

Figure S1. Measurement of acetate assimilation. Acetate concentration (g/L) in the medium was measured for the cells cultivated at the 4 acetate concentrations. Three biological replicates were included in the experiments. Error bars indicate standard deviations.

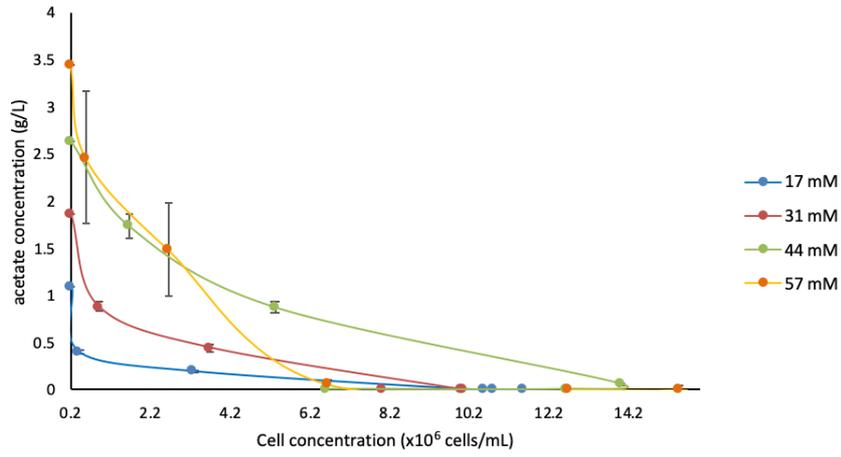


Figure S2. Fatty acid classes. Saturated (SAT), monounsaturated (MONOUNSAT), polyunsaturated (POLYUNSAT)

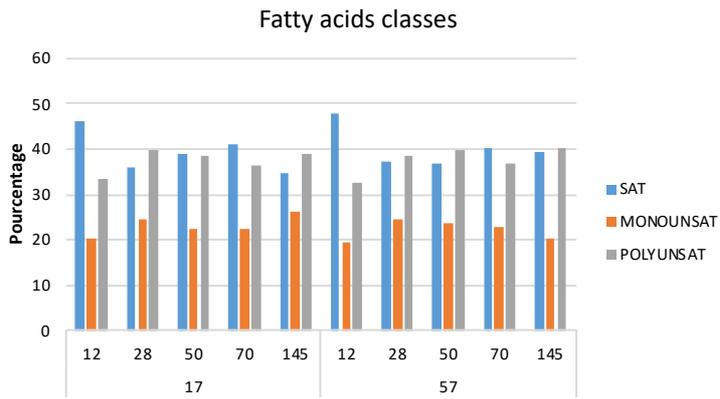


Figure S3. Boxplots of standard deviations. Between replicate variability of mean FPKM estimates per sample. Boxplots of log transformed standard deviation on the FPKM value per sample are depicted.

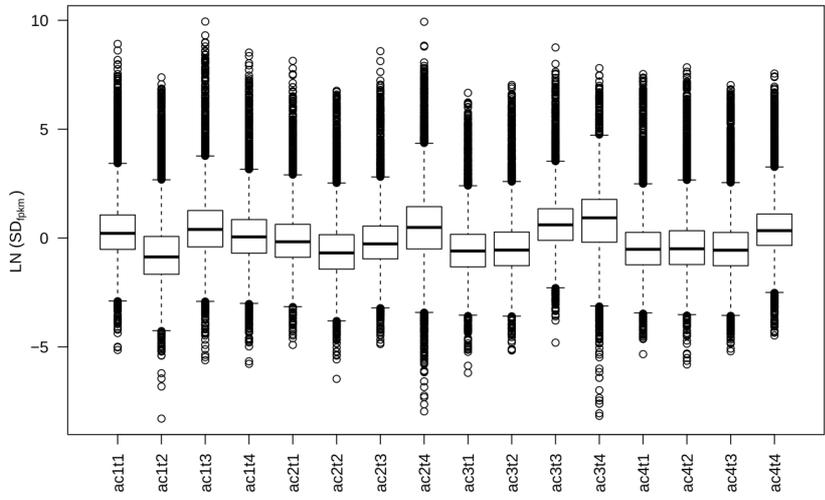


Figure S4. Comparison of 250 top-contributing genes according to surprisal analysis and K-means clustering of transcripts. (a) Centroid plots with mean and standard deviation of the expression values [Ln(meancenteredFPKM)] of the different genes belonging to the different clusters for each sample. Stationary-upregulated (cluster 1), high acetate (cluster 2), exponential-upregulated (cluster 3) and cluster 4. (b) Cumulative barplot describing how many of the 250 most contributing genes to the different phenotypes described according to the first 2 constraints belong to the 4 different clusters according to K-means clustering.

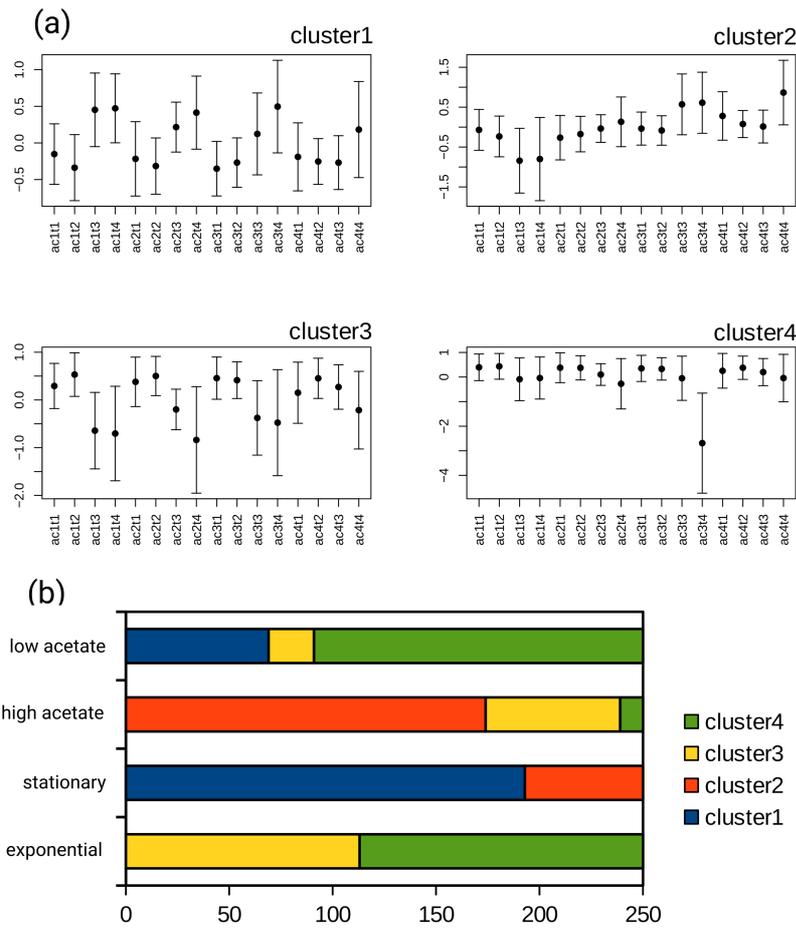


Figure S5. FPKM values for transcripts Cre08.g377550 encoding a Yippee-type zinc-binding protein and *APX1* (Cre02.g087700).

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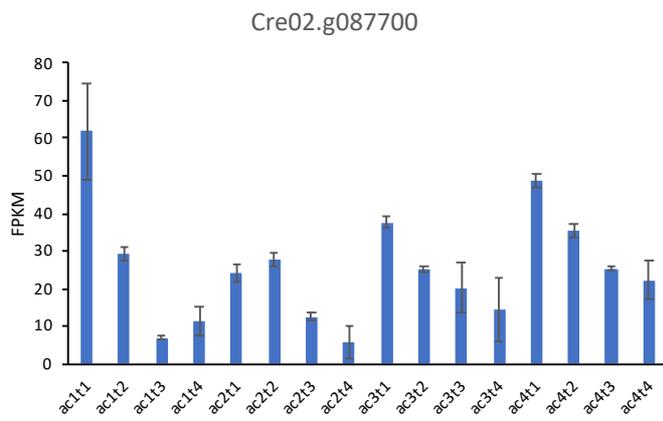
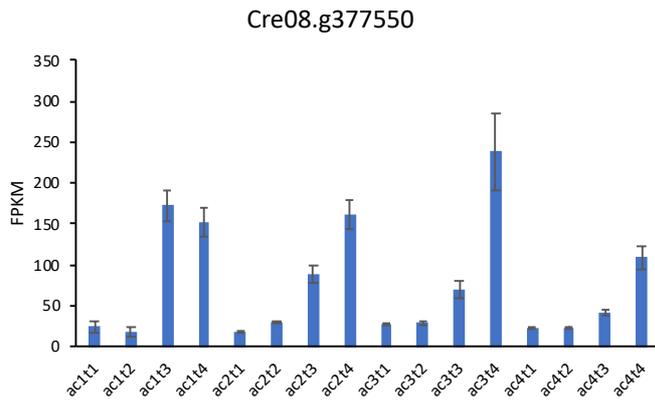


Table S1. Growth rates of WT and *iclC*. Number of doublings per day in exponential phase for cells cultivated in flasks at 50 $\mu\text{mol. m}^{-2}\cdot\text{s}^{-1}$.

acetate	WT	<i>iclC</i>
17 mM	1.9 (1.9-1.9)	2.0 (1.8-2.3)
57 mM	1.0 (1.1-1.0)	1.1 (1.1-1.2)

Table S2. Percentage of the main fatty acids of *C. reinhardtii* (iclC strain). Cells are cultivated in 17 and 57 mM acetate, and sampled at time points 12h, 28h, 50h and 70h of the growth curve (mean \pm SD, on 3 biological replicates).

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Time point	[Acetate] (mM)	C16:0	C16:1	C16:3	C18:0	C18:1	C18:2	C18:3	C20:0
12h	17	31.7 \pm 7.7	3.6 \pm 0.2	2.2 \pm 0.7	15.1 \pm 5.3	17.3 \pm 5.7	7.2 \pm 0.6	20.3 \pm 8.6	2.5 \pm 1.0
	57	31.4 \pm 4.3	4.1 \pm 0.2	2.0 \pm 0.3	15.3 \pm 4.5	17.0 \pm 4.0	7.7 \pm 0.6	19.5 \pm 4.7	2.9 \pm 1.0
28h	17	27.4 \pm 5.1	3.9 \pm 0.3	3.4 \pm 0.1	8.3 \pm 1.7	21.8 \pm 3.0	9.4 \pm 0.4	24.8 \pm 4.0	1.1 \pm 0.4
	57	28.1 \pm 4.7	3.9 \pm 0.3	3.0 \pm 0.3	8.6 \pm 0.9	21.8 \pm 2.7	9.6 \pm 0.6	23.9 \pm 3.7	1.1 \pm 0.5
50h	17	25.8 \pm 4.5	4.8 \pm 0.4	3.0 \pm 0.3	10.2 \pm 1.1	20.3 \pm 1.9	10.5 \pm 0.8	22.2 \pm 2.4	3.3 \pm 1.2
	57	27.7 \pm 5.3	6.2 \pm 0.9	3.2 \pm 0.6	8.5 \pm 1.7	19.8 \pm 2.4	14.5 \pm 0.2	17.9 \pm 5.8	2.1 \pm 1.3
70h	17	28.9 \pm 5.2	4.2 \pm 0.3	2.5 \pm 0.1	10.8 \pm 1.7	20.2 \pm 2.8	8.1 \pm 0.4	22.7 \pm 4.6	2.5 \pm 0.8
	57	32.7 \pm 5.0	4.8 \pm 0.6	3.1 \pm 0.3	7.3 \pm 1.5	20.4 \pm 3.1	13.5 \pm 0.2	17.0 \pm 4.5	1.3 \pm 0.5

Table S3. Number of sequenced reads for 4 acetate concentrations and 4 timepoints (ac1=17 mM, ac2=31 mM, ac3=44 mM, ac4=57 mM) and 4 time points (t1=12h, t2=28h, t3=50h, t4=70h). Samples in italics were removed from the analysis, because they had too few uniquely mapping reads to the genome. *data available in [25] (<https://www.ncbi.nlm.nih.gov/Traces/study/?acc=SRP132684>).

Sample	Biological replicate	Acetate concentration (mM)	Time (hours)	Number of sequenced reads	number of trimmed reads	Number of uniquely mapped reads	Fraction of uniquely mapped reads
ac1t1*	1	17	12	27596703	25600013	22269444	86.99%
ac1t1*	2	17	12	30114986	28063350	22460172	80.03%
ac1t1*	3	17	12	28741589	26807561	22575552	84.21%
ac1t2*	1	17	28	26218763	24652570	22412128	90.91%
ac1t2*	2	17	28	27889515	26249741	23698788	90.28%
ac1t2*	3	17	28	26630091	24994681	22769422	91.10%
ac1t3	1	17	50	24818061	22130171	17485954	79.01%
ac1t3	2	17	50	26992479	25028973	22613353	90.35%
ac1t3	3	17	50	29937141	27743622	22533450	81.22%
ac1t4	1	17	70	28969256	26884722	15303367	56.92%
ac1t4	2	17	70	34291726	31593263	15336658	48.54%
ac1t4	3	17	70	28602705	26371812	14452537	54.80%
ac2t1	1	57	12	17490336	14345681	11605784	64.31%
ac2t1*	2	57	12	18295960	15367211	15345326	82.76%
ac2t1*	3	57	12	17594155	12572740	15349330	85.50%
ac2t2*	1	57	28	17636204	15865151	15595713	79.18%
ac2t2*	2	57	28	18105831	16393941	16736724	90.70%
ac2t2*	3	57	28	19490295	15448228	13787210	70.88%
ac2t3	1	57	50	20236476	14428833	16153442	85.78%
ac2t3	2	57	50	19987724	12434769	16327473	85.55%
ac2t3	3	57	50	19455896	16421430	16842275	92.62%
ac2t4	1	57	70	17159711	10394197	13754355	69.32%
ac2t4	2	57	70	18376883	11037934	10688319	57.52%
ac2t4	3	57	70	18042360	7104147	5663700	31.22%
ac3t1*	1	31	12	18047009	15595713	19335327	93.14%
ac3t1*	2	31	12	18541383	16736724	17216882	91.68%
ac3t1*	3	31	12	17952421	13787210	17147077	93.58%
ac3t2*	1	31	28	19695743	11605784	16323251	86.84%
ac3t2*	2	31	28	18453200	15345326	14403003	74.24%
ac3t2*	3	31	28	19452219	15349330	14137670	75.26%
ac3t3	1	31	50	18831301	16153442	10982341	71.86%
ac3t3	2	31	50	19085569	16327473	12882313	71.85%
ac3t3	3	31	50	18184329	16842275	16201118	89.03%
ac3t4	1	31	70	19843257	13754355	10638497	81.09%
ac3t4	2	31	70	18580719	10688319	6568536	42.59%
ac3t4	3	31	70	18141774	5663700	3875397	24.90%
ac4t1*	1	44	12	20759397	16323251	15865151	90.71%
ac4t1*	2	44	12	18779332	14403003	16393941	89.60%
ac4t1*	3	44	12	18322514	14137670	15448228	87.80%
ac4t2*	1	44	28	18797355	19335327	14345681	81.34%
ac4t2*	2	44	28	19400482	17216882	15367211	84.87%
ac4t2*	3	44	28	18784045	17147077	12572740	64.51%
ac4t3	1	44	50	15281988	10982341	14428833	71.30%
ac4t3	2	44	50	17929166	12882313	12434769	62.21%

ac4t3	3	44	50	18197263	16201118	16421430	84.40%
ac4t4	1	44	70	13119628	10638497	10394197	60.57%
ac4t4	2	44	70	15421089	6568536	11037934	60.06%
ac4t4	3	44	70	15565195	3875397	7104147	39.37%

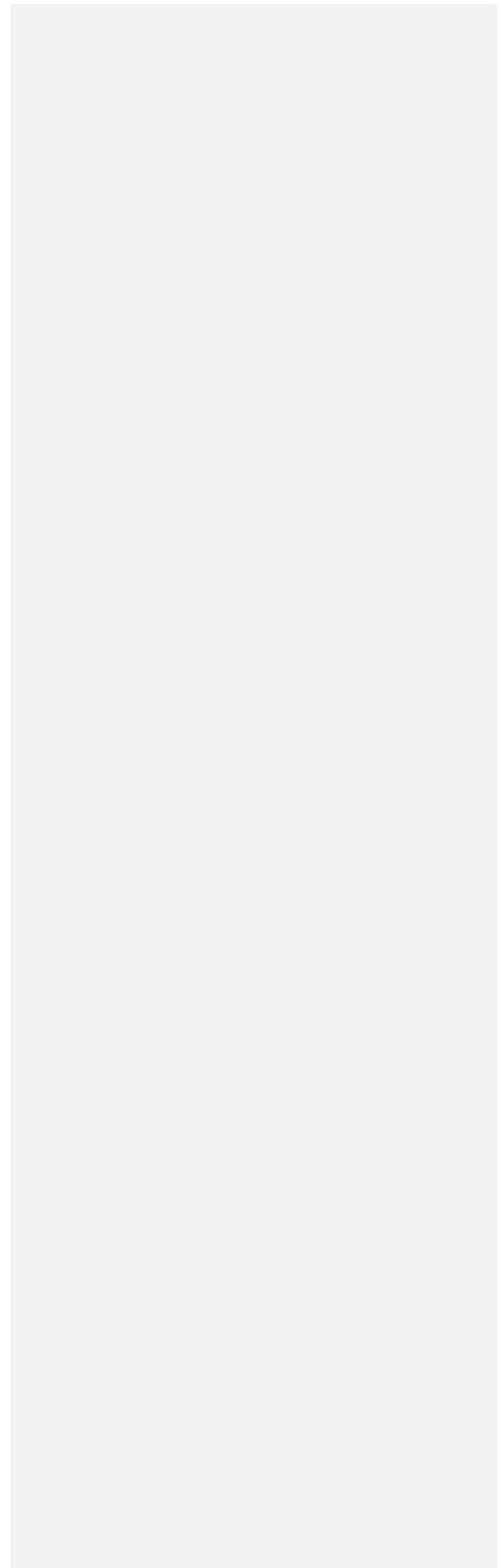


Table S4. Variation in λ_n explained by the variables growth mode (stationary/exponential) and acetate. Asterisks denote a significant relationship between λ_n and the environmental (acetate) or biological (growth mode) variable (One Way ANOVA, F-value, Df=3, P < 0.05).

time phenotype	F-statistic	p value
Constraint 1	8.7678	0.00237*
Constraint 2	0.0481	0.98536
Constraint 3	1.3264	0.31160
Constraint 4	0.5494	0.65808
Constraint 5	0.8671	0.48483
acetate phenotype	statistic	p value
Constraint 1	0.3747	0.77285
Constraint 2	5.5548	0.01263*
Constraint 3	0.3321	0.80238
Constraint 4	1.4531	0.27647
Constraint 5	0.6338	0.60733

Table S5. KEGG pathways ranked from low SR or high negative sum (more stable) to high SR (less stable). Bold pathways denote top 10 stable pathways.

Rank	Stability	names	Set size	Positive G subsets		Negative G subsets		SR
				Positive sum(G ²)	Negative sum(G ²)			
1		Oxidative phosphorylation	66	0	0	66	0.000355350995421	0
2		Carbon fixation in photosynthetic organisms	37	0	0	37	0.000332510146488	0
3		Phagosome	29	0	0	29	0.000316364886226	0
4		Citrate cycle (TCA cycle)	33	0	0	33	0.000304635822267	0
5		2-Oxocarboxylic acid metabolism	30	0	0	30	0.000255010881357	0
6		Valine, leucine and isoleucine biosynthesis	12	0	0	12	0.000242451697368	0
7		alpha-Linolenic acid metabolism	10	0	0	10	0.000231253920433	0
8		Lysine biosynthesis	10	0	0	10	0.000204109091004	0
9		Pyruvate metabolism	45	0	0	45	0.000195837928556	0
10		Fatty acid biosynthesis	19	0	0	19	0.000183795645287	0
11		Phenylalanine, tyrosine and tryptophan biosynthesis	21	0	0	21	0.000172490951702	0
12		Proteasome	34	0	0	34	0.000172007302702	0
13		Fructose and mannose metabolism	13	0	0	13	0.000155514506612	0
14		Sulfur metabolism	21	0	0	21	0.000147669898776	0
15		Pentose and glucuronate interconversions	10	0	0	10	0.000144653113935	0
16		Valine, leucine and isoleucine degradation	20	0	0	20	0.000139348141097	0
17		Steroid biosynthesis	11	0	0	11	0.000139320875242	0
18		Plant hormone signal transduction	11	0	0	11	0.000134375917837	0
19		Selenocompound metabolism	14	0	0	14	0.000130176048551	0
20		Pantothenate and CoA biosynthesis	19	0	0	19	0.000127134335054	0
21		Spliceosome	106	0	0	106	0.000123788577504	0
22		Protein export	29	0	0	29	0.000122962639836	0
23		mRNA surveillance pathway	42	0	0	42	0.000120693674893	0
24		Histidine metabolism	11	0	0	11	0.000118329890379	0
25		SNARE interactions in vesicular transport	14	0	0	14	0.00011803194921	0
26		Ascorbate and aldarate metabolism	17	0	0	17	0.000103718029108	0
27		Terpenoid backbone biosynthesis	21	0	0	21	9.80703801866992E-05	0
28		Regulation of autophagy	11	0	0	11	8.37812440043619E-05	0
29		Aminoacyl-tRNA biosynthesis	42	0	0	42	8.17559119495921E-05	0
30		Carotenoid biosynthesis	12	0	0	12	7.02912559110478E-05	0
31		Nucleotide excision repair	30	0	0	30	4.58930871398967E-05	0
32		Mismatch repair	17	0	0	17	4.39849088741505E-05	0
33		Base excision repair	13	0	0	13	4.34949898251257E-05	0
34		Glycerolipid metabolism	23	1	3.5097645464952E-12	22	6.45336431669079E-05	5.43865861937725E-08
35		Inositol phosphate metabolism	24	1	5.8689138694192E-12	23	7.79941753971541E-05	7.52481046120958E-08
36		Phosphatidylinositol signaling system	35	2	6.34994573690113E-12	33	8.38130119063243E-05	7.57632447811124E-08
37		Fatty acid metabolism	35	1	1.35100799446707E-10	34	0.000180398860024	7.48900516492723E-07
38		Biosynthesis of unsaturated fatty acids	16	1	3.2086439868593E-10	15	0.000196849537302	1.62999823664201E-06
39		Nicotinate and nicotinamide metabolism	17	1	2.61011084719169E-10	16	8.06066179301011E-05	3.23808505333281E-06
40		N-Glycan biosynthesis	20	1	2.11220645643598E-10	19	6.46800031775959E-05	3.26562515873161E-06
41		Ribosome	124	1	4.72303160637398E-09	123	0.000866811096156	5.44874382356074E-06
42		Carbon metabolism	131	2	5.70294205970845E-09	129	0.000235277792368	2.42391855274987E-05
43		Propanoate metabolism	18	1	5.54414498365616E-09	17	0.000183457568984	3.02203120555556E-05
44		Basal transcription factors	20	1	1.46466437276582E-09	19	4.7728335166987E-05	3.06875238426955E-05
45		Photosynthesis - antenna proteins	23	1	2.02441726380731E-08	22	0.000460832981165	4.39295221164656E-05
46		Protein processing in endoplasmic reticulum	80	3	6.27418290808014E-09	77	0.000134897169935	4.65108564627932E-05
47		Arachidonic acid metabolism	10	1	3.33546317662889E-09	9	6.41143784123809E-05	5.20236374308324E-05

48 RNA transport	89	1	7.45691588374356E-09	88	0.00013141471952	5.67433839299559E-05
49 Ubiquitin mediated proteolysis	54	1	5.12329571780646E-09	53	8.225902918128E-05	6.22824724385683E-05
50 RNA degradation	53	1	5.41173505621507E-09	52	8.16377759907414E-05	6.62895943763683E-05
51 Peroxisome	47	4	1.66419929907805E-08	43	0.000154269100457	0.000107876385754
52 Endocytosis	53	3	1.25609275370062E-08	50	0.000115238113204	0.000108999767418
53 Porphyrin and chlorophyll metabolism	40	1	1.18867896458742E-08	39	0.000104156816259	0.00011412397261
54 Fatty acid degradation	17	1	2.33817017604982E-08	16	0.000198615854243	0.000117723239414
55 Ribosome biogenesis in eukaryotes	57	1	1.16132296550105E-08	56	9.63850864350657E-05	0.000120487827366
56 Glutathione metabolism	32	2	2.15000277517205E-08	30	0.000118117246006	0.000182022765334
57 Biosynthesis of amino acids	120	1	4.11713195458188E-08	119	0.000195681099858	0.000210400082459
58 Arginine and proline metabolism	32	1	3.65316803913018E-08	31	0.00013282595145	0.000275034208243
59 Glycolysis / Gluconeogenesis	45	2	6.34994237357837E-08	43	0.000203203255585	0.000312492157436
60 Pentose phosphate pathway	24	1	1.0438395512019E-07	23	0.000217727580251	0.000479424586448
61 Glyoxylate and dicarboxylate metabolism	36	2	1.51040789762267E-07	34	0.000311460980794	0.000484942895181
62 Amino sugar and nucleotide sugar metabolism	36	2	7.34055378678352E-08	34	0.00013798279026	0.000531990531062
63 Alanine, aspartate and glutamate metabolism	27	1	1.92132824547154E-07	26	0.000234687309359	0.000818675816225
64 Homologous recombination	13	1	3.53177467327263E-08	12	4.09222528783088E-05	0.000863045024372
65 One carbon pool by folate	14	1	1.20974535093299E-07	13	0.000126319251077	0.000957688824643
66 RNA polymerase	26	1	7.88033409662853E-08	25	6.91206363966133E-05	0.001140084135136
67 Pyrimidine metabolism	76	4	1.06043114944306E-07	72	9.00796388985311E-05	0.001177215142522
68 Starch and sucrose metabolism	41	4	1.55042790314208E-07	37	0.000125609029266	0.001234328385624
69 Sphingolipid metabolism	15	1	7.37314758910123E-08	14	4.91164076160397E-05	0.001501157748901
70 Arginine biosynthesis	21	2	3.09653655088573E-07	19	0.000201555016631	0.001536323234539
71 Glycerophospholipid metabolism	32	2	1.32723750078467E-07	30	6.10950457180683E-05	0.002172414285291
72 ABC transporters	12	2	9.2529112951528E-08	10	3.54705573915424E-05	0.002608617393015
73 Purine metabolism	101	8	2.48508622430845E-07	93	8.95674656925117E-05	0.002774541185345
74 Photosynthesis	33	2	1.63228474516247E-06	31	0.000519266443881	0.003143443533466
75 Galactose metabolism	13	2	4.33469468910448E-07	11	9.41729568103144E-05	0.004602908134058
76 Ubiquinone and other terpenoid-quinone biosynthesis	17	2	4.14602087947335E-07	15	6.85879235348066E-05	0.006044826356887
77 DNA replication	28	4	3.30550443727272E-07	24	3.53124674172003E-05	0.009360729167463
78 Nitrogen metabolism	10	2	1.65656726365839E-06	8	0.000154399166856	0.010729120482935
79 Glycine, serine and threonine metabolism	35	1	2.83265308139074E-06	34	0.000158284511702	0.01789558681777
80 Cysteine and methionine metabolism	42	2	3.33441854992681E-06	40	0.000172904498725	0.019284741429649
81 Tyrosine metabolism	14	2	6.92943494401046E-06	12	0.000110182223635	0.062890679779266
82 Phenylalanine metabolism	10	1	9.20612251451991E-06	9	0.000131671732299	0.069917227895429
83 beta-Alanine metabolism	12	2	9.21490074407737E-06	10	0.000118507289164	0.077758092426824

Table S6. KEGG pathways ranked from low SR (stationary state) to high SR (exponential state) from the first constraint. Bold pathways denote the top 10 pathways contributing the most to either state. SR values <0.5 or >2 (grey background) indicate KEGG pathways where the sum of the positive contributions (G^2) of containing genes are at least double or less than half of the sum of the negative contributions.

Rank	KEGG pathway names	Set size	Positive G ² subset	Positive sum(G ²)	Negative G ² subsets	Negative sum(G ²)	SR
1	83 Regulation of autophagy	11	0	0	11	7.7566114627055E-05	0
2	82 Valine, leucine and isoleucine degradation	20	5	5.54342207234786E-06	15	5.5737851207342E-05	0.09945524920632
3	81 Endocytosis	53	17	1.87791840126372E-06	36	1.37474291350847E-05	0.136601424368946
4	80 Plant hormone signal transduction	11	4	1.92311671378083E-06	7	1.36469201698926E-05	0.140919466798344
5	79 Peroxisome	47	8	8.77502736124042E-06	39	3.62611942208702E-05	0.241994990782458
6	78 Propanoate metabolism	18	6	1.44650270373447E-05	12	4.60629635148019E-05	0.314027277743355
7	77 beta-Alanine metabolism	12	3	2.08791962473789E-05	9	5.69587536722822E-05	0.366566943643279
8	76 SNARE interactions in vesicular transport	14	5	6.49822069890119E-06	9	1.46704504769261E-05	0.442946227801367
9	75 Selenocompound metabolism	14	5	2.03738375099447E-05	9	3.73587275321166E-05	0.54535683776782
10	74 Pentose and glucuronate interconversions	10	4	7.64833874271331E-06	6	1.24103030098983E-05	0.616289444070226
11	73 alpha-Linolenic acid metabolism	10	2	1.44060522561005E-05	8	1.90411801952735E-05	0.756573495359099
12	72 Cysteine and methionine metabolism	42	25	3.64701686794292E-05	17	4.11246031796287E-05	0.886821169316352
13	71 Base excision repair	13	6	1.46887558288418E-05	7	1.54808386346216E-05	0.948834631994138
14	70 Ribosome	124	42	2.96973606304024E-05	82	2.98595361187222E-05	0.994568720435743
15	69 Glyoxylate and dicarboxylate metabolism	36	16	1.1915428378493E-05	20	1.19625489466162E-05	0.996060992658552
16	68 Fatty acid degradation	17	2	3.0847376956461E-05	15	3.07043819700765E-05	1.00465715240658
17	67 Arginine and proline metabolism	32	10	3.2666908337155E-05	22	2.76203486283993E-05	1.18271165859097
18	66 Ubiquitin mediated proteolysis	54	17	2.60044362425567E-05	37	1.74108892173597E-05	1.49357312644484
19	65 Starch and sucrose metabolism	41	16	3.35644223717635E-05	25	2.18872178100128E-05	1.53351708120749
20	64 Pyruvate metabolism	45	27	2.68270534836927E-05	18	1.57083171023985E-05	1.70782479808715
21	63 Galactose metabolism	13	9	7.90391604290231E-05	4	3.92662146792397E-05	2.01290501451905
22	62 Tyrosine metabolism	14	9	0.000118426799386	5	5.50685574518761E-05	2.15053389567942
23	61 Valine, leucine and isoleucine biosynthesis	12	6	1.87433765392686E-05	6	7.95943819599509E-06	2.35486174749113
24	60 Arachidonic acid metabolism	10	5	6.64840530608746E-05	5	2.5064580856565E-05	2.65251006754661
25	59 Nitrogen metabolism	10	3	3.22038383352851E-05	7	1.18469954621349E-05	2.71831270959917
26	58 ABC transporters	12	6	7.45209220923073E-05	6	2.61099901604096E-05	2.85411528822798
27	57 Ribosome biogenesis in eukaryotes	57	32	2.433559720558E-05	25	8.51607186942815E-06	2.85760824693629
28	56 Fructose and mannose metabolism	13	10	2.76752976509033E-05	3	9.58767394836722E-06	2.88654973040843
29	55 Phagosome	29	19	1.61703872464896E-05	10	5.5922498850236E-06	2.89157093816479
30	54 Alanine, aspartate and glutamate metabolism	27	13	4.77656226486358E-05	14	1.62093398091941E-05	2.94679630453196
31	53 Carbon fixation in photosynthetic organisms	37	23	5.96445524354843E-05	14	1.9737212234638E-05	3.02193398573333
32	52 Glycerophospholipid metabolism	32	17	4.86915715689258E-05	15	1.60794985090323E-05	3.0281772495314
33	51 Nucleotide excision repair	30	13	2.08062507113927E-05	17	6.75041590676193E-06	3.08221759944465
34	50 mRNA surveillance pathway	42	27	1.81637909145652E-05	15	5.71911185339432E-06	3.17598105793033
35	49 Phenylalanine metabolism	10	6	8.88670517134741E-05	4	2.73532745278459E-05	3.24886337184261
36	48 2-Oxocarboxylic acid metabolism	30	13	3.15678884257914E-05	17	9.03612529045881E-06	3.49352044278578
37	47 Pantothenate and CoA biosynthesis	19	6	6.74461193408085E-05	13	1.91458628188293E-05	3.52275162415129
38	46 Citrate cycle (TCA cycle)	33	16	2.92184470137691E-05	17	8.26915338333957E-06	3.53342665920764
39	45 Mismatch repair	17	6	2.04404535571122E-05	11	5.4584051943244E-06	3.74476661761314
40	44 Fatty acid biosynthesis	19	12	4.06595622686739E-05	7	1.04501746664177E-05	3.89080216997098
41	43 One carbon pool by folate	14	9	7.84068716710907E-05	5	1.93900986805211E-05	4.04365511300139
42	42 Glycerolipid metabolism	23	11	9.19121709764475E-05	12	2.22041889575659E-05	4.13940680977357
43	41 Fatty acid metabolism	35	15	6.41467760254326E-05	20	1.47509476984419E-05	4.3486545635443
44	40 Protein processing in endoplasmic reticulum	80	45	4.57048539672092E-05	35	1.02469388983873E-05	4.46034219784431
45	39 Phenylalanine, tyrosine and tryptophan biosynthesis	21	16	6.74649165981001E-05	5	1.46782499143288E-05	4.596250710532

46	38	Carbon metabolism	131	77	5.11354114806906E-05	54	1.09875501657145E-05	4.6539411160327
47	37	Glutathione metabolism	32	18	9.77371293331979E-05	14	2.07595905937399E-05	4.70804705381189
48	36	Glycine, serine and threonine metabolism	35	21	5.27812076571822E-05	14	1.07852587780657E-05	4.89382858059232
49	35	RNA transport	89	55	4.04787482994702E-05	34	7.95713290432183E-06	5.08710219952271
50	34	Basal transcription factors	20	11	4.96816583055217E-05	9	9.41328342735687E-06	5.27782454325521
51	33	Arginine biosynthesis	21	11	7.8116200179021E-05	10	1.37565966525879E-05	5.67845391936569
52	32	Spliceosome	106	72	3.50500733094166E-05	34	5.42196367938373E-06	6.46446110339871
53	31	Purine metabolism	101	62	6.8441892104463E-05	39	1.03861508112397E-05	6.58972639126289
54	30	Biosynthesis of unsaturated fatty acids	16	6	0.000100095772727	10	1.41556367045121E-05	7.07108940531341
55	29	RNA degradation	53	30	5.88916489082065E-05	23	8.06309370527E-06	7.30385272215244
56	28	Nicotinate and nicotinamide metabolism	17	9	7.96574468720383E-05	8	1.06647231774838E-05	7.46924655674304
57	27	Proteasome	34	24	6.54707102457124E-06	10	8.10772959540296E-07	8.07509790198652
58	26	Homologous recombination	13	6	5.34300669218936E-05	7	5.80274998408841E-06	9.20771480218914
59	25	Inositol phosphate metabolism	24	12	0.000151634631205	12	1.62994204805232E-05	9.30306886590089
60	24	Amino sugar and nucleotide sugar metabolism	36	21	8.87686991839296E-05	15	8.33788635932352E-06	10.646427086964
61	23	Oxidative phosphorylation	66	47	2.45507724794666E-05	19	2.21578396397889E-06	11.0799486225095
62	22	Pyrimidine metabolism	76	45	7.86468694260353E-05	31	6.97415119086303E-06	11.2769091569268
63	21	Aminoacyl-tRNA biosynthesis	42	34	7.59466408182134E-05	8	6.30445596291615E-06	12.0465019130824
64	20	Sphingolipid metabolism	15	8	9.53524929417924E-05	7	7.90159321503573E-06	12.0675021286022
65	19	Phosphatidylinositol signaling system	35	19	0.000111335921137	16	9.13587189491506E-06	12.1647854102092
66	18	Biosynthesis of amino acids	120	79	8.44770130293984E-05	41	6.34289640461107E-06	13.3183655605642
67	17	Ascorbate and aldarate metabolism	17	10	9.19563005787522E-05	7	6.43172251340224E-06	14.2973053310581
68	16	Protein export	29	22	4.78269360695944E-05	7	3.17830168812098E-06	15.047953518179
69	15	Sulfur metabolism	21	14	6.37188166222858E-05	7	4.02922526450064E-06	15.8141608968052
70	14	Pentose phosphate pathway	24	19	0.000106860728166	5	5.7543464795044E-06	18.5669258192087
71	13	Glycolysis / Gluconeogenesis	45	34	9.47992236237634E-05	11	4.58773195553766E-06	20.6636360935027
72	12	Terpenoid backbone biosynthesis	21	14	0.000131423957674	7	6.30495258837856E-06	20.8445592305032
73	11	Steroid biosynthesis	11	8	0.000151371825159	3	6.5968999615227E-06	22.9455896169092
74	10	Porphyrin and chlorophyll metabolism	40	31	0.00023502101665	9	9.8001626523729E-06	23.9813383705813
75	9	DNA replication	28	15	9.61736514076376E-05	13	3.92971382633096E-06	24.4734491257934
76	8	Carotenoid biosynthesis	12	11	4.81795322217881E-05	1	1.7915948444206E-06	26.8919797192162
77	7	N-Glycan biosynthesis	20	16	0.000104388928645	4	3.69991613604256E-06	28.2138634517583
78	6	RNA polymerase Ubiquinone and other terpenoid-quinone biosynthesis	26	18	5.85100042637253E-05	8	1.77798477333666E-06	32.908045749977
79	5	Lysine biosynthesis	17	13	0.000183713857725	4	5.05361047219889E-06	36.3529913387764
80	4	Lysine biosynthesis	10	8	0.00014362695846	2	3.68935052376957E-06	38.9301470637196
81	3	Histidine metabolism	11	6	0.000146351790137	5	3.33003018761552E-06	43.9490881137679
82	2	Photosynthesis - antenna proteins	23	22	0.000942091209597	1	2.22239770512546E-07	4239.07569479725
83	1	Photosynthesis	33	32	0.000484202173356	1	9.36900361348169E-09	51681.2879290016

Table S7. KEGG pathways ranked from low SR (low acetate) to high SR (high acetate) from the second constraint. Bold pathways denote the top 10 pathways contributing the most to either state. SR values <0.5 or >2 (grey background) indicate KEGG pathways where the sum of the positive contributions (G^2) of containing genes are at least double or less than half of the sum of the negative contributions.

Rank	Rank	Low Acetate	High Acetate	names	Set size	Positive subset	Positive sum(G^2)	Negative subset	Negative sum(G^2)	SR
1	83			alpha-Linolenic acid metabolism	10	0	0	10	3.71606353666472E-05	0
2	82			Photosynthesis - antenna proteins	23	1	1.29977127077725E-06	22	0.000222967613709	0.005829417327284
3	81			Fatty acid biosynthesis	19	4	2.53568479025119E-06	15	8.81899569903032E-05	0.02875253460584
4	80			Carotenoid biosynthesis	12	3	2.07406766610321E-06	9	4.22282095973124E-05	0.049115690337845
5	79			Photosynthesis	33	2	1.4921138092381E-05	31	0.000174360180435	0.085576523579996
6	78			Ribosome	124	19	4.45724858226991E-06	105	3.89963681019487E-05	0.114299069354799
7	77			Pyruvate metabolism	45	17	4.53309118929998E-06	28	3.14976778080882E-05	0.143918266512204
8	76			Lysine biosynthesis	10	3	5.84030696034789E-06	7	3.25485714319654E-05	0.179433588124001
9	75			Porphyrin and chlorophyll metabolism	40	17	1.0297009733194E-05	23	4.88237249390238E-05	0.210901764378978
10	74			Carbon fixation in photosynthetic organisms	37	9	1.17010884172259E-05	28	5.41218403961604E-05	0.216199011925249
11	73			Fatty acid metabolism	35	13	1.32076669015663E-05	22	6.00524708061381E-05	0.21993544519098
12	72			Regulation of autophagy	11	6	4.25400853413254E-06	5	1.86755847317052E-05	0.227784489495025
13	71			Propanoate metabolism	18	8	1.193298985184E-05	10	4.60004111880338E-05	0.259410702578419
14	70			Biosynthesis of unsaturated fatty acids	16	6	1.73401497461809E-05	10	4.40435833069922E-05	0.393704336573088
15	69			Terpenoid backbone biosynthesis	21	9	1.6001447923201E-05	12	3.31754678620265E-05	0.482327724502619
16	68			Fatty acid degradation	17	6	6.89061770839154E-06	11	1.41958523488842E-05	0.485396546754951
17	67			Carbon metabolism	131	55	1.98249280513014E-05	76	3.64555133915484E-05	0.543811517297064
18	66			Nicotinate and nicotinamide metabolism	17	10	1.73595362729729E-05	7	2.93785618483568E-05	0.590891288776406
19	65			Ribosome biogenesis in eukaryotes	57	21	8.8664405149457E-06	36	1.33815706782274E-05	0.662566129319914
20	64			Valine, leucine and isoleucine degradation	20	7	1.43168479624328E-05	13	1.96903915699469E-05	0.727088184491384
21	63			Inositol phosphate metabolism	24	13	1.00497919583491E-05	11	1.30826127100369E-05	0.768179275890273
22	62			Glyoxylate and dicarboxylate metabolism	36	12	2.64156194001291E-05	24	3.26242869472674E-05	0.809691854501715
23	61			Glycerolipid metabolism	23	11	1.82161364409318E-05	12	2.15286708449432E-05	0.8461338171841
24	60			Pentose phosphate pathway	24	11	4.0510157574217E-05	13	4.35952728686872E-05	0.929232802287117
25	59			Oxidative phosphorylation	66	38	1.2654558380013E-05	28	1.33415234842045E-05	0.948509245963943
26	58			Citrate cycle (TCA cycle)	33	15	1.73802258623453E-05	18	1.72334562041166E-05	1.00851655387581
27	57			Phosphatidylinositol signaling system	35	18	1.25378475447452E-05	17	1.22614055535686E-05	1.02254570163012
28	56			Glycolysis / Gluconeogenesis	45	20	3.34775825552621E-05	25	3.26922069801772E-05	1.02402332689136
29	55			Glycine, serine and threonine metabolism	35	15	3.18792776785898E-05	20	2.98115862446294E-05	1.06935865193463
30	54			Peroxisome	47	21	2.59107706126714E-05	26	2.40176979736783E-05	1.07881990360057
31	53			Steroid biosynthesis	11	5	9.19795390821098E-06	6	7.60473907550286E-06	1.20950289245825
32	52			Histidine metabolism	11	4	1.79318496103497E-05	7	1.44540798585274E-05	1.24060817332281
33	51			Valine, leucine and isoleucine biosynthesis	12	5	1.50461873422053E-05	7	1.10567439275E-05	1.36081539383244
34	50			Phenylalanine, tyrosine and tryptophan biosynthesis	21	7	1.93802677188277E-05	14	1.39722997860493E-05	1.38704923424117
35	49			Ubiquinone and other terpenoid-quinone biosynthesis	17	9	1.84486663681333E-05	8	1.26749002869749E-05	1.4555275347682
36	48			Basal transcription factors	20	13	9.56108494399651E-06	7	6.02392488322312E-06	1.58718528689236
37	47			Alanine, aspartate and glutamate metabolism	27	15	4.65416897560201E-05	12	2.81035735751866E-05	1.65607728253865
38	46			Biosynthesis of amino acids	120	54	3.8702745120734E-05	66	2.10845192275101E-05	1.83560007715217
39	45			RNA degradation	53	36	1.98840269097261E-05	17	1.03138538558489E-05	1.92789496415542
40	44			Tyrosine metabolism	14	7	4.39964781414467E-05	7	2.20922920315559E-05	1.99148545015626
41	43			Fructose and mannose metabolism	13	7	7.84342169885776E-05	6	3.46627928036226E-05	2.2627783465959
42	42			Phenylalanine metabolism	10	5	5.79014643844681E-05	5	2.30607313402472E-05	2.5108251568507
43	41			One carbon pool by folate	14	7	4.89636967101774E-05	7	1.85169729363939E-05	2.64426031610937
44	40			Aminoacyl-tRNA biosynthesis	42	26	1.51209291839449E-05	16	5.61174390936557E-06	2.69451518603855

45	39 Nitrogen metabolism	10	5	5.22351166445619E-05	5	1.83810312611197E-05	2.84179466878182
46	38 Ascorbate and aldarate metabolism	17	11	6.57964858240712E-05	6	1.92975801577917E-05	3.40957183678311
47	37 Selenocompound metabolism	14	6	2.58646413187865E-05	8	6.70376042067926E-06	3.85822876948305
48	36 Protein processing in endoplasmic reticulum	80	61	6.86595453139012E-05	19	1.74238374181285E-05	3.94055245502146
49	35 2-Oxocarboxylic acid metabolism	30	16	3.66002783870423E-05	14	8.87999674118398E-06	4.12165448409414
50	34 Purine metabolism	101	71	7.57549990959627E-05	30	1.75600313383829E-05	4.31405830867606
51	33 Starch and sucrose metabolism	41	24	8.6046668737767E-05	17	1.70989174039547E-05	5.03228752469881
52	32 Pyrimidine metabolism	76	57	7.79230072202996E-05	19	1.49822221170585E-05	5.20103136981114
53	31 Arginine and proline metabolism	32	21	5.01546437693255E-05	11	9.47920084455454E-06	5.29102026550451
54	30 Cysteine and methionine metabolism	42	23	7.7751811058141E-05	19	1.42095712137113E-05	5.4717915050889
55	29 Protein export	29	20	4.62900354431182E-05	9	8.24128646775005E-06	5.61684581943137
56	28 RNA polymerase	26	22	3.03102824124316E-05	4	5.23314425209737E-06	5.7919829747257
57	27 Spliceosome	106	85	2.10129752054405E-05	21	3.41578562480917E-06	6.15172540478572
58	26 Sulfur metabolism	21	12	5.59796181839274E-05	9	8.69441657830765E-06	6.43857097020117
59	25 Arachidonic acid metabolism	10	6	7.70841630425342E-05	4	1.13588487920981E-05	6.78626544409663
60	24 Arginine biosynthesis	21	14	0.000141834094132	7	1.8716321775867E-05	7.5780965849172
61	23 Pantothenate and CoA biosynthesis	19	7	8.61623073843592E-05	12	1.1259388152816E-05	7.65248574921987
62	22 Phagosome	29	16	3.39860369101962E-05	13	4.01004596601329E-06	8.47522377504925
63	21 Pentose and glucuronate interconversions	10	7	9.82960924208138E-05	3	1.13131499736608E-05	8.68865812348166
64	20 Glycerophospholipid metabolism	32	21	0.000121941488685	11	1.33257729688922E-05	9.15080040530887
65	19 RNA transport	89	71	3.47716591582055E-05	18	3.54546918141468E-06	9.80735055898335
66	18 Glutathione metabolism	32	23	0.00010155938134	9	8.47754299851394E-06	11.9798131790626
67	17 ABC transporters	12	7	2.56353356554724E-05	5	1.84415341980058E-06	13.9008692987401
68	16 mRNA surveillance pathway	42	32	1.87233218082622E-05	10	1.25322288901998E-06	14.9401371234959
69	15 Plant hormone signal transduction	11	8	1.73100930290953E-05	3	1.08625225832246E-06	15.9356106249463
70	14 Amino sugar and nucleotide sugar metabolism	36	29	0.000143682703211	7	6.50540254597104E-06	22.0866736832287
71	13 Endocytosis	53	47	5.80242121689035E-05	6	2.60810005145992E-06	22.2476941160381
72	12 Mismatch repair	17	16	0.000138524725787	1	4.91576275271565E-06	28.1797012498592
73	11 Galactose metabolism	13	12	0.000114525358523	1	3.96671931989986E-06	28.871555884629
74	10 Nucleotide excision repair	30	28	8.52340177432852E-05	2	2.32634066581331E-06	36.6386656072517
75	9 Sphingolipid metabolism	15	13	6.57564028834992E-05	2	1.78192936050591E-06	36.9018011268585
76	8 Ubiquitin mediated proteolysis	54	46	5.30105246036578E-05	8	1.17865534727564E-06	44.9754245175971
77	7 N-Glycan biosynthesis	20	17	0.000103380592831	3	2.18623598004475E-06	47.2870238047137
78	6 Base excision repair	13	12	9.49449634465281E-05	1	8.16144217818975E-07	116.333561365238
79	5 beta-Alanine metabolism	12	9	0.000168933865656	3	9.18839776430373E-07	183.855629663883
80	4 Homologous recombination	13	12	9.3113922773353E-05	1	2.06205852160388E-07	451.558099820215
81	3 DNA replication	28	28	0.00029906817796	0	0 Inf	
82	2 Proteasome	34	34	7.31794255700302E-05	0	0 Inf	
83	1 SNARE interactions in vesicular transport	14	14	3.89955852497964E-05	0	0 Inf	

Table S8. The 100 genes contributing most to the stable state including annotation.

identifier	GO	Gene Name	Most stable	
			define	description
Cre03.g207050.v5.5	-0.042413480576196	RPL29	Ribosomal protein L29, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L29; Cytosolic 60S large ribosomal subunit protein L29
Cre10.g420750.v5.5	-0.041379104310284	RPL30	Ribosomal protein L30, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L30; Cytosolic 60S large ribosomal subunit protein L30
Cre12.g514500.v5.5	-0.041144011219975	RPS11	Ribosomal protein S11, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S11; Cytosolic 40S small ribosomal subunit protein S11
Cre03.g203450.v5.5	-0.039587294504537	RPS21	Ribosomal protein S21, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S21; Cytosolic 40S small ribosomal subunit protein S21
Cre16.g682300.v5.5	-0.039132107680568	RPS26	Ribosomal protein S26, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S26; Cytosolic 40S small ribosomal subunit protein S26
Cre06.g310700.v5.5	-0.038952974045301	RPL36a	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
Cre12.g494050.v5.5	-0.038932448380835	RPL9	Ribosomal protein L9, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L9; Cytosolic 60S large ribosomal subunit protein L9
Cre12.g529400.v5.5	-0.038903314666547	RPS27e1	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 annotated as RPS27-A
Cre04.g211800.v5.5	-0.038865984694867	RPL23	Ribosomal protein L23, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L23; Cytosolic 60S large ribosomal subunit protein L23
Cre08.g359750.v5.5	-0.038845210540143	RPS9	Ribosomal protein S9, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S9; Cytosolic 40S small ribosomal subunit protein S9
Cre12.g498250.v5.5	-0.038528701001097	RPS17	Ribosomal protein S17, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S17; Cytosolic 40S small ribosomal subunit protein S17
Cre06.g282500.v5.5	-0.038515638730758	RPL23a	Ribosomal protein L23a, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L23a; Cytosolic 60S large ribosomal subunit protein L23a
Cre07.g325746.v5.5	-0.038513828597268	RPL38	Ribosomal protein L38, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L38; Cytosolic 60S large ribosomal subunit protein L38
Cre02.g120150.v5.5	-0.038503986885013	RBC52	Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit 2	RuBisCO small subunit 2, chloroplast precursor [PMID: 3820291]
Cre16.g666301.v5.5	-0.038314522325419	RPS30	Ribosomal protein S30, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S30; Cytosolic 40S small ribosomal subunit protein S30
Cre02.g143050.v5.5	-0.03824270621377	RPP2	Acidic ribosomal protein P2	Cytosolic 80S ribosomal protein P2; Cytosolic 60S large ribosomal subunit protein P2
Cre13.g568900.v5.5	-0.038132207964292	RPL17	Ribosomal protein L17, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L17; Cytosolic 60S large ribosomal subunit protein L17
Cre08.g382500.v5.5	-0.037980841499137	RPS25	Ribosomal protein S25, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S25; Cytosolic 40S small ribosomal subunit protein S25
Cre12.g489153.v5.5	-0.037976726888621	#N/A	#N/A	#N/A
Cre08.g360900.v5.5	-0.037617077547882	RPS15	Ribosomal protein S15, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S15; Cytosolic 40S small ribosomal subunit protein S15
Cre12.g532550.v5.5	-0.037077567747368	RPL13a	Ribosomal protein L13a, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L13a; Cytosolic 60S large ribosomal subunit protein L13a
Cre01.g027000.v5.5	-0.037001845227908	RPL11	Ribosomal protein L11, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L11; Cytosolic 60S large ribosomal subunit protein L11
Cre06.g273600.v5.5	-0.036944474092164	RPS27a	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
Cre04.g214503.v5.5	-0.036763936390851	#N/A	#N/A	#N/A
Cre09.g391097.v5.5	-0.036670114320081	RPL24	Ribosomal protein L24, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L24; Cytosolic 60S large ribosomal subunit protein L24
Cre10.g456200.v5.5	-0.03664927693843	RPS24	Ribosomal protein S24, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S24; Cytosolic 40S small ribosomal subunit protein S24. Possible locus for PR1 (paromomycin resistance) genetic marker
Cre14.g617900.v5.5	-0.036604397300632	RPL35	Ribosomal protein L35, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L35; Cytosolic 60S large ribosomal subunit protein L35
Cre10.g459250.v5.5	-0.036601471139178	RPL35a	Ribosomal protein L35a, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L35a; Cytosolic 60S large ribosomal subunit protein L35a
Cre10.g430400.v5.5	-0.036549933605961	RPL37	Ribosomal protein L37, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L37; Cytosolic 60S large ribosomal subunit protein L37
Cre02.g106600.v5.5	-0.03646274041787	RPS19	Ribosomal protein S19, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S19; Cytosolic 40S small ribosomal subunit protein S19

Cre12.g528750.v5.5	-0.036435012799071	RPL12	Ribosomal protein L12, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L12; Cytosolic 60S large ribosomal subunit protein L12
Cre08.g358556.v5.5	-0.036248750146842	RPS29	Ribosomal protein S29, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S29; Cytosolic 40S small ribosomal subunit protein S29
Cre06.g272800.v5.5	-0.035916232912405	RPS8	Ribosomal protein S8, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S8; Cytosolic 40S small ribosomal subunit protein S8
Cre17.g738300.v5.5	-0.03584918683167	RPP1	Acidic ribosomal protein P1	Cytosolic 80S ribosomal protein P1; Cytosolic 60S large ribosomal subunit protein P1
Cre16.g660150.v5.5	-0.035737613566746	#N/A	#N/A	#N/A
Cre02.g102250.v5.5	-0.03561429953238	RPS3	Ribosomal protein S3, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S3; Cytosolic 40S small ribosomal subunit protein S3
Cre06.g290950.v5.5	-0.03559280766374	RPS5	Ribosomal protein S5, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S5; Cytosolic 40S small ribosomal subunit protein S5
Cre06.g257150.v5.5	-0.03554370524704	RPL37a	Ribosomal protein L37a, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L37a; Cytosolic 60S large ribosomal subunit protein L37a
Cre14.g621450.v5.5	-0.035398032897396	RPL5	Ribosomal protein L5, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L5; Cytosolic 60S large ribosomal subunit protein L5
Cre12.g512600.v5.5	-0.035038175500325	RPL18	Ribosomal protein L18, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L18; Cytosolic 60S large ribosomal subunit protein L18
Cre02.g115200.v5.5	-0.034996292191571	RPL27a	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.
Cre02.g075700.v5.5	-0.034878863304563	RPL19	Ribosomal protein L19, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L19; Cytosolic 60S large ribosomal subunit protein L19
Cre01.g007051.v5.5	-0.034947921258339	#N/A	#N/A	#N/A
Cre07.g331900.v5.5	-0.034920690387241	RPS13	Ribosomal protein S13, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S13; Cytosolic 40S small ribosomal subunit protein S13
Cre17.g701650.v5.5	-0.034874742420666	RPL27	Ribosomal protein L27, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L27; Cytosolic 60S large ribosomal subunit protein L27
Cre09.g388200.v5.5	-0.034794257456671	RPL10	Ribosomal protein L10, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L10; Cytosolic 60S large ribosomal subunit protein L10
Cre12.g498900.v5.5	-0.034719764220557	RPS7	Ribosomal protein S7, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S7; Cytosolic 40S small ribosomal subunit protein S7
Cre02.g091100.v5.5	-0.034719444120971	RPL15	Ribosomal protein L15, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L15; Cytosolic 60S large subunit ribosomal protein L15
Cre10.g417700.v5.5	-0.034652304538003	RPL3	Ribosomal protein L3, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L3; Cytosolic 60S large ribosomal subunit protein L3
Cre09.g405106.v5.5	-0.034634630358681	#N/A	#N/A	#N/A
Cre12.g537800.v5.5	-0.03458260358644	RPL7	Ribosomal protein L7, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L7; Cytosolic 60S large ribosomal subunit protein L7
Cre12.g504200.v5.5	-0.034550459414828	RPS23	Ribosomal protein S23, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S23; Cytosolic 40S small ribosomal subunit protein S23
Cre06.g278135.v5.5	-0.034524745728077	RPL21	Ribosomal protein L21, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L21; Cytosolic 60S large ribosomal subunit protein L21
Cre06.g278222.v5.5	-0.034360678909814	RCK1	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: 2116589]
Cre16.g661050.v5.5	-0.033918227742958	RPL34	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
Cre09.g402219.v5.5	-0.033849999760451	LCI3	Low-CO ₂ -inducible protein	Regulated by CCM1 [PMID: 15235119]. Acclimation to changing CO ₂ concentrations and light intensities was studied by Yamano et al. 2008 [PMID: 18322145].
Cre12.g529651.v5.5	-0.033764842424319	#N/A	#N/A	#N/A
Cre06.g272950.v5.5	-0.03370671310797	RPS18	Ribosomal protein S18, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S18; Cytosolic 40S small ribosomal subunit protein S18
Cre12.g520500.v5.5	-0.03352743568126	RPP0	Acidic ribosomal protein P0, Ribosomal protein L10	Cytosolic 80S acidic ribosomal protein P0; Cytosolic 60S large ribosomal subunit protein P0. Ribosomal protein L10
Cre13.g568650.v5.5	-0.033525675237866	RPS3a	Ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S3a; Cytosolic 40S small ribosomal subunit protein S3a
Cre07.g357850.v5.5	-0.033435738845439	RPL22	Ribosomal protein L22, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L22; Cytosolic 60S large ribosomal subunit protein L22
Cre06.g249250.v5.5	-0.033424997844404	RPL7ae	Ribosomal protein L7Ae	Cytosolic 80S ribosomal protein L7Ae; Cytosolic 60S large ribosomal subunit protein L7ae
Cre06.g261000.v5.5	-0.033370970149946	PSBR	10 kDa photosystem II polypeptide	Similar to At1g79040, chloroplast-targeted
Cre11.g467578.v5.5	-0.03331154318676	#N/A	#N/A	#N/A

Cre01.g040000.v5.5	-0.033138221316172	RPL26	Ribosomal protein L26, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L26; Cytosolic 60S large ribosomal subunit protein L26
Cre17.g701200.v5.5	-0.033058019581648	RPL14	Ribosomal protein L14, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L14; Cytosolic 60S large ribosomal subunit protein L14
Cre01.g047750.v5.5	-0.033045067712998	RPL18a	Ribosomal protein L18a, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L18a; Cytosolic 60S large ribosomal subunit protein L18a
Cre06.g308250.v5.5	-0.033024373977157	RPS4	Ribosomal protein S4, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S4; Cytosolic 40S small ribosomal subunit protein S4
Cre12.g484050.v5.5	-0.032758780612405	RPL36	Ribosomal protein L36, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L36; Cytosolic 60S large ribosomal subunit protein L36
Cre03.g182551.v5.5	-0.03250281882078	PCY1	Pre-apoplastocyanin	Pre-apoplastocyanin copper binding protein, PETE [PMID: 2165059; PMID: 8940133]; structure of plastocyanin PDB: 2PLT; mutant = ac208 [PMID: 8463310]
Cre01.g039250.v5.5	-0.032452807781255	RPS2	Ribosomal protein S2, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S2; Cytosolic 40S small ribosomal subunit protein S2
Cre14.g62700.v5.5	-0.032402639703491	PETF	Ferredoxin	2Fe-2S containing redox protein involved in photosynthetic electron transfer, chloroplast localization [PMID: 16656453]
Cre09.g400650.v5.5	-0.03220916822848	RPS6	Ribosomal protein S6, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S6; Cytosolic 40S small ribosomal subunit protein S6
Cre02.g101350.v5.5	-0.032187682328782	RPL10a	Ribosomal protein L10a, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L10a; Cytosolic 60S large ribosomal subunit protein L10a
Cre09.g411100.v5.5	-0.031850354389245	RPS10	Ribosomal protein S10, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S10; Cytosolic 40S small ribosomal subunit protein S10
Cre12.g498600.v5.5	-0.031848443989171	#N/A	Eukaryotic translation elongation factor 1 alpha	Flagellar Associated Protein, found in the flagellar proteome [PMID: 15998802]. Previously annotated as just EEF1
Cre12.g535851.v5.5	-0.031698709415264	#N/A	#N/A	#N/A
Cre10.g432800.v5.5	-0.03140255910603	RPSa	Ribosomal protein Sa, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein Sa; Cytosolic 40S small ribosomal subunit protein Sa
Cre06.g289550.v5.5	-0.031357587761394	RPL32	Ribosomal protein L32, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L32; Cytosolic 60S large ribosomal subunit protein L32
Cre01.g011000.v5.5	-0.0313480234275	RPL6	Ribosomal protein L6, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L6; Cytosolic 60S large ribosomal subunit protein L6
Cre01.g066917.v5.5	-0.031269557867695	LHCBM1	Chlorophyll a/b binding protein of LHClI	Chlorophyll a-b binding protein of LHClI
Cre03.g190950.v5.5	-0.031200648389157	TUA1	Alpha tubulin 1	Alpha tubulin 1
Cre10.g452350.v5.5	-0.031153722520479	#N/A	#N/A	#N/A
Cre11.g480150.v5.5	-0.031026695131996	RPS14	Ribosomal protein S14, component of cytosolic 80S ribosome and 40S small subunit	Cytosolic 80S ribosomal protein S14; Cytosolic 40S small ribosomal subunit protein S14
Cre05.g234637.v5.5	-0.03096127351989	#N/A	#N/A	#N/A
Cre08.g372200.v5.5	-0.030773403723922	#N/A	#N/A	#N/A
Cre05.g234550.v5.5	-0.03067184285381	FBA3	Fructose-1,6-bisphosphate aldolase	Fructose-1,6-bisphosphate aldolase 1 [EC:4.1.2.13]; probably plastidic, but predicted mitochondrial by Target-P; 87% identical to cDNA (Q42690); glycolytic enzyme that catalyses the reversible aldol cleavage or condensation of fructose-1,6-bisphosphate in
Cre06.g263450.v5.5	-0.030619375917674	#N/A	#N/A	#N/A
Cre16.g659700.v5.5	-0.030458018527192	#N/A	#N/A	#N/A
Cre13.g580000.v5.5	-0.030163619982343	#N/A	#N/A	#N/A
Cre07.g337100.v5.5	-0.030146050506178	#N/A	#N/A	#N/A
Cre10.g420350.v5.5	-0.030119630592311	PSAE	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]
Cre07.g323800.v5.5	-0.029959977080676	#N/A	#N/A	#N/A
Cre06.g282800.v5.5	-0.029680494422761	ICL1	Isocitrate lyase	Isocitrate lyase [EC 4.1.3.1]; isocitrate: 98% identical to cDNA (AAB61446) [PMID: 9049260]; PMID: 19847013; Listed by Rolland et al. 2008 [PMID: 19451016] in a table of putative redox-regulated proteins identified by proteomic methods
Cre17.g724300.v5.5	-0.029565205566247	PSAK	Photosystem I reaction center subunit psak	8.4 kD subunit of photosystem I (polypeptide 37) [PMID: 2693938]
Cre13.g579450.v5.5	-0.029524400126888	CST1	Chlamy-specific membrane transporter of unknown function	Transmembrane protein; shows similarity to various transporters and permeases; highly expressed; small gene family appears specific to Chlamydomonas
Cre06.g298650.v5.5	-0.029339168655577	#N/A	#N/A	#N/A
Cre13.g573351.v5.5	-0.029311290088974	#N/A	#N/A	#N/A
Cre09.g397697.v5.5	-0.029287916533883	RPL4	Ribosomal protein L4, component of cytosolic 80S ribosome and 60S large subunit	Cytosolic 80S ribosomal protein L4; Cytosolic 60S large ribosomal subunit protein L4
Cre12.g546150.v5.5	-0.029236218915832	PETM	Cytochrome b6f complex PetM subunit	Cytochrome b6f complex chain PetM, chloroplast precursor; GI:2493687; PMID: 8631873, PMID: 8616155, PMID: 7493968

Table S9. The 100 genes contributing the most to the exponential state including annotation.

100 genes contributing most to the exponential state				
Identifier	G1	Gene Name	define	description
Cre06.g284250.v5.5	0.055996613203082	LHCBM8	Chlorophyll a/b binding protein of LHCl	Chlorophyll a-b binding protein of LHCl
Cre06.g278213.v5.5	0.050465962662738	LHCA6	Light-harvesting protein of photosystem I	#N/A
Cre16.g675550.v5.5	0.050058582384222	#N/A	Peptidyl-prolyl cis-trans isomerase, FKBP-type	FKBP-type peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase), orthologous to At5g45680; isoform a of gene FKBP-2, probably directed to thylakoid lumen (TP length 26, RR motif); other splicing isoforms possibly directed to stroma or mito
Cre12.g546550.v5.5	0.049154804201197	FEA1	Fe-assimilating protein	High-CO ₂ inducible, iron-deficiency inducible, periplasmic protein. Changes in expression with light intensity were studied by Long and Merchant 2008 [PMID: 19067961]. Cis-acting regulatory elements were characterized by Fei et al. 2009 [PMID: 19351705].
Cre06.g257601.v5.5	0.048187442158047	PRX1	2-cys peroxiredoxin, chloroplastic	2-cys Peroxiredoxin, thioredoxin dependent peroxidase, chloroplast precursor, PMID: 11784321. Protein processed at aa 39 to produce N-terminus of SHAEPKPL as determined by Edman degradation
Cre07.g334550.v5.5	0.04807240094068	PSAO	Photosystem I subunit O	Photosystem I subunit O; similar to 10-kDa subunit of eukaryotic photosystem I [PMID: 11801243]; microarray element: 894019E07
Cre17.g700950.v5.5	0.047246862010625	FDX5	Apoferrredoxin	Fe2S2 containing redox protein, predicted chloroplast localization
Cre03.g207800.v5.5	0.044642888826623	#N/A	#N/A	#N/A
Cre12.g548950.v5.5	0.044459325609396	LHCBM7	Chlorophyll a/b binding protein of LHCl	Chlorophyll a-b binding protein of LHCl
Cre12.g516700.v5.5	0.044074477466568	#N/A	#N/A	#N/A
Cre02.g082750.v5.5	0.04400684293239	PSBX	4.1 kDa photosystem II subunit	Encoding a 4.1 kDa subunit for PS2 with a single TMH [PMID: 16143838].
Cre12.g559800.v5.5	0.04378386752357	#N/A	#N/A	#N/A
Cre06.g283950.v5.5	0.043524311561079	LHCBM4	Chlorophyll a/b binding protein of LHCl	PSII-associated chlorophyll a/b-binding protein. Identified in the eyespot phosphoproteome by Wagner et al. 2008 [PMID: 18065559]
Cre02.g145050.v5.5	0.043109825830372	CMK1	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplast precursor	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase) (CDPMEK) (ispE) (ychB), chloroplast precursor
Cre09.g407600.v5.5	0.041749395967091	#N/A	#N/A	#N/A
Cre12.g548955.v5.5	0.041409361376581	#N/A	#N/A	#N/A
Cre12.g516717.v5.5	0.040259081203751	#N/A	#N/A	#N/A
Cre02.g101700.v5.5	0.040116763680551	#N/A	#N/A	#N/A
Cre01.g013100.v5.5	0.04006858029322	PRL10	Predicted extracellular protein	Similar to pathogenesis-related protein 1, extracellular
Cre04.g226600.v5.5	0.039958289511076	#N/A	#N/A	#N/A
Cre06.g268600.v5.5	0.039908483445275	NAB1	Nucleic acid binding protein	Nucleic acid binding protein; RNA binding protein involved in the light-regulated differential expression of the light-harvesting antenna of <i>Chlamydomonas reinhardtii</i> [PMID: 16284312, Genbank entry AY157846]. Studied by Wobbe et al. 2009 [PMID: 19666611]
Cre06.g280750.v5.5	0.039745072457031	#N/A	#N/A	#N/A
Cre12.g497300.v5.5	0.039533890589178	#N/A	Rhodanese-like Ca-sensing receptor	Rhodanese-like, Ca-sensing receptor, chloroplast location proposed; present in thylakoid-enriched fraction based on mass spectrometric peptide identification [PMID: 17078018]. Busch et al. (2010) [Chlamy 2010 Meeting abstract] proposed that this protein
Cre04.g232104.v5.5	0.038910075857458	LHCBM3	Light-harvesting complex II chlorophyll a/b binding protein M3	#N/A
Cre02.g089000.v5.5	0.038755308995787	#N/A	#N/A	#N/A
Cre17.g708750.v5.5	0.038713873474805	#N/A	#N/A	#N/A
Cre08.g370401.v5.5	0.038576546257935	#N/A	#N/A	#N/A
Cre06.g302950.v5.5	0.03837884156655	#N/A	#N/A	#N/A
Cre07.g330250.v5.5	0.038295956000591	PSAH	Subunit H of photosystem I	Formerly called protein P28. See PMID: 2693938.
Cre12.g503900.v5.5	0.038050905747892	#N/A	#N/A	#N/A
Cre02.g076300.v5.5	0.038002231932874	UPD2	Uroporphyrinogen decarboxylase	Uroporphyrinogen decarboxylase, chloroplast precursor (URO-D) (UPD) (HemE). Previously annotated as UROD2
Cre06.g300700.v5.5	0.037865179312019	#N/A	#N/A	#N/A
Cre02.g089650.v5.5	0.037860567143789	#N/A	#N/A	#N/A
Cre01.g011630.v5.5	0.037668718712836	#N/A	#N/A	#N/A
Cre03.g158000.v5.5	0.037441522612527	GSA1	Glutamate-1-semialdehyde aminotransferase	Glutamate-1-semialdehyde aminotransferase (GSA-AT); Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor; PMID: 16126849; PMID: 15890644; PMID: 12228605; PMID: 10872234; PMID: 10080695; PMID: 8989881; PMID: 8155881; PMID: 1985889; predicted chl
Cre13.g602650.v5.5	0.037406078310922	#N/A	#N/A	#N/A
Cre14.g626750.v5.5	0.037381936460096	#N/A	#N/A	#N/A
Cre05.g240300.v5.5	0.037210154464508	#N/A	#N/A	#N/A
Cre17.g720350.v5.5	0.037153349383248	MINE1	Chloroplast division site-determinant MinE	Helps define position of the chloroplast division ring [PMID: 11743109]; conserved in plants and eubacteria. Characterized by Adams et al. 2008 [PMID: 18270733].

Cre12.g519850.v5.5	0.037095363699312	#N/A	#N/A	#N/A
Cre12.g551950.v5.5	0.037085722779803	CGL38	Predicted protein	Conserved expressed protein of unknown function; similar to protein of unknown function in Arabidopsis and rice. cd00204. Contains 4 consecutive ankyrin repeats
Cre01.g004700.v5.5	0.036847423640864	#N/A	#N/A	#N/A
Cre10.g442750.v5.5	0.036835435315033	#N/A	#N/A	#N/A
Cre02.g143450.v5.5	0.036745385184473	#N/A	#N/A	#N/A
Cre06.g266550.v5.5	0.036581419186997	#N/A	#N/A	#N/A
Cre07.g334800.v5.5	0.036465372420429	FDX4	Ferredoxin	Fe2S2 containing redox protein, predicted chloroplast localization
Cre17.g313143.v5.5	0.036365423967029	#N/A	#N/A	#N/A
Cre02.g080250.v5.5	0.036283300772534	#N/A	#N/A	#N/A
Cre09.g412400.v5.5	0.036218450020991	#N/A	#N/A	#N/A
Cre16.g673650.v5.5	0.036190978660225	LHC85	Minor chlorophyll a/b binding protein of photosystem II	Minor chlorophyll a-b binding protein of photosystem II. Included among genes whose expression levels changed significantly during hydrogen production in sulfur-deficient cells; Nguyen et al. 2008 [PMID: 18708561]. Protein product also known as CP26
Cre17.g696350.v5.5	0.036080622900095	#N/A	#N/A	#N/A
Cre09.g397623.v5.5	0.036007137767625	#N/A	#N/A	#N/A
Cre12.g522950.v5.5	0.03582923308604	MIND1	Chloroplast septum site-determining protein	Putative chloroplast septum site-determining protein MinD. Chloroplast-encoded in other Chlorophyte algae. Characterized by Adams et al. 2008 [PMID: 18270733].
Cre03.g170550.v5.5	0.035814790741702	#N/A	#N/A	#N/A
Cre02.g078507.v5.5	0.035802445018855	#N/A	#N/A	#N/A
Cre06.g302500.v5.5	0.035777715077089	#N/A	#N/A	#N/A
Cre13.g602450.v5.5	0.03575673401548	#N/A	#N/A	#N/A
Cre16.g674300.v5.5	0.035720655932985	FAP269	Flagellar Associated Protein	Conserved uncharacterized Flagellar Associated Protein with ankyrin repeats; found in the flagellar proteome [PMID: 15998802]
Cre02.g085450.v5.5	0.035697346180366	CPX1	Coproporphyrinogen III oxidase	Coproporphyrinogen III oxidase, chloroplast precursor; GI:837299; CPO1; HEM13; HEM6 [PMID: 15849308]; Predicted chloroplast transit peptide 1-31
Cre09.g414000.v5.5	0.035672135809172	#N/A	#N/A	#N/A
Cre07.g325736.v5.5	0.035563644694878	#N/A	#N/A	#N/A
Cre08.g372550.v5.5	0.035563502305416	CDKB1	Plant specific cyclin dependent kinase	Plant specific cyclin dependent kinase; CDKB subfamily; PSTTLRE motif; mitotic regulator. Putative function in G2/M
Cre14.g625000.v5.5	0.035147448461403	#N/A	#N/A	#N/A
Cre01.g049000.v5.5	0.035032939569305	#N/A	Pterin dehydratase	4a-hydroxytetrahydrobiopterin dehydratase. Green-lineage conserved expressed protein. Previously annotated as CGL31
Cre06.g259450.v5.5	0.03480485696617	#N/A	#N/A	#N/A
Cre16.g678650.v5.5	0.034741292189895	#N/A	#N/A	#N/A
Cre03.g199450.v5.5	0.034718282134375	MINE2	Chloroplast division site determinant	Putative MinE homolog, chloroplast division site-determinant A homolog of ELIP (early light-inducible protein) gene which was originally identified as transiently expressed during the early phase of greening in etiolated pea seedlings [PMID: 6692824]. It has three TMH, whose sequences are closely related to LHC pro
Cre09.g393173.v5.5	0.034631473744295	ELI2	Early light-inducible protein	Conserved expressed protein of unidentified function; some similarity to Arabidopsis protein gi 18402865 ref NP_564561.1 - Also a domain COG0741: Soluble lytic murein transglycosylase and related regulatory proteins in Rickettsia
Cre02.g086100.v5.5	0.034619268349099	CGL40	Predicted protein	
Cre12.g501250.v5.5	0.034498413144327	#N/A	#N/A	#N/A
Cre05.g237150.v5.5	0.034492306250579	#N/A	#N/A	#N/A
Cre03.g201500.v5.5	0.034452458193624	#N/A	#N/A	#N/A
Cre12.g523900.v5.5	0.034444764717794	#N/A	#N/A	#N/A
Cre16.g693200.v5.5	0.034355236761613	#N/A	#N/A	#N/A
Cre14.g627850.v5.5	0.034266018343334	#N/A	#N/A	#N/A
Cre03.g179820.v5.5	0.034216235085678	#N/A	#N/A	#N/A
Cre07.g354976.v5.5	0.034111588271749	#N/A	#N/A	#N/A
Cre05.g238600.v5.5	0.034110524484057	#N/A	#N/A	#N/A
Cre12.g520050.v5.5	0.034092236484209	#N/A	#N/A	#N/A
Cre12.g497850.v5.5	0.034085974668822	#N/A	#N/A	#N/A
Cre09.g403071.v5.5	0.034084338406364	#N/A	#N/A	#N/A
Cre16.g688800.v5.5	0.034052616582133	#N/A	#N/A	#N/A
Cre10.g441250.v5.5	0.033988880568631	#N/A	#N/A	#N/A
Cre01.g003850.v5.5	0.03397038688887	#N/A	Cytochrome P450, CYP197 superfamily	Cytochrome P450, CYP197 superfamily, CYP197B family. Previously annotated as CYP747A1
Cre14.g619450.v5.5	0.033969577948411	#N/A	#N/A	#N/A
Cre17.g732250.v5.5	0.033933393338647	#N/A	#N/A	#N/A

Cre09.g386167.v5.5	0.033773497208234	#N/A	#N/A	#N/A
Cre17.g726400.v5.5	0.033763914731162	#N/A	#N/A	#N/A
Cre11.g482700.v5.5	0.033612210891776	#N/A	#N/A	#N/A
Cre06.g278104.v5.5	0.033607118426563	#N/A	#N/A	#N/A
Cre03.g181550.v5.5	0.033601138820279	#N/A	#N/A	#N/A
Cre10.g439250.v5.5	0.033499830723557	#N/A	#N/A	#N/A
Cre01.g066917.v5.5	0.033474616717733	LHCBM1	Chlorophyll a/b binding protein of LHCII	Chlorophyll a-b binding protein of LHCII
Cre06.g278204.v5.5	0.033427881822105	#N/A	#N/A	#N/A
Cre03.g156050.v5.5	0.033353830595088	#N/A	#N/A	#N/A
Cre16.g667850.v5.5	0.033303898546312	#N/A	#N/A	#N/A
Cre06.g273450.v5.5	0.03327151925858	#N/A	#N/A	#N/A
Cre11.g467672.v5.5	0.033159917703381	#N/A	#N/A	#N/A
Cre10.g436500.v5.5	0.033098193533785	#N/A	#N/A	#N/A
Cre09.g386155.v5.5	0.033023182733131	#N/A	#N/A	#N/A

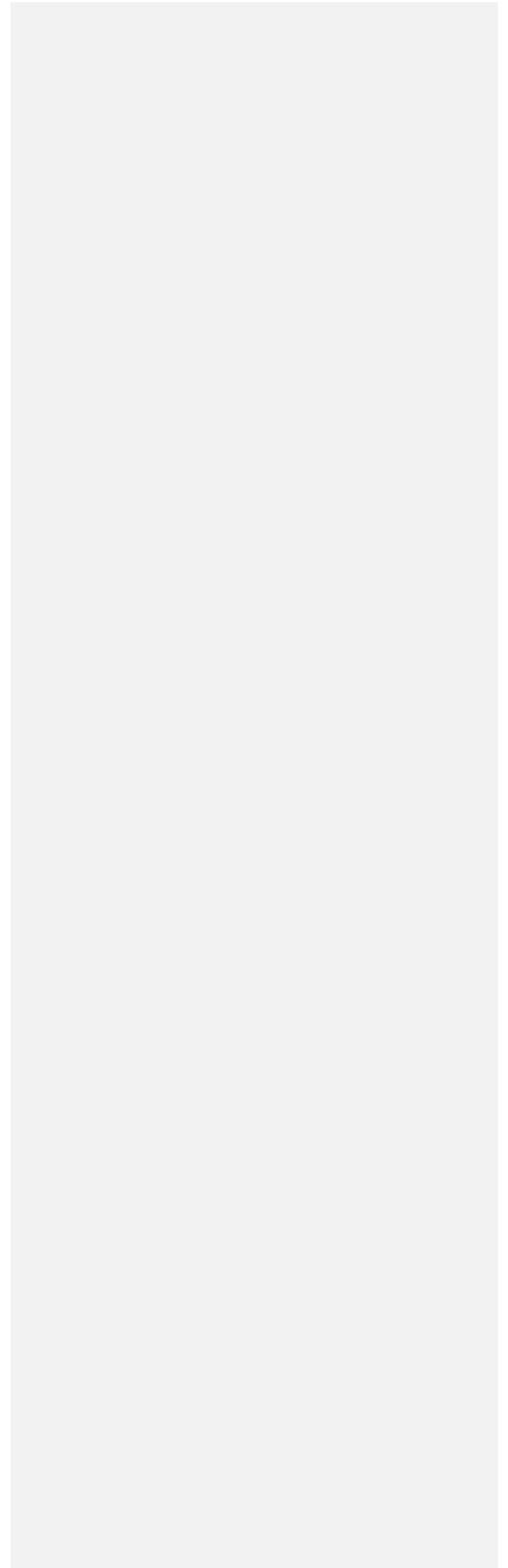


Table S10. The 100 genes contributing the most to the stationary state including annotation.

100 genes contributing most to the stationary state				
Identifer	GO	Gene Name	define	description
Cre02.g144650.v5.5	-0.039092277585641	PTB12	Sodium/phosphate symporter	Putative phosphate transporter, similar to yeast Pho89 and Neurospora PHO4 probable Na ⁺ /Pi symporters; present in a cluster of four highly related PTB family members on scaffold 24, including PTB9, PTB5 and PTB4.
Cre24.g755547.v5.5	-0.037814401767473	#N/A	#N/A	#N/A
Cre17.g713700.v5.5	-0.035629644054225	#N/A	#N/A	#N/A
Cre02.g085500.v5.5	-0.032200883433109	#N/A	#N/A	#N/A
Cre08.g379800.v5.5	-0.030624807628227	#N/A	#N/A	#N/A
Cre01.g030350.v5.5	-0.028948703123221	CGL41	Predicted protein	Conserved expressed protein of unknown function
Cre12.g495952.v5.5	-0.027695403816197	#N/A	#N/A	#N/A
Cre03.g163950.v5.5	-0.027496470120439	CDO2	Cysteine dioxygenase	Cysteine dioxygenase Predicted to contain 3 transmembrane helices and 4 Armadillo repeats; expressed exclusively during gametogenesis, at a late stage [PMID: 15459796]. Identified by Abe et al. 2004 [PMID: 15459796] as NSG13, a gene expressed during nitrogen-starved gametoge
Cre07.g328800.v5.5	-0.027066349440318	NSG13	Protein expressed during nitrogen-starved gametogenesis	
Cre12.g518800.v5.5	-0.026556562718769	#N/A	#N/A	#N/A
Cre14.g630350.v5.5	-0.026442135732279	#N/A	#N/A	#N/A
Cre16.g690319.v5.5	-0.026043091119337	#N/A	#N/A	#N/A
Cre08.g380800.v5.5	-0.026009818158272	#N/A	#N/A	#N/A
Cre11.g468800.v5.5	-0.025713632066336	#N/A	#N/A	#N/A
Cre12.g545101.v5.5	-0.025358074085579	#N/A	#N/A	#N/A
Cre06.g279450.v5.5	-0.024469338365996	MUT68	Polyadenylate polymerase beta nucleotidyltransferase	Noncanonical polyadenylate polymerase that adds untemplated adenines to the 5' RNA fragments after siRNA-mediated cleavage and appears to stimulate their exosome-dependent degradation. Discussed by Zimmer et al. 2008 [PMID: 18493045]. The role of MUT68 i
Cre02.g096250.v5.5	-0.023618451139756	FMO9	Flavin-containing monooxygenase	Flavin-containing monooxygenase. This family includes diverse enzymes that utilise FAD - 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases [Coenzyme metabolism/Energy production and conversion - this gene is about 20 kb aw
Cre02.g144700.v5.5	-0.023536524058637	PTB5	Sodium/phosphate symporter	Putative phosphate transporter, similar to yeast Pho89 and Neurospora PHO4 probable Na ⁺ /Pi symporters; present in a cluster of four highly related PTB family members on scaffold 24, including PTB9, PTB12 and PTB4.
Cre03.g204465.v5.5	-0.022973589795245	#N/A	#N/A	#N/A
Cre09.g400750.v5.5	-0.022956997799386	AMT5	Ammonium transporter	Belongs to AMT1 family (Amt1.5 or Amt1.5); two different splicing variants have been found for this gene, this one is AMT5b, the shorter one with additional intron [AYS88243]; was AMT1EB; belongs to AMT1 family (Amt1.5 or Amt1.5); two different splicing va
Cre02.g095500.v5.5	-0.022608409238979	#N/A	#N/A	#N/A
Cre12.g488450.v5.5	-0.022415726479985	VSP3	Extracellular matrix protein	Extracellular matrix protein (vegetative cell wall protein) similar to ISG (Volvox carterii) [PMID: 1600938], both are glycoproteins with a hydroxyproline-rich (HR) domain. [PMID: 800007. ISG Genbank entry X65165; VSP3, L29029; C. incerta ortholog, AY7950
Cre12.g531000.v5.5	-0.022344377616321	AMT8	Ammonium transporter	Belongs to AMT1 family (Amt1.8); corresponds to AY548754, mRNA complete cds [PMID: 15821986]. Previously annotated as AMT1H
Cre06.g284150.v5.5	-0.022310191578858	RHP2	Rh protein	Similar to Rh50 gene product of Drosophila melanogaster
Cre17.g707750.v5.5	-0.02208774284382	#N/A	#N/A	#N/A
Cre03.g145787.v5.5	-0.021966383347445	HSP22C	Heat shock protein 22C	Small heat shock protein containing an alpha-crystallin domain; N-terminus by TargetP weakly predicted to be chloroplast transit peptide; PMID: 16143837
Cre06.g271900.v5.5	-0.02183714786302	#N/A	#N/A	#N/A
Cre17.g701000.v5.5	-0.021691986731389	#N/A	#N/A	#N/A
Cre15.g636950.v5.5	-0.021589869279906	#N/A	#N/A	#N/A
Cre12.g528600.v5.5	-0.020953907848077	#N/A	#N/A	#N/A
Cre01.g053300.v5.5	-0.020862794824919	AIH1	Agmatine iminohydrolase	Converts agmatin to N-carbamoyl-putrescine; involved in agmatine pathway of polyamine (putrescine) biosynthesis; could be organelle-targeted
Cre08.g380700.v5.5	-0.020424054650379	#N/A	#N/A	#N/A
Cre09.g413350.v5.5	-0.020422473627258	#N/A	#N/A	#N/A
Cre06.g260700.v5.5	-0.020335186921844	XUV1	Xanthine/uracil/vitamin C permease-like	Xanthine/uracil/vitamin C permease-like. Related to plants and fungi; also related to bacterial inner membrane proteins
Cre12.g541500.v5.5	-0.020089454421164	#N/A	#N/A	#N/A
Cre10.g448400.v5.5	-0.020034684258556	#N/A	#N/A	#N/A
Cre12.g551700.v5.5	-0.01985844789748	#N/A	#N/A	#N/A
Cre10.g424750.v5.5	-0.019811343425543	PPD1	Pyruvate phosphate dikinase	Pyruvate phosphate dikinase (PPDK) (EC 2.7.9.1); Pyruvate orthophosphate dikinase (PODK); Target-P predicts no organelle

Accession	Score	Gene	Protein	Description	Notes
targeting sequence, similar to PPK from Phytophthora (GenBank AAK74150)					
Cre10.g429500.v5.5	-0.019784618414886	#N/A	#N/A	#N/A	#N/A
Cre05.g243358.v5.5	-0.019602737549601	#N/A	#N/A	#N/A	#N/A
Cre10.g427896.v5.5	-0.019422697764296	#N/A	#N/A	#N/A	#N/A
Cre12.g488050.v5.5	-0.019382291007925	#N/A	#N/A	#N/A	#N/A
Cre10.g426152.v5.5	-0.019286634853558	#N/A	#N/A	#N/A	#N/A
Cre03.g152600.v5.5	-0.019274381175217	#N/A	#N/A	#N/A	#N/A
Cre06.g297049.v5.5	-0.019020794649341	#N/A	#N/A	#N/A	#N/A
Cre06.g285950.v5.5	-0.019018567393163	#N/A	#N/A	#N/A	#N/A
Cre03.g202785.v5.5	-0.019009776425972	#N/A	#N/A	#N/A	#N/A
Cre08.g368300.v5.5	-0.018914752574756	#N/A	#N/A	#N/A	#N/A
Cre08.g360550.v5.5	-0.018893806271714	ERM3	ERD4-related membrane protein	NO-forming, copper-containing nitrite reductase. N-terminus: transmembrane protein with a DUF221 domain of unknown function; this domain is present in many eukaryotes, in particular in Arabidopsis ERD4 (early response to dehydration); belongs to a cluster	#N/A
Cre17.g714300.v5.5	-0.018768629837689	#N/A	#N/A	#N/A	#N/A
Cre16.g694206.v5.5	-0.018723517437475	#N/A	#N/A	#N/A	#N/A
Cre09.g395213.v5.5	-0.01869721389458	#N/A	#N/A	#N/A	#N/A
Cre02.g073600.v5.5	-0.018692213822661	#N/A	#N/A	#N/A	#N/A
Cre09.g392208.v5.5	-0.018668745590115	#N/A	#N/A	#N/A	#N/A
Cre03.g194700.v5.5	-0.018568347907587	AGL1	Alpha glucosidase	Putative alpha-glucosidase (EC 3.2.1.20); similarity to arabidopsis [Aglu1; GenBank AAB82656] and sugar beet [GenBank BAA20343; PMID: 9178565] secreted alpha-glucosidase gene products Hypothetical protein highly conserved with protein on chromosome 5 of Arabidopsis and also with mammalian protein. Putative TGF (transforming growth factor) beta inducible nuclear protein TINP1 [Oryza sativa (japonica cultivar-group)]; May be associated	#N/A
Cre12.g507300.v5.5	-0.018535977372492	LCI30	Low-CO2-inducible protein		#N/A
Cre03.g166150.v5.5	-0.018484614597907	#N/A	#N/A	#N/A	#N/A
Cre08.g384285.v5.5	-0.01839453932041	#N/A	#N/A	#N/A	#N/A
Cre06.g311050.v5.5	-0.018353092980533	#N/A	#N/A	#N/A	#N/A
Cre24.g755597.v5.5	-0.018250815226267	#N/A	#N/A	#N/A	#N/A
Cre17.g714750.v5.5	-0.018226207681113	#N/A	#N/A	#N/A	#N/A
Cre06.g278137.v5.5	-0.018204881705646	#N/A	#N/A	#N/A	#N/A
Cre14.g627950.v5.5	-0.018187150949366	#N/A	#N/A	#N/A	#N/A
Cre17.g732802.v5.5	-0.01818019212802	#N/A	#N/A	#N/A	#N/A
Cre09.g399912.v5.5	-0.018052928316054	#N/A	#N/A	#N/A	#N/A
Cre16.g668700.v5.5	-0.017961039819676	#N/A	#N/A	#N/A	#N/A
Cre12.g541450.v5.5	-0.017868208201403	#N/A	#N/A	#N/A	#N/A
Cre01.g029250.v5.5	-0.017640238731458	AAH1	Aromatic amino acid hydroxylase-related protein	Related to phenylalanine hydroxylase and tryptophan monooxygenase, not usually found in angiosperms	#N/A
Cre07.g342552.v5.5	-0.017631386684605	#N/A	#N/A	#N/A	#N/A
Cre07.g323800.v5.5	-0.017619830970618	#N/A	#N/A	#N/A	#N/A
Cre17.g739350.v5.5	-0.017581331654029	#N/A	#N/A	#N/A	#N/A
Cre13.g605500.v5.5	-0.017546639306976	#N/A	#N/A	#N/A	#N/A
Cre02.g118100.v5.5	-0.01754631115597	#N/A	#N/A	#N/A	#N/A
Cre12.g498750.v5.5	-0.017454886359882	LIP2	Triacylglycerol lipase	Triacylglycerol lipase. Related to gastric lipase. Previously annotated as LIPG2	#N/A
Cre01.g013500.v5.5	-0.01741983587509	#N/A	#N/A	#N/A	#N/A
Cre08.g360200.v5.5	-0.01735897614015	DUR3	Urea active transporter	Na+/solute symporter. Previously annotated as DUR3A	#N/A
Cre06.g310950.v5.5	-0.017290198191368	#N/A	#N/A	#N/A	#N/A
Cre10.g428966.v5.5	-0.017192513633351	#N/A	#N/A	#N/A	#N/A
Cre08.g364600.v5.5	-0.017124153488005	#N/A	#N/A	#N/A	#N/A
Cre12.g522250.v5.5	-0.01710798041914	#N/A	#N/A	#N/A	#N/A
Cre06.g249500.v5.5	-0.017030661942123	#N/A	Cytosine-C5 specific DNA methyltransferase	Dnmt1 class (cytosine-5-)DNA methyltransferase, ChromDB DMT3403; allelic to the previously published sequence AB108536 at the DMT1 locus [also published as MET1; PMID: 11983892, PMID: 15514055], which was sequenced from strain CC-683, a strain carrying th	#N/A
Cre08.g358600.v5.5	-0.017019688005888	#N/A	#N/A	#N/A	#N/A
Cre02.g074200.v5.5	-0.016917876146775	#N/A	#N/A	#N/A	#N/A
Cre05.g234653.v5.5	-0.016904274739522	#N/A	#N/A	#N/A	#N/A
Cre02.g106250.v5.5	-0.016868605691789	LAL2	La-like RNA-binding protein	La-like RNA-binding protein. Contains an N-terminal La domain and a RRM motif; its closest homologues in Arabidopsis are La-like proteins	#N/A

Accession	Score	Gene	Protein	Notes
Cre06.g269908.v5.5	-0.016826262114682	#N/A	#N/A	#N/A
Cre17.g710871.v5.5	-0.016797543379032	#N/A	#N/A	#N/A
Cre16.g691150.v5.5	-0.016691564055034	#N/A	#N/A	#N/A
Cre08.g368850.v5.5	-0.016660880915618	#N/A	#N/A	#N/A
Cre06.g301750.v5.5	-0.016637028161296	#N/A	#N/A	#N/A
Cre07.g325748.v5.5	-0.016547462531392	#N/A	#N/A	#N/A
Cre08.g377550.v5.5	-0.016537525967757	#N/A	#N/A	#N/A
Cre01.g029050.v5.5	-0.016397388226313	#N/A	#N/A	#N/A
Cre06.g307750.v5.5	-0.016394596414928	#N/A	#N/A	#N/A
Cre06.g278098.v5.5	-0.016317510342748	MCC1	Methylcrotonoyl-CoA carboxylase alpha subunit	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial precursor; 3-methylcrotonyl-CoA carboxylase; biotin-dependent carboxylase. Previously annotated as MCCA. Contains a very short LSU-rRNA motif on the opposite strand (4456221-4456270), in intro
Cre02.g099900.v5.5	-0.016306662791335	#N/A	#N/A	#N/A
Cre11.g469800.v5.5	-0.016249167382437	#N/A	#N/A	#N/A
Cre01.g004750.v5.5	-0.016152860428728	#N/A	#N/A	#N/A
Cre17.g730350.v5.5	-0.016093309341154	#N/A	#N/A	#N/A
Cre07.g355500.v5.5	-0.01597037299039	#N/A	#N/A	#N/A

with a single RRM and an N-terminal extension (AT5G46250, AT3G19090), believed not to fulfill the stabilization func

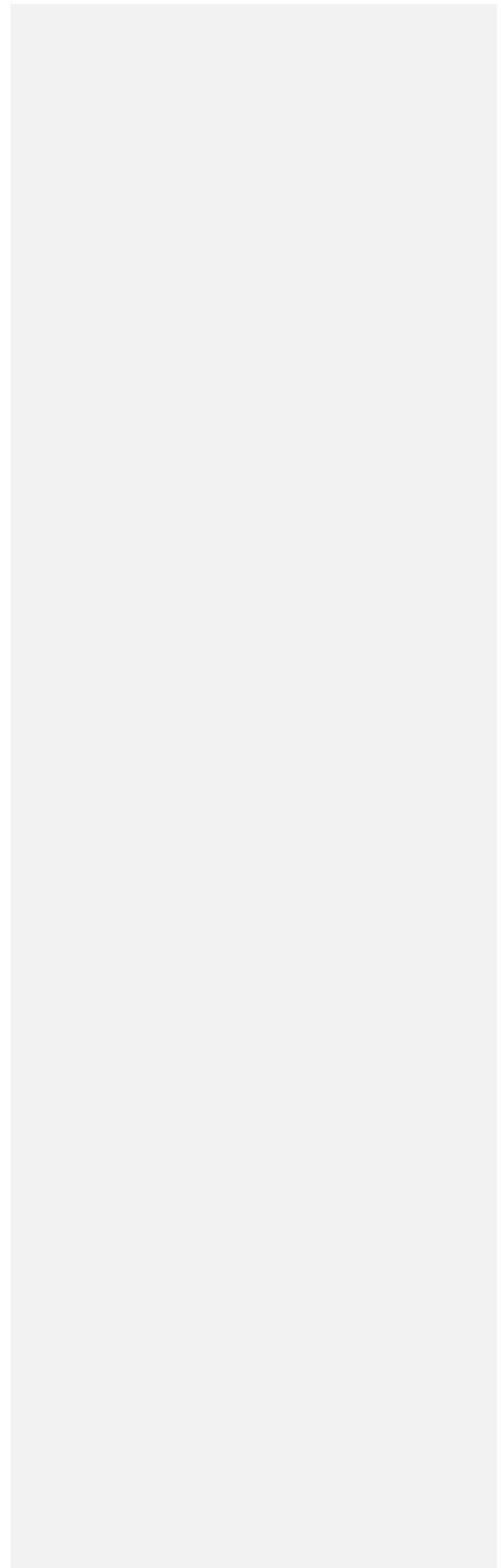


Table S11. The 100 genes contributing the most to the high acetate state including annotation.

100 genes contributing most to the high acetate state				
Identifier	GO	Gene Name	define	description
Cre13.g569850.v5.5	0.061692255360913	AMT4	Ammonium transporter	Belongs to AMT1 family (AMT1.4 or AMT1.4); corresponds to AY542491_mRNA complete cds (PMID: 15821986). Previously annotated as AMT1D
Cre03.g177800.v5.5	0.057760166294872	#N/A	#N/A	#N/A
Cre13.g563950.v5.5	0.052615672164696	#N/A	#N/A	#N/A
Cre16.g690319.v5.5	0.050997473486197	#N/A	#N/A	#N/A
Cre03.g204500.v5.5	0.050778844806041	#N/A	#N/A	#N/A
Cre12.g551352.v5.5	0.050382528068324	#N/A	#N/A	#N/A
Cre07.g321800.v5.5	0.048700331031005	#N/A	#N/A	#N/A
Cre06.g253000.v5.5	0.048148326339707	MTA1	Gamete-specific protein	Protein of unknown function; the mRNA is induced in plus gametes; the gene exists only in the mt+ locus (PMID: 1180505). The gene was originally called A1. Independently sequenced, see AF417571.
Cre04.g217944.v5.5	0.047981880431855	#N/A	#N/A	#N/A
Cre01.g008300.v5.5	0.047883621966319	#N/A	#N/A	#N/A
Cre17.g704100.v5.5	0.047395374663271	#N/A	#N/A	#N/A
Cre02.g089500.v5.5	0.047209429364108	#N/A	#N/A	#N/A
Cre10.g423850.v5.5	0.04714687361269	SRR26	Scavenger receptor cysteine rich (SRCR) protein	Scavenger receptor cysteine-rich protein; contains ligand-binding SRCR domain found in speract/scavenger receptor (PMID: 14995912) proteins.
Cre08.g382575.v5.5	0.046643645346606	#N/A	#N/A	#N/A
Cre17.g714100.v5.5	0.04663033548602	HTA21	Histone H2A	Replication-linked Histone H2A Belongs to AMT1 family (Amt1.5 or Amt1.5) two different splicing variants have been found for this gene, this one is AMT5b, the shorter one with additional intron (AY588243); was AMT1EB; belongs to AMT1 family (Amt1.5 or Amt1.5); two different splicing variants
Cre09.g400750.v5.5	0.045659061228502	AMT5	Ammonium transporter	
Cre02.g081700.v5.5	0.045657504854803	#N/A	#N/A	#N/A
Cre02.g077750.v5.5	0.045508174837251	FAP211	Flagellar Associated Protein	Flagellar Associated Protein, found in the flagellar proteome (PMID: 15998802)
Cre02.g102200.v5.5	0.045194819032043	#N/A	#N/A	#N/A
Cre15.g635376.v5.5	0.04493704580035	#N/A	#N/A	#N/A
Cre05.g235850.v5.5	0.044298841443097	#N/A	#N/A	#N/A
Cre16.g686750.v5.5	0.043982211792315	PTA3	Proton/phosphate symporter	Putative phosphate transporter homolog type A-4, similar to yeast Pho84 H+/Pi symporter; clusters with PTA2 and PTA4 on scaffold 14. gi 21218043 dbj AB074876.1
Cre12.g516700.v5.5	0.043981747920903	#N/A	#N/A	#N/A
Cre10.g442800.v5.5	0.043964241655341	XUV6	Xanthine/uracil/vitamin C permease-like	Xanthine/uracil/vitamin C permease-like. Previously annotated as UAPA1
Cre09.g390875.v5.5	0.043953908290605	#N/A	#N/A	#N/A
Cre04.g220700.v5.5	0.04369856428454	ALK2	Aurora-like kinase	Possible role in mitotic regulation. Note that the ALK1 model (originally called CALK) and several other kinase models in the genome are much weaker hits to the aurora family.
Cre12.g559900.v5.5	0.043672195877131	#N/A	#N/A	#N/A
Cre05.g238450.v5.5	0.043634396138197	#N/A	#N/A	#N/A
Cre03.g204129.v5.5	0.043515039196616	#N/A	#N/A	#N/A
Cre12.g549500.v5.5	0.043413626262504	#N/A	#N/A	#N/A
Cre08.g360200.v5.5	0.04333950831122	DUR3	Urea active transporter	Na+/solute symporter. Previously annotated as DUR3A Hydroxyproline-rich glycoprotein, putative component of the zygote ECM; contains PPSX repeats, described in PMID: 11258910. This gene is called A2 in some publications. The mRNA is gamete-specific; there is no protein localization data. A pseudogene copy
Cre16.g668850.v5.5	0.043250290885929	MTA2	Hydroxyproline-rich glycoprotein	
Cre12.g545703.v5.5	0.043078366443266	#N/A	#N/A	#N/A
Cre01.g013769.v5.5	0.04269225070094	#N/A	#N/A	#N/A
Cre13.g569150.v5.5	0.042076113255347	#N/A	#N/A	#N/A
Cre05.g239700.v5.5	0.042009967190307	#N/A	#N/A	#N/A
Cre14.g629920.v5.5	0.041970658842226	#N/A	#N/A	#N/A
Cre09.g404201.v5.5	0.041825977180628	#N/A	#N/A	#N/A
Cre08.g365150.v5.5	0.04165818651621	#N/A	#N/A	#N/A
Cre02.g142366.v5.5	0.041384860459346	#N/A	#N/A	#N/A
Cre08.g365065.v5.5	0.041279103338676	#N/A	#N/A	#N/A
Cre11.g479950.v5.5	0.041231584367213	#N/A	Triose phosphate transporter	Triose phosphate transporter. Conserved protein related to chloroplast P translocator
Cre48.g761247.v5.5	0.041043002732586	#N/A	#N/A	#N/A

Cre07.g320800.v5.5	0.040997674659227	#N/A	#N/A	#N/A
Cre03.g207900.v5.5	0.040914039960444	CYCA1	A-type cyclin	Cyclin A homolog; A-type cyclin homolog. Putative function in S/G2/M Replication-linked Histone H2A. PMID: 8590479. Identified as nitrogen-controlled-gene NCG10 expressed upon nitrogen starvation. PMID:11469597
Cre17.g714500.v5.5	0.040783531336268	HTA1	Histone H2A	
Cre07.g338000.v5.5	0.040726710631976	MCM2	Minichromosome maintenance protein	Homologous to MCM2 DNA replication protein
Cre14.g620702.v5.5	0.040481933781484	#N/A	#N/A	#N/A
Cre08.g365100.v5.5	0.040358328093199	FAP242	Flagellar Associated Protein	Coiled-Coil Flagellar Associated Protein, found in the flagellar proteome [PMID: 15998802]
Cre11.g468800.v5.5	0.040308728638527	#N/A	#N/A	#N/A
Cre01.g010300.v5.5	0.038957731407512	#N/A	#N/A	#N/A
Cre09.g399363.v5.5	0.038820527992884	#N/A	#N/A	#N/A
Cre17.g735550.v5.5	0.038142448918727	#N/A	#N/A	#N/A
Cre17.g719050.v5.5	0.038129850925043	#N/A	#N/A	#N/A
Cre02.g090150.v5.5	0.037935194072724	PAN3	Pantothenate synthetase	Pantothenate synthetase; Pantoate-beta-alanine ligase. Previously annotated as PANC Cyclin dependent kinase; Chlamydomonas specific subfamily; AASTLRE motif. Novel CDK subfamily. Also identified from nitrogen starvation experiments as nitrogen-controlled-gene NCG9 [PMID: 11469597]
Cre17.g742250.v5.5	0.037889614494085	CDKG2	Cyclin dependent kinase	
Cre03.g199090.v5.5	0.03775503845625	#N/A	#N/A	#N/A
Cre09.g394065.v5.5	0.037447529418686	#N/A	#N/A	#N/A
Cre06.g281750.v5.5	0.037388884671213	#N/A	#N/A	#N/A
Cre06.g249500.v5.5	0.037359519462329	#N/A	Cytosine-C5 specific DNA methyltransferase	Dnmt1 class (cytosine-5-)DNA methyltransferase, ChromDB DMT3403; allelic to the previously published sequence AB108536 at the DMT1 locus [also published as MET1; PMID: 11983892, PMID: 15514055], which was sequenced from strain CC-683, a strain carrying th
Cre02.g145950.v5.5	0.037327378657702	#N/A	#N/A	#N/A
Cre17.g699800.v5.5	0.037291317274302	#N/A	#N/A	#N/A
Cre09.g412400.v5.5	0.037263595226669	#N/A	#N/A	#N/A
Cre05.g233350.v5.5	0.037159463750446	#N/A	#N/A	#N/A
Cre11.g481750.v5.5	0.036997912664017	GAS30	Hydroxyproline-rich glycoprotein, stress-induced	Belongs to the large perophorin-family, a family of extracellular matrix glycoproteins (cell wall glycoproteins) with a central hydroxyproline-rich (HR) domain. The mRNA is up-regulated in gametes. In zygotes, by agglutination/cAMP treatment, by osmotic 1,3-beta-D-glucan synthase and glycosyl transferase. Previously annotated as GTR12
Cre06.g302050.v5.5	0.036948046300439	#N/A	1,3-beta-D-glucan synthase	
Cre11.g467586.v5.5	0.036887593916565	#N/A	#N/A	#N/A
Cre07.g322250.v5.5	0.036867365815112	#N/A	#N/A	#N/A
Cre17.g714150.v5.5	0.036716039049479	KUP1	Potassium ion uptake transporter	Potassium ion uptake transporter. Linked to related KUP2 and KUP3
Cre12.g489700.v5.5	0.036685890670675	OTC1	Ornithine carbamoyltransferase	Ornithine carbamoyltransferase (OTC) (ARG3 in yeast); chloroplast-targeted (by homology to At1g75330); arg4 is probably a mutant in that gene; note however that arg4 is not rescued by citrulline, whereas an OTC mutant should be.
Cre06.g258850.v5.5	0.036684665678723	#N/A	#N/A	#N/A
Cre03.g159254.v5.5	0.036604164877308	#N/A	#N/A	#N/A
Cre04.g226550.v5.5	0.036508096315657	#N/A	#N/A	#N/A
Cre06.g288100.v5.5	0.036206286196298	#N/A	#N/A	#N/A
Cre04.g212450.v5.5	0.036185666064818	#N/A	#N/A	#N/A
Cre06.g278250.v5.5	0.036002756917705	#N/A	#N/A	#N/A
Cre10.g420200.v5.5	0.035891435729852	#N/A	#N/A	#N/A
Cre17.g706000.v5.5	0.035854384890403	#N/A	#N/A	#N/A
Cre12.g551353.v5.5	0.035799147330193	#N/A	#N/A	#N/A
Cre13.g589450.v5.5	0.035664542073721	#N/A	#N/A	#N/A
Cre12.g544450.v5.5	0.035627281537301	#N/A	#N/A	#N/A
Cre08.g368650.v5.5	0.035520820478213	#N/A	#N/A	#N/A
Cre03.g160250.v5.5	0.035518899708229	#N/A	#N/A	#N/A
Cre01.g053000.v5.5	0.03548085387363	GPD2	Glycerol-3-phosphate dehydrogenase/dihydroxyacetone-3-phosphate reductase	Glycerol-3-phosphate dehydrogenase/dihydroxyacetone-3-phosphate reductase
Cre12.g524350.v5.5	0.035449666691746	HUS1	DNA damage checkpoint protein	Forms a sliding clamp complex with Rad9 and Rad1 that mediates repair at sites of DNA damage.
Cre11.g483351.v5.5	0.035364833585524	#N/A	#N/A	#N/A
Cre08.g365103.v5.5	0.035035813567334	#N/A	#N/A	#N/A
Cre13.g563050.v5.5	0.034963935381537	#N/A	#N/A	#N/A
Cre07.g324500.v5.5	0.034812923576204	#N/A	#N/A	#N/A

Cre07.g332275.v5.5	0.034789675800128	#N/A	#N/A	#N/A
Cre12.g488500.v5.5	0.034749173404391	#N/A	#N/A	#N/A
Cre12.g523900.v5.5	0.034587000479747	#N/A	#N/A	#N/A
Cre09.g405350.v5.5	0.034565146851294	#N/A	#N/A	#N/A
Cre03.g177600.v5.5	0.034470672864949	#N/A	#N/A	#N/A
Cre13.g605200.v5.5	0.034380590353668	#N/A	#N/A	#N/A
Cre07.g342551.v5.5	0.034246479004594	#N/A	#N/A	#N/A
Cre01.g053150.v5.5	0.034225330740729	GPD3	Glycerol-3-phosphate dehydrogenase/dihydroxyacetone-3-phosphate reductase	Glycerol-3-phosphate dehydrogenase/dihydroxyacetone-3-phosphate reductase
Cre03.g190800.v5.5	0.034184717197988	#N/A	#N/A	#N/A
Cre12.g488450.v5.5	0.034165995801455	VSP3	Extracellular matrix protein	Extracellular matrix protein (vegetative cell wall protein) similar to ISG (Volvox carterii) [PMID: 1600938], both are glycoproteins with a hydroxyproline-rich (HR) domain. [PMID: 8000007. ISG Genbank entry X65165; VSP3, L29029; C. incerta ortholog, AY7950
Cre08.g385550.v5.5	0.034154628165592	#N/A	#N/A	#N/A

Table S12. The 100 genes contributing the most to the low acetate state including annotation.

100 genes contributing most to the low acetate state				
identifier	GO	Gene Name	define	description
Cre16.g661750.v5.5	-0.054019122079341	#N/A		#N/A
Cre06.g274750.v5.5	-0.040920443227048	#N/A	Histone H2B	Replication-linked Histone H2B. Also annotated as HTB26
Cre04.g223300.v5.5	-0.040082055187707	CCP1	Low-CO2-inducible chloroplast envelope protein	Low-CO2-inducible 36kDa chloroplast envelope protein (LIP36-1), CO2-responsive gene; related to mitochondrial carriers; Chen et al. 1997 [PMID: 9159951]. CCP1 and LCIE are located in head-to-head orientation; regulated by CCM1 [PMID: 15235119]. Acclimatio
Cre05.g236650.v5.5	-0.039720630250885	#N/A		#N/A
Cre04.g223100.v5.5	-0.037952321087351	CAH1	Carbonic anhydrase	Carbonate dehydratase 1 in Chlamydomonas reinhardtii, also known as CA1; gi:115447; Carbonic anhydrase 1 precursor (Carbonate dehydratase 1) (CA1); alpha type - Carbonic anhydrase 1 localized in the periplasmic space and low-CO2 inducible gene regulated b
Cre11.g467615.v5.5	-0.037922370340832	#N/A		#N/A
Cre06.g271550.v5.5	-0.036248101030833	#N/A		#N/A
Cre16.g661850.v5.5	-0.035944431122288	#N/A		#N/A
Cre05.g248400.v5.5	-0.035911736348512	CAH4	Mitochondrial carbonic anhydrase, beta type	Mitochondrial carbonic anhydrase, beta type. Probably regulated by CCM1 [PMID: 15235119]; Acclimation to changing CO2 concentrations and light intensities was studied by Yamano et al. 2008 [PMID: 18322145], identified in their table as MCA. The inorganic
Cre17.g717400.v5.5	-0.035665935540261	#N/A		#N/A
Cre05.g239600.v5.5	-0.035124737862376	#N/A		#N/A
Cre14.g608093.v5.5	-0.03445216943993	#N/A		#N/A
Cre09.g395288.v5.5	-0.033847285887188	NHA1	Sodium ion/proton transporter protein	Sodium:hydrogen antiporter NhaD. Previously annotated as NHA01
Cre09.g393953.v5.5	-0.032110499918333	#N/A		#N/A
Cre12.g554100.v5.5	-0.031127312035748	#N/A		#N/A
Cre06.g265500.v5.5	-0.030488940019009	#N/A		#N/A
Cre08.g367400.v5.5	-0.030246260273157	LHCSR3	Stress-related chlorophyll a/b binding protein 3	Stress-related chlorophyll a/b binding protein, similar to LH818-1/LHCSR1. Peers et al. (2009) [PMID: 19940928] call this gene LHCSR3.2; this apparently codes for the same protein as LHCSR3.1
Cre02.g085500.v5.5	-0.029500384828609	#N/A		#N/A
Cre16.g683954.v5.5	-0.029462157345945	#N/A		#N/A
Cre10.g436400.v5.5	-0.029208393263428	#N/A		#N/A
Cre06.g257601.v5.5	-0.028480704657127	PRX1	2-cys peroxidoredoxin, chloroplastic	2-cys Peroxiredoxin, thioredoxin dependent peroxidase, chloroplast precursor, PMID: 11784321. Protein processed at aa 39 to produce N-terminus of SHAEKPL as determined by Edman degradation
Cre05.g248450.v5.5	-0.027947979045768	CAH5	Mitochondrial carbonic anhydrase	Mitochondrial carbonic anhydrase, also called CA2. Matches exons 5 and 6 of CRU41190 Chlamydomonas reinhardtii carbonic anhydrase precursor (beta-CA2). The inorganic carbon-concentrating mechanism has been reviewed by Spalding (2008) [PMID: 17597098]
Cre02.g084350.v5.5	-0.027802545686327	CGLD1	Predicted protein	Putative plastid protein
Cre09.g402219.v5.5	-0.027739427116643	LCI3	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].
Cre06.g268600.v5.5	-0.027302269714369	NAB1	Nucleic acid binding protein	Nucleic acid binding protein; RNA binding protein involved in the light-regulated differential expression of the light-harvesting antenna of Chlamydomonas reinhardtii [PMID: 15284312, Genbank entry AY157846]. Studied by Wobbe et al. 2009 [PMID: 19666611]
Cre16.g649433.v5.5	-0.027185128671149	#N/A		#N/A
Cre05.g244400.v5.5	-0.027053516245648	#N/A		#N/A
Cre13.g590500.v5.5	-0.026816023498735	#N/A	Omega-6-fatty acid desaturase, chloroplast isoform	Omega-6-FAD, chloroplast isoform [PMID: 9498569]. Also known as DES6
Cre10.g422300.v5.5	-0.02676157159526	PRX6	Thioredoxin dependent peroxidase	Peroxiredoxin Q, chloroplastic thioredoxin dependent peroxidase, chloroplast precursor. Attached to thylakoids in Arabidopsis [PMID: 16507087; PMID: 15531707; PMID: 14976238; PMID: 12529539; PMID: 15890615]
Cre08.g367500.v5.5	-0.026749524569554	LHCSR2	Stress-related chlorophyll a/b binding protein 2	Stress-related chlorophyll a/b binding protein, similar to LH818-1/LHCSR1. Peers et al. (2009) [PMID: 19940928] call this gene LHCSR3.1; this apparently codes for the same protein as LHCSR3.2
Cre03.g205100.v5.5	-0.026668440061125	#N/A		#N/A
Cre02.g082750.v5.5	-0.02588328417187	PSBX	4.1 kDa photosystem II subunit	Encoding a 4.1 kDa subunit for PS2 with a single TMH [PMID: 16143838].
Cre17.g730550.v5.5	-0.025589387617479	#N/A		#N/A
Cre06.g309000.v5.5	-0.025221321480339	NAR1.2	Anion transporter	Nitrite transporter-homologue, possibly chloroplastic [PMID: 11912227, AY612639]; significant similarities with two anion transporters, the chloroplastic nitrite transporter NAR1 and formate transporters in bacteria; also known as LCIA. induced by CO2-limi

Cre10.g436550.v5.5	-0.025219816823229	LCI5	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].
Cre08.g361150.v5.5	-0.025199379733876	#N/A	#N/A	#N/A
Cre13.g570851.v5.5	-0.02511429017738	#N/A	#N/A	#N/A
Cre06.g284600.v5.5	-0.025100404062781	RBD2	Rubredoxin	Rubredoxin A homolog of ELIP (early light-inducible protein) gene which was originally identified as transiently expressed during the early phase of greening in etiolated pea seedlings [PMID: 6692824]. It has three TMH, whose sequences are closely related to LHC pro
Cre09.g393173.v5.5	-0.024886886710214	ELI2	Early light-inducible protein	
Cre14.g621650.v5.5	-0.024085396477217	#N/A	#N/A	#N/A
Cre06.g271250.v5.5	-0.02390039989252	HTR8	Histone H3	Replication-linked Histone H3
Cre13.g573250.v5.5	-0.023885616757612	#N/A	#N/A	#N/A
Cre04.g227700.v5.5	-0.023723543686113	#N/A	#N/A	#N/A
Cre12.g540351.v5.5	-0.023656334169586	#N/A	#N/A	#N/A
Cre09.g399908.v5.5	-0.023274356939811	#N/A	#N/A	#N/A
Cre02.g117175.v5.5	-0.023145502197924	#N/A	#N/A	#N/A
Cre02.g141786.v5.5	-0.023070884389193	PDE25	3',5'-cyclic-nucleotide phosphodiesterase	Calmodulin dependent PDE1B1 protein from Homo Sapiens is closest relative
Cre03.g195410.v5.5	-0.022893590308439	#N/A	#N/A	#N/A
Cre26.g756747.v5.5	-0.022446823611193	#N/A	#N/A	#N/A
Cre14.g610400.v5.5	-0.02242292916985	#N/A	#N/A	#N/A
Cre06.g288900.v5.5	-0.022366681834002	#N/A	#N/A	#N/A
Cre17.g732250.v5.5	-0.022356458174544	#N/A	#N/A	#N/A
Cre03.g180450.v5.5	-0.02222906564093	#N/A	5'-nucleotidase and Flagellar Associated Protein	5'-nucleotidase and conserved uncharacterized Flagellar Associated Protein; found in the flagellar proteome [PMID: 15998802]. Previously annotated as FAP215
Cre16.g650250.v5.5	-0.022144510134672	HFO39	Histone H4	Replication-linked Histone H4
Cre03.g195200.v5.5	-0.022082119500335	#N/A	Haloalkane dehalogenase-like hydrolase	Haloalkane dehalogenase, an alpha/beta hydrolase. Green-lineage conserved expressed protein with epoxide hydrolase / esterase motif. Previously annotated as CGL76
Cre12.g485438.v5.5	-0.021937903206539	#N/A	#N/A	#N/A
Cre16.g672609.v5.5	-0.021779493531215	#N/A	#N/A	#N/A
Cre13.g571520.v5.5	-0.021591768598954	#N/A	#N/A	#N/A
Cre07.g334550.v5.5	-0.021435755434016	PSAO	Photosystem I subunit O	Photosystem I subunit O; similar to 10-kDa subunit of eukaryotic photosystem I [PMID: 11801243]; microarray element: 894019E07
Cre14.g626700.v5.5	-0.021202150904888	PETF	Ferredoxin	2Fe-2S containing redox protein involved in photosynthetic electron transfer, chloroplast localization [PMID: 16656453]
Cre09.g13200.v5.5	-0.021046649492915	#N/A	Serine/threonine protein kinase	Serine/Threonine protein kinase. Previously annotated as STPK22
Cre13.g603550.v5.5	-0.020905830560223	#N/A	#N/A	#N/A
Cre11.g477733.v5.5	-0.02075707991942	#N/A	#N/A	#N/A
Cre08.g358558.v5.5	-0.020743283567865	#N/A	#N/A	#N/A
Cre14.g613800.v5.5	-0.020727379700084	#N/A	#N/A	#N/A
Cre01.g025150.v5.5	-0.020586154775489	CPLD15	Predicted protein	Conserved organelle protein with lipase active site
Cre13.g565311.v5.5	-0.020485822017577	#N/A	#N/A	#N/A
Cre24.g755197.v5.5	-0.020425338769253	RBD3	Putative rubredoxin-like protein	Putative rubredoxin-like protein
Cre12.g546150.v5.5	-0.020400170256475	PETM	Cytochrome b6f complex PetM subunit	Cytochrome b6f complex chain PetM, chloroplast precursor; GI:2493687; PMID: 8631873, PMID: 8616155, PMID: 7493968
Cre13.g590750.v5.5	-0.020144350381864	HTB37	Histone H2B	Replication-linked Histone H2B
Cre06.g273150.v5.5	-0.020063931852885	#N/A	#N/A	#N/A
Cre06.g274700.v5.5	-0.020048876896628	#N/A	#N/A	#N/A
Cre01.g010900.v5.5	-0.020047832755341	GAP3	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,
Cre16.g694500.v5.5	-0.019843518083654	#N/A	DnaI-like protein	DnaI-like protein
Cre10.g435800.v5.5	-0.019521949980616	#N/A	NAD-dependent epimerase/dehydratase	NAD-dependent epimerase/dehydratase, possibly with UDP-glucose 4-epimerase activity. Possible chloroplast stem-loop-binding protein 41b, cp ribosome-associated protein RAP38. Previously annotated as CSP41b
Cre16.g662600.v5.5	-0.019495986597625	#N/A	#N/A	#N/A
Cre09.g392867.v5.5	-0.019489822746428	FMG1-B	Flagella membrane glycoprotein, major form	Flagella membrane protein, major form. Only one expressed in Chlamydomonas during vegetative growth (and likely even in gametes). A gene model for this was present in v2, lost in v3, and recovered with Augustus (first noticed in Au5 update). This g
Cre02.g118550.v5.5	-0.019384856416699	#N/A	#N/A	#N/A
Cre11.g479900.v5.5	-0.01935289596692	#N/A	#N/A	#N/A
Cre02.g076250.v5.5	-0.019315977311994	EFG1	Chloroplast elongation factor G	Putative chloroplast elongation factor G (fusA), GTP binding; likely locus for previously described C. reinhardtii fsr1 (fus-1) mutant

				resistant to fusidic acid [Carbonera et al. 1981, FEBS Lett. 132, 227-230]	
Cre13.g58000.v5.5	-0.019286458448033	#N/A	#N/A	#N/A	#N/A
Cre08.g362100.v5.5	-0.019226279510258	#N/A	Similar to Flagellar Associated Protein FAP154	Similar to Flagellar Associated Protein FAP154 with PAS sensory domain that was found in the flagellar proteome [PMID: 15998802]. This may be a duplication of FAP154; overlaps FAP154 gene model from v3	#N/A
Cre17.g716613.v5.5	-0.019217126718573	#N/A	#N/A	#N/A	#N/A
Cre12.g494850.v5.5	-0.019102669807173	ADK3	Adenylate kinase	Adenylate kinase; probably chloroplast-targeted (by homology to KADD_ARATH); contains a C-terminal domain with two Cys residues, homologous to that found in CP12 linking GAPDH and PRK [PMID: 8980547]	#N/A
Cre17.g734725.v5.5	-0.0189252325252117	#N/A	#N/A	#N/A	#N/A
Cre12.g550850.v5.5	-0.018901346748483	PSBP1	Oxygen-evolving enhancer protein 2 of photosystem II	Oxygen-evolving enhancer protein 2, chloroplast precursor (OEE2) (23 kDa subunit of oxygen evolving complex of photosystem II) (OEC 23 kDa subunit) (23 kDa thylakoid membrane protein) [OEC23]; PMID: 3468511; targeted to thylakoid lumen by TAT pathway	#N/A
Cre14.g630500.v5.5	-0.018868137929669	#N/A	#N/A	#N/A	#N/A
Cre16.g687900.v5.5	-0.018829786157859	LHCA7	Light-harvesting protein of photosystem I	#N/A	#N/A
Cre06.g272650.v5.5	-0.0188227595825	LHCA8	Light-harvesting protein of photosystem I	#N/A	#N/A
Cre17.g15250.v5.5	-0.01872897479201	BCC1	Acetyl-CoA biotin carboxyl carrier	Biotin-containing subunit of the chloroplastic acetyl-coenzyme A carboxylase; N-terminal sequence identified by Edman degradation is AAKT....	#N/A
Cre04.g229536.v5.5	-0.018668394080494	#N/A	#N/A	#N/A	#N/A
Cre30.g758247.v5.5	-0.018613225768048	#N/A	#N/A	#N/A	#N/A
Cre17.g724300.v5.5	-0.018595939640892	PSAK	Photosystem I reaction center subunit psaK	8.4 kD subunit of photosystem I (polypeptide 37) [PMID: 2693938]	#N/A
Cre10.g439450.v5.5	-0.018577484500267	#N/A	#N/A	#N/A	#N/A
Cre12.g517681.v5.5	-0.018503104482783	#N/A	#N/A	#N/A	#N/A
Cre11.g479100.v5.5	-0.018446195005692	#N/A	#N/A	#N/A	#N/A
Cre03.g156050.v5.5	-0.018364483020047	#N/A	#N/A	#N/A	#N/A
Cre12.g486300.v5.5	-0.018341711035851	PSAL	Photosystem I reaction center subunit XI	#N/A	#N/A
Cre17.g720250.v5.5	-0.018333822887126	LHCB4	Chlorophyll a/b binding protein of photosystem II	Chlorophyll a-b binding protein of photosystem II. Protein product also known as CP29	#N/A
Cre16.g679750.v5.5	-0.018283244057131	#N/A	#N/A	#N/A	#N/A

Table S13. The 100 most stable regulatory genes (Protein Kinase (PPC), transcriptional regulators and transcription factors from the iTAK database) including annotation.

G ₀ sorted identifier	G ₀	geneName	define	description	name	type
Cre17.g742250.v5.5	0.01041097245589	CDKG2	Cyclin dependent kinase	Cyclin dependent kinase; Chlamydomonas specific subfamily; AASTLRE motif. Novel CDK subfamily. Also identified from nitrogen starvation experiments as nitrogen-controlled-gene NCG9 [PMID: 11469597]	CDC2 Like Kinase Family Unknown Function Kinase	PPC
Cre12.g537400.v5.5	0.008975762021363					PPC
Cre02.g087900.v5.5	0.008517079870007				GmpPK6/AtMRK1 Family IRE/NPH/PI dependent/S6 Kinase	PPC
Cre03.g199050.v5.5	0.007667285114936					PPC
Cre09.g404351.v5.5	0.004374692184443				SET Unknown Function Kinase	transcriptional regulator
Cre11.g467585.v5.5	0.004098069082157				WNK like kinase - with no lysine kinase	PPC
Cre01.g040150.v5.5	0.002847075293308				Unknown Function Kinase	PPC
Cre03.g187300.v5.5	0.002735088965977					PPC
Cre11.g475100.v5.5	0.002397327965001				GNAT	transcriptional regulator
Cre17.g710000.v5.5	0.00219402281228				GmpPK6/AtMRK1 Family	PPC
Cre09.g392300.v5.5	0.002049160165836				GNAT	transcriptional regulator
Cre03.g182700.v5.5	0.001995879628658				Others	transcriptional regulator
Cre04.g221900.v5.5	0.001988289255229				TRAF Unknown Function Kinase	transcriptional regulator
Cre09.g396065.v5.5	0.001477899973287	ALK5	Aurora-like kinase	Aurora-like kinase High mobility group protein, histone-like transcription factor. Has homology to DNA polymerase epsilon subunit	CTR1/EDR1 Kinase	PPC
Cre03.g193900.v5.5	0.001431393329984		High mobility group protein, histone-like transcription factor		HMG	transcriptional regulator
Cre01.g036900.v5.5	0.001406308390395					PPC
Cre01.g009550.v5.5	0.001398986719746				GNAT	transcriptional regulator
Cre13.g564100.v5.5	0.001227531617411	PTK2	Putative tyrosine kinase	Putative tyrosine kinase identified through multi-level HMM library for kinase classification [PMID: 17557329]	GmpPK6/AtMRK1 Family Receptor Like Cytoplasmic Kinase VI	PPC
Cre02.g141886.v5.5	0.001120333419833					PPC
Cre07.g346550.v5.5	0.00110089267122				GmpPK6/AtMRK1 Family	PPC
Cre03.g212977.v5.5	0.001097555154075				TAZ	transcriptional regulator
Cre12.g522400.v5.5	0.000968871816103				MYB->MYB	transcription factor
Cre09.g404050.v5.5	0.00096155299405				GmpPK6/AtMRK1 Family	PPC
Cre03.g149400.v5.5	0.000867665028949	RWP11	RWP-RK transcription factor	Putative RWP-RK domain transcription factor [PMID: 15785851]. Tandem pair with RWP4 with which there is amino acid homology around the RWP-RK domain and some intron conservation. Part of the model is tentative.	RWP-RK	transcription factor
Cre03.g153050.v5.5	0.000832014625406	RWP1	RWP-RK transcription factor	Putative RWP-RK domain transcription factor [PMID: 15785851]; model is very tentative	RWP-RK Leucine Rich Repeat Kinase XI & XII	transcription factor
Cre11.g467586.v5.5	0.000802498836637					PPC
Cre03.g174150.v5.5	0.000758383160517				TRAF	transcriptional regulator
Cre06.g296200.v5.5	0.000680302938973				Calcium Dependent Protein Kinase	PPC

Cre16.g674065.v5.5	0.0006594199191695		Unknown Function Kinase	PPC
Cre17.g741900.v5.5	0.000611332851719		GmpPK6/AtMRK1 Family	PPC
			DnaJ-like protein and Myb-like transcription factor; probably nuclear/cytosolic; similar to Chlamy Q6JX09_CHLRE GlsA-related protein and to Volvox GLSA; contains J-domain (pfam00226) at the N-terminus and Myb_DNA-binding-Domain (pfam00249) at the C-termin	
Cre16.g695600.v5.5	0.000603702350472	DNJ10	DnaJ-like protein and Myb-like transcription factor	MYB->MYB-related transcription factor
Cre03.g198800.v5.5	0.00059970392788			MYB->MYB-related transcription factor
Cre12.g500900.v5.5	0.000572617608828			PHD transcriptional regulator
Cre06.g281000.v5.5	0.000554160134835			SET transcriptional regulator
Cre11.g479800.v5.5	0.000499613088264			TRAF transcriptional regulator
Cre13.g583217.v5.5	0.000445885477054			GNAT transcriptional regulator
Cre14.g632700.v5.5	0.000445486354914			GmpPK6/AtMRK1 Family PPC
Cre03.g149201.v5.5	0.000414498173279			MYB->MYB transcription factor
Cre03.g151050.v5.5	0.000399184765747			TRAF transcriptional regulator
Cre06.g278265.v5.5	0.000394102435955			Unknown Function Kinase PPC
Cre06.g249050.v5.5	0.000369830647426			MYB->MYB-related transcription factor
Cre01.g048501.v5.5	0.000363116408629			TRAF transcriptional regulator
Cre09.g413050.v5.5	0.00034191802918			bZIP transcription factor
Cre04.g223500.v5.5	0.000303538132762			IRE/NPH/PI dependent/S6 Kinase PPC
			Serine/Threonine protein kinase. Previously annotated as two models, STPK21 and PTK26 (for protein tyrosine kinase)	
Cre10.g435750.v5.5	0.000277896379824		Serine/Threonine protein kinase	S Domain Kinase (Type 2) PPC
Cre07.g339100.v5.5	0.000263287665261			Unknown Function Kinase PPC
Cre10.g423200.v5.5	0.000250619291515			GmpPK6/AtMRK1 Family PPC
Cre16.g679893.v5.5	0.00024222034113			GmpPK6/AtMRK1 Family PPC
Cre08.g361400.v5.5	0.000211782404239			CPP transcription factor
Cre16.g679781.v5.5	0.000202345081449			SET transcriptional regulator
Cre16.g676300.v5.5	0.000189597638901			CTR1/EDR1 Kinase PPC
Cre14.g623926.v5.5	0.000181476854579			GmpPK6/AtMRK1 Family PPC
Cre06.g289900.v5.5	0.00015150859582			MYB->MYB-related transcription factor
Cre09.g398750.v5.5	0.000144576027389			GmpPK6/AtMRK1 Family PPC
Cre10.g446850.v5.5	0.00012999954551			Jumonji transcriptional regulator
Cre13.g579650.v5.5	0.000116187358545			GmpPK6/AtMRK1 Family PPC
Cre12.g558300.v5.5	0.000112337818414			GmpPK6/AtMRK1 Family PPC
			Histone-lysine N-methyltransferase. Green-lineage and diatoms conserved protein contains a SET domain with similarity to Arabidopsis thaliana ATXR3, SET2, SDG2 (At4g15180) and Oryza sativa SDG701. Previously annotated as CGLD30. ChromoDB SDG3401. Poss	
Cre17.g742700.v5.5	6.00227749121812E-05		Histone-lysine N-methyltransferase	SET SNF1 Related Protein Kinase (SnRK) transcriptional regulator
Cre12.g485600.v5.5	3.92449728784609E-05			PPC
Cre02.g084550.v5.5	1.83366549863245E-05			GNAT transcriptional regulator
Cre17.g745447.v5.5	1.1736317940689E-05	MAPK4	Mitogen-Activated Protein Kinase	Hypothetical Mitogen-Activated Protein Kinase Homolog 4 MAPK Family PPC
Cre16.g649700.v5.5	-3.70053686262777E-05			SET transcriptional regulator
Cre06.g297150.v5.5	-3.72629725971905E-05	RWP9	RWP-RK transcription factor	Putative RWP-RK domain transcription factor; model is very tentative RWP-RK transcription factor
Cre08.g385300.v5.5	-5.22266199978947E-05			SET transcriptional regulator

Cre03.g169100.v5.5	-5.7092248941272E-05		Calcium Dependent Protein Kinase	PPC
Cre11.g482700.v5.5	-6.20517468967167E-05		HMG	transcriptional regulator
Cre12.g541777.v5.5	-6.7969519535387E-05		SET	transcriptional regulator
Cre07.g353000.v5.5	-8.22281675553122E-05		CDC2 Like Kinase Family	PPC
Cre02.g111950.v5.5	-0.000106612282938		GmPK6/AtMRK1 Family	PPC
Cre17.g747397.v5.5	-0.000113598036014		SNF1 Related Protein Kinase (SnRK)	PPC
Cre04.g228850.v5.5	-0.000159677180812		Unknown Function Kinase	PPC
Cre07.g340250.v5.5	-0.00016443144292	Serine/threonine protein kinase	Serine/Threonine protein kinase. Previously annotated as STPK8	GmPK6/AtMRK1 Family
Cre17.g738600.v5.5	-0.000169517826765	RegA/RlsA-like protein	Member of a family of proteins [PMID: 16720695, 16622701] related to Volvox carteri RegA, which is a putative transcription repressor [PMID: 9895312] containing a SAND domain [IPRO00770 SAND; PFD1342].	VARL
Cre12.g514250.v5.5	-0.000184383320232			ARID
Cre11.g467577.v5.5	-0.00018927664782			MADS->MADS-M-type
Cre13.g583150.v5.5	-0.000195184448698			TRAF
Cre12.g495100.v5.5	-0.000201080193084	PSR1	Myb-like DNA binding domain and coiled-coil domain containing transcription factor required for phosphate deficiency-inducible gene expression; nuclear-localized [AF174480 (mRNA), AF174532 (gene); PMID: 10611385]	GARP->GARP-G2-like
Cre01.g023100.v5.5	-0.000265974543283			AP2/ERF->AP2/ERF-ERF
Cre06.g302150.v5.5	-0.0002948867918			VARL
Cre10.g464264.v5.5	-0.000304949630244			GNAT
Cre02.g083750.v5.5	-0.000308953213645			GARP->GARP-G2-like
Cre14.g633789.v5.5	-0.000336585456635			MYB->MYB-related
Cre03.g160700.v5.5	-0.000342610305972			C2C2->C2C2-GATA
Cre09.g393062.v5.5	-0.000352145182434			GmPK6/AtMRK1 Family
Cre06.g264400.v5.5	-0.000389891953958			MYB->MYB-related Legume Lectin Domain Kinase
Cre10.g425350.v5.5	-0.000391465295682			TRAF
Cre04.g219400.v5.5	-0.000429581454051			GmPK6/AtMRK1 Family
Cre09.g390300.v5.5	-0.000440910377274			SET
Cre03.g201332.v5.5	-0.000452380211715			GmPK6/AtMRK1 Family
Cre17.g709900.v5.5	-0.00045463495611			SET
Cre03.g186450.v5.5	-0.000488355403593	Lysine N-methylase	Putative SET domain lysine N-methylase, possibly involved in histone modification. ChromoDB SDG3414	SET
Cre16.g653258.v5.5	-0.000492505083718			TRAF
Cre09.g387950.v5.5	-0.000500106323684			GmPK6/AtMRK1 Family
Cre14.g617151.v5.5	-0.000501050154693			VARL
Cre13.g581150.v5.5	-0.000519148538138			GNAT
Cre12.g552150.v5.5	-0.000599821271365			GmPK6/AtMRK1 Family
Cre13.g604350.v5.5	-0.000604134233214			GmPK6/AtMRK1 Family
Cre16.g694550.v5.5	-0.000604879259672			CTR1/EDR1 Kinase
Cre09.g394400.v5.5	-0.000613320827055			GmPK6/AtMRK1 Family
Cre11.g481104.v5.5	-0.000657628702137			Calcium Dependent Protein Kinase

Table S14. The 100 regulatory genes (Protein Kinase (PPC), transcriptional regulators and transcription factors from iTAK) contributing the most to the stationary state including annotation.

G ₁ sorted identifier	G ₁	geneName	define	description	name	type
Cre12.g537400.v5.5	-0.0153139799596				Unknown Function Kinase	PPC
Cre14.g623926.v5.5	-0.014037006930749				GmPK6/AtMRK1 Family	PPC transcriptional regulator
Cre17.g700550.v5.5	-0.014028236140407				TRAF	PPC transcriptional regulator
Cre02.g087850.v5.5	-0.013976687167056	PTK19	Protein tyrosine kinase	Putative protein tyrosine kinase identified through multi-level HMM library for kinase classification (PMID: 17557329)	GmPK6/AtMRK1 Family	PPC transcriptional regulator
Cre01.g022950.v5.5	-0.013813258535296				TRAF	transcriptional regulator
Cre02.g146629.v5.5	-0.013582671144331				MYB->MYB-related	transcription factor
Cre09.g396065.v5.5	-0.013195390689521	ALK5	Aurora-like kinase	Aurora-like kinase	Unknown Function Kinase	PPC transcriptional regulator
Cre07.g330650.v5.5	-0.013065600052316				mTERF	transcriptional regulator
Cre07.g322450.v5.5	-0.013048875869342				SET	transcriptional regulator
Cre03.g144747.v5.5	-0.013037898584037				MYB->MYB	transcription factor
Cre04.g221900.v5.5	-0.012742978771397				TRAF	transcriptional regulator
Cre08.g384250.v5.5	-0.012361622963537				SNF1 Related Protein Kinase (SnRK)	PPC
Cre13.g579200.v5.5	-0.012246720946781	S6K1	Ribosomal protein S6 kinase	Protein kinase that phosphorylates rp56, mediating ribosomal processivity; activation is TOR-dependent	IRE/NPH/PI dependent/S6 Kinase	PPC
Cre12.g558300.v5.5	-0.012222969092559				GmPK6/AtMRK1 Family	PPC
Cre06.g278265.v5.5	-0.012045943763679				Unknown Function Kinase	PPC transcriptional regulator
Cre03.g173165.v5.5	-0.012043120975247				TRAF	transcriptional regulator
Cre06.g262800.v5.5	-0.0115004632112				PHD	transcriptional regulator
Cre16.g666300.v5.5	-0.010748454059189				CTR1/EDR1 Kinase	PPC
Cre09.g395658.v5.5	-0.010360815447916				CDC2 Like Kinase Family	PPC
Cre12.g554051.v5.5	-0.010351788575901				Leucine Rich Repeat Kinase XI & XII	PPC transcriptional regulator
Cre03.g212641.v5.5	-0.0102192552022				TAZ	transcriptional regulator
Cre17.g713750.v5.5	-0.010091968072999		Serine/threonine protein kinase	Serine/Threonine protein kinase. Previously annotated as STPK16	Leucine Rich Repeat Kinase XI & XII	PPC
Cre17.g715700.v5.5	-0.009973716207746		Phosphoprotein phosphatase 2C	Phosphoprotein phosphatase 2C. Previously annotated as PP2CS	Leucine Rich Repeat Kinase XI & XII	PPC
Cre02.g074850.v5.5	-0.009973296925905				Unknown Function Kinase	PPC
Cre10.g425350.v5.5	-0.009916285411942				Legume Lectin Domain Kinase	PPC transcription factor
Cre02.g108350.v5.5	-0.00974188645036				MYB->MYB	transcriptional regulator
Cre03.g174200.v5.5	-0.009720532250253				TRAF	transcriptional regulator
Cre02.g111200.v5.5	-0.009568225446873				MYB->MYB-related	transcription factor
Cre06.g253250.v5.5	-0.009446911674628				MADS->MADS-M-type	transcription factor
Cre16.g674291.v5.5	-0.009368281300386				Unknown Function Kinase	PPC
Cre02.g141966.v5.5	-0.009342031776893				Other Protein Kinase	PPC transcription factor
Cre09.g410450.v5.5	-0.009276865481252				GARP->GARP-G2-like	transcription factor
Cre10.g423200.v5.5	-0.009236112009984				GmPK6/AtMRK1 Family	PPC
Cre03.g146067.v5.5	-0.009201916377806				Receptor Like Cytoplasmic Kinase VII	PPC
Cre03.g169100.v5.5	-0.009160690696399				Calcium Dependent Protein Kinase	PPC transcription factor
Cre13.g566200.v5.5	-0.00910756841831				C3H	transcription factor
Cre16.g684450.v5.5	-0.009016392387422				SNF1 Related Protein Kinase (SnRK)	PPC
Cre11.g481104.v5.5	-0.008988630319524				Calcium Dependent Protein Kinase	PPC
Cre03.g187300.v5.5	-0.008964876052803				Unknown Function Kinase	PPC
Cre04.g228800.v5.5	-0.008948543205183				Unknown Function Kinase	PPC
Cre12.g527000.v5.5	-0.008947861378061				Calcium Dependent Protein Kinase	PPC

Cre01.g040150.v5.5	-0.008831965899736			WNK like kinase - with no lysine kinase	PPC transcription factor
Cre12.g489000.v5.5	-0.008797969618033			bZIP	PPC transcription factor
Cre02.g113600.v5.5	-0.008742108768305			Unknown Function Kinase	PPC
Cre02.g108650.v5.5	-0.008653709081121			GmPK6/AtMRK1 Family	PPC transcription factor
Cre08.g378800.v5.5	-0.008640000779984			C2C2->C2C2-GATA	PPC transcription factor
Cre07.g349000.v5.5	-0.00850084482242			GmPK6/AtMRK1 Family	PPC
Cre16.g674403.v5.5	-0.008475010356836			Unknown Function Kinase	PPC transcriptional regulator
Cre03.g167850.v5.5	-0.008442356799696			TRAF	PPC transcriptional regulator
Cre05.g236216.v5.5	-0.008419516724107			CTR1/EDR1 Kinase	PPC
Cre02.g111550.v5.5	-0.008347964848881			GmPK6/AtMRK1 Family	PPC
Cre01.g016570.v5.5	-0.008320275341583			MAP3K	PPC transcriptional regulator
Cre02.g096700.v5.5	-0.00830655193286			TRAF	PPC transcriptional regulator
Cre09.g391245.v5.5	-0.008282322230684			APG1 Like Kinase	PPC
Cre07.g314500.v5.5	-0.008180370305148			GmPK6/AtMRK1 Family	PPC
Cre09.g388875.v5.5	-0.008146633058495			GmPK6/AtMRK1 Family	PPC transcriptional regulator
Cre17.g46247.v5.5	-0.008110023975363			SET	transcriptional regulator
Cre09.g407373.v5.5	-0.008068967983454			GNAT Leucine Rich Repeat Kinase VII	transcriptional regulator PPC
Cre13.g575300.v5.5	-0.008025247910782				PPC
				Putative tyrosine kinase identified through multi-level HMM library for kinase classification (PMID: 17557329)	
Cre06.g303150.v5.5	-0.007952757912858	PTK4	Putative tyrosine kinase	Other Protein Kinase	PPC transcription factor
Cre03.g198800.v5.5	-0.007942807877213			MYB->MYB-related	PPC transcription factor
Cre17.g719450.v5.5	-0.007915148855948			Unknown Function Kinase	PPC transcription factor
Cre07.g335150.v5.5	-0.007864031689273			SBP	transcriptional regulator
Cre13.g5712150.v5.5	-0.007860617988991			GNAT	transcriptional regulator
Cre01.g046237.v5.5	-0.007853050587333			SNF2	transcriptional regulator
Cre12.g514250.v5.5	-0.007778703987475			ARID	transcriptional regulator
Cre02.g113350.v5.5	-0.007744675509264			GmPK6/AtMRK1 Family	PPC
Cre09.g390171.v5.5	-0.007732186954417			GmPK6/AtMRK1 Family	PPC
Cre02.g098600.v5.5	-0.007723510774605			GmPK6/AtMRK1 Family	PPC transcriptional regulator
Cre14.g611200.v5.5	-0.007608718306512			mTERF Leucine Rich Repeat Kinase XI & XII	PPC
Cre11.g467586.v5.5	-0.007564301791407			GmPK6/AtMRK1 Family	PPC
Cre16.g687800.v5.5	-0.007549492200267			GmPK6/AtMRK1 Family	PPC
Cre10.g425000.v5.5	-0.007546712637035			GmPK6/AtMRK1 Family	PPC
				MAPKKK4; MAP (Mitogen-Activated) Kinase Kinase Kinase Homolog 4; MEK Kinase 4; MAP3K4	
Cre01.g030600.v5.5	-0.007492223112921	MAPKKK4	Mitogen-Activated Protein Kinase Kinase Kinase	GmPK6/AtMRK1 Family	PPC
Cre02.g117813.v5.5	-0.007485562450212			GmPK6/AtMRK1 Family	PPC transcriptional regulator
Cre06.g249700.v5.5	-0.00744459001675			mTERF	transcriptional regulator
Cre09.g393650.v5.5	-0.00744205763404			GmPK6/AtMRK1 Family	PPC
Cre16.g687400.v5.5	-0.007439836681871			MAPK Family	PPC transcription factor
Cre11.g467581.v5.5	-0.007403829468578			C2C2->C2C2-GATA Calcium Dependent Protein Kinase	PPC
Cre03.g144484.v5.5	-0.007401156645307			CTR1/EDR1 Kinase	PPC
Cre02.g102650.v5.5	-0.007344295373998			CTR1/EDR1 Kinase	PPC
Cre12.g551250.v5.5	-0.007336626358299			CDC2 Like Kinase Family	PPC
Cre01.g014500.v5.5	-0.007326156010086			GmPK6/AtMRK1 Family	PPC transcriptional regulator
Cre10.g446850.v5.5	-0.007270314828662			Jumonji	transcriptional regulator
Cre12.g516600.v5.5	-0.007259396365441		Serine/threonine protein kinase	S Domain Kinase (Type 2)	PPC transcriptional regulator
Cre03.g189650.v5.5	-0.007242073207127			TAZ	transcriptional regulator
Cre09.g387023.v5.5	-0.007207878577996			CTR1/EDR1 Kinase	PPC transcription factor
Cre01.g012200.v5.5	-0.007189387202965			SBP	transcription factor
Cre02.g145500.v5.5	-0.007182366018145	PTK24	Protein tyrosine kinase	Putative protein tyrosine kinase identified through	GmPK6/AtMRK1 Family PPC

Accession	Score	Gene	Protein	Family	Function
Cre11.g480950.v5.5	-0.007126399120634			HMG	transcriptional regulator
Cre05.g236400.v5.5	-0.007111411456278			GNAT	transcriptional regulator
					multi-level HMM library for kinase classification (PMID: 17557329)
					Mixed lineage protein kinase with a GAF domain, which is a domain present in phytochrome and CGMP-specific phosphodiesterases. A serine/threonine protein kinase which has a GAF domain, a potential chromophore binding domain.
Cre10.g436100.v5.5	-0.007086173398982	MLK1	Mixed lineage protein kinase	CTR1/EDR1 Kinase	PPC transcription factor
Cre03.g176651.v5.5	-0.007036590984859			MYB->MYB-related	PPC transcriptional regulator
Cre03.g169500.v5.5	-0.006968449818209			CDC2 Like Kinase Family	PPC transcriptional regulator
Cre12.g551201.v5.5	-0.006958075665117			GNAT	PPC
Cre14.g630750.v5.5	-0.006936886965706	MAPKKK10	Mitogen-Activated Protein Kinase Kinase	GmPK6/ATMRK1 Family	PPC transcription factor
Cre12.g530000.v5.5	-0.006935350214384			MAPK Family	PPC
Cre03.g145407.v5.5	-0.006879727167364			C3H	PPC
Cre04.g230438.v5.5	-0.006876403391352		Serine/threonine protein kinase	GmPK6/ATMRK1 Family	PPC
Cre04.g211600.v5.5	-0.006824962617891			SNF1 Related Protein Kinase (SnRK)	PPC
					Serine/threonine protein kinase. Previously annotated as SRR25

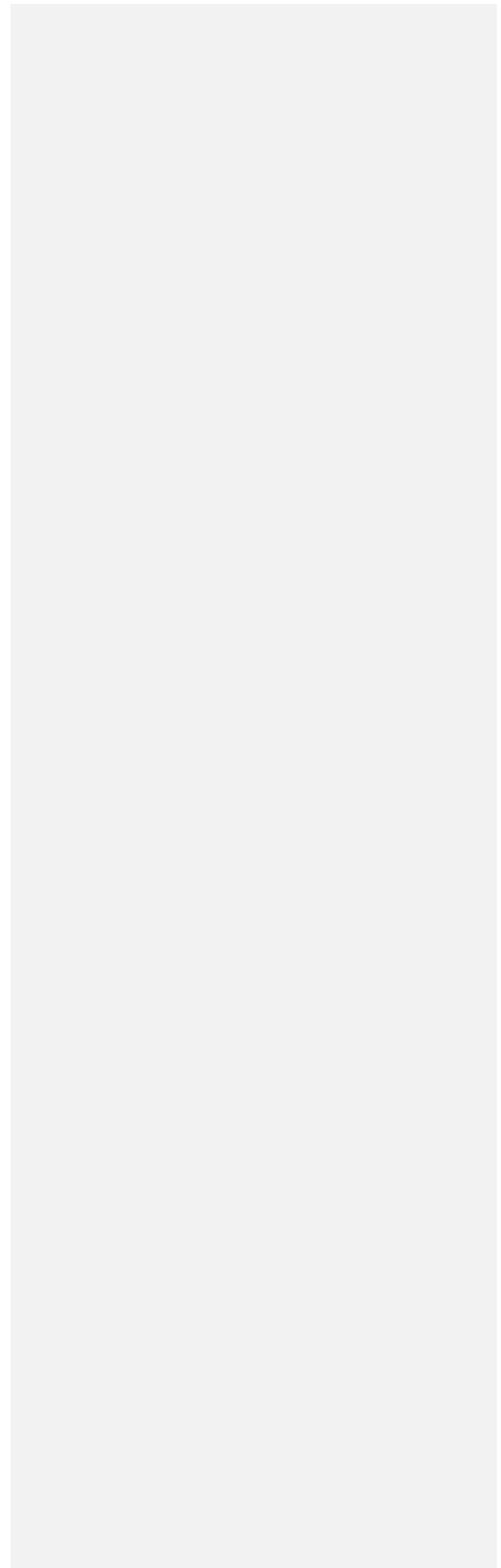


Table S14. The 100 regulatory genes (Protein Kinase (PPC), transcriptional regulators and transcription factors from the iTAK database) contributing the most to the exponential state including annotation.

G_i sorted identifier	G_i	geneName	define	description	name	type
Cre06.g268600.v5.5	0.039908483445275	NAB1	Nucleic acid binding protein	Nucleic acid binding protein; RNA binding protein involved in the light-regulated differential expression of the light-harvesting antenna of <i>Chlamydomonas reinhardtii</i> [PMID: 16284312, Genbank entry AY157846]. Studied by Wobbe et al. 2009 [PMID: 19666611]	CSD	transcription factor
Cre08.g372550.v5.5	0.035563502305416	CDK81	Plant specific cyclin dependent kinase	Plant specific cyclin dependent kinase, CDKB subfamily, PSTLRE motif, mitotic regulator. Putative function in G2/M	CDC2 Like Kinase Family	PPC
Cre11.g482700.v5.5	0.033612210891776				HMG	transcriptional regulator
Cre02.g101850.v5.5	0.031070869487763				GNAT	transcriptional regulator
Cre06.g249050.v5.5	0.030183593199477				MYB->MYB-related	transcription factor
Cre07.g355250.v5.5	0.028273139105171	WEE1	CDK inhibitory kinase	WEE1 kinase, CDK inhibitory kinase, dual specificity for serine/threonine and tyrosine. Putative function in G2/M High mobility group protein, histone-like transcription factor. Has homology to DNA polymerase epsilon subunit	Unknown Function Kinase	PPC
Cre03.g193900.v5.5	0.027693079946812		High mobility group protein, histone-like transcription factor		HMG	transcriptional regulator
Cre09.g404351.v5.5	0.026791782506516				SET	transcriptional regulator
Cre14.g623800.v5.5	0.026162507109669				GNAT	transcriptional regulator
Cre02.g084550.v5.5	0.025910433782552				GNAT	transcriptional regulator
Cre16.g664000.v5.5	0.025337358268807				SET	transcriptional regulator
Cre09.g386350.v5.5	0.025234838850502				IWS1	transcriptional regulator
Cre09.g392300.v5.5	0.024804574025502				GNAT	transcriptional regulator
Cre08.g383150.v5.5	0.024464248392691	NAT5	N-acetyl-transferase-like protein	Contains similarity to N-acetyl-transferase 5 that catalyzes the first step of melatonin biosynthesis	GNAT	transcriptional regulator
Cre11.g475100.v5.5	0.023966496934803				GNAT	transcriptional regulator
Cre17.g710000.v5.5	0.022629722541365				GmPK6/AtMRK1 Family	PPC
Cre12.g560200.v5.5	0.022216320224439	NAT2	Glucosamine 6-phosphate N-acetyltransferase	Glucosamine 6-phosphate N-acetyltransferase. N-acetyltransferase related to GCN5, a histone acetyltransferase	GNAT	transcriptional regulator
Cre16.g649700.v5.5	0.022037439373744				SET	transcriptional regulator
Cre06.g304050.v5.5	0.022034103795788				IRE/NPH/PI dependent/S6 Kinase	PPC
Cre11.g467659.v5.5	0.021979422748045				MED6	transcriptional regulator
Cre12.g541777.v5.5	0.021190311122856				SET	transcriptional regulator
Cre16.g679893.v5.5	0.020610979058654				GmPK6/AtMRK1 Family	PPC
Cre17.g696300.v5.5	0.020596959512559				C2H2	transcription factor
Cre13.g574300.v5.5	0.020484673312893				GmPK6/AtMRK1 Family	PPC
Cre03.g185950.v5.5	0.020429852944815				C2H2	transcription factor
Cre10.g446450.v5.5	0.020376339125738				Others	transcriptional regulator
Cre01.g062902.v5.5	0.019477568346997				MED7	transcriptional regulator
Cre06.g296200.v5.5	0.018912691095976				Calcium Dependent Protein Kinase	PPC
Cre17.g745447.v5.5	0.018304189223532	MAPK4	Mitogen-Activated Protein Kinase	Hypothetical Mitogen-Activated Protein Kinase Homolog 4	MAPK Family	PPC
Cre13.g583150.v5.5	0.018079120923344				TRAF	transcriptional regulator

Cre09.g399552.v5.5	0.017540041480506	LCR1	Low-CO2 response regulator, Myb-like transcription factor	Myb-DNA binding transcriptional factor induced under low CO2 stress condition [PMID: 15155888]; regulates CO2-responsive genes, Cah1, Lci1, and Lci6; regulated by CCM1 [PMID: 15235119]	MYB->MYB-related	transcription factor
Cre01.g035150.v5.5	0.017300174655929				C3H	transcription factor
Cre02.g141886.v5.5	0.017039048729257				Receptor Like Cytoplasmic Kinase VI	PPC
Cre06.g281000.v5.5	0.016808522946978				SET	transcriptional regulator
Cre01.g036900.v5.5	0.016554583618468				CTR1/EDR1 Kinase	PPC
Cre13.g572600.v5.5	0.015685849133613		SET	transcriptional regulator		
Cre04.g220700.v5.5	0.015573876084009	ALK2	Aurora-like kinase	Possible role in mitotic regulation. Note that the ALK1 model (originally called CALK) and several other kinase models in the genome are much weaker hits to the aurora family.	Unknown Function Kinase	PPC
Cre10.g429880.v5.5	0.015236286129495				ARID	transcriptional regulator
Cre16.g653258.v5.5	0.014480545791998				TRAF	transcriptional regulator
Cre11.g479800.v5.5	0.0144310459798				TRAF	transcriptional regulator
Cre03.g151050.v5.5	0.014415456539851				TRAF	transcriptional regulator
Cre07.g346550.v5.5	0.014157329633439				GmpK6/AtMRK1 Family	PPC
Cre09.g386753.v5.5	0.013175490225302				S1Fa-like IRE/NPH/PI dependent/S6 Kinase	transcription factor
Cre11.g467568.v5.5	0.013165977452692				TRAF	transcriptional regulator
Cre03.g174150.v5.5	0.012783797897047				C3H	transcription factor
Cre06.g293750.v5.5	0.012525763735153				mTERF	transcriptional regulator
Cre12.g522400.v5.5	0.011160977899072				MYB->MYB	transcription factor
Cre16.g657150.v5.5	0.01101988050037				GNAT	transcriptional regulator
Cre12.g483650.v5.5	0.010985338671687				CDC2 Like Kinase Family	PPC
Cre08.g364450.v5.5	0.010604522469592	NAT1			Peptide alpha-N-acetyltransferase	transcriptional regulator
Cre11.g467577.v5.5	0.010084139266638				MADS->MADS-M-type	transcription factor
Cre12.g514400.v5.5	0.009959907677424		MYB->MYB-related	transcription factor		
Cre03.g184600.v5.5	0.009735486613113	RWP7	RWP-RK transcription factor	Putative RWP-RK domain transcription factor [PMID: 15785851]. The model is partly based on an unpublished cDNA sequence. Member of a family of proteins [PMID: 16720695, 16622701] related to Volvox carteri RegA, which is a putative transcription repressor [PMID: 9895312] containing a SAND domain [PRO00770 SAND; PF01542].	RWP-RK	transcription factor
Cre17.g738600.v5.5	0.009668530174794	RL55	RegA/RlsA-like protein		VARL	transcription factor
Cre03.g152150.v5.5	0.009628239590313			C2H2	transcription factor	
Cre17.g741900.v5.5	0.009523467962478			GmpK6/AtMRK1 Family	PPC	
Cre11.g469400.v5.5	0.00933063889287			Others	transcriptional regulator	
Cre06.g261450.v5.5	0.009177111710038			HMG	transcriptional regulator	
Cre03.g160700.v5.5	0.008641167583391			C2C2->C2C2-GATA	transcription factor	
Cre12.g509000.v5.5	0.008610992303841	MAPK3	Mitogen-Activated Protein Kinase	Mitogen-Activated Protein Kinase Homolog 3; downstream kinase in the canonical MAP kinase pathway	MAPK Family	PPC
Cre02.g083750.v5.5	0.008418137238237				GARP->GARP-G2-like	transcription factor
Cre13.g564100.v5.5	0.008321980401547	PTK2	Putative tyrosine kinase	Putative tyrosine kinase identified through multi-level HMM library for kinase classification [PMID: 17557329]	GmpK6/AtMRK1 Family	PPC
Cre17.g702650.v5.5	0.00816436039123				HMG	transcriptional regulator

Cre07.g329900.v5.5	0.008100937101493		Others	transcriptional regulator
Cre06.g250950.v5.5	0.007465533037693		C3H	transcription factor
Cre09.g414650.v5.5	0.007453161915058		MAPK Family	PPC
Cre24.g755647.v5.5	0.007404580992485		C3H	transcription factor
Cre09.g393728.v5.5	0.007153142101581		SET	transcriptional regulator
Cre13.g580450.v5.5	0.007098461746361		TRAF	transcriptional regulator
Cre14.g614750.v5.5	0.007000082618185		GNAT	transcriptional regulator
Cre01.g009550.v5.5	0.00697787481571		GNAT	transcriptional regulator
Cre10.g441000.v5.5	0.006615330409794		IWS1	transcriptional regulator
Cre16.g668200.v5.5	0.006569799502889		PHD	transcriptional regulator
Cre16.g679781.v5.5	0.006549082382677		SET	transcriptional regulator
			DnaJ-like protein and Myb-like transcription factor; probably nuclear/cytosolic; similar to Chlamy Q6JX09_CHLRE GlsA-related protein and to Volvox GLSA; contains J-domain (pfam00226) at the N-terminus and Myb_DNA-binding-Domain (pfam00249) at the C-termin	
Cre16.g695600.v5.5	0.006065239052822	DNU10	MYB->MYB-related	transcription factor
Cre08.g384900.v5.5	0.006051425181334		CTR1/EDR1 Kinase	PPC
			Serine/Threonine protein kinase. Previously annotated as STPK22	
Cre09.g413200.v5.5	0.00601748891563		CDC2 Like Kinase Family	PPC
			Myb-like DNA binding domain and coiled-coil domain containing transcription factor required for phosphate deficiency-inducible gene expression; nuclear-localized	
Cre12.g495100.v5.5	0.005995003197363	PSR1	GARP->GARP-G2-like	transcription factor
			[AF174480 (mRNA), AF174532 (gene); PMID: 10611385]	
			Putative protein tyrosine kinase identified through multi-level HMM library for kinase classification (PMID: 17557329)	
Cre07.g351800.v5.5	0.005922088588887	PTK12	Leucine Rich Repeat Kinase XI & XII SNF1 Related Protein Kinase (SnRK)	PPC
Cre04.g217943.v5.5	0.005831391164752			PPC
Cre12.g516150.v5.5	0.005604776246164		GNAT	transcriptional regulator
Cre10.g464100.v5.5	0.005570306505474		MAP3K	PPC
Cre12.g552150.v5.5	0.005450527856794		GmPK6/AtMRK1 Family	PPC
Cre03.g152500.v5.5	0.005418958848952		SET	transcriptional regulator
Cre02.g087900.v5.5	0.005389371956976		GmPK6/AtMRK1 Family	PPC
Cre06.g278184.v5.5	0.005262334037598		TRAF	transcriptional regulator
Cre16.g657350.v5.5	0.005211155683758		SNF1 Related Protein Kinase (SnRK)	PPC
			Member of a family of proteins [PMID: 16720695, 16622701] related to Volvox carteri RegA, which is a putative transcription repressor [PMID: 9895312] containing a SAND domain [IPR000770 SAND; PFD1342]	
Cre15.g643700.v5.5	0.004881063623466	RLS6	VARL	transcription factor
Cre02.g114750.v5.5	0.004838103865249		Calcium Dependent Protein Kinase	PPC
Cre10.g461150.v5.5	0.004730929539725		Unknown Function Kinase	PPC
Cre01.g002250.v5.5	0.004729128330598		GNAT	transcriptional regulator
Cre03.g149201.v5.5	0.004690048643646		MYB->MYB	transcription factor
Cre05.g241636.v5.5	0.004628246484063		bHLH	transcription factor
Cre06.g275500.v5.5	0.004571205294254		AP2/ERF->AP2/ERF-ERF	transcription factor
Cre04.g229948.v5.5	0.004508260969292		C3H	transcription factor
Cre06.g264400.v5.5	0.004493653030072		MYB->MYB-related	transcription factor
			RegA/RlsA-like protein	

Cre07.g334250.v5.5 0.004438307594955
Cre13.g581150.v5.5 0.004433757486765
Cre10.g441300.v5.5 0.004411205748618

SET transcriptional regulator
GNAT transcriptional regulator
AP2/ERF->AP2/ERF-AP2 transcription factor

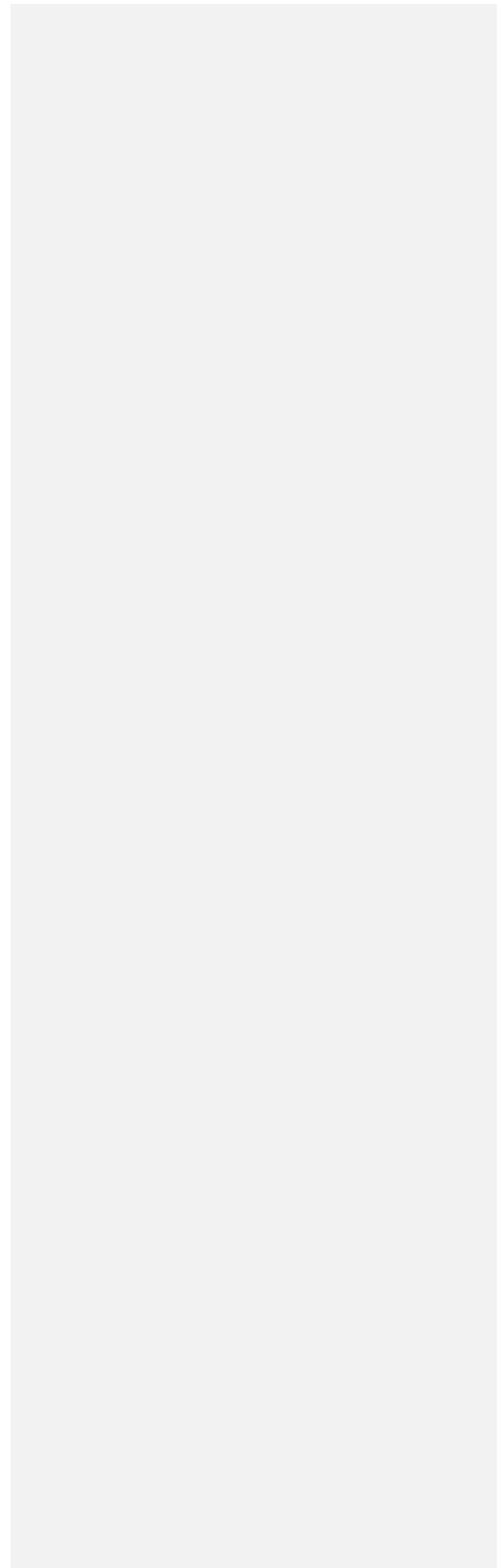


Table S16. The 100 regulatory genes (Protein Kinase (PPC), transcriptional regulators and transcription factors from the iTAK database) contributing the most to the low acetate state including annotation.

G ₂ sorted identifier	G ₂	geneName	define	description	name	type
Cre06.g268600.v5.5	-0.027302269714369	NAB1	Nucleic acid binding protein	Nucleic acid binding protein; RNA binding protein involved in the light-regulated differential expression of the light-harvesting antenna of <i>Chlamydomonas reinhardtii</i> [PMID: 16284312, Genbank entry AY157846]. Studied by Wobbe et al. 2009 [PMID: 19666611]	CSD	transcription factor
Cre09.g413200.v5.5	-0.021046649492915		Serine/threonine protein kinase	Serine/Threonine protein kinase. Previously annotated as STPK22	CDC2 Like Kinase Family GmPK6/AtMRK1 Family	PPC
Cre17.g736250.v5.5	-0.018223227537334					PPC
Cre17.g746547.v5.5	-0.016249335901147				bZIP	transcription factor
Cre12.g534100.v5.5	-0.016193518159343				Others	transcriptional regulator
Cre12.g501600.v5.5	-0.015124413229956				bZIP	transcription factor
Cre01.g036250.v5.5	-0.014328805837334				SNF1 Related Protein Kinase (SnRK)	PPC
Cre02.g141886.v5.5	-0.013957054506091				Receptor Like Cytoplasmic Kinase VI	PPC
Cre09.g391245.v5.5	-0.013424886692029				APG1 Like Kinase	PPC
Cre13.g604350.v5.5	-0.013331687571319				GmPK6/AtMRK1 Family	PPC
Cre01.g036900.v5.5	-0.013235999161154				CTR1/EDR1 Kinase	PPC
Cre12.g514400.v5.5	-0.013135346823895			Chloroplast protein kinase required for LHClI phosphorylation and state transition [PMID: 12624266]. Identified in the eyespot phosphoproteome by Wagner et al. 2008 [PMID: 18065559].	MYB->MYB-related	transcription factor
Cre02.g120250.v5.5	-0.01297102375006		Calcium/calmodulin-dependent protein kinase		GSK3/Shaggy Like Protein Kinase Family	PPC
Cre10.g438850.v5.5	-0.012691686899621				bZIP	transcription factor
Cre17.g696950.v5.5	-0.012505381418891				CTR1/EDR1 Kinase	PPC
Cre13.g574300.v5.5	-0.012405643730999				GmPK6/AtMRK1 Family	PPC
Cre02.g141966.v5.5	-0.012396296290734				Other Protein Kinase	PPC
Cre13.g579650.v5.5	-0.012314850197403				GmPK6/AtMRK1 Family	PPC
Cre09.g407373.v5.5	-0.01225238653361				GNAT	transcriptional regulator
Cre09.g404050.v5.5	-0.01115596269779				GmPK6/AtMRK1 Family	PPC
Cre16.g677382.v5.5	-0.011091748087841				MYB->MYB	transcription factor
Cre14.g628237.v5.5	-0.011020858940682				GmPK6/AtMRK1 Family	PPC
Cre14.g623800.v5.5	-0.010908756141582				GNAT	transcriptional regulator
Cre12.g521150.v5.5	-0.010830271484854	CGL19	Predicted protein	Conserved expressed protein with Dof type zinc finger	C2C2->C2C2-Dof	transcription factor
Cre01.g064362.v5.5	-0.010746413189694				GmPK6/AtMRK1 Family	PPC
Cre10.g446450.v5.5	-0.010596984000128				Others	transcriptional regulator
Cre02.g102650.v5.5	-0.010469666812559				CTR1/EDR1 Kinase	PPC
Cre17.g707650.v5.5	-0.010402589999402				SNF1 Related Protein Kinase (SnRK)	PPC
Cre08.g368700.v5.5	-0.010319015633982				SET	transcriptional regulator
Cre01.g030600.v5.5	-0.010313735045169	MAPKKK4	Mitogen-Activated Protein Kinase Kinase	MAPKKK4; MAP (Mitogen-Activated) Kinase Kinase Homolog 4; MEK Kinase 4; MAP3K4	GmPK6/AtMRK1 Family	PPC
Cre13.g603600.v5.5	-0.010292462091995				GmPK6/AtMRK1 Family	PPC
Cre14.g633789.v5.5	-0.010223854894053				MYB->MYB-related	transcription factor
Cre04.g219600.v5.5	-0.010223435035738				TRAF	transcriptional regulator
Cre01.g009500.v5.5	-0.010168612017048				Calcium Dependent Protein Kinase	PPC
Cre06.g293300.v5.5	-0.009941098217323				GmPK6/AtMRK1 Family	PPC
Cre09.g399552.v5.5	-0.009689302228528	LCR1	Low-CO2 response regulator, Myb-like transcription factor	Myb-DNA binding transcriptional factor induced under low CO2 stress condition [PMID: 15155888]; regulates CO2-responsive genes, Cah1, Lcl1, and Lcl6; regulated by CCM1 [PMID: 15235119]	MYB->MYB-related	transcription factor

Cre02.g106650.v5.5	-0.009644378292513			Calcium Dependent Protein Kinase	PPC
Cre16.g674403.v5.5	-0.009387021995572			Unknown Function Kinase	PPC
Cre16.g684400.v5.5	-0.009171921358055			CDC2 Like Kinase Family	PPC
Cre17.g719450.v5.5	-0.009153569432369			Unknown Function Kinase	PPC transcriptional regulator
Cre02.g094150.v5.5	-0.009091012961225			Pseudo ARR-B	transcription factor
Cre09.g411950.v5.5	-0.008985472638715			MYB->MYB-related	transcription factor
Cre06.g278159.v5.5	-0.008893021565106	CON1	B-box zinc finger protein; contains CONSTANS-type zinc finger, conserved in <i>Ostreococcus</i> and involved in circadian rhythms. Previously annotated as CGLD18 for being conserved in the Green lineage and diatoms, as well as CO for CONSTANS by Serrano et al.	C2C2->C2C2-CO-like	transcription factor
Cre06.g275350.v5.5	-0.00888302160813			MYB->MYB-related	transcription factor transcriptional regulator
Cre16.g649700.v5.5	-0.008836324387629			SET	transcriptional regulator
Cre07.g346550.v5.5	-0.008814478568924			GmPK6/AtMRK1 Family	PPC
Cre06.g291500.v5.5	-0.008785813463926	RWP6	Putative RWP-RK domain transcription factor, however the domain is non-canonical in this gene (NWP5RK). The model is based on an unpublished cDNA sequence.	RWP-RK GmPK6/AtMRK1 Family	transcription factor
Cre14.g632750.v5.5	-0.008596876626975				PPC transcriptional regulator
Cre04.g212100.v5.5	-0.008511059293967			TRAF	transcriptional regulator
Cre06.g253200.v5.5	-0.008508846081655		Protein tyrosine kinase	GmPK6/AtMRK1 Family	PPC
Cre10.g418900.v5.5	-0.008414450733		Protein tyrosine kinase. Previously annotated as PKY1	Calcium Dependent Protein Kinase	PPC
Cre03.g185950.v5.5	-0.008348510621441			C2H2	transcription factor
Cre02.g108350.v5.5	-0.0083204398687			MYB->MYB	transcription factor
Cre12.g535100.v5.5	-0.008220041356359			Unknown Function Kinase	PPC
Cre07.g334950.v5.5	-0.008218586476192			GmPK6/AtMRK1 Family	PPC
Cre17.g741900.v5.5	-0.008126861634032			GmPK6/AtMRK1 Family	PPC
Cre17.g717100.v5.5	-0.007981998690485			GmPK6/AtMRK1 Family	PPC
Cre03.g168150.v5.5	-0.007935450648337			Ankyrin Repeat Domain Kinase	PPC
Cre13.g568050.v5.5	-0.007878854692396			SNF1 Related Protein Kinase (SnRK)	PPC
Cre09.g390134.v5.5	-0.007863637406822			GmPK6/AtMRK1 Family	PPC transcriptional regulator
Cre03.g212641.v5.5	-0.007818519350491			TAZ	transcriptional regulator
Cre06.g275500.v5.5	-0.00765115277588			AP2/ERF->AP2/ERF-ERE	transcription factor
Cre04.g223350.v5.5	-0.007638105844873			IRE/NPH/PI dependent/56 Kinase	PPC
Cre06.g304050.v5.5	-0.007612500089536			IRE/NPH/PI dependent/56 Kinase	PPC
Cre04.g228800.v5.5	-0.007542158896205			Unknown Function Kinase	PPC
Cre07.g345350.v5.5	-0.007472833742064			MYB->MYB	transcription factor
Cre03.g157200.v5.5	-0.007368151766934			GmPK6/AtMRK1 Family	PPC
Cre04.g230438.v5.5	-0.007364921018793	Serine/threonine protein kinase	Serine/threonine protein kinase. Previously annotated as SRR25	GmPK6/AtMRK1 Family	PPC
Cre07.g314500.v5.5	-0.007295585184967			GmPK6/AtMRK1 Family	PPC
Cre06.g278265.v5.5	-0.00723095279127			Unknown Function Kinase	PPC
Cre02.g141946.v5.5	-0.007212205384675			GmPK6/AtMRK1 Family	PPC
Cre16.g679893.v5.5	-0.007101367987538			GmPK6/AtMRK1 Family	PPC
Cre16.g659400.v5.5	-0.007011279564238			GmPK6/AtMRK1 Family	PPC
Cre17.g710000.v5.5	-0.006903614474124			GmPK6/AtMRK1 Family	PPC
Cre02.g096300.v5.5	-0.006888842365639	CCM1	Master regulator of CO2-responsive genes including low-CO2 inducible genes necessary for carbon-concentrating mechanism; CCM1-A and CCM1-B, are generated by an alternative splicing between 3rd and 4th exons, CCM1B=CIA5=698aa, CCM1A=699aa, Zn-finger domain	C2H2	transcription factor
Cre08.g381950.v5.5	-0.006883370556937			Unknown Function Kinase	PPC
Cre08.g378800.v5.5	-0.006817237538094			C2C2->C2C2-GATA	transcription factor

Cre02.g107800.v5.5	-0.006791650764685	CNK9	NimA-related protein kinase	Contains a NIMA (never-in-mitosis) kinase domain and a C-terminal region with no database similarity except in Volvox	Unknown Function Kinase	PPC
Cre04.g211600.v5.5	-0.006751758501643				SNF1 Related Protein Kinase (SnRK)	PPC
Cre02.g074150.v5.5	-0.006710321246721	COP5	Chlamyopsin, light-gated proton channel rhodopsin	Chlamyopsin 5, sensory rhodopsin with histidine kinase domain; has histidine kinase, response regulator receiver domains like a two-component hybrid sensor and regulator [PMID: 15143209]	Others	transcriptional regulator
Cre10.g462350.v5.5	-0.006671127727761				GmPK6/ATMRK1 Family	PPC
Cre17.g700166.v5.5	-0.006594659331304				WNK like kinase - with no lysine kinase	PPC
Cre06.g296200.v5.5	-0.00658872868935				Calcium Dependent Protein Kinase	PPC transcriptional regulator
Cre06.g278200.v5.5	-0.006575462559263				Others	transcriptional regulator
Cre01.g001200.v5.5	-0.006572241676701				GmPK6/ATMRK1 Family	PPC transcriptional regulator
Cre16.g664000.v5.5	-0.00652833780901				SET	transcriptional regulator
Cre12.g529550.v5.5	-0.006344181846351	ALK1	Aurora-like kinase	Aurora-Like Kinase; formerly known as CALK (Chlamydomonas Aurora-Like Kinase [g:9716372; PMID: 11121779]. Serine/threonine protein kinase; regulates chromosome segregation and cytokinesis in mammals. Previously annotated as CALK1	Unknown Function Kinase	PPC
Cre10.g451450.v5.5	-0.006327485750599				GmPK6/ATMRK1 Family	PPC
Cre03.g146067.v5.5	-0.006297562013251				Receptor Like Cytoplasmic Kinase VII	PPC
Cre12.g527000.v5.5	-0.006291010292426				Calcium Dependent Protein Kinase	PPC
Cre01.g031300.v5.5	-0.006276252802679				Calcium Dependent Protein Kinase	PPC
Cre02.g083750.v5.5	-0.006264831531365				GARP->GARP-G2-like	transcription factor
Cre09.g395658.v5.5	-0.006234290816226				CDC2 Like Kinase Family	PPC
Cre06.g278230.v5.5	-0.006211933426252				SNF1 Related Protein Kinase (SnRK)	PPC
Cre02.g099550.v5.5	-0.006141757577895				CTR1/EDR1 Kinase	PPC
Cre03.g181700.v5.5	-0.006116544444264				SNF1 Related Protein Kinase (SnRK)	PPC
Cre01.g025050.v5.5	-0.00607780258381				C2C2->C2C2-GATA	transcription factor transcriptional regulator
Cre13.g571200.v5.5	-0.006046128199868				Others	transcriptional regulator
Cre19.g750597.v5.5	-0.006025743752457				Calcium Dependent Protein Kinase	PPC
Cre09.g402478.v5.5	-0.006015473173604				GmPK6/ATMRK1 Family	PPC

Table S17. The 100 regulatory genes (Protein Kinase (PPC), transcriptional regulators and transcription factors from the iTAK database) contributing the most to the high acetate state including annotation.

G ₂ sorted identifier	G ₂	geneName	define	description	name	type
Cre04.g220700.v5.5	0.04369856428454	ALK2	Aurora-like kinase	Possible role in mitotic regulation. Note that the ALK1 model (originally called CALK) and several other kinase models in the genome are much weaker hits to the aurora family.	Unknown Function Kinase	PPC
Cre17.g735550.v5.5	0.038142448918727				MAP3K	PPC
Cre17.g742250.v5.5	0.037889614494085	CDK2	Cyclin dependent kinase	Cyclin dependent kinase; Chlamydomonas specific subfamily; AASTLRE motif. Novel CDK subfamily. Also identified from nitrogen starvation experiments as nitrogen-controlled-gene NCG9 [PMID: 11469597]	CDC2 Like Kinase Family Kinase XI & XII	PPC
Cre11.g467586.v5.5	0.036887593916565				Unknown Function Kinase	PPC
Cre12.g537400.v5.5	0.03366555387022				MYB->MYB	transcription factor
Cre12.g522400.v5.5	0.032256067453098					
Cre02.g075350.v5.5	0.03167216753854	CNK1	NimA-related protein kinase	NimA (never-in-mitosis) related kinase homolog 1 [gi:34334391, PMID: 15068267]	Unknown Function Kinase	PPC
Cre16.g666300.v5.5	0.031519331060252				CTR1/EDR1 Kinase	PPC
Cre08.g372550.v5.5	0.031133415301622	CDKB1	Plant specific cyclin dependent kinase	Plant specific cyclin dependent kinase; CDKB subfamily; PSTLRE motif; mitotic regulator. Putative function in G2/M	CDC2 Like Kinase Family	PPC
Cre17.g705950.v5.5	0.031059150316697				GNAT	transcriptional regulator
Cre03.g187300.v5.5	0.030935825910406				Unknown Function Kinase	PPC
Cre13.g572600.v5.5	0.030570220382922				SET	transcriptional regulator
Cre12.g498650.v5.5	0.029003464255077	ALK3	Aurora-like kinase	Aurora-like kinase	Unknown Function Kinase	PPC
Cre03.g169100.v5.5	0.028742136016912				Calcium Dependent Protein Kinase	PPC
Cre03.g182700.v5.5	0.028052873091894				Others	transcriptional regulator
Cre11.g482700.v5.5	0.028038098173913				HMG	transcriptional regulator
Cre03.g199050.v5.5	0.02800482677449				IRE/NPH/PI dependent/S6 Kinase	PPC
Cre17.g745447.v5.5	0.02751613604963	MAPK4	Mitogen-Activated Protein Kinase	Hypothetical Mitogen-Activated Protein Kinase Homolog 4	MAPK Family	PPC
Cre02.g087900.v5.5	0.027124369689123				GmpPK6/AtMRK1 Family	PPC
Cre17.g713750.v5.5	0.027024657578258		Serine/threonine protein kinase	Serine/threonine protein kinase. Previously annotated as STPK16	Leucine Rich Repeat Kinase XI & XII	PPC
Cre12.g489000.v5.5	0.026820573804038				bZIP	transcription factor
Cre09.g404351.v5.5	0.025028037620979				SET	transcriptional regulator
Cre13.g564100.v5.5	0.024892825207606	PTK2	Putative tyrosine kinase	Putative tyrosine kinase identified through multi-level HMM library for kinase classification [PMID: 17557329]	GmpPK6/AtMRK1 Family	PPC
Cre03.g144747.v5.5	0.024128903679894				MYB->MYB	transcription factor
Cre01.g040150.v5.5	0.023806999139333				WNK like kinase - with no lysine kinase	PPC
Cre03.g193900.v5.5	0.022721087924103		High mobility group protein, histone-like transcription factor	High mobility group protein, histone-like transcription factor. Has homology to DNA polymerase epsilon subunit	HMG	transcriptional regulator
Cre07.g355250.v5.5	0.022551713493427	WEE1	CDK inhibitory kinase	WEE1 kinase, CDK inhibitory kinase, dual specificity for serine/threonine and	Unknown Function Kinase	PPC

			tyrosine. Putative function in G2/M		
Cre06.g249050.v5.5	0.022478731610186			MYB->MYB-related	transcription factor
Cre10.g464100.v5.5	0.022245176210763			MAP3K	PPC
Cre08.g361400.v5.5	0.021409446323135			CPP	transcription factor
Cre08.g384250.v5.5	0.020226886646373			SNF1 Related Protein Kinase (SnRK)	PPC
Cre09.g392300.v5.5	0.01986259129437			GNAT	transcriptional regulator
Cre11.g475100.v5.5	0.019194016407485			GNAT	transcriptional regulator
Cre11.g467585.v5.5	0.018165527752851			Unknown Function Kinase	PPC
Cre01.g023100.v5.5	0.018017488906327			AP2/ERF->AP2/ERF-ERF	transcription factor
Cre03.g197100.v5.5	0.017657577665787			MYB->MYB	transcription factor
			Putative protein tyrosine kinase identified through multi-level HMM library for kinase classification (PMID: 17557329)		
Cre07.g351800.v5.5	0.016934310833512	PTK12	Protein tyrosine kinase	Leucine Rich Repeat Kinase XI & XII	PPC
Cre09.g393728.v5.5	0.016375168970236			SET	transcriptional regulator
Cre10.g460700.v5.5	0.016083358935205			Phosphoenolpyruvate Carboxylase Kinase	PPC
Cre06.g261450.v5.5	0.015962678575517			HMG	transcriptional regulator
			Tubby-like protein 2. Transcript upregulated during flagellar regeneration [PMID: 15738400].		
Cre16.g667450.v5.5	0.01558522033987	TLP2	Tubby-like protein	TUB	transcription factor
Cre06.g283200.v5.5	0.015324395523501			SET	transcriptional regulator
Cre17.g746247.v5.5	0.015232020701777			SET	transcriptional regulator
Cre02.g117813.v5.5	0.015203078587366			GmPK6/AtMRK1 Family	PPC
			DnaJ-like protein and Myb-like transcription factor; probably nuclear/cytosolic; similar to Chlamy Q6JX09_CHLRE GlsA-related protein and to Volvox GLSA; contains J-domain (pfam00226) at the N-terminus and Myb_DNA-binding-Domain (pfam00249) at the C-termin		
Cre16.g695600.v5.5	0.014654984163563	DNJ10	DnaJ-like protein and Myb-like transcription factor	MYB->MYB-related	transcription factor
Cre04.g224600.v5.5	0.014629159987299			bHLH	transcription factor
Cre14.g623926.v5.5	0.01446039477115			GmPK6/AtMRK1 Family	PPC
Cre05.g242600.v5.5	0.01415835584217			C2C2->C2C-GATA	transcription factor
Cre11.g467526.v5.5	0.013719307845917			GNAT	transcriptional regulator
Cre16.g657150.v5.5	0.013555133173296			GNAT	transcriptional regulator
Cre12.g503450.v5.5	0.013421546206617			SET	transcriptional regulator
Cre09.g396065.v5.5	0.01341461110065	ALK5	Aurora-like kinase	Unknown Function Kinase	PPC
Cre04.g221900.v5.5	0.013150257227062			TRAF	transcriptional regulator
Cre17.g702650.v5.5	0.013073394790848			HMG	transcriptional regulator
			Putative RWP-RK domain transcription factor [PMID: 15785851]; model is very tentative		
Cre01.g004600.v5.5	0.0129389265082	RWP12	RWP-RK transcription factor	RWP-RK	transcription factor
Cre09.g408051.v5.5	0.012931101922438			mTERF	transcriptional regulator
Cre16.g694550.v5.5	0.012930777767894			CTR1/EDR1 Kinase	PPC
Cre06.g275450.v5.5	0.012562050108774			Leucine Rich Repeat Kinase XI & XII	PPC
Cre14.g614400.v5.5	0.012520823209283			SNF2	transcriptional regulator
Cre01.g009550.v5.5	0.01251539694958			GNAT	transcriptional regulator
			Mitogen-activated protein kinase 1 (gi:32130552); Long Flagella 4 (MOK homolog). Characterized by Berman et al. 2003 [PMID: 12842015]. Previously annotated as LF4		
Cre13.g582650.v5.5	0.012426311340379	LF4	Mitogen-activated protein kinase, Long-flagella mutant LF4 protein	CDC2 Like Kinase Family	PPC
Cre04.g231124.v5.5	0.012339484381277			C3H	transcription factor

Cre09.g413050.v5.5	0.012157585620051			bZIP	transcription factor
Cre03.g174200.v5.5	0.012132002166181			TRAF	transcriptional regulator
Cre16.g668200.v5.5	0.011942779577514			PHD Leucine Rich Repeat Kinase XI & XII	transcriptional regulator PPC
Cre12.g554051.v5.5	0.011837541293272			PHD Unknown Function Kinase	transcriptional regulator PPC
Cre06.g262800.v5.5	0.011797399692414			CDC2 Like Kinase Family	PPC
Cre06.g266150.v5.5	0.01176600192014			CSD IRE/NPH/PI dependent/S6 Kinase	transcription factor PPC
Cre13.g575650.v5.5	0.011682514006965			GmPK6/AtMRK1 Family	PPC
Cre02.g078831.v5.5	0.011551034764689			NF-Y-Y-NF-YB	transcription factor
Cre06.g267650.v5.5	0.011346126996628			Others	transcriptional regulator
Cre13.g574350.v5.5	0.011308614054252			C3H	transcription factor
Cre07.g341800.v5.5	0.011196114543812			AP2/ERF->AP2/ERF-ERF SNF1 Related Protein Kinase (SnRK)	transcription factor PPC
Cre10.g424350.v5.5	0.011176784085381			GNAT	transcriptional regulator
Cre06.g293750.v5.5	0.011149197368497			SET	transcriptional regulator
Cre08.g385350.v5.5	0.010933488967516			Serine/threonine protein kinase. Previously annotated as STPK2	
Cre01.g054750.v5.5	0.010823019438999			Phosphoenolpyruvate Carboxylase Kinase	PPC
Cre07.g351850.v5.5	0.01081648362717			CPP Unknown Function Kinase	transcription factor PPC
Cre03.g152500.v5.5	0.010692920533889			TRAF	transcriptional regulator
Cre12.g555800.v5.5	0.010502245058688			GmPK6/AtMRK1 Family	PPC
Cre11.g481800.v5.5	0.010421386653772			Putative RWP-RK domain transcription factor [PMID: 15785851]; model is tentative	
Cre06.g278140.v5.5	0.010384656634527			RWP-RK Unknown Function Kinase	transcription factor PPC
Cre01.g022950.v5.5	0.0103564795353			SET Unknown Function Kinase	transcriptional regulator PPC
Cre02.g104450.v5.5	0.010355576639216			RWP-RK transcription factor	
Cre04.g218050.v5.5	0.010344137514302	RWP8		RWP-RK Unknown Function Kinase	transcription factor PPC
Cre16.g674065.v5.5	0.010327271131356			SET Unknown Function Kinase	transcriptional regulator PPC
Cre06.g281000.v5.5	0.010218034899874			Putative RWP-RK domain transcription factor [PMID: 15785851]; tandem pair with RWP4 with which there is amino acid homology around the RWP-RK domain and some intron conservation. Part of the model is tentative.	
Cre08.g380452.v5.5	0.010046387101046			RWP-RK	transcription factor
Cre03.g149400.v5.5	0.010042867680205	RWP11		Tousled like kinase	PPC
Cre11.g481400.v5.5	0.010036797796712			S Domain Kinase (Type 2)	PPC
Cre12.g517000.v5.5	0.010030075179578	MAPKKK7		CTR1/EDR1 Kinase	PPC
Cre09.g387023.v5.5	0.009929715119873			SET	transcriptional regulator
Cre12.g503800.v5.5	0.009920099064303			E2F family transcription factor. Putative function in G1/S and S/M. Positive regulator that controls commitment and S/M size checkpoints. Mutations at this locus suppress the small-cell phenotype of mutants in the MAT3 gene encoding a retinoblastoma-like Putative RWP-RK domain transcription factor [PMID: 15785851]; model is very tentative	
Cre01.g052300.v5.5	0.00976963470837	E2F1		RWP-RK Unknown Function Kinase	transcription factor PPC
Cre03.g153050.v5.5	0.009688480817284	RWP1		GNAT	transcriptional regulator
Cre06.g266100.v5.5	0.00968760449846			Putative protein tyrosine kinase identified	
Cre02.g084550.v5.5	0.009627351224876			GmPK6/AtMRK1 Family	PPC
Cre02.g116700.v5.5	0.009546499621585	PTK11			

through multi-level
HMM library for kinase
classification (PMID:
17557329)

Cre11.g467577.v5.5 0.00945790317502
Cre16.g683650.v5.5 0.009283807669016

MADS->MADS-M-type transcription factor
CTR1/EDR1 Kinase PPC

