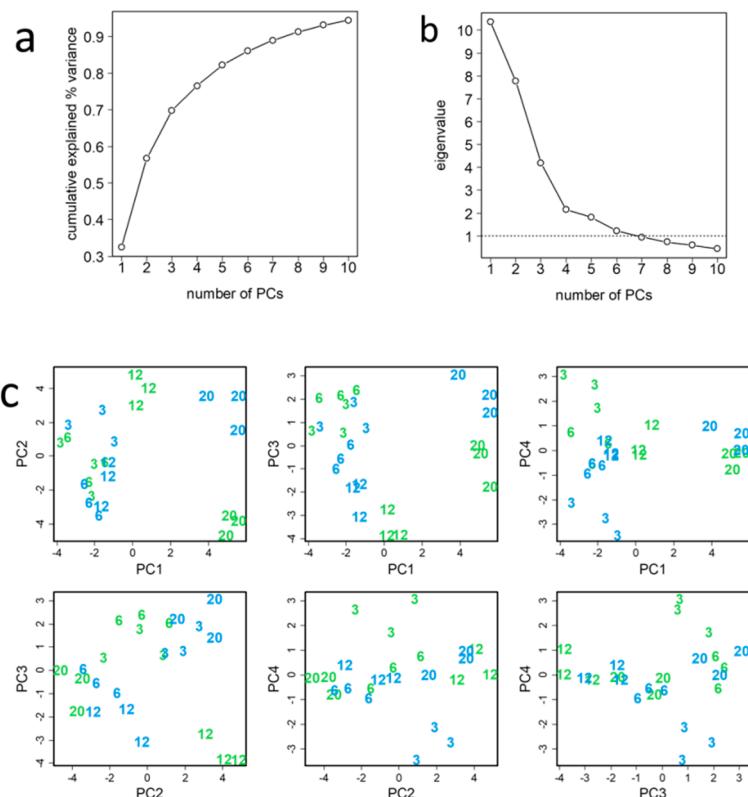
	1 days			2 days			4 days			6 days		
gene	FC	MM/MA	FDR	FC	MM/MA	FDR	FC	MM/MA	FDR	FC	MM/MA	FDR
<i>CPK4</i>	0.4	0.031		0.26	0.0012		1.42	0.5		0.68	0.52	
<i>CARB1</i>	4.49	0.023		0.12	0.096		1.51	0.37		3.83	0.48	
<i>KASIII</i>	0.53	0.11		0.37	0.00096		0.25	0.37		1.29	0.65	
<i>PHOB</i>	2.04	0.013		0.6	0.011		0.83	0.73		1.1	0.89	
<i>ACX2</i>	0.68	0.25		0.13	0.0051		0.27	0.37		0.48	0.48	
<i>TRE1</i>	27.16	0.037		0.1	0.0051		1.48	0.37		1.7	0.068	
<i>ACK1</i>	1.73	0.16		0.18	0.015		1.29	0.7		0.89	0.71	
<i>ACK2</i>	0.43	0.063		0.38	0.027		0.29	0.37		0.49	0.48	
<i>ACLA1</i>	0.55	0.077		0.48	0.16		1.03	0.95		0.39	0.28	
<i>ACLB1</i>	0.89	0.64		0.6	0.072		1.11	0.9		1.13	0.71	
<i>ACS1</i>	8.65	0.022		1.92	0.039		1.16	0.73		1.01	0.99	
<i>ACS2</i>	1.73	0.02		0.51	0.015		0.81	0.7		1.13	0.71	
<i>AGA1</i>	0.97	0.85		0.05	0.0014		1.67	0.37		0.98	0.92	
<i>AMYB1</i>	2.04	0.047		0.15	0.0037		0.68	0.38		0.95	0.86	
<i>APE2</i>	0.56	0.057		0.21	0.0051		0.84	0.73		0.88	0.65	
<i>BCC1</i>	0.58	0.043		0.14	0.046		0.47	0.37		0.6	0.5	
<i>CIS2</i>	2.76	0.015		0.1	0.012		0.87	0.7		1.13	0.71	
<i>FBA3</i>	0.5	0.03		0.09	0.012		0.31	0.082		0.83	0.65	
<i>HXK1</i>	0.29	0.015		0.37	0.046		0.47	0.7		0.1	0.28	
<i>HXT1</i>	0.29	0.03		0.32	0.029		0.78	0.37		0.85	0.65	
<i>DIT</i>	6.14	0.016		0.06	0.046		1.56	0.37		1.63	0.52	
<i>MEX1</i>	0.37	0.03		0.33	0.0033		0.93	0.37		0.61	0.48	
<i>OMT1</i>	0.24	0.019		0.23	0.0012		0.18	0.37		0.54	0.48	
<i>PCK1</i>	0.88	0.32		0.19	0.0018		0.26	0.082		1.07	0.86	
<i>TPT</i>	2.86	0.022		0.28	0.012		2.1	0.35		1.7	0.5	
<i>RBCS1</i>	3.01	0.12		1.67	0.046		5.43	0.37		2.05	0.52	
<i>SBE3</i>	1.57	0.015		0.18	0.0072		0.79	0.7		1.21	0.65	
<i>STA11</i>	0.78	0.33		0.21	0.0067		0.48	0.37		0.71	0.65	
<i>TAL2</i>	5.63	0.016		0.18	0.0087		1.24	0.73		2.83	0.19	
<i>TPIC1</i>	1.22	0.38		0.86	0.039		1.14	0.7		0.98	0.95	
<i>PPT2</i>	0.84	0.51		0.25	0.033		1.72	0.38		1.34	0.65	
<i>TRK1</i>	4.48	0.022		0.35	0.18		0.53	0.7		1.54	0.4	

**Table S4.** Fold changes in relative gene expression and adjusted *p*-value from *t*-test for autotrophic cultures.

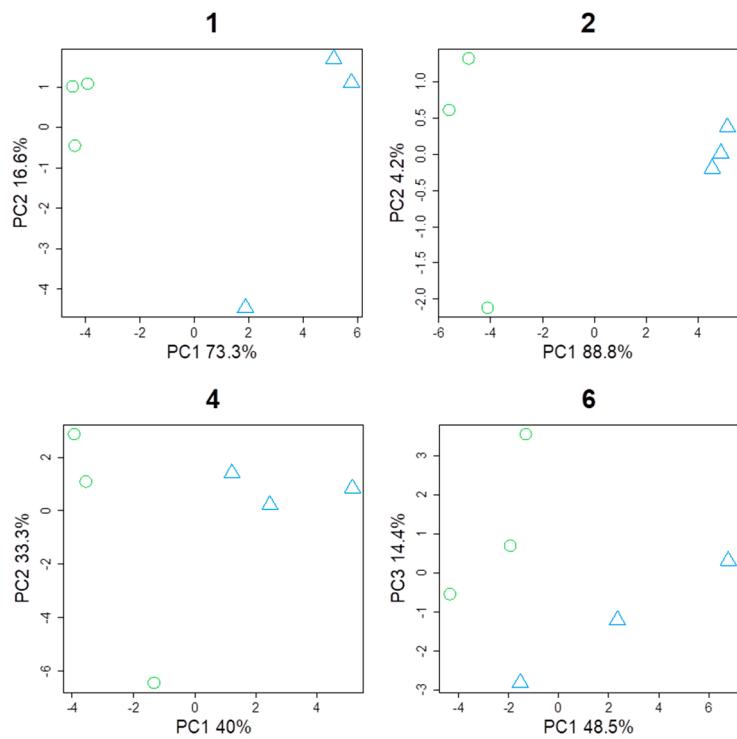
3 days			6 days		12 days		20 days	
gene	FC AM/AA	FDR	FC AM/A	FDR	FC AM/AA	FDR	FC AM/A	FDR
<i>CPK4</i>	0	0.12	0.31	0.11	0.57	0.2	0.01	0.15
<i>CARB1</i>	5.23	0.12	1.45	0.67	0.54	0.24	3.02	0.48
<i>KASIII</i>	0.98	0.96	0.78	0.35	1	1	103.11	0.014
<i>PHOB</i>	0.72	0.57	0.84	0.7	0.08	0.18	2.71	0.33
<i>ACX2</i>	1.66	0.77	0.14	0.11	0.26	0.064	6.51	0.0072
<i>TRE1</i>	0.01	0.57	6.02	0.35	31.43	0.064	NA	NA
<i>ACK1</i>	0.75	0.84	0.94	0.91	2.06	0.14	1.41	0.66
<i>ACK2</i>	0.94	0.96	0.78	0.42	1.45	0.36	1.65	0.64
<i>ACLA1</i>	1.04	0.96	0.91	0.9	3.59	0.19	0.94	0.93
<i>ACLB1</i>	1.39	0.77	0.28	0.3	0.72	0.2	2.86	0.42
<i>ACS1</i>	0.18	0.14	0.45	0.38	1.09	0.89	0.62	0.42
<i>ACS2</i>	1.26	0.77	0.89	0.83	0.26	0.12	1.54	0.32
<i>AGA1</i>	3.3	0.12	0.49	0.38	0.04	0.24	9.91	0.071
<i>AMYB1</i>	1.32	0.77	0.84	0.7	0.8	0.25	2.12	0.067
<i>APE2</i>	1.17	0.87	0.72	0.52	1.09	0.3	6.15	0.13
<i>BCC1</i>	2.12	0.57	0.89	0.7	1.81	0.2	1.92	0.5
<i>CIS2</i>	0.95	0.96	0.34	0.19	0.76	0.25	2.12	0.066
<i>FBA3</i>	0.93	0.96	0.66	0.3	1.23	0.44	1.05	0.93
<i>HXK1</i>	0.74	0.77	0.95	0.91	0.74	0.36	2.44	0.46
<i>HXT1</i>	0.26	0.46	0.87	0.7	0.55	0.064	3.56	0.071
<i>DIT</i>	4.31	0.31	0.22	0.0043	0.46	0.36	4.03	0.067
<i>MEX1</i>	1.3	0.8	0.26	0.11	0.93	0.92	3.76	0.41
<i>OMT1</i>	0.77	0.77	0.68	0.52	1.61	0.25	0.58	0.44
<i>PCK1</i>	0.87	0.92	0.42	0.18	0.69	0.25	3.32	0.039
<i>TPT</i>	2.82	0.031	1.09	0.91	0.37	0.11	2.25	0.014
<i>RBCS1</i>	1.01	0.96	1.86	0.35	0.39	0.31	2.75	0.39
<i>SBE3</i>	5.62	0.18	0.34	0.29	0.2	0.064	3.15	0.08
<i>STA11</i>	0.75	0.84	0.37	0.35	0.15	0.25	0	0.014
<i>TAL2</i>	0.44	0.49	0.81	0.73	0.33	0.24	3.87	0.039
<i>TPIC1</i>	1.44	0.37	1.04	0.94	0.38	0.25	2.48	0.24
<i>PPT2</i>	8.57	0.031	1.55	0.35	1.01	1	1.09	0.93
<i>TRK1</i>	1.05	0.96	0.77	0.7	0.4	0.1	2.23	0.42



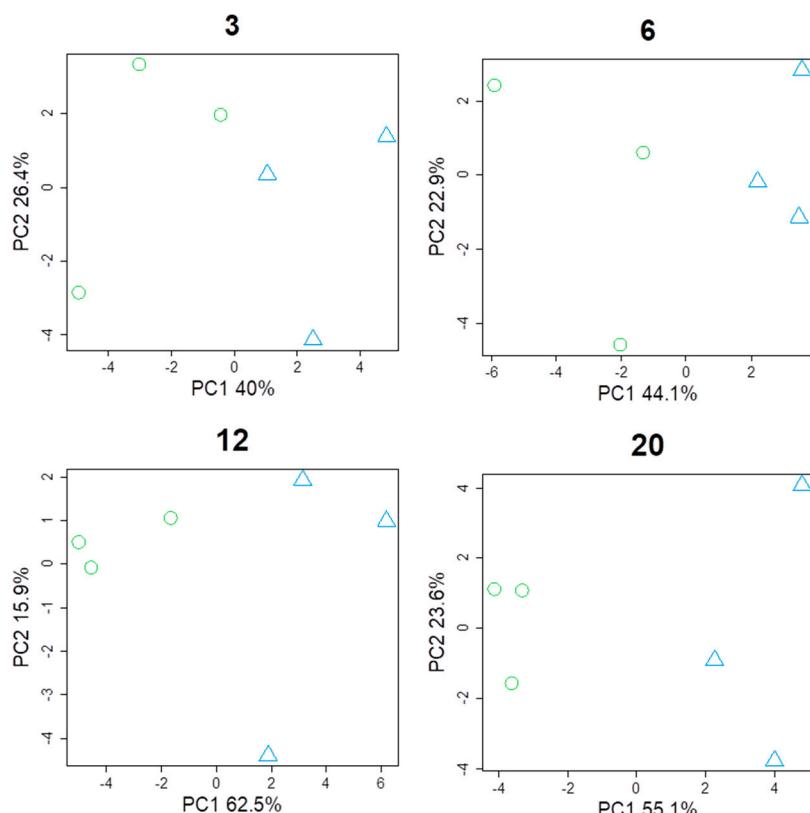
**Figure S1.** PCA of expression profiles from mixotrophic *C. reinhardtii* cultures. Curves showing the dependence of the explained variance (**a**) on the number of principal components and the eigenvalues of the components (**b**), (**c**) scores plots of the first 3 principal components. Numbers—time after inoculation, days; color—type of acclimation: green indicates autotrophy, blue indicates mixotrophy.



**Figure S2.** PCA of expression profiles from autotrophic *C. reinhardtii* cultures. Curves showing the dependence of the explained variance (**a**) on the number of principal components and the eigenvalues of the components (**b**), (**c**) scores plots of the first 4 principal components. Numbers—time after inoculation, days; color—type of acclimation: green indicates autotrophy, blue indicates mixotrophy.



**Figure S3.** PCA score plots derived from the analysis of the expression profiles from mixotrophic batch cultures of *C. reinhardtii* of four ages acclimated to mixotrophy (blue triangles) and autotrophy (green circles). Samples were taken at 1, 2, 4, and 6 days after inoculation (numbers above plots).



**Figure S4.** PCA score plots derived from the analysis of the expression profiles from autotrophic batch cultures of *C. reinhardtii* of four ages acclimated to mixotrophy (blue triangles) and autotrophy (green circles). Samples were taken at 3, 6, 12, and 20 days after inoculation (numbers above plots).

**Table S5.** *t*-test of differences in PC1 values in pairwise comparison of cultures with different acclimation at each time point (Figures S3 and S4 above).

DAI	<i>p</i>	fdr
mixotrophy		
1	0.018	0.029
2	0.00056	0.0045
4	0.018	0.029
6	0.16	0.16
autotrophy		
3	0.032	0.044
6	0.039	0.045
12	0.012	0.029
20	0.0061	0.024