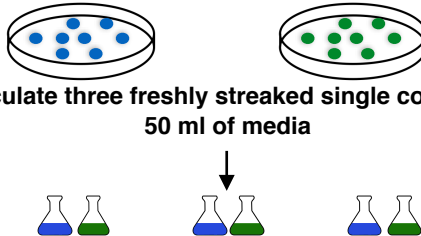
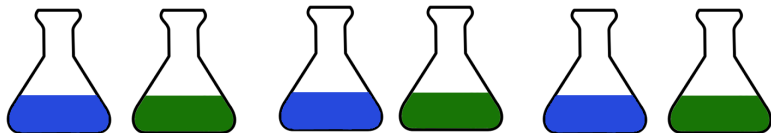


Inoculate three freshly streaked single colony to 50 ml of media



Ribosome profiling and RNA-Seq

Grow till OD750=0.6 (mid-log phase).
Sub-culture into 750ml media



OD750=0.6

filter cells > snap freeze in liquid nitrogen

Pulverise in liquid nitrogen with buffer containing cycloheximide

Thaw powder on ice

Clarify lysate, discard pellet and proceed with supernatants



RNase1 digest



38,000 rpm, 18hr, 4C,
35% sucrose cushion

Extract RNA from pellet

Total RNA extraction

rRNA subtraction
by ribo-zero

Alkaline hydrolysis

Size selection (26-34nt)

3' adaptor ligation

5' adaptor ligation

RT-PCR

PCR

2X DSN treatment to remove rRNA

Pool libraries into one tube, sequence all in four lanes of HiSeq2000

N15 quantitative proteomics

Inoculate 0.25ml into 20ml of either 14N or 15N media



Subculture 0.25ml OD750=0.6, 5 more times for full N15 incorporation

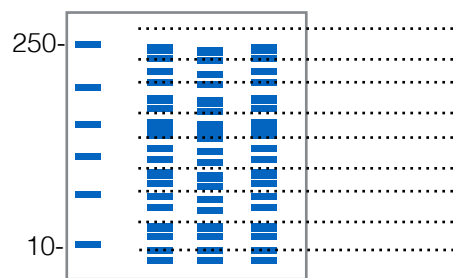


Mix equal number of cells
(Complement N14 + Mutant N15)



TCA-acetone protein extraction

Denaturing protein gel > Stain >
Divide lanes into 16 size fractions
(between 250 and 10 kDa)



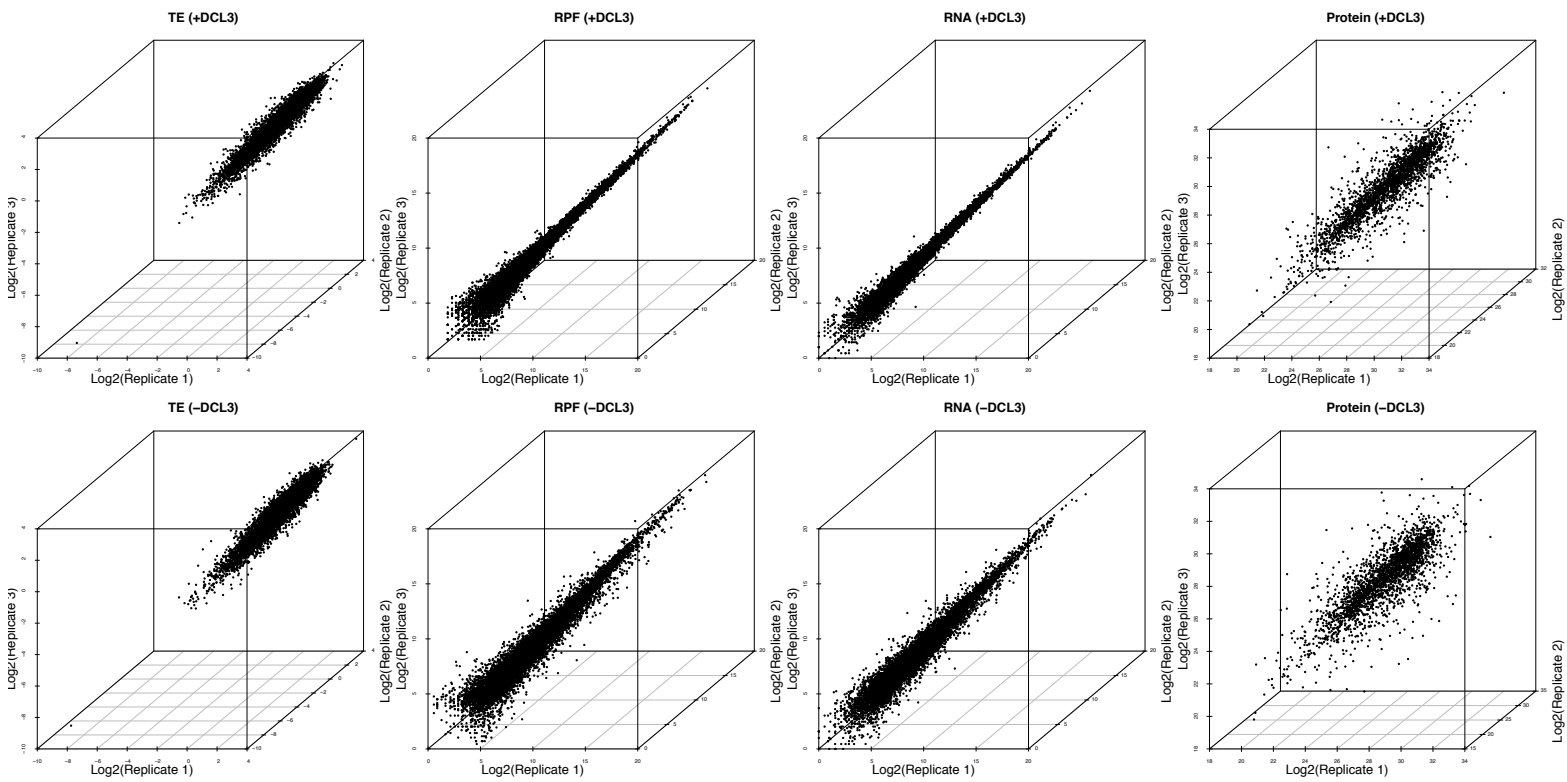
Trypsin digest > LC-MS etc...

Figure legends

- DCL3 mutant in N14 media
- DCL3 complement N14 media
- DCL3 mutant in N15 media
- 35% sucrose

Supplementary figure 1. Experimental workflow

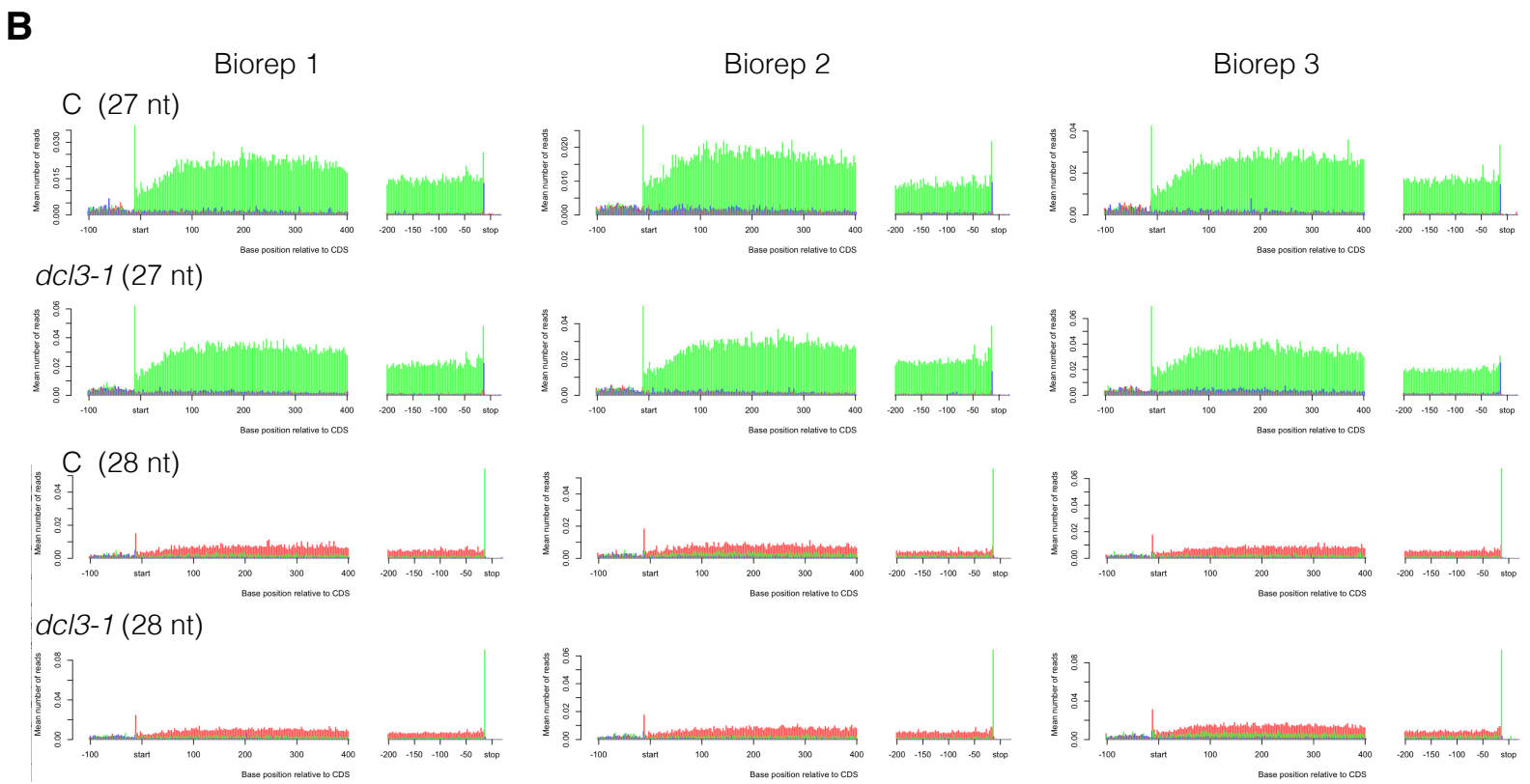
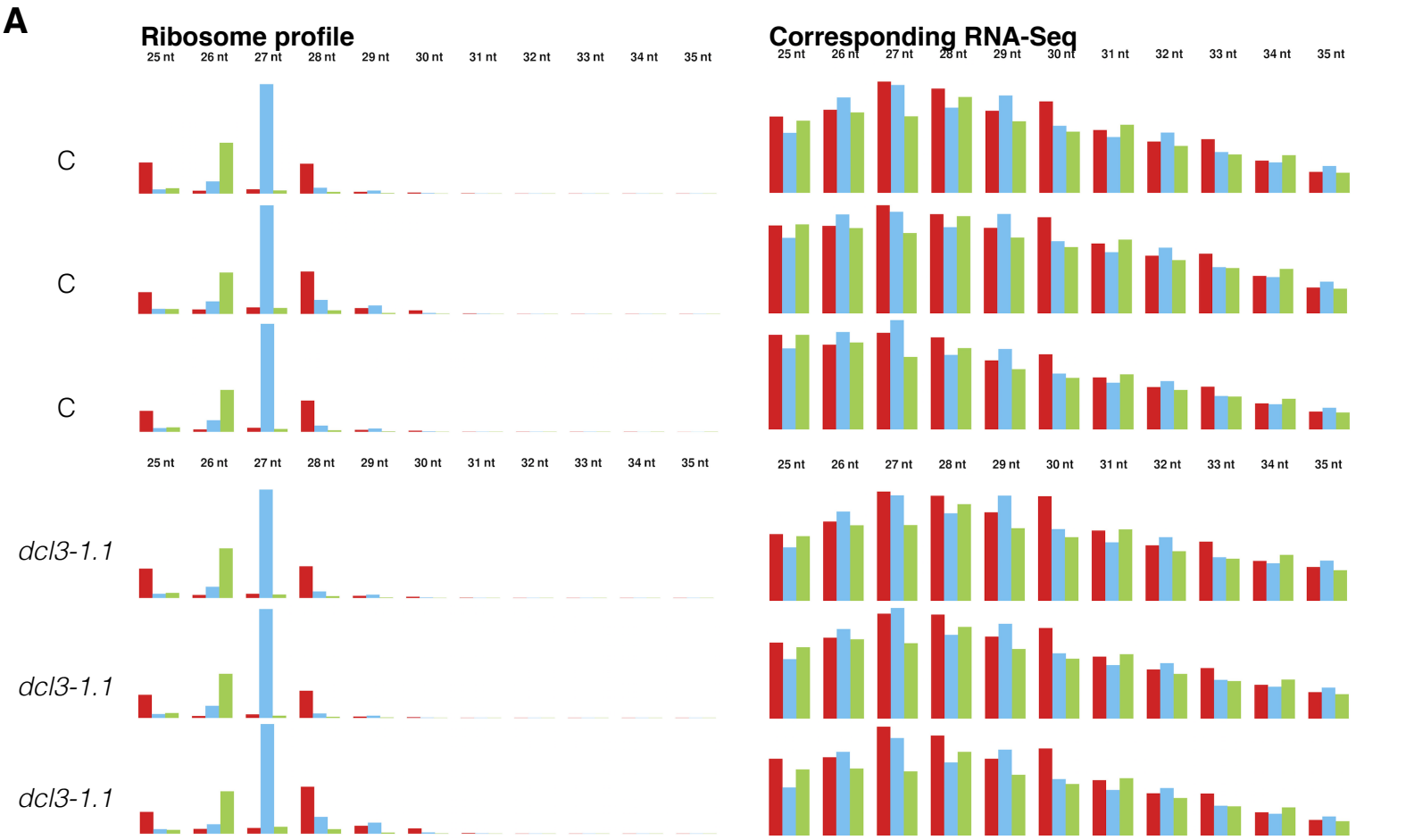
Three independent single colonies from freshly streaked *Chlamydomonas* Δ DCL3 (green) or complement (blue) were inoculated into 50ml of TAP media and grown until OD₇₅₀=0.6 (mid-log phase). 0.25 ml of each culture was used for N15 incorporation for whole cell proteomics and the remaining culture was used to sub-culture 750ml of TAP for ribosome profiling.

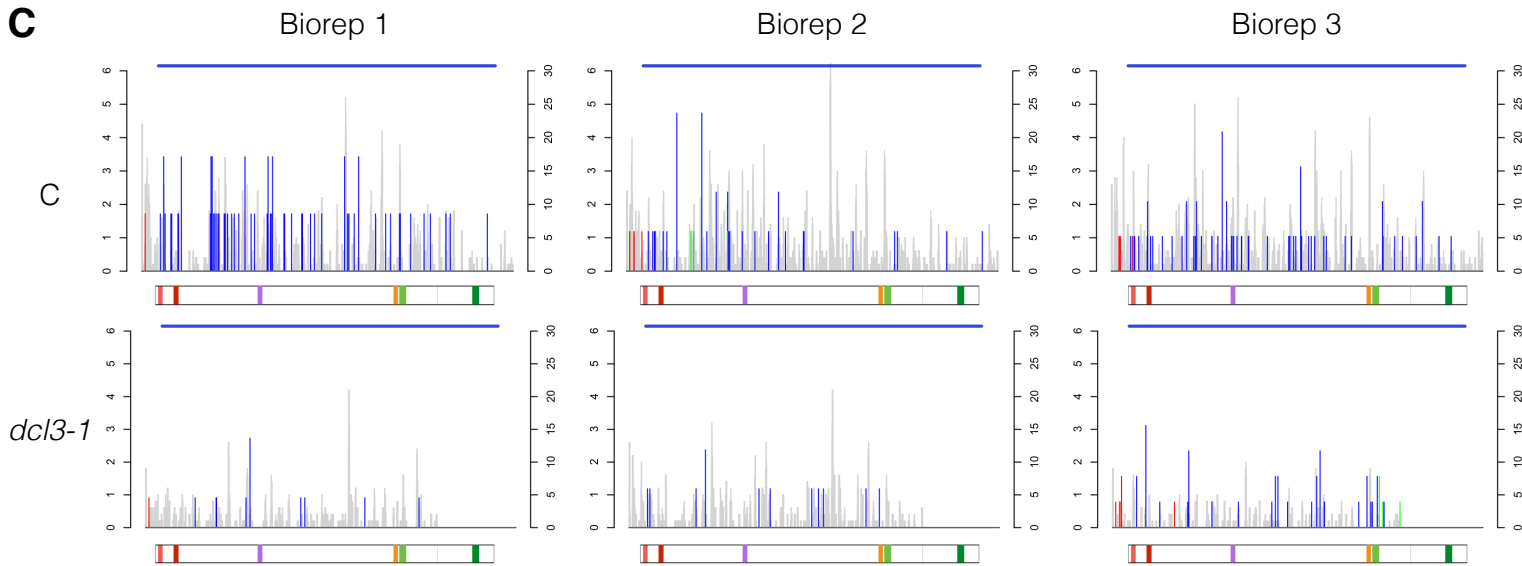


Supplementary Figure 2. Reproducibility of TE, Ribosome profiling, RNA-Seq and N15 Proteomics
 (A)-(D) Correspondence between biological triplicates for DCL3-complements
 (E)-(H) Correspondence between biological triplicates for DCL3-mutants

	library sizes	biorep 1	biorep 2	biorep 3
RiboSeq	Complement	368,613	291,373	444,768
	DCL3	515,717	461,013	590,953
RNA-seq	Complement	908,865	1,114,867	1,223,427
	DCL3	1,166,393	1,183,071	679,375

Supplementary table 1: Alignment statistics for each library that maps to the nuclear-encoded transcripts (Phytozome 281).





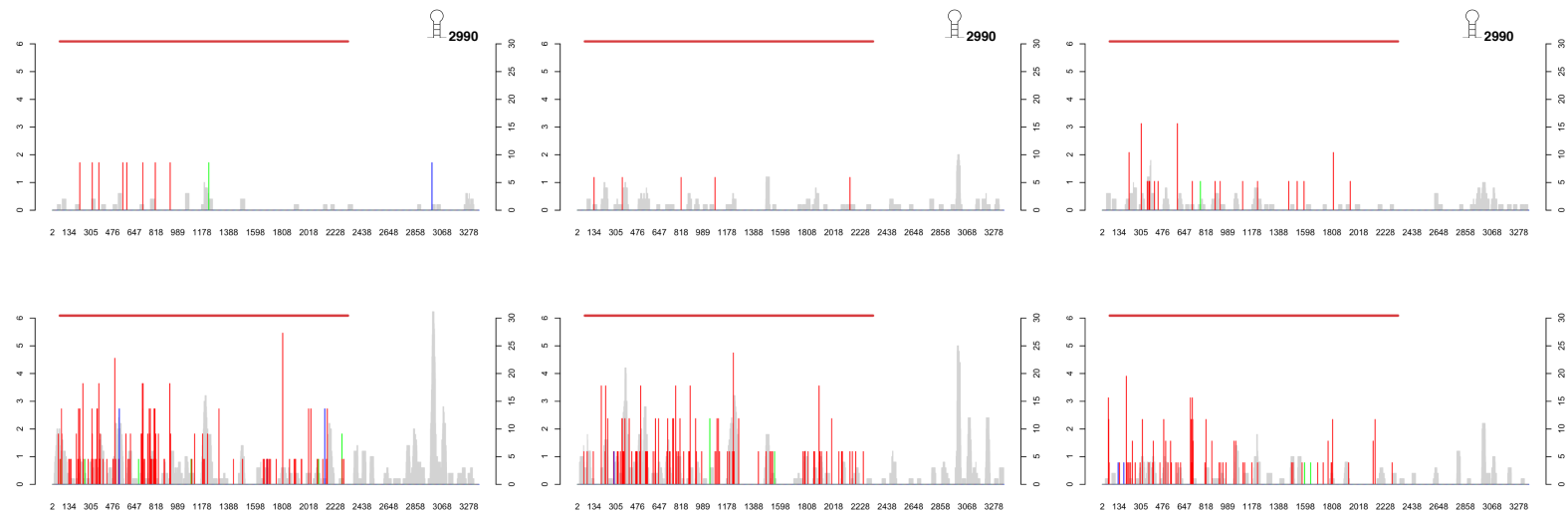
Supplementary Figure 3: Generation of precise ribosome profiling data:

- (A) Histogram of positions for all biological triplicates to which the 5' ends of ribosome profile footprints (RPFs) and corresponding RNA-Seq reads map, respectively, as a function of read size class (nt), for reads mapping to the interior region of nuclear-encoded coding ORFs. Red, green and blue bars indicate the proportion of reads that map to codon positions 0, 1 and 2 (respectively).
- (B) Histogram of 5' end positions of 27 and 28-nt RPFs relative to start and stop codons for all biological triplicates. Reads were derived from the complement or DCL3 mutant (respectively) and summed over all transcripts. Phasing is indicated using the same colours as in panels A and B. Histogram of 5' end positions of RPF (coloured, left-axis) and RNA-Seq (grey, right-axis)
- (C) 27-nt reads mapped to DCL3 transcripts in all biological triplicates. The blue horizontal line indicates the *de novo* defined ORF by ribosome profiling of the DCL3 gene (12,219 nt), which corresponds to the annotated CDS (612-12,830 nt). The schematic below the plot shows the domain organisation of DCL3 which contains two DEAD/DEAH box helicase domains (light and dark red boxes), a Helicase C domain (purple box), a proline-rich domain (orange box) and two Ribonuclease III domains a and b (light and dark green boxes, respectively). The thin grey line and the corresponding red arrow indicates the Hygromycin insertion site (nt 10,193) (replicates are shown in Figure S1).

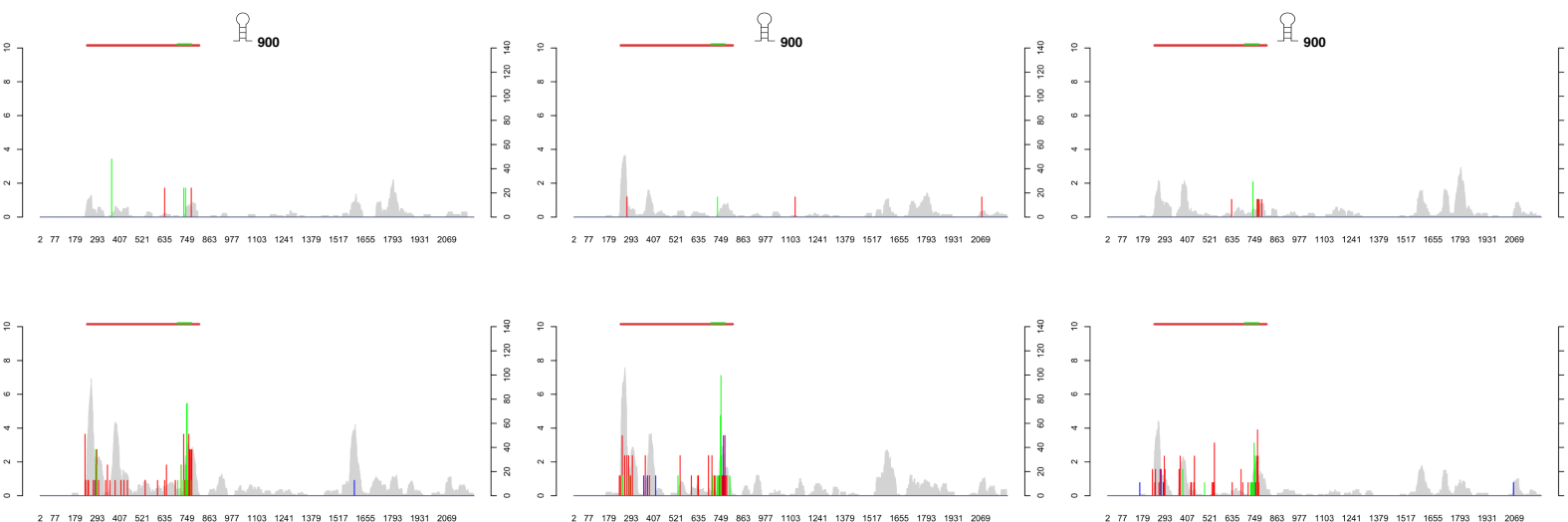
3'UTR	Intron	CDS	3'UTR intron
Cre14.g623850	Cre04.g229050	Cre05.g239950	Cre08.g358535
Cre02.g089850	Cre01.g035500		
Cre02.g143427	Cre04.g225700		
Cre02.g143527	Cre06.g274550		
Cre03.g195950	Cre06.g296983		
Cre05.g242301	Cre07.g328400		
Cre10.g465000	Cre07.g354150		
Cre13.g576700	Cre12.g537671		
Cre13.g585175	Cre14.g629200		
Cre13.g585200	Cre01.g035500		
Cre16.g694950	Cre02.g143327		
Cre02.g143527	Cre04.g217925		
Cre24.g755697	Cre04.g229050		
Cre02.g143527	Cre08.g358537		
Cre13.g576700	Cre09.g406983		
Cre16.g694950	Cre16.g647602		
Cre24.g755697	Cre07.g341100		
Cre07.g352150			
Cre06.g294776			
Cre10.g444300			
Cre01.g051050			

Supplementary table 2: Re-annotation of miRNA precursor-containing mRNA.

D Cre24.g755697.t1.1_136..2328



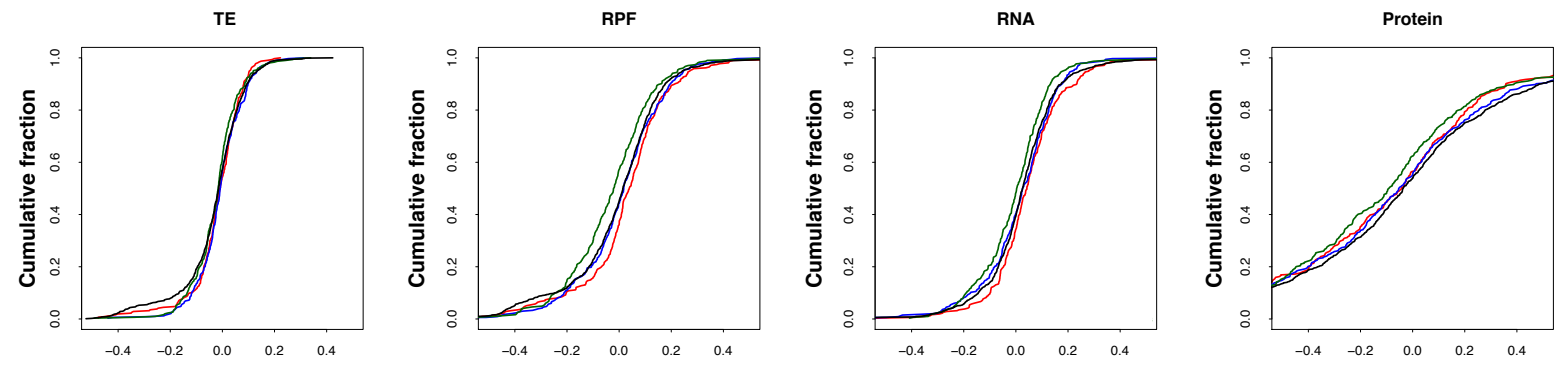
E Cre10.g444300.t1.2_241..810



Supplementary figure 6. DCL3-dependent processing of miRNA occurs in the cytoplasm and down regulates translation efficiency

(A) New annotation for precursor containing transcripts. Yellow circle = precursor-containing CDS, white circle = precursor-containing 3'UTR, orange circle = precursor-containing intron, white circle with red outline = transcripts previously annotated as non-coding transcript but is intact coding and contains miRNA precursor in the 3'UTR. Pearson correlation = 0.07186134 and 0.4858507 for intron and exon-containing transcripts respectively.

(B)-(E) Histogram of normalised 5' end positions of 27-nt RPFs relative to start and stop codons (colour) and corresponding RNA-seq reads (grey). Reads were derived from the complement or DCL3 mutant (top and bottom in biological triplicates, respectively) and summed over all transcripts.



p-value with non-target (n=911) comparisons	TE	RPF	RNA	Protein
1 target site (n = 471)	0.07	0.0042	0.17	0.18
2 target sites (n = 297)	0.12	0.55	0.48	0.81
≥ 4 target sites (n = 187)	0.22	0.0019	0.024	0.047

Supplementary Figure 7:

Cumulative *dcl3-1* vs C fold-change distributions of TE, RPF, RNA, protein for genes with both NGS and proteomic support and with 0 (black), 1 (red), 2-3 (blue) and 4 or more (green) target sites with corresponding K.S. p-values in the table below.

Supplementary table3

All mRNAs and their annotation within box A, A', B, B', C and C'. Annotations associated with the translation machinery are highlighted in green, other RNA binding proteins in red. Messenger RNAs with detectable protein in the N15 proteomics data are highlighted in blue

A (30)	
Cre01.g034600.t1.2	
Cre03.g165215.t1.1	ubiquitin-like modifier-activating enzyme ATG7
Cre04.g222700.t1.2	Elongation factor 3
Cre09.g408950.t1.1	Autophagy-specific Gee 2, isoform A
Cre09.g397450.t1.1	Dimethylaniline Mnoxygenase
Cre12.g504200.t1.2	Ribosomal protein S23, component of cytosolic 80S ribosome and 40S small subunit
Cre17.g701200.t1.2	Ribosomal protein L14, component of cytosolic 80S ribosome and 60S large subunit
Cre08.g359450.t1.2	D-Alanine Ligase
Cre02.g093850.t1.1	Ras supressor protein (contains leucine-rich repeats)
Cre11.g468353.t1.1	SF14-voltage-gated potassium channel
Cre04.g214503.t1.1	Ribosomal protein S12, component of cytosolic 80S ribosome and 40S small subunit
Cre02.g091100.t1.2	Ribosomal protein L15, component of cytosolic 80S ribosome and 60S large subunit
Cre02.g106600.t1.2	Ribosomal protein S19, component of cytosolic 80S ribosome and 40S small subunit
Cre12.g498900.t1.2	Ribosomal protein S7, component of cytosolic 80S ribosome and 40S small subunit
Cre06.g299450.t1.2	
Cre06.g280800.t1.2	Nuclear auto antigenic sperm protein
Cre07.g349950.t1.1	Transcription initiation factor RFIID subunit 6
Cre12.g521200.t1.2	DNA replication factor C complex subunit 1
Cre17.g720300.t1.2	Non-specific serine/threonine protein kinase
Cre06.g272950.t1.1	Ribosomal protein S18, component of cytosolic 80S ribosome and 40S small subunit
Cre08.g385800.t1.1	
Cre03.g174900.t1.1	SARM1 (protein binding)
Cre12.g494050.t1.2	Ribosomal protein L9, component of cytosolic 80S ribosome and 60S large subunit
Cre09.g399141.t1.1	MFS transporter, ACS family, solute carrier family 17
Cre11.g467560.t1.1	TPR repeat containing protein
Cre16.g660750.t1.1	coiled-coil and C2 domain-containing protein 2A
Cre07.g357850.t1.2	Ribosomal protein L22, component of cytosolic 80S ribosome and 60S large subunit
Cre01.g040850.t1.2	G Protein-coupled receptor-related protein
Cre01.g036800.t1.1	Diacylglycerol kinase
Cre16.g661588.t1.1	FAST Leu-Rich Domain-containing protein

B (2)	
Cre16.g675200.t1.1	
Cre06.g281450.t1.1	Scavenger receptor cysteine rich (SRCR) protein

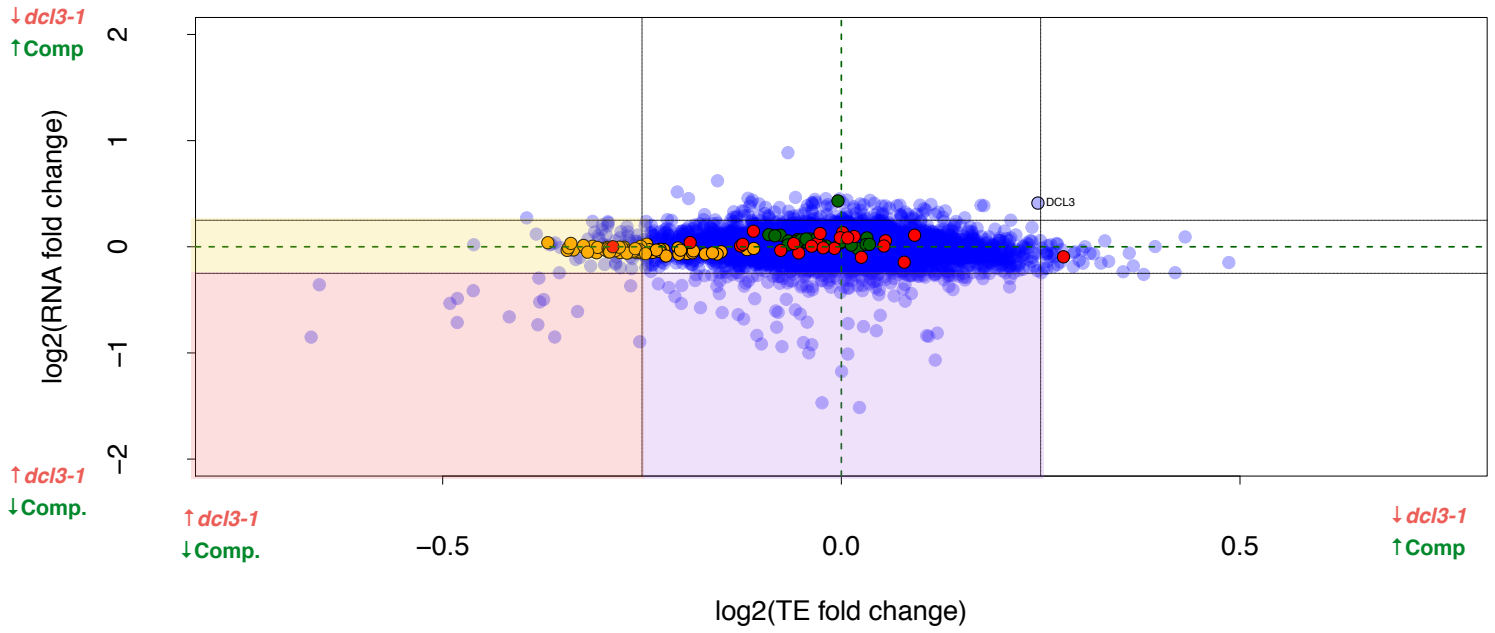
C (59)	
Cre01.g022650.t1.2	SF9 - BETA-UREIDOPROPIONASE
Cre01.g057061.t1.1	rRNA processing/ ribosome biogenesis (RIX1)
Cre02.g074800.t2.1	Adenylate/guanylate cyclase
Cre02.g082300.t1.2	
Cre02.g089500.t1.2	
Cre02.g093750.t1.2	Nucleoredoxin 2
Cre02.g095080.t1.1	MAJOR VAULT PROTEIN
Cre02.g109100.t1.1	3',5'-cyclic-nucleotide phosphodiesterase
Cre03.g155950.t1.2	
Cre03.g170750.t1.2	Small nucleolar ribonucleoprotein U3 component
Cre03.g198400.t1.2	
Cre03.g199800.t1.1	Iron hydrogenase
Cre03.g200431.t1.1	
Cre03.g205450.t1.1	
Cre04.g212800.t1.1	
Cre04.g224931.t1.1	
Cre05.g235700.t1.2	SAPOSIN-RELATED
Cre06.g271200.t1.2	NADH oxidase (H(2)O(2)-forming) / H(2)O(2)-forming NADH oxidase
Cre06.g278098.t1.1	Methylcrotonoyl-CoA carboxylase alpha subunit
Cre06.g281450.t1.1	Scavenger receptor cysteine rich (SRCR) protein
Cre06.g288600.t1.1	
Cre06.g296700.t1.2	Hydrogenase assembly factor/biotin synthase
Cre07.g324500.t1.2	Gametolysin / Lysin
Cre07.g330900.t1.2	RNA polymerase II transcription factor TFIIA, large chain
Cre07.g348250.t1.2	GLIOMA SUPPRESSOR CANDIDATE REGION GENE 2
Cre08.g358564.t1.1	
Cre08.g373650.t1.1	
Cre09.g388800.t1.2	Glutamate dehydrogenase
Cre09.g396438.t1.1	
Cre09.g398250.t1.1	
Cre09.g398400.t1.2	Transient receptor potential ion channel protein
Cre09.g402663.t1.1	
Cre09.g405100.t2.1	
Cre10.g452250.t1.1	
Cre10.g466450.t1.1	Splicing factor 3b, subunit 4
Cre11.g467531.t1.1	Flagellar Associated Protein
Cre11.g477050.t1.1	

C (59)	
Cre12.g496400.t1.1	
Cre12.g499700.t1.1	MATE efflux family protein
Cre12.g542350.t1.2	SUGAR UTILIZATION REGULATORY PROTEIN IMP2
Cre13.g572272.t1.2	Collagens (type IV and type XIII), and related proteins
Cre13.g580900.t1.1	SERINE/THREONINE-PROTEIN KINASE RIO1
Cre14.g623900.t1.1	
Cre15.g643503.t1.1	
Cre16.g648350.t1.1	PROLINE OXIDASE
Cre16.g677920.t1.2	
Cre16.g683793.t1.1	
Cre17.g696950.t1.1	
Cre17.g701050.t1.2	CELL GROWTH-REGULATING NUCLEOLAR PROTEIN
Cre17.g701884.t1.1	
Cre17.g701950.t1.2	
Cre17.g717600.t1.2	
Cre17.g718650.t1.2	
Cre17.g727801.t1.1	T-type voltage-gated Ca ²⁺ channel, pore-forming alpha1I subunit
Cre17.g731800.t1.2	
Cre17.g740950.t1.2	High intensity light-inducible Lhc-like gene
Cre18.g748297.t1.1	
Cre18.g749547.t1.1	
Cre24.g755997.t1.1	Cell wall protein pherophorin-C18

A' (15)	
Cre16.g668050.t1.1	Aspartyl protease (Asp_protease_2)
Cre06.g265850.t1.1	Tail-specific/C-terminal processing peptidase protease
Cre03.g191950.t1.2	RimM N-terminal domain (RimM)
Cre14.g614950.t1.2	Putative mitochondrial ribosomal protein S2, imported to mitochondria
Cre12.g554300.t1.1	Sodium:solute symporter
Cre15.g639050.t1.1	ZINC FINGER MYND DOMAIN CONTAINING PROTEIN 10
Cre14.g626800.t1.1	
Cre14.g610663.t1.1	
Cre06.g271950.t1.2	GENERAL VESICULAR TRANSPORT FACTOR P115
Cre07.g318300.t1.1	CAMP-DEPENDENT PROTEIN KINASE REGULATORY CHAIN
Cre17.g739850.t1.2	
Cre10.g429200.t1.1	RuBisCO methyltransferase
Cre17.g703450.t1.1	
Cre14.g623439.t1.1	Pyrrolidone-carboxylate peptidase
Cre14.g626800.t1.1	

C' (36)	
Cre43.g760497.t1.1	
Cre17.g734644.t1.1	
Cre17.g734100.t1.2	
Cre17.g733650.t1.1	7-keto-8-aminopelargonic acid synthase
Cre12.g561350.t1.1	
Cre12.g502250.t1.2	Plastid lipid associated protein
Cre09.g396300.t1.2	Protoporphyrinogen oxidase
Cre02.g143547.t1.1	
Cre02.g083800.t2.1	dTDP-glucose 4,6-dehydratase
Cre02.g076300.t1.1	Uroporphyrinogen decarboxylase
Cre01.g024050.t1.2	
Cre43.g760547.t1.1	
Cre17.g734200.t1.2	L,L-diaminopimelate aminotransferase
Cre09.g386137.t1.1	
Cre03.g158000.t1.2	Glutamate-1-semialdehyde aminotransferase
Cre02.g143467.t1.1	
Cre02.g079650.t1.1	
Cre26.g756597.t1.1	
Cre17.g733950.t1.2	
Cre16.g695850.t1.2	
Cre11.g480250.t1.1	
Cre10.g465550.t1.1	ClpD chaperone, Hsp100 family
Cre06.g299800.t1.2	
Cre03.g166500.t1.2	
Cre01.g050950.t1.2	
Cre01.g048600.t1.1	
Cre04.g214650.t1.1	1,3-beta-D-glucan synthase
Cre06.g292249.t1.1	
Cre17.g734709.t1.1	
Cre17.g734400.t1.1	Ubiquitin ligase SCF complex subunit Cullin
Cre16.g668300.t1.1	
Cre26.g756897.t1.1	
Cre17.g734350.t1.1	
Cre17.g733800.t1.1	
Cre05.g242000.t1.2	Magnesium chelatase subunit D
Cre17.g734250.t1.1	

All expressed genes



Supplementary figure 8

Correspondence between TE and RNA fold-changes of *dcl3-1* and its corresponding complement for expressed all nuclear encode genes. All mRNAs within box A, B and C are highlighted in yellow, red and purple respectively.

Table 4

All expressed mRNAs and their annotation within box A, A', B, B', C and C' in supplementary figure 9. Annotations associated with the translation machinery are highlighted in green, other RNA binding proteins in red. Messenger RNAs with detectable protein in the N15 proteomics data are highlighted in blue

A (109)	
Cre02.g074370.t1.2	Protein tyrosine kinase
Cre07.g312650.t1.2	
Cre02.g075700.t1.2	Ribosomal protein L19, component of cytosolic 80S ribosome and 60S large subunit
Cre06.g267550.t1.2	Bardet-Biedl syndrome-5 associated protein
Cre01.g018750.t1.2	
Cre01.g016350.t1.1	
Cre03.g179941.t1.1	
Cre01.g034600.t1.2	WD40 repeat protein
Cre07.g325746.t1.1	Ribosomal protein L38, component of cytosolic 80S ribosome and 60S large subunit Ribosomal protein L38
Cre13.g568650.t1.2	Ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit
Cre04.g222700.t1.2	Elongation Factor 3
Cre17.g701200.t1.2	Ribosomal protein L14, component of cytosolic 80S ribosome and 60S large subunit
Cre06.g282500.t1.2	Ribosomal protein L23a, component of cytosolic 80S ribosome and 60S large subunit
Cre03.g165215.t1.1	Ubiquitin-like modifier activating enzyme ATG7
Cre03.g174900.t1.1	SARM1
Cre10.g420750.t1.2	Ribosomal protein L30, component of cytosolic 80S ribosome and 60S large subunit
Cre08.g359450.t1.2	D-Alanine ligase
Cre01.g047750.t1.2	Ribosomal protein L18a, component of cytosolic 80S ribosome and 60S large subunit
Cre13.g573351.t1.2	Ribosomal protein S16, component of cytosolic 80S ribosome and 40S small subunit
Cre12.g504200.t1.2	Ribosomal protein S23, component of cytosolic 80S ribosome and 40S small subunit
Cre02.g093850.t1.1	Ras supressor protein
Cre09.g408950.t1.1	Autophagy-specific Gee 2, isoform A
Cre12.g493350.t1.1	
Cre08.g359200.t1.1	Regulator of chromosome condensation
Cre02.g091100.t1.2	Ribosomal protein L15, component of cytosolic 80S ribosome and 60S large subunit
Cre05.g246550.t1.2	L-amino-acid oxidase
Cre06.g289550.t1.2	Ribosomal protein L32, component of cytosolic 80S ribosome and 60S large subunit
Cre12.g498250.t1.2	Ribosomal protein S17, component of cytosolic 80S ribosome and 40S small subunit
Cre06.g278253.t1.1	
Cre11.g467772.t1.1	D-type cyclin D-type cyclin

A cont.	
Cre02.g106600.t1.2	Ribosomal protein S19, component of cytosolic 80S ribosome and 40S small subunit
Cre09.g397450.t1.1	Dimethylaniline Mnooxygenase
Cre12.g521200.t1.2	DNA replication factor C complex subunit 1
Cre03.g203850.t1.2	ATP-sulfurylase
Cre11.g468353.t1.1	Voltage-gated potassium channel
Cre07.g331900.t1.2	Ribosomal protein S13, component of cytosolic 80S ribosome and 40S small subunit
Cre24.g755647.t1.1	YTH YT521-B homology domain-containing
Cre04.g214503.t1.1	Ribosomal protein S12, component of cytosolic 80S ribosome and 40S small subunit
Cre16.g660150.t1.2	30S ribosomal protein S10 family member
Cre06.g290950.t1.2	Ribosomal protein S5, component of cytosolic 80S ribosome and 40S small subunit
Cre01.g024900.t1.1	RNA-binding region RNP-1 domain containing protein
Cre06.g280800.t1.2	Nuclear auto antigenic sperm protein NASP-related
Cre12.g514500.t1.2	Ribosomal protein S11, component of cytosolic 80S ribosome and 40S small subunit
Cre10.g424150.t1.2	Transcription initiation factor IIA subunit 2
Cre06.g310700.t1.2	Ribosomal protein L36a, component of cytosolic 80S ribosome and 60S large subunit
Cre12.g529400.t1.2	Ribosomal protein S27e isoform 1, component of 80S ribosome and 40S small subunit
Cre13.g568900.t1.2	Ribosomal protein L17, component of cytosolic 80S ribosome and 60S large subunit
Cre17.g701650.t1.2	Ribosomal protein L27, component of cytosolic 80S ribosome and 60S large subunit
Cre08.g359750.t2.1	Ribosomal protein S9, component of cytosolic 80S ribosome and 40S small subunit
Cre12.g512600.t1.2	Ribosomal protein L18, component of cytosolic 80S ribosome and 60S large subunit
Cre12.g510450.t1.2	Ribosomal protein S28, component of cytosolic 80S ribosome and 40S small subunit
Cre07.g322500.t1.2	Mitochondrial ribosomal protein L19
Cre05.g234637.t1.1	Ribosomal protein S15A, component of cytosolic 80S ribosome and 40S small subunit
Cre06.g272950.t1.1	Ribosomal protein S18, component of cytosolic 80S ribosome and 40S small subunit
Cre12.g498900.t1.2	Ribosomal protein S7, component of cytosolic 80S ribosome and 40S small subunit
Cre07.g349950.t1.1	Transcription initiation factor TFIID subunit 6
Cre02.g143527.t1.1	
Cre17.g714800.t1.2	Hydroxyproline-rich cell wall protein
Cre07.g335200.t1.1	Translation elongation factor EFG/EF2 related to membrane GTP-binding protein LepA
Cre02.g115200.t1.2	Ribosomal protein L27a, component of cytosolic 80S ribosome and 60S large subunit
Cre11.g480150.t1.2	Ribosomal protein S14, component of cytosolic 80S ribosome and 40S small subunit
Cre12.g537800.t1.2	Ribosomal protein L7, component of cytosolic 80S ribosome and 60S large subunit
Cre08.g374100.t1.1	
Cre12.g494050.t1.2	Ribosomal protein L9, component of cytosolic 80S ribosome and 60S large subunit
Cre17.g699500.t1.2	Tubulin tyrosine ligase
Cre01.g035500.t1.2	Phosphatidylinositol-3-kinase, probably vacuolar
Cre17.g720300.t1.2	Leucine-rich repeat containing protein DDB_G0281931-related
Cre09.g399141.t1.1	Anion transporter 5-related
Cre09.g400650.t1.2	Ribosomal protein S6, component of cytosolic 80S ribosome and 40S small subunit
Cre09.g397697.t1.1	Ribosomal protein L4, component of cytosolic 80S ribosome and 60S large subunit Ribosomal protein L4
Cre06.g257150.t1.2	Ribosomal protein L37a, component of cytosolic 80S ribosome and 60S large subunit
Cre12.g560400.t1.1	DnaJ-like protein

A Cont.	
Cre12.g535851.t1.1	Ribosomal protein L8, component of cytosolic 80S ribosome and 60S large subunit
Cre03.g203450.t1.2	Ribosomal protein S21, component of cytosolic 80S ribosome and 40S small subunit
Cre04.g211800.t1.2	Ribosomal protein L23, component of cytosolic 80S ribosome and 60S large subunit
Cre12.g528750.t1.2	Ribosomal protein L12, component of cytosolic 80S ribosome and 60S large subunit
Cre06.g299450.t1.2	
Cre03.g193400.t1.2	RNA polymerase sigma factor RPO
Cre06.g249200.t1.2	Actin-related protein, putative SWR-C component
Cre08.g360900.t1.2	Ribosomal protein S15, component of cytosolic 80S ribosome and 40S small subunit
Cre10.g427750.t1.2	Kinesis-Like protein KIF9
Cre09.g404500.t1.1	Spindle pole body protein
Cre01.g018900.t1.2	E3-ubiquitin-protein ligase RNF14
Cre16.g678550.t1.1	
Cre03.g177550.t1.2	Integral membrane ankyrin-repeat protein Kidins220/26S proteasome regulatory complex, subunit PSMD10
Cre16.g660750.t1.1	MKS-6
Cre10.g459250.t1.2	Ribosomal protein L35a, component of cytosolic 80S ribosome and 60S large subunit
Cre11.g467560.t1.1	TPR repeat containing protein
Cre01.g039250.t2.1	Ribosomal protein S2, component of cytosolic 80S ribosome and 40S small subunit
Cre14.g630100.t1.2	Ribosomal protein L13, component of cytosolic 80S ribosome and 60S large subunit
Cre07.g312400.t1.1	Diacylglycerol kinase
Cre06.g278135.t1.1	Ribosomal protein L21, component of cytosolic 80S ribosome and 60S large subunit Ribosomal protein L21, component of cytosolic 80S ribosome and 60S large subunit
Cre07.g313950.t1.1	
Cre02.g110000.t1.1	Caspase regulator
Cre01.g036800.t1.1	KIF6 Kinesin-like protein
Cre10.g435400.t1.2	
Cre01.g040000.t1.2	Ribosomal protein L26, component of cytosolic 80S ribosome and 60S large subunit
Cre12.g489153.t1.1	Ribosomal protein L31, component of cytosolic 80S ribosome and 60S large subunit
Cre14.g608452.t1.1	Ubiquitin C-terminal hydrolase
Cre02.g142066.t1.1	IQ calmodulin-binding motif
Cre01.g039300.t1.2	Polyadenylate-binding protein RB47
Cre02.g103550.t1.2	Eukaryotic translation initiation factor 1A, eIF-1A
Cre10.g417700.t1.2	Ribosomal protein L3, component of cytosolic 80S ribosome and 60S large subunit
Cre08.g358556.t1.1	Ribosomal protein S29, component of cytosolic 80S ribosome and 40S small subunit Ribosomal protein S29, component of cytosolic 80S ribosome and 40S small subunit
Cre09.g391097.t1.1	Ribosomal protein L24, component of cytosolic 80S ribosome and 60S large subunit Ribosomal protein L24, component of cytosolic 80S ribosome and 60S large subunit
Cre09.g388200.t1.1	Ribosomal protein L10, component of cytosolic 80S ribosome and 60S large subunit
Cre07.g357850.t1.2	Ribosomal protein L22, component of cytosolic 80S ribosome and 60S large subunit
Cre16.g692200.t1.1	Metalloproteinase of VMP family
Cre06.g272800.t1.2	Ribosomal protein S8, component of cytosolic 80S ribosome and 40S small subunit

B (17)	
Cre07.g329950.t1.1	
Cre15.g634900.t1.2	
Cre16.g673200.t1.2	
Cre05.g239950.t1.1	
Cre10.g444300.t1.2	
Cre17.g704251.t1.1	
Cre13.g576700.t1.1	
Cre16.g675200.t1.1	
Cre12.g486450.t1.2	
Cre07.g325757.t1.1	
Cre11.g477700.t1.1	
Cre24.g755697.t1.1	
Cre11.g467650.t1.1	
Cre13.g585200.t1.2	
Cre12.g541400.t1.2	Las17-binding protein actin regulator (Ysc84)
Cre07.g317601.t1.1	
Cre06.g281450.t1.1	Scavenger receptor cysteine rich (SRCR) protein

C (150)	
Cre07.g317350.t1.2	
Cre10.g459100.t1.1	
Cre08.g379800.t1.2	Alpha-2 macroglobulin family (A2M)
Cre16.g677920.t1.2	
Cre06.g294776.t1.1	
Cre03.g156850.t1.1	Sphingomyelin phosphodiesterase related
Cre12.g551700.t1.2	
Cre13.g578750.t1.2	PsbA translation factor
Cre07.g334150.t1.1	Tumor necrosis factor receptor superfamily member
Cre14.g623900.t1.1	
Cre03.g143967.t1.1	
Cre03.g182800.t1.1	Alanine-glyoxylate transaminase
Cre06.g271200.t1.2	NADH oxidase / H2O2-forming NADH oxidase
Cre02.g095080.t1.1	Major vault protein
Cre17.g719450.t1.1	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily // Serine/threonine protein kinase
Cre13.g580900.t1.1	SERINE/THREONINE-PROTEIN KINASE RIO1
Cre16.g694950.t1.1	Non-specific serine/threonine protein kinase / Threonine-specific protein kinase
Cre07.g317450.t1.1	
Cre08.g358535.t1.1	
Cre06.g278098.t1.1	Methylcrotonoyl-CoA carboxylase alpha subunit Methylcrotonoyl-CoA carboxylase alpha subunit
Cre12.g496400.t1.1	
Cre14.g623850.t1.1	

C cont.	
Cre06.g296700.t1.2	Hydrogenase assembly factor/biotin synthase
Cre16.g648350.t1.1	PROLINE OXIDASE
Cre18.g748297.t1.1	
Cre07.g330900.t1.2	RNA polymerase II transcription initiation factor TFIIA, large chain
Cre09.g396438.t1.1	
Cre02.g074800.t2.1	Adenylate/guanylate cyclase
Cre15.g638400.t1.2	Universal stress protein family
Cre04.g229050.t1.1	INOSITOL POLYPHOSPHATE KINASE 1
Cre35.g759297.t1.1	
Cre14.g613800.t1.1	
Cre03.g199800.t1.1	Iron hydrogenase
Cre02.g096200.t1.2	PROTEIN MEMO1
Cre04.g212800.t1.1	
Cre17.g701950.t1.2	
Cre09.g398450.t1.1	
Cre11.g477050.t1.1	
Cre11.g467531.t1.1	Flagellar Associated Protein Flagellar Associated Protein
Cre12.g499700.t1.1	MATE efflux family protein
Cre17.g727801.t1.1	T-type voltage-gated Ca ²⁺ channel, pore-forming alpha1I subunit
Cre01.g001250.t1.2	
Cre03.g145307.t2.1	
Cre04.g225800.t1.2	ANKYRIN REPEAT PROTEIN
Cre06.g278229.t1.1	SF1 - SQUAMOSA PROMOTER-BINDING-LIKE PROTEIN 10-RELATED
Cre01.g022650.t1.2	SF9 - BETA-UREIDOPROPIONASE
Cre03.g170850.t1.1	Gametolysin / Lysin
Cre09.g398250.t1.1	
Cre12.g487200.t1.1	Angio-associated migratory cell protein (contains WD40 repeats)
Cre12.g499000.t1.2	Cgr1 family (Cgr1)
Cre07.g348250.t1.2	GLIOMA SUPPRESSOR CANDIDATE REGION GENE 2
Cre05.g232150.t1.2	Glutamate dehydrogenase
Cre10.g452250.t1.1	
Cre09.g388800.t1.2	Glutamate dehydrogenase
Cre09.g398500.t1.1	
Cre18.g748097.t1.1	
Cre08.g360450.t1.1	LEUCINE-RICH REPEAT-CONTAINING PROTEIN
Cre10.g452350.t1.1	
Cre11.g468050.t1.2	SF6 - MEMBRANE-ASSOCIATED PROTEIN VIPP1, CHLOROPLASTIC
Cre24.g755997.t1.1	Cell wall protein pherophorin-C18
Cre12.g555000.t1.1	
Cre14.g612950.t1.1	Adenylate/guanylate cyclase
Cre10.g423250.t1.2	NAD-dependent malate dehydrogenase
Cre09.g393543.t1.1	Hybrid-cluster protein Hybrid-cluster protein
Cre16.g683793.t1.1	PESCADILLO - RELATED
Cre09.g393506.t1.1	Hybrid-cluster protein

C cont.	
Cre12.g542350.t1.2	SF26 - SUGAR UTILIZATION REGULATORY PROTEIN IMP2
Cre08.g358564.t1.1	Heterokaryon incompatibility protein (HET) (HET)
Cre16.g680700.t1.2	Asparagine synthase (glutamine-hydrolyzing) / Glutamine-dependent asparagine synthetase
Cre07.g315750.t1.2	D-arabinitol dehydrogenase (NADP(+)) / NADP(+)-dependent D-arabinitol dehydrogenase
Cre09.g399400.t1.1	Triacylglycerol lipase
Cre17.g696950.t1.1	MEKK and related serine/threonine protein kinases
Cre08.g367500.t1.1	Stress-related chlorophyll a/b binding protein 2
Cre07.g324500.t1.2	Gametolysin / Lysin
Cre15.g640200.t1.1	KH domain (KH_1)
Cre15.g643503.t1.1	Response regulator receiver domain (Response_reg)
Cre17.g701050.t1.2	CELL GROWTH-REGULATING NUCLEOLAR PROTEIN
Cre21.g752247.t1.1	
Cre08.g365900.t1.2	Stress-related chlorophyll a/b binding protein 1
Cre03.g173550.t1.2	F15H11.13 PROTEIN
Cre11.g467632.t1.1	
Cre04.g224931.t1.1	
Cre17.g725250.t1.1	
Cre15.g644051.t1.1	AAA domain (dynein-related subfamily) (AAA_5)
Cre02.g095076.t1.1	Major facilitator superfamily transporter, involved in circadian rhythm control Major facilitator superfamily transporter, involved in circadian rhythm control
Cre06.g296300.t1.1	Scavenger receptor cysteine rich (SRCR) protein
Cre02.g118300.t1.2	DEAD box ATP-dependent RNA helicase
Cre02.g089500.t1.2	
Cre18.g749547.t1.1	
Cre02.g089650.t1.1	U1 snRNP-specific protein C
Cre10.g458850.t1.2	
Cre01.g057061.t1.1	rRNA processing/ribosome biogenesis (RIX1)
Cre01.g042502.t1.1	SF299 - LYSYL OXIDASE-RELATED
Cre03.g159900.t1.1	SF36 - SERINE/THREONINE-PROTEIN KINASE RIO2
Cre01.g055400.t1.2	NUCLEOLAR AND COILED-BODY PHOSPHOPROTEIN 1
Cre05.g235700.t1.2	SAPOSIN-RELATED
Cre04.g217962.t1.1	Low-CO2-inducible protein Low-CO2-inducible protein
Cre10.g466450.t1.1	Splicing factor 3b, subunit 4
Cre12.g539100.t1.1	DEAD-BOX ATP-DEPENDENT RNA HELICASE 5
Cre03.g170750.t1.2	Small nucleolar ribonucleoprotein U3 component
Cre02.g141986.t1.1	SERINE-THREONINE PROTEIN KINASE
Cre02.g095087.t1.1	Cysteine endopeptidase Cysteine endopeptidase
Cre03.g155950.t1.2	
Cre11.g468850.t1.2	Flagellar Associated Protein
Cre14.g622150.t1.1	
Cre17.g731800.t1.2	FOLLISTATIN-RELATED
Cre17.g721553.t1.2	
Cre06.g288600.t1.1	
Cre07.g347300.t1.1	L-methionine (R)-S-oxide reductase / FRMsr

C cont.	
Cre17.g744697.t1.1	
Cre02.g107200.t1.1	
Cre17.g701884.t1.1	
Cre09.g391726.t1.1	
Cre17.g705300.t2.1	Cellulase / Endoglucanase
Cre17.g740950.t1.2	High intensity light-inducible Lhc-like gene
Cre12.g549000.t1.2	Cell wall protein pherophorin-C4
Cre17.g696500.t1.1	Cell wall protein pherophorin-C19
Cre06.g288908.t1.2	SF79 - NITROGEN NETWORK KINASE 1
Cre02.g082300.t1.2	SURFEIT LOCUS PROTEIN 6
Cre17.g718650.t1.2	NOP SEVEN ASSOCIATED PROTEIN 1
Cre02.g093750.t1.2	Nucleoredoxin 2
Cre14.g624900.t1.2	Flagellar Associated Protein
Cre02.g109050.t1.2	FAST LEU-RICH DOMAIN-CONTAINING
Cre10.g426250.t1.1	PRE-RRNA-PROCESSING PROTEIN TSR2 HOMOLOG
Cre19.g751047.t1.1	
Cre09.g405100.t2.1	
Cre03.g177600.t1.1	L-gulonolactone oxidase
Cre03.g200431.t1.1	
Cre01.g051250.t1.2	Flagellar outer dynein arm 18 kDa light chain LC4
Cre09.g398400.t1.2	Transient receptor potential ion channel protein
Cre02.g087150.t1.2	
Cre17.g719150.t1.2	
Cre03.g198400.t1.2	
Cre09.g402663.t1.1	
Cre08.g373650.t1.1	
Cre01.g004900.t1.2	SF1 - THIJ/PFPI
Cre11.g478100.t1.2	SnoaL-like domain (SnoaL_2)
Cre08.g368500.t1.2	Nucleolar RNA-binding protein NIFK
Cre17.g739350.t1.1	
Cre06.g264500.t1.2	TBP-binding protein, activator of basal transcription (contains rrm motif)
Cre03.g192201.t1.1	Pherophorin (DUF3707)
Cre16.g675400.t1.1	
Cre06.g300050.t1.1	FAST LEU-RICH DOMAIN-CONTAINING
Cre06.g302950.t1.1	Gametolysin peptidase M11 (Peptidase_M11)
Cre03.g205450.t1.1	
Cre13.g587300.t1.1	
Cre13.g567200.t1.1	SF513 - SERINE-THREONINE PROTEIN KINASE
Cre11.g480551.t1.2	
Cre17.g717600.t1.2	
Cre07.g314500.t1.1	Mitogen-activated protein kinase kinase kinase / MLTK

A' (40)	
Cre03.g191950.t1.2	RimM N-terminal domain (RimM)
Cre06.g248900.t1.1	Leucine-rich repeat (LRR) protein associated with apoptosis in muscle tissue
Cre12.g490700.t1.2	Mini-eyespot protein
Cre14.g610663.t1.1	Protein Y56A3A.33
Cre14.g618600.t1.2	ABC transporter, multidrug resistance associated protein
Cre12.g486000.t1.2	PCDC2 PROGRAMMED CELL DEATH PROTEIN 2 -RELATED
Cre06.g287200.t1.2	
Cre05.g232550.t1.2	Phosphoglycerate mutase
Cre02.g119850.t1.1	3',5'-cyclic-nucleotide phosphodiesterase
Cre09.g411751.t1.1	
Cre08.g363050.t1.2	
Cre10.g451450.t1.1	SERINE-THREONINE PROTEIN KINASE
Cre05.g241655.t1.1	
Cre14.g608400.t1.2	
Cre12.g548152.t1.1	SF0 - GRAVES DISEASE CARRIER PROTEIN
Cre10.g429200.t1.1	RuBisCO methyltransferase
Cre02.g087300.t1.1	Hydroxypyruvate reductase / D-glycerate dehydrogenase
Cre06.g306250.t1.1	Receptor protein-tyrosine kinase / Receptor protein tyrosine kinase
Cre01.g052150.t1.1	Flagellar Associated Protein with ankyrin repeats
Cre06.g269350.t1.2	GC-RICH SEQUENCE DNA-BINDING FACTOR
Cre14.g614950.t1.2	Putative mitochondrial ribosomal protein S2, imported to mitochondria
Cre12.g554300.t1.1	Sodium:solute symporter
Cre17.g740390.t1.1	
Cre02.g081300.t1.1	MUTT-NUDIX-RELATED
Cre12.g546900.t1.1	F-BOX/LEUCINE RICH REPEAT PROTEIN
Cre13.g606200.t1.1	SF34 - METHYLTRANSFERASE NSUN6-RELATED
Cre13.g603400.t1.1	RING-FINGER, DEAD-LIKE HELICASE, PHD AND SNF2 DOMAIN-CONTAINING PROTEIN
Cre01.g043700.t1.2	Tubulin-Related protein
Cre03.g190550.t1.2	MEDIATOR COMPLEX SUBUNIT
Cre06.g271950.t1.2	General vesicular transport factor P115
Cre07.g313350.t1.2	Acyl-lysine deacylase
Cre02.g076000.t1.2	Serine/threonine protein kinase
Cre06.g276300.t1.1	
Cre07.g318300.t1.1	Camp-Dependent protein kinase regulatory chain
Cre17.g739850.t1.2	Predicted protein: Identified by comparative genomics as being present only in organisms having motile (MOT) cilia
Cre03.g198450.t1.2	
Cre15.g639050.t1.1	Zinc finger MYND domain containing protein 10
Cre17.g703450.t1.1	
Cre14.g623439.t1.1	Pyroglutamyl-peptidase
Cre14.g626800.t1.1	

C' (118)	
Cre09.g389900.t1.1	Hydroxyproline-rich glycoprotein
Cre26.g756847.t1.1	SF27 - CALCIUM-INDEPENDENT PHOSPHOLIPASE A2 IPLA2 -RELATED
Cre07.g345750.t1.1	Acetyltransferase (GNAT) domain (Acetyltransf_10)
Cre03.g207150.t1.1	NAD(P)-binding Rossmann-like domain (NAD_binding_8)
Cre12.g542202.t1.1	MGC174333 PROTEIN
Cre06.g288850.t1.2	
Cre07.g345850.t1.2	
Cre17.g733400.t1.2	Fusaric acid resistance protein-like (FUSC_2)
Cre04.g214650.t1.1	1,3-beta-D-glucan synthase
Cre16.g650050.t1.2	SF112 - RHODANESE-LIKE DOMAIN-CONTAINING PROTEIN 14, CHLOROPLASTIC
Cre13.g569600.t1.2	Antibiotic biosynthesis monooxygenase (ABM)
Cre07.g336900.t1.1	
Cre17.g733950.t1.2	CALCOFLUOR WHITE HYPERSENSITIVE PROTEIN PRECURSOR
Cre09.g386137.t1.1	
Cre17.g728550.t1.2	
Cre07.g345700.t1.2	Coenzyme Q-binding protein
Cre03.g200650.t1.1	SF200 - CHITINASE
Cre26.g756897.t1.1	PHD finger protein AF10
Cre17.g734000.t1.2	INNER MEMBRANE PROTEIN
Cre10.g422300.t1.2	Thioredoxin dependent peroxidase
Cre11.g480250.t1.1	Predicted lipase
Cre02.g143487.t1.1	
Cre07.g328075.t1.1	
Cre17.g734596.t1.1	
Cre10.g454250.t1.2	Peptidyl-prolyl cis-trans isomerase, FKBP-type
Cre07.g335700.t1.2	
Cre07.g355750.t1.2	F-BOX AND WD40 DOMAIN PROTEIN
Cre03.g184250.t1.2	EF-hand domain pair (EF-hand_7)
Cre02.g079650.t1.1	SF6 - SOLUTE CARRIER FAMILY 35 MEMBER G1
Cre12.g502250.t1.2	Plastid lipid associated protein
Cre12.g544450.t1.2	
Cre03.g168950.t1.2	
Cre07.g345500.t1.2	
Cre10.g463150.t1.1	SF43 - DELTA(3,5)-DELTA(2,4)-DIENOYL-COA ISOMERASE, MITOCHONDRIAL
Cre17.g707350.t1.2	
Cre17.g734200.t1.2	L,L-diaminopimelate aminotransferase
Cre07.g327450.t1.2	DnaJ-like protein
Cre13.g562526.t1.1	
Cre17.g734050.t1.1	
Cre17.g734150.t1.1	SF16 - TIP41-LIKE PROTEIN
Cre17.g734628.t1.1	SF2 - ZINC FINGER PROTEIN 593
Cre02.g143307.t1.1	ClpC chaperone, Hsp100 family
Cre02.g143587.t1.1	GENERAL TRANSCRIPTION FACTOR 3C POLYPEPTIDE 2
Cre12.g537250.t1.2	

C' cont.	
Cre17.g734612.t1.1	ABC transporter, multidrug resistance associated protein ABC transporter, multidrug resistance associated protein
Cre02.g143467.t1.1	Ulp1 peptidase / Ulp1 protease
Cre02.g076300.t1.1	Uroporphyrinogen decarboxylase
Cre17.g734548.t1.1	Pyruvate phosphate dikinase, chloroplastic
Cre17.g734516.t1.1	26S proteasome regulatory subunit 26S proteasome regulatory subunit
Cre02.g076466.t1.1	
Cre12.g561350.t1.1	SF8 - ZINC FINGER MYND DOMAIN CONTAINING PROTEIN 10
Cre17.g734400.t1.1	Ubiquitin ligase SCF complex subunit Cullin
Cre17.g734300.t1.1	SF47 - TRANSLOCASE OF CHLOROPLAST 120, CHLOROPLASTIC-RELATED
Cre02.g085450.t1.2	Coproporphyrinogen III oxidase
Cre02.g143567.t1.1	
Cre12.g551950.t1.2	Predicted protein
Cre01.g032000.t1.1	BETA CATENIN-RELATED ARMADILLO REPEAT-CONTAINING
Cre04.g227400.t1.2	Ferric-chelate reductase/ oxidoreductase
Cre17.g734450.t1.2	Plastid ribosomal protein L19
Cre17.g734100.t1.2	Adenylosuccinate synthase / Succinoadenylic kinosynthetase
Cre03.g156200.t1.1	Lectin C-type domain (Lectin_C)
Cre03.g156600.t1.2	
Cre02.g103100.t1.1	SF631 - SHORT-CHAIN DEHYDROGENASE/REDUCTASE FAMILY PROTEIN
Cre17.g734500.t1.2	Vacuolar ATP synthase subunit E
Cre09.g398050.t1.1	DIMETHYLANILINE MONOOXYGENASE
Cre01.g050950.t1.2	Geranylgeranyl diphosphate reductase / Geranylgeranyl reductase
Cre12.g553500.t1.1	Predicted protein with ankyrin repeats
Cre11.g467700.t1.1	Uroporphyrinogen-III decarboxylase
Cre10.g460150.t1.2	ERD4-related membrane protein
Cre01.g015350.t1.1	Light-dependent protochlorophyllide reductase
Cre26.g756747.t1.1	
Cre05.g242000.t1.2	Magnesium chelatase subunit D
Cre01.g045650.t1.2	DnaJ-like zinc-finger protein
Cre17.g734644.t1.1	Squalene monooxygenase / Squalene epoxidase
Cre17.g734250.t1.1	Non-specific protein-tyrosine kinase / Cytoplasmic protein tyrosine kinase
Cre17.g734709.t1.1	
Cre03.g167924.t1.1	SF3 - VERY-LONG-CHAIN (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] DEHYDRATASE HPO-8
Cre16.g663900.t1.2	Porphobilinogen deaminase
Cre17.g734350.t1.1	
Cre09.g396300.t1.2	Protoporphyrinogen oxidase
Cre43.g760497.t1.1	SF96 - ATP-DEPENDENT CLP PROTEASE
Cre09.g409650.t1.2	RING-variant domain (RINGv)
Cre01.g048600.t1.1	
Cre10.g443500.t1.2	SF1 - EXPRESSED PROTEIN-RELATED
Cre16.g695850.t1.2	
Cre02.g143367.t1.1	
Cre26.g756797.t1.1	SF59 - PROTEASOME SUBUNIT BETA TYPE-1

C' cont.	
Cre02.g083800.t2.1	dTDP-glucose 4,6-dehydratase
Cre16.g674300.t1.1	Flagellar Associated Protein
Cre03.g166500.t1.2	
Cre05.g241450.t1.2	Chloroplast SRP Receptor
Cre43.g760647.t1.1	
Cre02.g143667.t1.1	Plastid lipid associated protein Plastid lipid associated protein
Cre08.g358546.t1.1	
Cre26.g756597.t1.1	Scaffold protein Shank and related SAM domain proteins
Cre16.g668300.t1.1	
Cre12.g554400.t1.1	
Cre10.g465550.t1.1	ClpD chaperone, Hsp100 family
Cre43.g760547.t1.1	
Cre02.g110050.t1.1	SF160 - WD40 REPEAT-CONTAINING PROTEIN
Cre01.g003850.t1.1	Cytochrome P450, CYP197 superfamily
Cre11.g468250.t1.1	
Cre02.g105100.t1.2	
Cre07.g337100.t1.2	
Cre11.g467644.t1.1	ClpB chaperone, Hsp100 family ClpB chaperone, Hsp100 family
Cre03.g155250.t1.2	
Cre17.g733800.t1.1	
Cre09.g403367.t1.1	SF57 - MCG1031578
Cre02.g143547.t1.1	UBX-RELATED
Cre10.g455350.t1.2	
Cre06.g299800.t1.2	Long-chain-fatty-acid--[acyl-carrier-protein] ligase / Acyl-[acyl-carrier-protein] synthetase
Cre03.g191300.t1.2	Low-CO2-inducible protein
Cre12.g535100.t1.2	Ribosomal protein S6 kinase and related proteins
Cre17.g733650.t1.1	7-keto-8-aminopelargonic acid synthase
Cre01.g024050.t1.2	SF3 - PROTEIN RMD-2, ISOFORM B-RELATED
Cre46.g761047.t1.1	Sulfotransferase family (Sulfotransfer_3)
Cre04.g228208.t1.2	Serine/threonine protein kinase
Cre07.g345900.t1.1	Dicer-like protein (DCL3)