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R. Willamme, K.A. Bogaert, F. Remacle, C. Remacle

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RNA-seq data and surprisal analysis of *icl* mutant and control strain of the green microalga *Chlamydomonas reinhardtii* during day/night cycles

Willamme R[1], Bogaert KA[2], Remacle F[2], Remacle C[1*]

[1]Genetics and Physiology of Microalgae, UR InBios, Chemin de la Vallée, 4, University of Liège, 4000 Liège, Belgium

[2]Theoretical Physical Chemistry, UR MOLSYS, Allée du 6 Août, 11, University of Liège, 4000 Liège, Belgium

Remi.Willamme@doct.uliege.be;

bogaert.kenny@gmail.com

fremacle@uliege.be

c.remacle@ulg.ac.be

Abstract

The data presented in this article are associated to the research article *"***Surprisal analysis of the transcriptomic response of the green microalga *Chlamydomonas* to the addition of acetate during day/night cycles"** (R. Willamme, K.A. Bogaert, F. Remacle, C. Remacle, 2018) [1]. Here the RNA-seq data of the *icl* mutant, a null mutant of the isocitrate lyase gene, and its control are summarized and the FPKM values are listed. The data were analysed using surprisal analysis and the genes contributing the strongest to the mutant and wild type phenotype are listed. The raw data are accessible at BioProject PRJNA437393 with SRA accession number SRP136101 (experiments SRX3824204-SRX3824249). The raw data set and expression values used for surprisal analysis are made public to enable critical or extended analyses.

Specifications Table

Subject area	*Biology*
More specific subject area	*transcriptomic data (RNA-seq) on the microalga* Chlamydomonas reinhardtii
Type of data	*Tables*
How data was acquired	*Next generation sequencing (NGS)*
Data format	*tables (doc files and csv files)*
Experimental factors	*NA*
Experimental features	*Two strains of the microalga* Chlamydomonas *have been submitted to day/night cycles in a cultivation medium containing acetate as*

	organic carbon source and sampled every 4 hours for transcriptomic analysis by RNA-seq during 28 hours. Three biological replicates of each strain and for each time point have been analysed. One strain is a null mutant of the isocitrate lyase gene (icl) and the other strain is a control strain (iclC). The isocitrate lyase enzyme is essential for the glyoxylate cycle, required for acetate metabolization. Surprisal analysis has been used to understand the transcriptomic response of both strains to the diurnal rhythm and the presence of acetate.
Data source location	*NA*
Data accessibility	Raw data of RNA seq analysis are available on Sequence Read Archive (SRA) database and connected to bioproject PRJNA437393.
Related research article	**Surprisal analysis of the transcriptomic response of the green microalga *Chlamydomonas* to the addition of acetate during day/night cycles in revision**

Value of the Data

- FPKM values of the raw data of the transcriptomics analysis performed in the associated research paper are found (Tables 2 and 3) and allow comparison with other transcriptomic data obtained in the microalga *Chlamydomonas*.
- KEGG pathways used for the surprisal analysis are found (Table 4) and allow comparison with other papers dealing with differential gene expression analyses.
- All the data supplied here are impossible to display in the accompanying research paper because of their size.

Data

The dataset of this article provides information on raw RNA-seq reads obtained from the *icl* mutant and and the control strain over the diurnal cycle. Data shared concerns the reads information for each biological replicate (Data in Brief 1), the FPKM values of the processed data (data in Brief 2 and 3), the number of KEGG pathways used in the surprisal analysis (Data in Brief 4), the list of genes relevant for the surprisal analysis of the transcriptomics data (Data in Brief 5,6,7).
List is found below

Data in Brief

Data in Brief 1. Reads information for each sample.

Data in Brief 2. FPKM values per replicate.

Data in Brief 3. FPKM values per sample.

Data in Brief 4. KEGG pathways defined for *C. reinhardtii* (http://www.kegg.jp/kegg/). Names of the pathways (ko indexes), number of genes contained in the pathway and number of genes of the pathway detected in our transcriptomic data are mentioned.

Data in Brief 5. List of the 100 most highly expressed genes in the balance constraint when all 16 samples are grouped together. *C. reinhardtii* genome version v5.5. #N/A means the function of the gene is unknown.

Data in Brief 6. List of the 100 most positive expressed genes (*iclC* phenotype) (right) and of the 100 most negative expressed genes (*icl* phenotype) of the first constraint (left) when 8 light samples are analysed separately. *C. reinhardtii* genome version v5.5. #N/A means the function of the gene is unknown.

Data in Brief 7. List of the 100 most positive expressed genes (*iclC* phenotype) (right) and 100 most negative genes (*icl* phenotype) (left) of the second constraint when 8 dark samples are analysed separately. *C. reinhardtii* genome version v5.5. #N/A means the function of the gene is unknown.

Experimental Design, Materials, and Methods

The experimental design has been described in the accompanying research paper ('Surprisal analysis of the transcriptomic response of the green microalga *Chlamydomonas* to the addition of acetate during day/night cycles' by Willamme et al.)

Acknowledgments

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References

[1] Willamme R, Bogaert KA, Remacle F, Remacle C. Surprisal analysis of the transcriptomic response of the green microalga *Chlamydomonas* to the addition of acetate during day/night cycles. Chem Phys. 2018 doi: 10.1016/j.chemphys.2018.04.015

	Identifier	Sample	Time	Run1	Run2	Run3	Total trimmed reads	Uniquely mapped reads	
E570	S1	icl-1	0	7,217,147	9,986,544	8,899,546	24,594,592	10,889,198	44.27%
E571	S2	icl-2	0	6,985,359	9,593,406	8,567,402	23,672,579	5,397,631	22.80%
E572	S3	icl-3	0	8,100,615	11,034,273	9,882,926	27,233,161	16,728,413	61.43%
E573	S4	icl-1	4	6,467,075	9,146,339	8,745,481	22,827,602	6,414,517	28.10%
E574	S5	icl-2	4	7,383,804	10,553,381	10,073,812	26,328,898	5,172,493	19.65%
E575	S6	icl-3	4	6,743,101	9,431,694	9,013,797	23,672,337	8,634,465	36.47%
E576	S7	icl-1	8	6,247,151	8,500,819	7,622,941	20,935,847	9,267,671	44.27%
E577	S8	icl-2	8	6,561,665	9,096,924	8,113,833	22,299,466	11,949,621	53.59%
E578	S9	icl-3	8	6,798,083	9,320,352	8,290,004	22,864,576	12,424,631	54.34%
F077	S10_merged	icl-1	12	32,755,414			29,897,157	28,340,363	94.79%
F078	S11_merged	icl-2	12	33,261,222			30,053,211	28,237,858	93.96%
F079	S12_merged	icl-3	12	34,400,218			31,270,607	29,713,890	95.02%
F080	S13_merged	icl-1	16	31,882,527			28,375,109	26,673,053	94.00%
F081	S14_merged	icl-2	16	34,901,956			31,731,913	26,074,281	82.17%
F082	S15_merged	icl-3	16	50,662,389			45,946,899	43,403,802	94.47%
E585	S16	icl-1	20	7,284,467	9,977,663	8,904,835	24,456,403	15,934,392	65.15%
E586	S17	icl-2	20	7,200,127	10,004,412	8,931,750	24,432,043	13,946,239	57.08%
E587	S18	icl-3	20	7,441,326	10,105,891	9,078,986	24,839,544	15,642,532	62.97%
E588	S19	icl-1	24	7,311,700	10,128,151	8,994,962	24,857,333	10,220,754	41.12%
E589	S20	icl-2	24	6,731,836	9,379,166	8,373,664	22,833,919	9,439,133	41.34%
E590	S21	icl-3	24	7,008,238	9,563,936	8,602,426	23,498,155	6,177,451	26.29%
E591	S22	icl-1	28	6,844,960	9,360,993	8,320,745	23,089,569	5,775,659	25.01%
E592	S23	icl-2	28	7,056,772	9,826,967	8,745,082	24,069,072	6,828,397	28.37%
E593	S24	icl-3	28	7,315,756	10,170,840	9,052,778	24,916,730	9,455,912	37.95%
E594	S25	iclC-1	0	5,991,675	7,940,724	7,155,052	19,251,804	12,949,495	67.26%
E595	S26	iclC-2	0	6,839,848	9,218,043	8,361,172	22,856,712	17,864,109	78.16%
E596	S27	iclC-3	0	7,254,089	10,014,821	9,636,648	25,176,694	15,836,513	62.90%
E597	S28	iclC-1	4	6,017,338	8,350,869	7,473,415	20,405,724	8,670,588	42.49%
E598	S29	iclC-2	4	6,546,781	9,009,950	8,748,220	22,560,512	9,900,506	43.88%
E599	S30	iclC-3	4	6,864,268	9,557,542	9,156,173	24,012,380	9,293,086	38.70%
E600	S31	iclC-1	8	7,327,088	9,855,745	8,902,573	24,320,636	19,309,180	79.39%
E601	S32	iclC-2	8	7,256,705	10,058,106	9,034,513	24,560,391	20,142,239	82.01%
E602	S33	iclC-3	8	7,423,799	10,226,270	9,043,798	25,081,167	8,072,448	32.19%
E603	S34	iclC-1	12	6,976,862	9,556,081	8,469,828	23,395,539	8,920,152	38.13%
E604	S35	iclC-2	12	7,780,492	10,572,880	9,398,663	25,931,665	19,266,856	74.30%
E607	S38	iclC-2	16	7,212,304	9,907,992	8,763,376	24,335,774	8,009,339	32.91%
E608	S39	iclC-3	16	7,725,427	10,495,602	9,337,691	25,786,338	15,740,171	61.04%
E609	S40	iclC-1	20	7,425,444	10,198,295	9,097,592	24,989,399	19,774,947	79.13%
E610	S41	iclC-2	20	7,582,576	10,550,976	9,460,866	25,936,035	20,327,813	78.38%
E611	S42	iclC-3	20	7,994,283	11,079,058	9,964,672	27,283,509	18,219,098	66.78%
E612	S43	iclC-1	24	8,570,183	11,827,426	10,616,979	29,080,836	26,421,509	90.86%
E613	S44	iclC-2	24	7,361,546	10,242,117	9,194,225	25,008,708	20,489,891	81.93%
E614	S45	iclC-3	24	7,427,254	10,310,636	9,284,406	25,280,845	13,996,128	55.36%
E615	S46	iclC-1	28	7,541,377	10,466,620	9,394,935	25,707,308	14,065,243	54.71%
E616	S47	iclC-2	28	7,941,287	11,178,096	9,952,481	27,369,675	13,964,405	51.02%
E617	S48	iclC-3	28	7,826,064	10,993,591	9,816,724	26,842,677	22,396,041	83.43%

Data in Brief 1. Reads information for each sample.

KEGG Pathway			Number of genes in our analysis	Total number of genes	KEGG Pathway			Number of genes in our analysis	Total number of genes
1	ko01200	Carbon metabolism	129	140	43	ko00196	Photosynthesis - antenna proteins	23	23
2	ko03010	Ribosome	123	125	44	ko00561	Glycerolipid metabolism	22	25
3	ko01230	Biosynthesis of amino acids	119	126	45	ko00900	Terpenoid backbone biosynthesis	22	23
4	ko03040	Spliceosome	107	110	46	ko00510	N-Glycan biosynthesis	21	22
5	ko00230	Purine metabolism	99	115	47	ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	21	21
6	ko03013	RNA transport	92	95	48	ko00920	Sulfur metabolism	21	21
7	ko04141	Protein processing in endoplasmic reticulum	77	82	49	ko00061	Fatty acid biosynthesis	20	22
8	ko00240	Pyrimidine metabolism	76	82	50	ko00280	Valine, leucine and isoleucine degradation	20	21
9	ko00190	Oxidative phosphorylation	66	69	51	ko00220	Arginine biosynthesis	20	21
10	ko03008	Ribosome biogenesis in eukaryotes	57	61	52	ko03022	Basal transcription factors	19	21
11	ko04120	Ubiquitin mediated proteolysis	55	64	53	ko00770	Pantothenate and CoA biosynthesis	18	20
12	ko03018	RNA degradation	54	61	54	ko03430	Mismatch repair	17	22
13	ko04144	Endocytosis	52	54	55	ko00640	Propanoate metabolism	17	19
14	ko04146	Peroxisome	45	50	56	ko00130	Ubiquinone and other terpenoid-quinone biosynthesis	17	19
15	ko03015	mRNA surveillance pathway	45	47	57	ko00760	Nicotinate and nicotinamide metabolism	17	19
16	ko00010	Glycolysis / Gluconeogenesis	44	49	58	ko00053	Ascorbate and aldarate metabolism	17	18
17	ko00620	Pyruvate metabolism	43	49	59	ko00071	Fatty acid degradation	17	17
18	ko00270	Cysteine and methionine metabolism	42	43	60	ko03410	Base excision repair	16	20
19	ko00970	Aminoacyl-tRNA biosynthesis	41	45	61	ko00600	Sphingolipid metabolism	16	18
20	ko00860	Porphyrin and chlorophyll metabolism	39	42	62	ko01040	Biosynthesis of unsaturated fatty acids	16	16
21	ko00500	Starch and sucrose metabolism	37	45	63	ko03440	Homologous recombination	15	22
22	ko00710	Carbon fixation in photosynthetic organisms	36	40	64	ko00350	Tyrosine metabolism	14	16
23	ko01212	Fatty acid metabolism	36	38	65	ko00450	Selenocompound metabolism	14	16
24	ko00520	Amino sugar and nucleotide sugar metabolism	35	37	66	ko04130	SNARE interactions in vesicular transport	14	15
25	ko04070	Phosphatidylinositol signaling system	35	36	67	ko00670	One carbon pool by folate	14	14
26	ko00260	Glycine, serine and threonine metabolism	34	39	68	ko00051	Fructose and mannose metabolism	13	19
27	ko00630	Glyoxylate and dicarboxylate metabolism	34	37	69	ko02010	ABC transporters	13	16
28	ko03050	Proteasome	34	34	70	ko00906	Carotenoid biosynthesis	13	15
29	ko00195	Photosynthesis	33	35	71	ko00340	Histidine metabolism	13	14
30	ko00330	Arginine and proline metabolism	32	36	72	ko00052	Galactose metabolism	12	16
31	ko00020	Citrate cycle (TCA cycle)	32	33	73	ko00590	Arachidonic acid metabolism	12	12

32	ko00480	Glutathione metabolism	32	32	74	ko00290	Valine, leucine and isoleucine biosynthesis	12	12
33	ko00564	Glycerophospholipid metabolism	31	38	75	ko04140	Regulation of autophagy	11	13
34	ko03420	Nucleotide excision repair	31	37	76	ko00360	Phenylalanine metabolism	11	12
35	ko01210	2-Oxocarboxylic acid metabolism	30	30	77	ko00100	Steroid biosynthesis	11	11
36	ko04145	Phagosome	29	30	78	ko04075	Plant hormone signal transduction	11	11
37	ko03060	Protein export	28	29	79	ko00410	beta-Alanine metabolism	10	12
38	ko03030	DNA replication	27	33	80	ko00592	alpha-Linolenic acid metabolism	10	11
39	ko00250	Alanine, aspartate and glutamate metabolism	26	27	81	ko00040	Pentose and glucuronate interconversions	10	11
40	ko03020	RNA polymerase	26	26	82	ko00300	Lysine biosynthesis	10	10
41	ko00030	Pentose phosphate pathway	24	26					
42	ko00562	Inositol phosphate metabolism	23	24	Total number of genes			2710	2937

Data in Brief 4. KEGG pathways defined for *C. reinhardtii* (http://www.kegg.jp/kegg/). Names of the pathways (ko indexes), number of genes contained in the pathway and number of genes of the pathway detected in our transcriptomic data are mentioned.

	balance state – all 16 samples together				
	Identifier	Name	G_{i0} value	Definition	Description
1	**Cre03.g207050.v5.5**	**RPL29**	**-0.0441087**	**Ribosomal protein L29, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L29; Cytosolic 60S large ribosomal subunit protein L29**
2	**Cre10.g420750.v5.5**	**RPL30**	**-0.0417273**	**Ribosomal protein L3-0. component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L30; Cytosolic 60S large ribosomal subunit protein L30**
3	**Cre12.g529400.v5.5**	**RPS27e 1**	**-0.0412797**	**Ribosomal protein S27e isoform 1, component of 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S27e, isoform 1; Cytosolic 40S small ribosomal subunit protein S27e, isoform 1. Previously annoated as RPS27-A**
4	**Cre16.g666301.v5.5**	**RPS30**	**-0.0401102**	**Ribosomal protein S3-0. component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S30; Cytosolic 40S small ribosomal subunit protein S30**
5	**Cre06.g310700.v5.5**	**RPL36a**	**-0.0400216**	**Ribosomal protein L36a, component of cytosolic 80S ribosome and 60S large subunit**	**This gene has also been annotated as RPL41 (according to the nomenclature used for the yeast ribosomal subunits) and shown to be the site of the cycloheximide resistance mutation ACT2. See PMID: 11254126. Cytosolic 80S ribosomal protein L36a; Cytosolic**
6	**Cre03.g203450.v5.5**	**RPS21**	**-0.0394877**	**Ribosomal protein S21, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S21; Cytosolic 40S small ribosomal subunit protein S21**
7	**Cre06.g282500.v5.5**	**RPL23a**	**-0.0394199**	**Ribosomal protein L23a, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L23a; Cytosolic 60S large ribosomal subunit protein L23a**
8	**Cre08.g382500.v5.5**	**RPS25**	**-0.0394116**	**Ribosomal protein S25, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S25; Cytosolic 40S small ribosomal subunit protein S25**
9	**Cre08.g360900.v5.5**	**RPS15**	**-0.039343**	**Ribosomal protein S15, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S15; Cytosolic 40S small ribosomal subunit protein S15**
10	**Cre16.g682300.v5.5**	**RPS26**	**-0.0389401**	**Ribosomal protein S26, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S26; Cytosolic 40S small ribosomal subunit protein S26**
11	**Cre02.g143050.v5.5**	**RPP2**	**-0.0388384**	**Acidic ribosomal protein P2**	**Cytosolic 80S ribosomal protein P2; Cytosolic 60S large ribosomal subunit protein P2**
12	Cre01.g066917.v5.5	LHCBM 1	-0.0383745	Chlorophyll a/b binding protein of LHCII	Chlorophyll a-b binding protein of LHCII
13	Cre02.g120150.v5.5	RBCS2	-0.0383725	Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit 2	RuBisCO small subunit 2, chloroplast precursor [PMID: 3820291]
14	**Cre12.g514500.v5.5**	**RPS11**	**-0.0383228**	**Ribosomal protein S11, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S11; Cytosolic 40S small ribosomal subunit protein S11**
15	Cre12.g489153.v5.5	#N/A	-0.0381789	#N/A	#N/A
16	**Cre07.g325746.v5.5**	**RPL38**	**-0.0380879**	**Ribosomal protein L38, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L38; Cytosolic 60S large ribosomal subunit protein L38**
17	**Cre08.g359750.v5.5**	**RPS9**	**-0.0379511**	**Ribosomal protein S9, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S9; Cytosolic 40S small ribosomal subunit protein S9**
18	**Cre10.g430400.v5.5**	**RPL37**	**-0.037616**	**Ribosomal protein L37, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L37; Cytosolic 60S large ribosomal subunit protein L37**
19	**Cre12.g494050.v5.5**	**RPL9**	**-0.037489**	**Ribosomal protein L9, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L9; Cytosolic 60S large ribosomal subunit protein L9**
20	**Cre09.g388200.v5.5**	**RPL10**	**-0.0373316**	**Ribosomal protein L1-0. component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L10; Cytosolic 60S large ribosomal subunit protein L10**
21	**Cre10.g456200.v5.5**	**RPS24**	**-0.0371878**	**Ribosomal protein S24,**	**Cytosolic 80S ribosomal protein S24;**

				component of cytosolic 80S ribosome and 40S small subunit	**Cytosolic 40S small ribosomal subunit protein S24. Possible locus for PR1 (paromomycin resistance) genetic marker**
22	**Cre04.g211800.v5.5**	**RPL23**	**-0.0371363**	**Ribosomal protein L23, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L23; Cytosolic 60S large ribosomal subunit protein L23**
23	**Cre12.g498250.v5.5**	**RPS17**	**-0.0370797**	**Ribosomal protein S17, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S17; Cytosolic 40S small ribosomal subunit protein S17**
24	Cre04.g214503.v5.5	#N/A	-0.0370682	#N/A	#N/A
24	**Cre06.g290950.v5.5**	**RPS5**	**-0.036391**	**Ribosomal protein S5, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S5; Cytosolic 40S small ribosomal subunit protein S5**
26	Cre03.g182551.v5.5	PCY1	-0.0362985	Pre-apoplastocyanin	Pre-apoplastocyanin copper binding protein, PETE [PMID: 2165059; PMID: 8940133]; structure of plastocyanin PDB: 2PLT; mutant = ac208 [PMID: 8463310]
27	**Cre12.g537800.v5.5**	**RPL7**	**-0.0360244**	**Ribosomal protein L7, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L7; Cytosolic 60S large ribosomal subunit protein L7**
28	Cre14.g626700.v5.5	PETF	-0.0360156	Ferredoxin	2Fe-2S containing redox protein involved in photosynthetic electron transfer, chloroplast localization [PMID: 16656453]
29	**Cre13.g568900.v5.5**	**RPL17**	**-0.0358546**	**Ribosomal protein L17, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L17; Cytosolic 60S large ribosomal subunit protein L17**
30	**Cre08.g358556.v5.5**	**RPS29**	**-0.0357983**	**Ribosomal protein S29, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S29; Cytosolic 40S small ribosomal subunit protein S29**
31	**Cre06.g272800.v5.5**	**RPS8**	**-0.0357831**	**Ribosomal protein S8, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S8; Cytosolic 40S small ribosomal subunit protein S8**
32	**Cre06.g273600.v5.5**	**RPS27a**	**-0.0357815**	**Ribosomal protein S27a, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S27a; Cytosolic 40S small ribosomal subunit protein S27a; ubiquitin region ends with amino acid residue 74. Has homology to ubiquitin superfamily**
33	**Cre12.g512600.v5.5**	**RPL18**	**-0.0356463**	**Ribosomal protein L18, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L18; Cytosolic 60S large ribosomal subunit protein L18**
34	**Cre10.g459250.v5.5**	**RPL35a**	**-0.0354754**	**Ribosomal protein L35a, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L35a; Cytosolic 60S large ribosomal subunit protein L35a**
35	**Cre17.g738300.v5.5**	**RPP1**	**-0.0354434**	**Acidic ribosomal protein P1**	**Cytosolic 80S ribosomal protein P1; Cytosolic 60S large ribosomal subunit protein P1**
36	Cre10.g420350.v5.5	PSAE	-0.0353805	Photosystem I 8.1 kDa reaction center subunit IV	Photosystem I reaction center subunit IV, chloroplast precursor (PSI-E) (Photosystem I 8.1 kDa protein) [PMID: 2693938]
37	**Cre01.g027000.v5.5**	**RPL11**	**-0.0353561**	**Ribosomal protein L11, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L11; Cytosolic 60S large ribosomal subunit protein L11**
38	**Cre17.g701650.v5.5**	**RPL27**	**-0.0352832**	**Ribosomal protein L27, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L27; Cytosolic 60S large ribosomal subunit protein L27**
39	**Cre14.g617900.v5.5**	**RPL35**	**-0.0352725**	**Ribosomal protein L35, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L35; Cytosolic 60S large ribosomal subunit protein L35**
40	**Cre02.g106600.v5.5**	**RPS19**	**-0.0352276**	**Ribosomal protein S19, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S19; Cytosolic 40S small ribosomal subunit protein S19**
41	**Cre12.g532550.v5.5**	**RPL13a**	**-0.0352177**	**Ribosomal protein L13a, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L13a; Cytosolic 60S large ribosomal subunit protein L13a**
42	**Cre02.g102250.v5.5**	**RPS3**	**-0.0351398**	**Ribosomal protein S3,**	**Cytosolic 80S ribosomal protein S3;**

				component of cytosolic 80S ribosome and 40S small subunit	**Cytosolic 40S small ribosomal subunit protein S3**
43	**Cre06.g257150.v5.5**	**RPL37a**	**-0.035103**	**Ribosomal protein L37a, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L37a; Cytosolic 60S large ribosomal subunit protein L37a**
44	**Cre12.g498900.v5.5**	**RPS7**	**-0.0350799**	**Ribosomal protein S7, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S7; Cytosolic 40S small ribosomal subunit protein S7**
45	**Cre12.g528750.v5.5**	**RPL12**	**-0.0350349**	**Ribosomal protein L12, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L12; Cytosolic 60S large ribosomal subunit protein L12**
46	**Cre07.g357850.v5.5**	**RPL22**	**-0.034811**	**Ribosomal protein L22, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L22; Cytosolic 60S large ribosomal subunit protein L22**
47	**Cre12.g504200.v5.5**	**RPS23**	**-0.0344687**	**Ribosomal protein S23, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S23; Cytosolic 40S small ribosomal subunit protein S23**
48	Cre09.g405106.v5.5	#N/A	-0.0343005	#N/A	#N/A
49	**Cre12.g484050.v5.5**	**RPL36**	**-0.0342738**	**Ribosomal protein L36, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L36; Cytosolic 60S large ribosomal subunit protein L36**
50	**Cre09.g391097.v5.5**	**RPL24**	**-0.0342292**	**Ribosomal protein L24, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L24; Cytosolic 60S large ribosomal subunit protein L24**
51	Cre01.g007051.v5.5	#N/A	-0.0341731	#N/A	#N/A
52	Cre09.g402219.v5.5	LCI3	-0.0341695	Low-CO2-inducible protein	Regulated by CCM1 [PMID: 15235119]. Acclimation to changing CO2 concentrations and light intensities was studied by Yamano et al. 2008 [PMID: 18322145].
53	**Cre14.g621450.v5.5**	**RPL5**	**-0.0337335**	**Ribosomal protein L5, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L5; Cytosolic 60S large ribosomal subunit protein L5**
54	Cre12.g498600.v5.5	#N/A	-0.0337325	Eukaryotic translation elongation factor 1 alpha	Flagellar Associated Protein, found in the flagellar proteome [PMID: 15998802]. Previously annotated as just EEF1
55	**Cre17.g701200.v5.5**	**RPL14**	**-0.0336314**	**Ribosomal protein L14, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L14; Cytosolic 60S large ribosomal subunit protein L14**
56	**Cre13.g568650.v5.5**	**RPS3a**	**-0.0334977**	**Ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S3a; Cytosolic 40S small ribosomal subunit protein S3a**
57	**Cre01.g047750.v5.5**	**RPL18a**	**-0.0334572**	**Ribosomal protein L18a, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L18a; Cytosolic 60S large ribosomal subunit protein L18a**
58	**Cre06.g278135.v5.5**	**RPL21**	**-0.0331582**	**Ribosomal protein L21, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L21; Cytosolic 60S large ribosomal subunit protein L21**
59	**Cre02.g101350.v5.5**	**RPL10a**	**-0.0331156**	**Ribosomal protein L10a, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L10a; Cytosolic 60S large ribosomal subunit protein L10a**
60	**Cre02.g115200.v5.5**	**RPL27a**	**-0.033038**	**Ribosomal protein L27a, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L27a; Cytosolic 60S large ribosomal subunit protein L27a. Candidate gene for the cycloheximide resistance mutation act1.**
61	Cre12.g546150.v5.5	PETM	-0.0329136	Cytochrome b6f complex PetM subunit	Cytochrome b6f complex chain PetM, chloroplast precursor; GI:2493687; PMID: 8631873, PMID: 8616155, PMID: 7493968
62	Cre06.g278222.v5.5	RCK1	-0.0327044	Receptor of activated protein kinase C	Receptor of activated protein kinase C 1, component of 40S small ribosomal subunit; Also cytosolic 40S small ribosomal subunit protein RACK1. Previously annotated as RACK1 and CBLP. Initially described [PMID: 2116589] as CBLP. Smith and Lee 2008 [PMID:

63	Cre12.g560950.v5.5	PSAG	-0.0325305	Photosystem I reaction center subunit V	(PSI-G) (P35 protein) [PMID: 2693938]
64	**Cre10.g417700.v5.5**	**RPL3**	**-0.0325262**	**Ribosomal protein L3, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L3; Cytosolic 60S large ribosomal subunit protein L3**
65	**Cre02.g075700.v5.5**	**RPL19**	**-0.0325095**	**Ribosomal protein L19, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L19; Cytosolic 60S large ribosomal subunit protein L19**
66	Cre12.g486300.v5.5	PSAL	-0.0324252	Photosystem I reaction center subunit XI	#N/A
67	Cre12.g529651.v5.5	#N/A	-0.0324189	#N/A	#N/A
68	Cre11.g467578.v5.5	#N/A	-0.0322713	#N/A	#N/A
69	**Cre07.g331900.v5.5**	**RPS13**	**-0.032224**	**Ribosomal protein S13, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S13; Cytosolic 40S small ribosomal subunit protein S13**
70	**Cre06.g272950.v5.5**	**RPS18**	**-0.0321851**	**Ribosomal protein S18, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S18; Cytosolic 40S small ribosomal subunit protein S18**
71	**Cre09.g411100.v5.5**	**RPS10**	**-0.032052**	**Ribosomal protein S1-0. component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S10; Cytosolic 40S small ribosomal subunit protein S10**
72	**Cre14.g630100.v5.5**	**RPL13**	**-0.0319474**	**Ribosomal protein L13, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L13; Cytosolic 60S large ribosomal subunit protein L13**
73	Cre13.g577100.v5.5	ACP2	-0.0317649	Acyl-carrier protein	Acyl-carrier protein
74	Cre12.g483850.v5.5	#N/A	-0.0317034	#N/A	#N/A
75	Cre06.g263450.v5.5	#N/A	-0.0315772	#N/A	#N/A
76	**Cre02.g091100.v5.5**	**RPL15**	**-0.031471**	**Ribosomal protein L15, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L15; Cytosolic 60S large subunit ribosomal protein L15**
77	**Cre01.g011000.v5.5**	**RPL6**	**-0.0314481**	**Ribosomal protein L6, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L6; Cytosolic 60S large ribosomal subunit protein L6**
78	Cre05.g234637.v5.5	#N/A	-0.031324	#N/A	#N/A
79	**Cre12.g520500.v5.5**	**RPP0**	**-0.0312926**	**Acidic ribosomal protein P-0. Ribosomal protein L10**	**Cytosolic 80S acidic ribosomal protein P0; Cytosolic 60S large ribosomal subunit protein P0. Ribosomal protein L10**
80	Cre12.g548950.v5.5	LHCBM 7	-0.0309816	Chlorophyll a/b binding protein of LHCII	Chlorophyll a-b binding protein of LHCII
81	**Cre06.g249250.v5.5**	**RPL7ae**	**-0.0309195**	**Ribosomal protein L7Ae**	**Cytosolic 80S ribosomal protein L7ae; Cytosolic 60S large ribosomal subunit protein L7ae**
82	**Cre16.g661050.v5.5**	**RPL34**	**-0.0307426**	**Ribosomal protein, L34e superfamily, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L34; Cytosolic 60S large ribosomal subunit protein L34. Belongs to Ribosomal_L34e superfamily**
83	Cre12.g548400.v5.5	LHCBM 2	-0.0307266	Light-harvesting protein of photosystem II	Encoding a light-harvesting antenna protein for PS2. This gene was reported under the name of LhcII-3 in PMID: 11522911, and the sequence has been deposited in Genbank (AB051205). Also designated as LhcbM2 in PMID: 16143838 and as Lhcbm2 in PMID: 14652691
84	Cre12.g535851.v5.5	#N/A	-0.0306301	#N/A	#N/A
85	Cre16.g660150.v5.5	#N/A	-0.0306154	#N/A	#N/A
86	**Cre01.g040000.v5.5**	**RPL26**	**-0.0306063**	**Ribosomal protein L26, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L26; Cytosolic 60S large ribosomal subunit protein L26**
87	**Cre01.g039250.v5.5**	**RPS2**	**-0.0305367**	**Ribosomal protein S2, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S2; Cytosolic 40S small ribosomal subunit protein S2**
88	**Cre09.g397697.v5.5**	**RPL4**	**-0.0302693**	**Ribosomal protein L4, component of cytosolic 80S ribosome and 60S large subunit**	**Cytosolic 80S ribosomal protein L4; Cytosolic 60S large ribosomal subunit protein L4**
89	Cre06.g285250.v5.5	LHCBM 6	-0.0301451	Chloropyll a/b binding protein of LHCII type I, chloroplast precursor	Chloropyll a-b binding protein of LHCII type I, chloroplast precursor

90	Cre17.g724300.v5.5	PSAK	-0.0301443	Photosystem I reaction center subunit psaK	8.4 kD subunit of photosystem I (polypeptide 37) [PMID: 2693938]
91	**Cre12.g510450.v5.5**	**RPS28**	**-0.0301316**	**Ribosomal protein S28, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S28; Cytosolic 40S small ribosomal subunit protein S28**
92	**Cre06.g308250.v5.5**	**RPS4**	**-0.0301189**	**Ribosomal protein S4, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S4; Cytosolic 40S small ribosomal subunit protein S4**
93	Cre06.g272650.v5.5	LHCA8	-0.0300836	Light-harvesting protein of photosystem I	#N/A
94	**Cre09.g400650.v5.5**	**RPS6**	**-0.0299611**	**Ribosomal protein S6, component of cytosolic 80S ribosome and 40S small subunit**	**Cytosolic 80S ribosomal protein S6; Cytosolic 40S small ribosomal subunit protein S6**
95	Cre01.g010900.v5.5	GAP3	-0.0299284	Glyceraldehyde-3-Phosphate Dehydrogenase	Glyceraldehyde 3-phosphate dehydrogenase A, chloroplast precursor (NADP-dependent glyceraldehyde phosphate dehydrogenase subunit A); corresponds to G3PA_CHLRE; found in the flagellar proteome [PMID: 15998802]. This enzyme is bispecific for NADP and NAD,
96	**Cre17.g734450.v5.5**	**PRPL19**	**-0.029736**	**Plastid ribosomal protein L19**	**Chloroplast ribosomal protein L19, imported to chloroplast; Chloroplast large ribosomal subunit protein L19**
97	Cre06.g261000.v5.5	PSBR	-0.0296755	10 kDa photosystem II polypeptide	Similar to At1g7904-0. chloroplast-targeted
98	Cre04.g214150.v5.5	THI4	-0.0296257	Thiazole biosynthetic enzyme; THI4 regulatory protein	Involved in the synthesis of the thiazole moiety of thiamine pyrophosphate. One of 2 splice variants.; Alternatively spliced variant of THI4 involved in the regulation of THI4a. Contains riboswitch THI RNA motif at positions 426525-426691. Regulatory p
99	Cre17.g702950.v5.5	#N/A	-0.0295457	#N/A	#N/A
100	Cre16.g650550.v5.5	FAP103	-0.0294053	Flagellar Associated Protein, nucleoside diphosphate kinase-like	Flagellar Associated Protein similar to nucleoside diphosphate kinase, found in the flagellar proteome [PMID: 15998802]

Data in Brief 5. List of the 100 most highly expressed genes in the balance constraint when all 16 samples are grouped together. Bold: transcripts encoding components of ribosome; underlined: transcripts encoding components of the photosynthetic machinery. *C. reinhardtii* genome version v5.5. #N/A means the function of the gene is unknown.

	Light samples – constraint 1 – 100 most positive genes- *icIC* phenotype				**Light samples – constraint 1 – 100 most negative genes- *icI* phenotype**			
	Identifier	Name	G_{i1} value	Definition	Identifier	Name	G_{i1} value	Definition
1	Cre02.g141206.v5.5	#N/A	6.20E-02	#N/A	Cre07.g321800.v5.5	#N/A	-5.76E-02	#N/A
2	Cre13.g577850.v5.5	#N/A	4.97E-02	Peptidyl-prolyl cis-trans isomerase, FKBP-type	Cre16.g674151.v5.5	#N/A	-5.69E-02	#N/A
3	Cre03.g179820.v5.5	#N/A	4.86E-02	#N/A	Cre06.g281600.v5.5	LCI23	-5.65E-02	Low-CO2-inducible protein, septin-like
4	Cre16.g659300.v5.5	#N/A	4.73E-02	Cytochrome b5 protein	Cre03.g155150.v5.5	#N/A	-5.42E-02	#N/A
5	Cre03.g144807.v5.5	**MAS1**	4.58E-02	**Malate synthase**	Cre10.g426800.v5.5	#N/A	-5.32E-02	#N/A
6	Cre12.g546550.v5.5	FEA1	4.03E-02	Fe-assimilating protein	Cre10.g463850.v5.5	#N/A	-5.28E-02	#N/A
7	Cre06.g282800.v5.5	**ICL1**	3.92E-02	**Isocitrate lyase**	Cre07.g328800.v5.5	NSG13	-5.15E-02	Protein expressed during nitrogen-starved gametogenesis
8	Cre17.g702900.v5.5	#N/A	3.84E-02	#N/A	Cre04.g220700.v5.5	ALK2	-5.12E-02	Aurora-like kinase
9	Cre01.g032650.v5.5	**TAL1**	3.53E-02	**Transaldolase**	Cre03.g207377.v5.5	#N/A	-5.06E-02	#N/A
10	Cre08.g364100.v5.5	#N/A	2.91E-02	#N/A	Cre02.g075350.v5.5	CNK1	-5.05E-02	NimA-related protein kinase
11	Cre12.g550500.v5.5	#N/A	2.87E-02	#N/A	Cre12.g528650.v5.5	#N/A	-5.01E-02	#N/A
12	Cre07.g353450.v5.5	**ACS3**	2.87E-02	**Acetyl-CoA synthetase/ligase**	Cre10.g464100.v5.5	#N/A	-4.99E-02	#N/A
13	Cre14.g630000.v5.5	KIR2	2.84E-02	Ketoacid isomerase-like protein	Cre14.g619450.v5.5	#N/A	-4.99E-02	#N/A
14	Cre16.g669600.v5.5	#N/A	2.76E-02	#N/A	Cre06.g278161.v5.5	#N/A	-4.95E-02	#N/A
15	Cre10.g428100.v5.5	#N/A	2.76E-02	#N/A	Cre06.g251750.v5.5	#N/A	-4.93E-02	#N/A
16	Cre02.g141166.v5.5	#N/A	2.68E-02	#N/A	Cre09.g395251.v5.5	#N/A	-4.90E-02	#N/A
17	Cre12.g540500.v5.5	#N/A	2.47E-02	#N/A	Cre09.g396772.v5.5	#N/A	-4.89E-02	#N/A
18	Cre02.g094250.v5.5	#N/A	2.43E-02	#N/A	Cre12.g519850.v5.5	#N/A	-4.88E-02	#N/A
19	Cre14.g623176.v5.5	#N/A	2.38E-02	#N/A	Cre14.g611250.v5.5	#N/A	-4.85E-02	#N/A
20	Cre12.g523900.v5.5	#N/A	2.37E-02	#N/A	**Cre14.g622850.v5.5**	**#N/A**	**-4.84E-02**	**DNA recombination protein**
21	Cre06.g263300.v5.5	#N/A	2.37E-02	#N/A	Cre11.g477350.v5.5	#N/A	-4.79E-02	#N/A
22	Cre02.g141400.v5.5	**PCK1**	2.32E-02	**Phosphoenolpyruvate carboxykinase**	Cre02.g098300.v5.5	#N/A	-4.78E-02	#N/A
23	Cre01.g044450.v5.5	#N/A	2.31E-02	#N/A	Cre05.g237150.v5.5	#N/A	-4,77E-02	#N/A

24	Cre12.g543400.v5.5	FDH1	2.27E-02	Formaldehyde dehydrogenase	Cre06.g249050.v5.5	#N/A	-4.77E-02	#N/A
24	Cre09.g387726.v5.5	**AST1**	2.23E-02	**Aspartate aminotransferase**	Cre17.g723350.v5.5	SUL2	-4.75E-02	Sulfate anion transporter
26	Cre13.g573000.v5.5	#N/A	2.19E-02	#N/A	Cre03.g155100.v5.5	#N/A	-4.74E-02	#N/A
27	Cre07.g315400.v5.5	#N/A	2.17E-02	Simlar to nitric oxide associated protein protein of CSG family	Cre03.g179450.v5.5	SRR7	-4.72E-02	Scavenger receptor cysteine rich (SRCR) protein
28	Cre12.g541250.v5.5	NAR 1.5	2.15E-02	Nitrite transporter	Cre07.g321750.v5.5	#N/A	-4.71E-02	#N/A
29	Cre15.g641200.v5.5	#N/A	2.14E-02	#N/A	Cre12.g535300.v5.5	#N/A	-4.71E-02	#N/A
30	Cre08.g358558.v5.5	#N/A	2.13E-02	#N/A	Cre10.g448977.v5.5	#N/A	-4.70E-02	#N/A
31	Cre50.g761397.v5.5	#N/A	2.13E-02	#N/A	Cre16.g693200.v5.5	#N/A	-4.69E-02	#N/A
32	Cre03.g149100.v5.5	**CIS2**	2.12E-02	**Citrate synthase**	Cre06.g278212.v5.5	CGL46	-4.69E-02	Predicted protein
33	Cre04.g214500.v5.5	**IDH3**	2.09E-02	**Isocitrate dehydrogenase, NADP-dependent**	Cre12.g500250.v5.5	#N/A	-4.68E-02	#N/A
34	Cre17.g731900.v5.5	#N/A	2.07E-02	#N/A	**Cre03.g199450.v5.5**	**MINE2**	**-4.67E-02**	**Chloroplast division site determinant**
35	Cre02.g108350.v5.5	#N/A	2.02E-02	#N/A	Cre16.g658600.v5.5	#N/A	-4.67E-02	#N/A
36	Cre17.g702950.v5.5	#N/A	1.96E-02	#N/A	Cre16.g693450.v5.5	FAP40	-4.65E-02	Flagellar Associated Protein
37	Cre07.g332800.v5.5	#N/A	1.93E-02	#N/A	Cre13.g569400.v5.5	#N/A	-4.64E-02	#N/A
38	Cre14.g626000.v5.5	#N/A	1.92E-02	#N/A	Cre01.g050700.v5.5	#N/A	-4.64E-02	#N/A
39	Cre03.g153400.v5.5	#N/A	1.88E-02	#N/A	Cre09.g402350.v5.5	#N/A	-4.61E-02	#N/A
40	Cre13.g563500.v5.5	#N/A	1.88E-02	#N/A	Cre03.g174400.v5.5	CDO1	-4.60E-02	Cysteine dioxygenase
41	Cre07.g346650.v5.5	#N/A	1.85E-02	#N/A	Cre12.g551700.v5.5	#N/A	-4.59E-02	#N/A
42	Cre07.g328075.v5.5	#N/A	1.83E-02	#N/A	Cre04.g226600.v5.5	#N/A	-4.57E-02	#N/A
43	Cre03.g198850.v5.5	#N/A	1.81E-02	#N/A	Cre13.g570450.v5.5	#N/A	-4.56E-02	#N/A
44	Cre03.g153450.v5.5	#N/A	1.80E-02	#N/A	Cre12.g491050.v5.5	RIR2	-4.55E-02	Ribonucleoside-diphosphate reductase R2 subunit
45	Cre06.g278136.v5.5	#N/A	1.77E-02	#N/A	Cre02.g145950.v5.5	#N/A	-4.54E-02	#N/A
46	Cre12.g523550.v5.5	#N/A	1.76E-02	#N/A	Cre09.g394065.v5.5	#N/A	-4.53E-02	#N/A
47	Cre01.g003200.v5.5	#N/A	1.73E-02	#N/A	Cre13.g569450.v5.5	#N/A	-4.52E-02	#N/A
48	Cre09.g411300.v5.5	#N/A	1.72E-02	#N/A	Cre06.g266550.v5.5	#N/A	-4.51E-02	#N/A
49	Cre03.g158100.v5.5	#N/A	1.68E-02	#N/A	Cre07.g342551.v5.5	#N/A	-4.51E-02	#N/A

50	Cre12.g541200.v5.5	#N/A	1.67E-02	#N/A	Cre17.g728750.v5.5	#N/A	-4.50E-02	#N/A
51	Cre08.g358553.v5.5	#N/A	1.67E-02	#N/A	Cre07.g344000.v5.5	#N/A	-4.50E-02	#N/A
52	Cre03.g164550.v5.5	#N/A	1.65E-02	#N/A	Cre12.g501250.v5.5	#N/A	-4.47E-02	#N/A
53	Cre01.g022283.v5.5	#N/A	1.64E-02	#N/A	Cre12.g551552.v5.5	#N/A	-4.47E-02	#N/A
54	Cre13.g591400.v5.5	#N/A	1.64E-02	#N/A	Cre10.g431900.v5.5	#N/A	-4.46E-02	#N/A
55	Cre13.g603750.v5.5	#N/A	1.62E-02	#N/A	Cre09.g387600.v5.5	#N/A	-4.46E-02	#N/A
56	Cre17.g705450.v5.5	LCI26	1.61E-02	Low-CO2-induced U-box protein	Cre12.g522400.v5.5	#N/A	-4.45E-02	#N/A
57	Cre01.g011630.v5.5	#N/A	1.60E-02	#N/A	Cre06.g299250.v5.5	#N/A	-4.45E-02	#N/A
58	Cre01.g043450.v5.5	#N/A	1.60E-02	#N/A	Cre12.g545750.v5.5	#N/A	-4.44E-02	#N/A
59	Cre07.g335700.v5.5	#N/A	1.56E-02	#N/A	Cre09.g413114.v5.5	#N/A	-4.44E-02	#N/A
60	Cre16.g679781.v5.5	#N/A	1.55E-02	#N/A	Cre02.g097800.v5.5	#N/A	-4.43E-02	ABC transporter
61	Cre06.g278215.v5.5	#N/A	1.53E-02	#N/A	Cre12.g550702.v5.5	TEF13	-4.43E-02	Predicted protein
62	Cre11.g479100.v5.5	#N/A	1.51E-02	#N/A	Cre09.g393600.v5.5	#N/A	-4.43E-02	#N/A
63	Cre13.g562300.v5.5	#N/A	1.51E-02	#N/A	**Cre02.g115250.v5.5**	**POC1**	**-4.43E-02**	**Centriole proteome protein**
64	Cre04.g215050.v5.5	#N/A	1.50E-02	Beta-carotene hydroxylase, putative chloroplast precursor	Cre02.g089650.v5.5	#N/A	-4.42E-02	#N/A
65	Cre10.g421800.v5.5	#N/A	1.49E-02	#N/A	Cre02.g107000.v5.5	#N/A	-4.40E-02	#N/A
66	Cre02.g076300.v5.5	UPD2	1.49E-02	Uroporphyrinogen decarboxylase	**Cre17.g720350.v5.5**	**MINE1**	**-4.39E-02**	**Chloroplast division site-determinant MinE**
67	Cre06.g278147.v5.5	#N/A	1.47E-02	#N/A	Cre12.g561601.v5.5	#N/A	-4.38E-02	#N/A
68	Cre09.g393150.v5.5	FOX1	1.47E-02	Multicopper ferroxidase	Cre08.g372550.v5.5	CDKB1	-4.36E-02	Plant specific cyclin dependent kinase
69	Cre03.g167250.v5.5	#N/A	1.47E-02	#N/A	Cre10.g423850.v5.5	SRR26	-4.36E-02	Scavenger receptor cysteine rich (SRCR) protein
70	Cre12.g495900.v5.5	#N/A	1.44E-02	#N/A	Cre03.g195950.v5.5	#N/A	-4.35E-02	#N/A
71	Cre08.g384700.v5.5	#N/A	1.44E-02	#N/A	Cre07.g341700.v5.5	#N/A	-4.35E-02	#N/A
72	Cre02.g116250.v5.5	#N/A	1.44E-02	#N/A	Cre04.g223100.v5.5	CAH1	-4.34E-02	Carbonic anhydrase
73	Cre06.g265900.v5.5	#N/A	1.43E-02	#N/A	Cre03.g194600.v5.5	#N/A	-4.34E-02	#N/A
74	Cre14.g630859.v5.5	#N/A	1.42E-02	#N/A	Cre11.g483250.v5.5	#N/A	-4.33E-02	#N/A

75	Cre09.g391400.v5.5	#N/A	1.41E-02	#N/A	Cre07.g325742.v5.5	#N/A	-4.32E-02	#N/A
76	Cre12.g487150.v5.5	#N/A	1.41E-02	#N/A	Cre01.g007350.v5.5	MOT42	-4.32E-02	Predicted protein
77	Cre02.g119000.v5.5	#N/A	1.40E-02	#N/A	Cre12.g512500.v5.5	#N/A	-4.30E-02	#N/A
78	Cre05.g241655.v5.5	#N/A	1.40E-02	#N/A	Cre16.g672497.v5.5	#N/A	-4.30E-02	#N/A
79	Cre14.g633903.v5.5	#N/A	1.40E-02	#N/A	Cre14.g616800.v5.5	#N/A	-4.29E-02	#N/A
80	Cre19.g751047.v5.5	#N/A	1.40E-02	#N/A	Cre03.g207900.v5.5	CYCA1	-4.29E-02	A-type cyclin
81	Cre06.g278148.v5.5	#N/A	1.39E-02	#N/A	**Cre06.g295700.v5.5**	**MCM3**	**-4.29E-02**	**Minichromosome maintenance protein**
82	Cre12.g495850.v5.5	#N/A	1.38E-02	#N/A	Cre09.g388100.v5.5	#N/A	-4.28E-02	#N/A
83	Cre02.g109600.v5.5	#N/A	1.36E-02	Inositol monophosphatase	Cre02.g108150.v5.5	#N/A	-4.28E-02	#N/A
84	Cre14.g630847.v5.5	#N/A	1.36E-02	#N/A	Cre17.g718400.v5.5	#N/A	-4.27E-02	#N/A
85	Cre17.g700750.v5.5	#N/A	1.36E-02	#N/A	Cre03.g204450.v5.5	#N/A	-4.27E-02	#N/A
86	Cre14.g615450.v5.5	#N/A	1.36E-02	#N/A	Cre18.g749747.v5.5	#N/A	-4.26E-02	Similar to Flagellar Associated Protein FAP281
87	Cre07.g346600.v5.5	#N/A	1.34E-02	#N/A	Cre10.g456350.v5.5	#N/A	-4.26E-02	#N/A
88	Cre50.g761447.v5.5	#N/A	1.34E-02	#N/A	Cre08.g376950.v5.5	MMP14	-4.25E-02	Matrix metalloproteinase
89	Cre17.g718150.v5.5	#N/A	1.34E-02	#N/A	Cre17.g723400.v5.5	#N/A	-4.24E-02	#N/A
90	Cre17.g700950.v5.5	FDX5	1.33E-02	Apoferredoxin	Cre17.g697500.v5.5	#N/A	-4.23E-02	#N/A
91	Cre17.g703700.v5.5	**SCL2**	1.33E-02	**Succinate-CoA ligase beta chain**	**Cre02.g104800.v5.5**	**HTV1**	**-4.23E-02**	**Histone H3 variant**
92	Cre06.g254150.v5.5	UTP1	1.32E-02	Nucleolar protein, component of the U3 processome	Cre01.g004750.v5.5	#N/A	-4.22E-02	#N/A
93	Cre12.g547650.v5.5	#N/A	1.32E-02	#N/A	Cre12.g505300.v5.5	#N/A	-4.21E-02	#N/A
94	Cre12.g548950.v5.5	LHCBM7	1.31E-02	Chlorophyll a/b binding protein of LHCII	Cre16.g666300.v5.5	#N/A	-4.21E-02	#N/A
95	Cre02.g073850.v5.5	CGL54	1.30E-02	Predicted protein	Cre03.g170550.v5.5	#N/A	-4.20E-02	#N/A
96	Cre01.g020305.v5.5	#N/A	1.30E-02	#N/A	Cre14.g632100.v5.5	#N/A	-4.19E-02	#N/A
97	Cre04.g232104.v5.5	LHCBM3	1.30E-02	Light-harvesting complex II chlorophyll a/b binding protein M3	Cre06.g298750.v5.5	AOT4	-4.19E-02	Amino acid transporter
98	Cre03.g182100.v5.5	#N/A	1.29E-02	#N/A	Cre01.g053800.v5.5	#N/A	-4.18E-02	#N/A
99	Cre09.g387875.v5.5	IPY3	1.29E-02	Soluble inorganic	Cre06.g311700.v5.5	#N/A	-4.16E-02	#N/A

				pyrophosphatase				
100	Cre07.g329767.v5.5	#N/A	1.28E-02	#N/A	Cre12.g502600.v5.5	SLT1	-4.15E-02	Sodium/sulfate co-transporter

Data in Brief 6. List of the 100 most positive expressed genes (*iclC* phenotype) (right) and of the 100 most negative expressed genes (*icl* phenotype) (left) of the first constraint when 8 light samples are analysed separately. Red: transcripts encoding components for acetate metabolization; bold: transcripts encoding components of cell division. *C. reinhardtii* genome version v5.5. #N/A means the function of the gene is unknown.

	Dark samples – constraint 2 – 100 most positive genes- *iclC* phenotype				**Dark samples – constraint 2 – 100 most negative genes- *icl* phenotype**			
	Identifier	Name	G_{i2} value	Definition	Identifier	Name	G_{i2} value	Definition
1	Cre02.g141206.v5.5	#N/A	5.24E-02	#N/A	**Cre04.g223100.v5.5**	**CAH1**	**-9.35E-02**	**Carbonic anhydrase**
2	Cre17.g700950.v5.5	FDX5	4.65E-02	Apoferredoxin	**Cre09.g399552.v5.5**	**LCR1**	**-8.04E-02**	**Low-CO2 response regulator, Myb-like transcription factor**
3	Cre02.g141166.v5.5	#N/A	4.40E-02	#N/A	Cre16.g674151.v5.5	#N/A	-7.45E-02	#N/A
4	Cre06.g282800.v5.5	ICL1	3.88E-02	Isocitrate lyase	Cre17.g723400.v5.5	#N/A	-7.26E-02	#N/A
5	Cre01.g011630.v5.5	#N/A	3.63E-02	#N/A	Cre26.g756747.v5.5	#N/A	-6.66E-02	#N/A
6	Cre12.g546550.v5.5	FEA1	3.62E-02	Fe-assimilating protein	Cre12.g554929.v5.5	#N/A	-6.47E-02	#N/A
7	Cre16.g659300.v5.5	#N/A	3.14E-02	Cytochrome b5 protein	*Cre17.g723350.v5.5*	*SUL2*	*-6.42E-02*	*Sulfate anion transporter*
8	Cre03.g180750.v5.5	MES1	3.12E-02	Cobalamin-independent methionine synthase	Cre16.g681351.v5.5	#N/A	-6.27E-02	#N/A
9	Cre08.g364100.v5.5	#N/A	3.10E-02	#N/A	Cre06.g298802.v5.5	#N/A	-6.22E-02	#N/A
10	Cre12.g546600.v5.5	FEA2	2.71E-02	Fe-assimilating protein	Cre07.g342551.v5.5	#N/A	-6.18E-02	#N/A
11	Cre01.g036950.v5.5	#N/A	2.70E-02	#N/A	Cre09.g392208.v5.5	#N/A	-6.11E-02	#N/A
12	Cre10.g417600.v5.5	#N/A	2.58E-02	#N/A	*Cre02.g144700.v5.5*	*PTB5*	*-6.09E-02*	*Sodium/phosphate symporter*
13	Cre09.g389356.v5.5	#N/A	2.57E-02	#N/A	Cre13.g579650.v5.5	#N/A	-5.84E-02	#N/A
14	Cre12.g543400.v5.5	FDH1	2.51E-02	Formaldehyde dehydrogenase	Cre07.g328800.v5.5	NSG13	-5.77E-02	Protein expressed during nitrogen-starved gametogenesis
15	Cre07.g356600.v5.5	#N/A	2.50E-02	#N/A	Cre05.g234661.v5.5	BCS1	-5.75E-02	Ubiquinol:cytochrome c oxidoreductase biogenesis factor
16	Cre12.g541400.v5.5	#N/A	2.42E-02	#N/A	*Cre12.g502600.v5.5*	*SLT1*	*-5.73E-02*	*Sodium/sulfate co-transporter*
17	Cre13.g586300.v5.5	FKB12	2.36E-02	Peptidyl-prolyl cis-trans isomerase, FKBP-type	Cre10.g447800.v5.5	#N/A	-5.71E-02	#N/A
18	Cre12.g555500.v5.5	#N/A	2.32E-02	#N/A	Cre17.g725750.v5.5	#N/A	-5.56E-02	#N/A
19	**Cre01.g062172.v5.5**	**HBV1**	**2.29E-02**	**Histone H2B variant**	Cre05.g236650.v5.5	#N/A	-5.50E-02	#N/A
20	Cre07.g344400.v5.5	#N/A	2.27E-02	#N/A	Cre03.g163950.v5.5	CDO2	-5.50E-02	Cysteine dioxygenase
21	Cre02.g080450.v	#N/A	2.22E-	#N/A	Cre03.g151650.v5	#N/A	-5.44E-	#N/A

	5.5		02		.5		02	
22	Cre03.g144967.v5.5	#N/A	2.21E-02	#N/A	**Cre09.g394473.v5.5**	**LCI9**	**-5.43E-02**	**Low-CO2-inducible protein**
23	Cre06.g293950.v5.5	SHMT2	2.19E-02	Serine hydroxymethyltransferase 2	Cre03.g155150.v5.5	#N/A	-5.32E-02	#N/A
24	Cre14.g632100.v5.5	#N/A	2.17E-02	#N/A	Cre06.g293100.v5.5	#N/A	-5.29E-02	#N/A
24	Cre12.g520050.v5.5	#N/A	2.15E-02	#N/A	Cre12.g551700.v5.5	#N/A	-5.28E-02	#N/A
26	**Cre09.g399911.v5.5**	**CDC20**	**2.12E-02**	**Activator and specificity subunit of anaphase promoting complex**	Cre10.g431900.v5.5	#N/A	-5.25E-02	#N/A
27	Cre14.g619450.v5.5	#N/A	2.11E-02	#N/A	Cre06.g301750.v5.5	#N/A	-5.23E-02	#N/A
28	Cre13.g586000.v5.5	#N/A	2.07E-02	#N/A	**Cre16.g663450.v5.5**	**#N/A**	**-5.15E-02**	**Low-CO2-inducible membrane protein**
29	Cre01.g053800.v5.5	#N/A	2.06E-02	#N/A	Cre10.g429000.v5.5	#N/A	-5.13E-02	#N/A
30	Cre17.g708750.v5.5	#N/A	2.03E-02	#N/A	Cre13.g570801.v5.5	#N/A	-5.01E-02	#N/A
31	Cre03.g204250.v5.5	SAH1	2.03E-02	S-Adenosyl homocysteine hydrolase	Cre11.g468050.v5.5	#N/A	-5.00E-02	#N/A
32	Cre02.g101700.v5.5	#N/A	2.02E-02	#N/A	Cre12.g505100.v5.5	#N/A	-4.99E-02	#N/A
33	Cre08.g358527.v5.5	#N/A	2.02E-02	#N/A	Cre09.g403550.v5.5	#N/A	-4.97E-02	#N/A
34	**Cre17.g726500.v5.5**	**ORC4**	**2.02E-02**	**Origin recognition complex subunit 4**	Cre07.g342552.v5.5	#N/A	-4.96E-02	#N/A
35	Cre02.g144750.v5.5	PTB4	2.02E-02	Sodium/phosphate symporter	Cre12.g505050.v5.5	#N/A	-4.96E-02	#N/A
36	Cre04.g215050.v5.5	#N/A	2.02E-02	Beta-carotene hydroxylase, putative chloroplast precursor	Cre07.g333350.v5.5	#N/A	-4.94E-02	#N/A
37	Cre12.g523900.v5.5	#N/A	2.01E-02	#N/A	Cre12.g518800.v5.5	#N/A	-4.90E-02	#N/A
38	Cre14.g618250.v5.5	#N/A	2.00E-02	#N/A	Cre10.g428966.v5.5	#N/A	-4.87E-02	#N/A
39	**Cre06.g295700.v5.5**	**MCM3**	**2.00E-02**	**Minichromosome maintenance protein**	Cre06.g287350.v5.5	#N/A	-4.86E-02	#N/A
40	**Cre06.g259150.v5.5**	**EFG8**	**2.00E-02**	**Mitochondrial translation factor Tu**	Cre16.g662600.v5.5	#N/A	-4.85E-02	#N/A
41	Cre12.g495050.v5.5	#N/A	1.99E-02	#N/A	Cre02.g106450.v5.5	#N/A	-4.82E-02	#N/A
42	Cre11.g482700.v5.5	#N/A	1.98E-02	#N/A	Cre05.g239450.v5.5	#N/A	-4.79E-02	#N/A
43	Cre03.g205750.v5.5	#N/A	1.98E-02	#N/A	Cre01.g029000.v5.5	#N/A	-4.76E-02	Ubiquinone/menaquinone biosynthesis methyltrans

								ferase
44	Cre12.g561601.v5.5	#N/A	1.95E-02	#N/A	Cre16.g681400.v5.5	#N/A	-4.76E-02	#N/A
45	Cre12.g559800.v5.5	#N/A	1.95E-02	#N/A	Cre12.g485600.v5.5	#N/A	-4.75E-02	#N/A
46	Cre16.g688190.v5.5	#N/A	1.95E-02	#N/A	Cre14.g617400.v5.5	HSP22F	-4.73E-02	Heat shock protein 22F
47	Cre50.g761397.v5.5	#N/A	1.92E-02	#N/A	Cre13.g585000.v5.5	#N/A	-4.72E-02	#N/A
48	Cre07.g339250.v5.5	#N/A	1.92E-02	#N/A	Cre12.g495952.v5.5	#N/A	-4.69E-02	#N/A
49	Cre10.g441250.v5.5	#N/A	1.91E-02	#N/A	Cre02.g107000.v5.5	#N/A	-4.69E-02	#N/A
50	Cre08.g377100.v5.5	ADK6	1.90E-02	Adenylate kinase	Cre01.g004750.v5.5	#N/A	-4.67E-02	#N/A
51	Cre09.g407600.v5.5	#N/A	1.89E-02	#N/A	Cre06.g278107.v5.5	#N/A	-4.67E-02	#N/A
52	Cre12.g523300.v5.5	GTR22	1.89E-02	Glycosyltransferase	Cre05.g238311.v5.5	#N/A	-4.63E-02	#N/A
53	Cre19.g751047.v5.5	#N/A	1.87E-02	#N/A	Cre03.g195950.v5.5	#N/A	-4.60E-02	#N/A
54	**Cre14.g622850.v5.5**	**#N/A**	**1.86E-02**	**DNA recombination protein**	Cre08.g367500.v5.5	LHCSR2	-4.60E-02	Stress-related chlorophyll a/b binding protein 2
55	Cre06.g261300.v5.5	#N/A	1.86E-02	#N/A	Cre13.g569450.v5.5	#N/A	-4.59E-02	#N/A
56	Cre14.g611250.v5.5	#N/A	1.85E-02	#N/A	Cre16.g686203.v5.5	#N/A	-4.55E-02	#N/A
57	Cre17.g702900.v5.5	#N/A	1.85E-02	#N/A	Cre07.g352550.v5.5	RDP3	-4.50E-02	Putative rhodanese domain phosphatase
58	Cre01.g010296.v5.5	#N/A	1.84E-02	#N/A	Cre13.g569500.v5.5	#N/A	-4.44E-02	#N/A
59	Cre12.g551050.v5.5	#N/A	1.84E-02	#N/A	Cre13.g569400.v5.5	#N/A	-4.43E-02	#N/A
60	Cre06.g251750.v5.5	#N/A	1.84E-02	#N/A	Cre02.g144734.v5.5	#N/A	-4.41E-02	#N/A
61	Cre17.g719900.v5.5	PWD1	1.84E-02	Phosphoglucan water dikinase	**Cre03.g162800.v5.5**	**LCI1**	**-4.40E-02**	**Low-CO2-inducible membrane protein**
62	Cre02.g092400.v5.5	#N/A	1.84E-02	#N/A	Cre13.g605500.v5.5	#N/A	-4.35E-02	#N/A
63	Cre13.g562475.v5.5	#N/A	1.83E-02	#N/A	Cre14.g617450.v5.5	HSP22E	-4.34E-02	Heat shock protein 22E
64	Cre05.g248150.v5.5	#N/A	1.83E-02	#N/A	Cre02.g093750.v5.5	NRX2	-4.34E-02	Nucleoredoxin 2
65	Cre01.g032650.v5.5	TAL1	1.82E-02	Transaldolase	Cre11.g477350.v5.5	#N/A	-4.33E-02	#N/A
66	Cre08.g365900.v5.5	LHCSR1	1.82E-02	Stress-related chlorophyll a/b binding protein 1	Cre03.g201417.v5.5	#N/A	-4.31E-02	#N/A
67	Cre16.g684700.v5.5	#N/A	1.82E-02	#N/A	Cre06.g310950.v5.5	#N/A	-4.30E-02	#N/A
68	Cre06.g261450.v5.5	#N/A	1.82E-02	#N/A	Cre15.g642865.v5.5	#N/A	-4.28E-02	#N/A
69	Cre17.g731900.v5.5	#N/A	1.81E-02	#N/A	Cre07.g343050.v5.5	#N/A	-4.22E-02	#N/A
70	Cre01.g024200.v	#N/A	1,81E-	#N/A	Cre06.g311050.v5	#N/A	-4.18E-	#N/A

	5.5		02		.5		02	
71	Cre17.g711150.v5.5	#N/A	1.80E-02	#N/A	Cre13.g583450.v5.5	#N/A	-4.17E-02	#N/A
72	Cre06.g278224.v5.5	MRPL16	1.80E-02	Putative mitochondrial ribosomal protein L16, imported to mitochondria	Cre04.g214750.v5.5	#N/A	-4.14E-02	Endosomal R-SNARE protein, VAMP-like family (R.III)
73	Cre12.g538150.v5.5	#N/A	1 .78E-02	#N/A	Cre07.g355500.v5.5	#N/A	-4.11E-02	#N/A
74	Cre12.g498150.v5.5	#N/A	1.78E-02	#N/A	*Cre02.g095076.v5.5*	*MFT10*	*-4.02E-02*	*Major facilitator superfamily transporter, involved in circadian rhythm control*
75	Cre09.g387875.v5.5	IPY3	1.77E-02	Soluble inorganic pyrophosphatase	Cre11.g467531.v5.5	FAP15	-3.99E-02	Flagellar Associated Protein
76	Cre14.g630859.v5.5	#N/A	1.77E-02	#N/A	*Cre06.g309000.v5.5*	*NAR1.2*	*-3.98E-02*	*Anion transporter*
77	Cre12.g550250.v5.5	#N/A	1.77E-02	#N/A	*Cre06.g298750.v5.5*	*AOT4*	*-3.97E-02*	*Amino acid transporter*
78	Cre13.g566626.v5.5	#N/A	1.76E-02	#N/A	Cre08.g366700.v5.5	#N/A	-3.94E-02	#N/A
79	Cre11.g467641.v5.5	#N/A	1.75E-02	#N/A	**Cre06.g281600.v5.5**	**LCI23**	**-3.94E-02**	**Low-CO2-inducible protein, septin-like**
80	Cre01.g026450.v5.5	#N/A	1.75E-02	Serine/arginine-rich pre-mRNA splicing factor	Cre13.g569150.v5.5	#N/A	-3.94E-02	#N/A
81	Cre16.g678150.v5.5	#N/A	1.75E-02	#N/A	Cre02.g077750.v5.5	FAP211	-3.87E-02	Flagellar Associated Protein
82	**Cre17.g746347.v5.5**	**UNG1**	**1.75E-02**	**Uracil DNA glycosylase**	Cre06.g278098.v5.5	MCC1	-3.87E-02	Methylcrotonoyl-CoA carboxylase alpha subunit
83	**Cre03.g172550.v5.5**	**PRM1**	**1.75E-02**	**Protein-/Histone-arginine N-methyltransferase**	Cre09.g393953.v5.5	#N/A	-3.86E-02	#N/A
84	Cre02.g102450.v5.5	#N/A	1.73E-02	#N/A	Cre08.g367400.v5.5	LHCSR3	-3.85E-02	Stress-related chlorophyll a/b binding protein 3
85	Cre06.g249050.v5.5	#N/A	1.73E-02	#N/A	Cre06.g259550.v5.5	#N/A	-3.82E-02	#N/A
86	Cre05.g244400.v5.5	#N/A	1.73E-02	#N/A	Cre12.g504900.v5.5	#N/A	-3.82E-02	#N/A
87	Cre14.g623176.v5.5	#N/A	1.73E-02	#N/A	Cre03.g176833.v5.5	#N/A	-3.81E-02	#N/A
88	Cre01.g019250.v5.5	#N/A	1.71E-02	Putative dTDP-glucose 4-6-dehydratase	Cre02.g095080.v5.5	#N/A	-3.74E-02	#N/A
89	**Cre12.g558100.v5.5**	**PRM2**	**1.71E-02**	**Protein-/Histone-**	Cre16.g685000.v5.5	#N/A	-3.74E-02	#N/A

				arginine N-methyltransferase				
90	Cre06.g298600.v5.5	#N/A	1.70E-02	#N/A	Cre01.g053288.v5.5	#N/A	-3.72E-02	#N/A
91	Cre12.g485150.v5.5	GAP1	1.70E-02	Glyceraldehyde 3-phosphate dehydrogenase	Cre11.g467693.v5.5	#N/A	-3.72E-02	#N/A
92	**Cre12.g515850.v5.5**	**PCN1**	**1.70E-02**	**Proliferating cell nuclear antigen homolog**	Cre12.g554400.v5.5	#N/A	-3.70E-02	#N/A
93	Cre03.g190800.v5.5	#N/A	1.70E-02	#N/A	Cre16.g694500.v5.5	#N/A	-3.69E-02	DnaJ-like protein
94	Cre17.g705550.v5.5	#N/A	1.70E-02	#N/A	Cre09.g396809.v5.5	#N/A	-3.68E-02	#N/A
95	Cre09.g403071.v5.5	#N/A	1.69E-02	#N/A	Cre04.g215900.v5.5	#N/A	-3.64E-02	#N/A
96	Cre16.g679350.v5.5	#N/A	1.69E-02	#N/A	Cre12.g516700.v5.5	#N/A	-3.62E-02	#N/A
97	Cre07.g318276.v5.5	#N/A	1.69E-02	#N/A	Cre04.g217925.v5.5	#N/A	-3.61E-02	#N/A
98	Cre16.g684850.v5.5	#N/A	1.69E-02	#N/A	Cre02.g093800.v5.5	NRX3	-3.61E-02	Nucleoredoxin
99	Cre06.g282850.v5.5	#N/A	1.69E-02	#N/A	Cre03.g144144.v5.5	#N/A	-3.60E-02	#N/A
100	Cre15.g635400.v5.5	ZYS3	1.69E-02	Zygote-specific protein	Cre17.g734725.v5.5	#N/A	-3.54E-02	#N/A

Data in Brief 7. List of the 100 most positive expressed genes (*iclC* phenotype) (right) and 100 most negative genes (*icl* phenotype) (left) of the second constraint when 8 dark samples are analysed separately. Bold: transcripts encoding components of the division machinery; red: transcripts encoding enzymes related to low carbon availability; underlined: transcripts related to stressful conditions; italis; transcripts encoding transporters. *C. reinhardtii* genome version v5.5. #N/A means the function of the gene is unknown.