Supplementary Information

Molecular toxicity of cerium oxide nanoparticles to the freshwater alga *Chlamydomonas reinhardtii* is associated with supra-environmental exposure concentrations

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Supplementary Experimental Section

Ceria NP synthesis and characterisation in exposure media

The PVP-coated ceria NPs tested in this study were synthesised and characterised as described previously (Merrifield et al. 213). Larger, 'bulk' particles of ca. 500-600 nm were prepared in a similar manner, with identical reagents, but produced by heating an unstirred suspension at 140°C for 4 hours. The determination of the rate of dissolution of Ce from the core of the PVP-coated ceria NPs was calculated by placing the NPs into 100mL of exposure media at a concentration of 1ppm, without the presence of *C. reinhardtii*, under otherwise identical conditions as those used for the exposure studies. Aliquots of 10mL were collected at four time-points, 0, 24, 48 and 72 hours and then ultra-filtered using a 10mL capacity stirred ultrafiltration cell and a 1kDa regenerated cellulose membrane (Millipore Corporation, USA). Filtration was carried out at a pressure of 100psi (nitrogen gas; BOC) using 10mL of solution added to the cell and filtered slowly to reduce the volume in the ultrafiltration cell down to 5mL. At no stage were the solutions left to dry. Nitric acid was added to the samples after separation to adjust to pH 2. The Ce ions were measured by ICP-MS using an Agilent 4500ce (Agilent Technologies). Ce ion standards were used to correct for membrane losses of dissolved cerium. Both retentate and filtrate were quantified, which were assumed to be the total and ionic concentrations respectively, and particle concentrations were calculated by difference. A correction was made for sorption of dissolved metal to the membranes and container walls.

Culture of *C. reinhardtii* and ceria NP exposure studies

C. reinhardtii cultures (CCAP strain 11/32c) were grown in modified Bolds Basal Medium (BBM; Table S4, below) in sterile 2L Erlenmeyer flasks and maintained in shaking (120rpm) growth incubators (Multitron, Infors HT; Switzerland) under a 12:12 light:dark regime at 22°C. Optical density at 660nm was used to determine cell density in comparison to a pre-determined growth curve for all measures of algal growth. For all exposure studies, *C. reinhardtii* cells in exponential growth phase were treated with the relevant nominal concentrations of the NPs in 50mL BBM. For the standard growth studies, cells were inoculated at a starting density of $5x10^4$ cells/mL, while for the molecular studies the starting density was increased to $1x10^6$cells/mL to allow for a suitable amount of biomass for subsequent analyses. All growth inhibition studies were of 72-hour duration, under continuous light as detailed in standard test guidelines (OECD, 2002), and a positive control of $CuSO_4$ (160µg/L) at a concentration known to induce 50% growth inhibition was used to validate each experiment.

Growth inhibition effect concentration (EC_{50}) studies were conducted over a wide range of ceria NP concentrations (0.5-80000µg/L), also for ionic Ce ($CeNO_3$; 0.5-32mg/L) and for free PVP (0.56-56.44mg/L). Further growth inhibition studies, combined with 'omics analyses, were performed at two different dosing regimens: firstly at supra-environmental levels (80, 400, 2000 and 10000µg/L; n=8) and secondly across predicted environmental concentrations (0.029, 0.144 and 0.72µg/L; n=4). Relevant controls were also incorporated into these studies, consisting of an ionic control ($CeNO_3$, corresponding to 0.01% of the highest ceria NP concentration used, i.e. 1µg/L; n=8), a free PVP control (1.94mg/L; n=4), bulk ceria (10000µg/L; n=8) and unexposed control samples.

Measurement of the uptake of ceria NPs by *C. reinhardtii*.

Aliquots containing 1 x10^4 algae cells were collected in parallel to the exposures used for the toxicity study due to logistical constraints. Each sample was filtered using a 0.45μm regenerated cellulose membrane, and the retentate re-dispersed in 10 mL of ultrapure water and gently agitated to remove any nanoparticles loosely bound to the exterior of the cells. The algal cells were then filtered again through a 0.45μm filter. The filtrate was collected and acidified to pH 2 and Ce concentrations measured by ICP-MS. The retentate, after similar acidification and ICP-MS measurement, was assumed to be ceria which had been internalised or strongly adhered to the walls of the algal cells, while the filtrate was assumed to be a measure of the free and weakly bound NPs. Aggregation was assumed to be minimal based on data here and elsewhere (Merrifield et al. 2013).

Scanning electron microscopy of *C. reinhardtii*

Following 72-hour exposures, as described above, the algal cells were centrifuged to form a pellet and the supernatant removed. The primary fixation of the pellet of algae cells was performed by adding 5mL of 2.5% glutaraldehyde in 100mM phosphate buffer (pH 7.0) and leaving to incubate for between 2-24 hours at 4°C. No staining was performed as preliminary studies indicated commonly used stains caused sample damage and/or problems with the imaging; in fact, contrast between the algal cells and ceria was enhanced in the absence of stains. Dehydration was performed in a sequential alcohol gradient of 50%, 70%, 80% and 100%, changing every 15 minutes. The 100% alcohol solution was drained and replaced with fresh 100% alcohol three times. Resin embedding was performed by replacing the alcohol by propylene oxide. This was changed twice at 15-minute intervals, and then exchanged by a 50:50 mixture of propylene oxide and resin (Agar 100 resin) on a rotator for 3 hours. Each sample was vacuum embedded in Mollenhauer epoxy resin (Epon 812) and 100nm thick sections were cut with a glass knife on a Reichert Ultracut ultra-microtome. These sections were imaged on a Jeol 7000 scanning electron microscope fitted with a Schottky FEG emitter, using an acceleration voltage of 20 keV and both backscatter and STEM modes. Viewing in backscatter mode allowed for a greater Z contrast to be observed with high atomic number nanoparticles showing as bright areas. Viewing in STEM mode caused the higher density nanoparticles to appear as dark, electron opaque areas. Other instrument parameters were chosen to achieve the highest possible resolution images while minimising sample damage. Elemental analysis was performed using an Oxford Instruments INCA EDS system with Si-Li x-sight detector.

Mass spectrometry based metabolomics

Following the 72-hour growth inhibition exposures at both the supra-environmental and predicted environmental dosing regimens, metabolites were extracted from each sample of *C. reinhardtii* using a modified version of published methods (Bölling & Fiehn 2005; Lee & Fiehn 2008). Briefly, a 400μL aliquot of *C. reinhardtii* cell suspension was retrieved from each exposure flask and added to 1.6mL of 70% methanol that was pre-cooled on dry ice in a 2mL Eppendorf tube, and mixed by inversion. Samples were then centrifuged as described in Bölling and Fiehn (2005), the supernatants carefully discarded, and then each pellet was flash frozen in liquid nitrogen and stored at -80 °C until metabolite extraction. Metabolites were extracted from *C. reinhardtii* samples as well as an extract blank (no biological material) using the methods described in Taylor et al. (2009) with an adjustment to the solvent volumes. Here, 500μL of ice-cold methanol with 200μL ice-cold water were used for the first stage of the extraction, followed by 500µL of ice-cold chloroform with a further 250µL of ice-cold water to yield a biphasic solution. All solvents used for the quenching and extraction procedures were of HPLC grade. Polar fractions were dried in a centrifugal concentrator; non-polar samples were not used in this study.

Dried polar extracts were resuspended for metabolomics analysis as previously described (Taylor et al. 2009) and then metabolites were measured using a hybrid 7-T Fourier transform ion cyclotron resonance (FT-ICR) mass spectrometer (LTQ FT Ultra, Thermo Fisher Scientific). Each sample was analysed in negative ion mode, in triplicate, using the SIM (selected ion monitoring)-stitching method from *m/z* 70–590, and the transient data processed using the methods reported previously using *m/z* 100 SIM windows with a *m/z* 30 overlap, and filtering parameters set at 2-out-of-3 replicate filter with 85% sample filter and a mass error margin of 1.5ppm (Weber et al. 2011; Southam et al 2007; Payne et al. 2009). Further data processing steps, including probabilistic quotient normalisation, k-nearest neighbour (KNN) imputation of missing values and generalized-log transformation, were as described previously (Taylor et al. 2009, 2010; Hrydziuszko & Viant 2012). Custom written software MI-Pack was used to putatively annotate the detected peaks with metabolite names (1.5ppm mass error margin), according to the Metabolomics Standards Initiative definitions (Weber et al. 2011; Weber & Viant 2010; Sumner et al. 2007). Subsequently, the putatively annotated metabolites were investigated using the web-based software MetaboAnalyst 2.0 for biochemical pathway enrichment analysis (Xia et al. 2012).

Both univariate and multivariate statistical analyses were conducted to investigate any metabolic perturbations in response to *C. reinhardtii* exposure to ceria NPs. Methods were as described in Taylor et al.(2009), briefly, MATLAB (version 7, The Mathworks) with PLS-Toolbox (Eigenvector Research) was used to conduct the principal components analysis (PCA) on the covariance matrix. The PCA was used to visually determine the metabolic similarities and differences between treatment groups and controls. Univariate t-tests were employed to discover if any peaks in the mass spectra changed intensity significantly, using a false discovery rate (FDR) of 5% to correct for multiple testing (Benjamini & Hochberg 1995).

Microarray based transcriptomics

RNA was extracted from each sample of *C. reinhardtii*. Briefly, a 15mL cell suspension was taken from each exposure flask, and centrifuged at 3000rpm for 10min at 4°C. The supernatant was carefully discarded and the cell pellet flash frozen in liquid nitrogen and stored at -80°C until RNA extraction. RNA was extracted using the Qiagen RNeasy Plant Mini kit (Qiagen Ltd) following the manufacturer's recommended protocol. Microarray analyses were conducted on the following sample groups: unexposed controls (n=4), ionic Ce control ($CeNO_3$; 0.008µg/L; n=7) free PVP control (1.94mg/L; n=4), and two ceria NP concentrations (0.144µg/L; n=4, and 10000µg/L; n=7).

The oligonucleotide microarray was designed via Agilent eArray (Agilent Technologies) using predicted transcript sequences derived from the JGI *Chlamydomonas reinhardtii* genome project v4.0 (downloaded in June 2010: Merchant et al. 2007). Annotation from JGI was supplemented from Phytozome via BioMart and by Blast2GO (Götz et al. 2008). The microarrays were printed in 8x15k format (Agilent-029192:8x15k BhamChlamy15k1). The array design is available from ArrayExpress under accession A-MEXP-2384. Labelling was achieved using the Agilent One Colour Low Input Linear

Amplification kit with Spike-ins (Agilent Technologies) according to the manufacturer's protocol. Total RNA was converted to cRNA and labelled with fluorophore Cy3. Uncoupled Cy3 was removed using the RNeasy Mini kit (Qiagen) following the manufacturer's instructions. Labelling efficiency was determined by NanoDrop ND-1000 UV-VIS Spectrophotometer, version 3.2.1 (NanoDrop, USA). A yield of 0.825µg cRNA, and a specific activity (Cy3 dye incorporation) of >6pmol Cy3/µg cRNA was considered sufficient. Microarray hybridisation was performed using an Agilent Gene Expression Hybridisation kit according to the manufacturer's protocol. Briefly, the hybridisation mixes were loaded onto 8x15k format slides (Agilent-029192:8x15k BhamChlamy15k1) hybridised overnight (65°C), washed, stabilised and dried. The dried slides were scanned using an Agilent G2565CA microarray scanner system (Agilent Technologies).

MIAME-compliant raw microarray data and experimental design are available at the ArrayExpress database (www.ebi.ac.uk/arrayexpress) under accession number E-MTAB-2454. GeneSpring vGX7.3 (Agilent Technologies) and MultiExperimental Viewer (MeV) v4.7 were used for analysing the processed signal data (where fluorescence intensities comprised of the background subtracted signal corrected by multiplicative de-trending). Agilent feature extraction software (FE) was used for quality control, both at sample and gene level (Saeed et al. 2003). Data flagged as present in at least 20 out of 25 samples and exceeding a raw fluorescence value of 114 were used for analysis. Data were quantile normalised with GE workbench, SAM (Statistical Analysis of Microarrays) analysis was carried out within MeV (Floratos et al. 2010; Tusher et al. 2001). PCA was used to visually determine the metabolic similarities and differences between treatment groups and controls. Annotation enrichment analyses were performed using the Algal Functional Annotation Tool (http://pathways.mcdb.ucla.edu/algal/about.html) and with Blast2GO (Götz et al. 2008). Annotation enrichment compared transcripts statistically significantly altered in expression, as determined by SAM, with the list of all detected transcripts.

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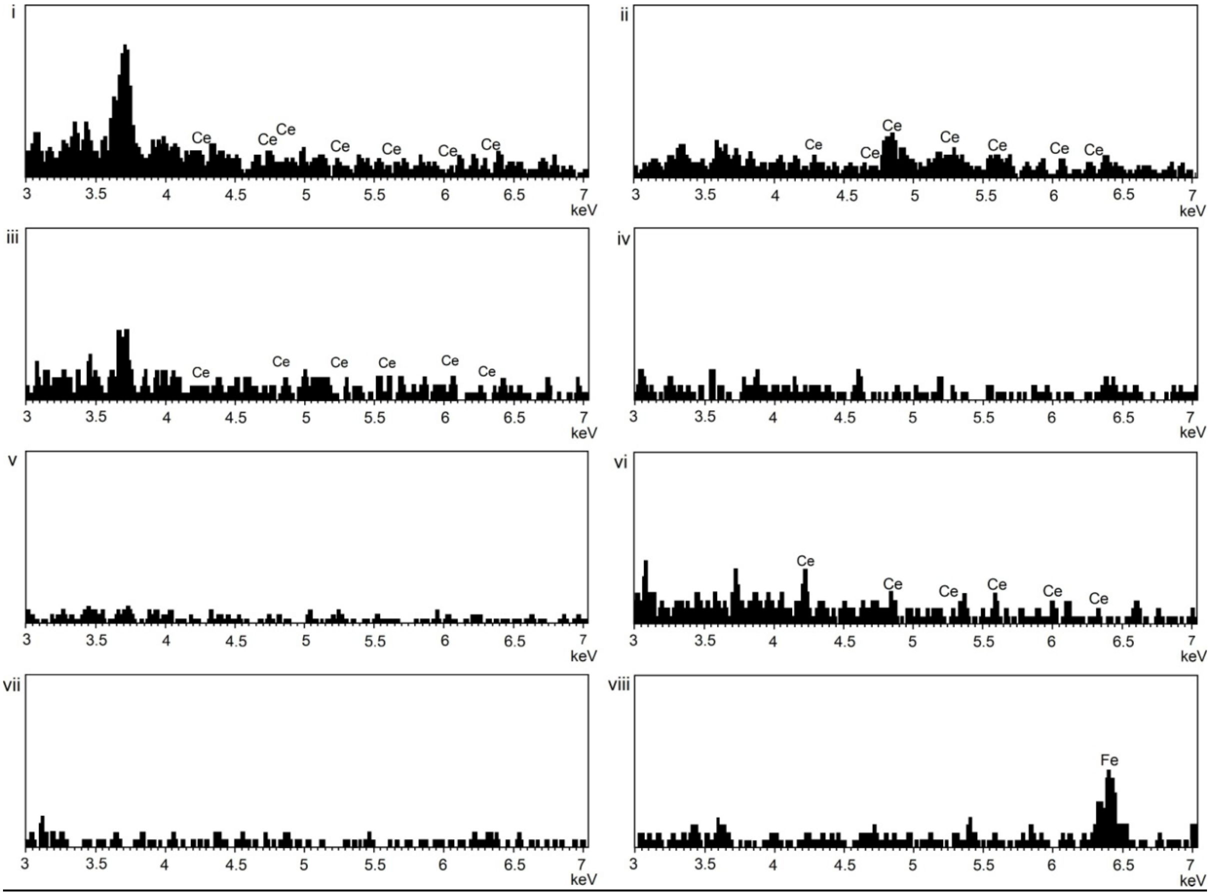

Figure S1. Energy dispersive spectra (EDS) corresponding to the arrows in Figure 4 following exposure of algal cells to a high (10000 µg/L) dose of ceria NPs (i and ii), a low dose (80 µg/L) of ceria NPs (iii and iv), bulk ceria (10000 µg/L) (v and vi), and unexposed control cells (no added cerium, vii and viii). Panels (i), (iii), (v) and (vii) show spectra collected from within the vesicles, indicating that the cells internalise and concentrate the cerium within the vesicles following ceria NP exposure but not following bulk or control exposures. Panels (ii), (iv), (vi) and (viii) show spectra collected from electron dense areas surrounding the cells indicating that ceria NPs are found within the media of the high dose exposure, that large aggregates can be identified on the cell surface in the bulk exposure, but no trace of cerium can be found in the low dose or control exposures.

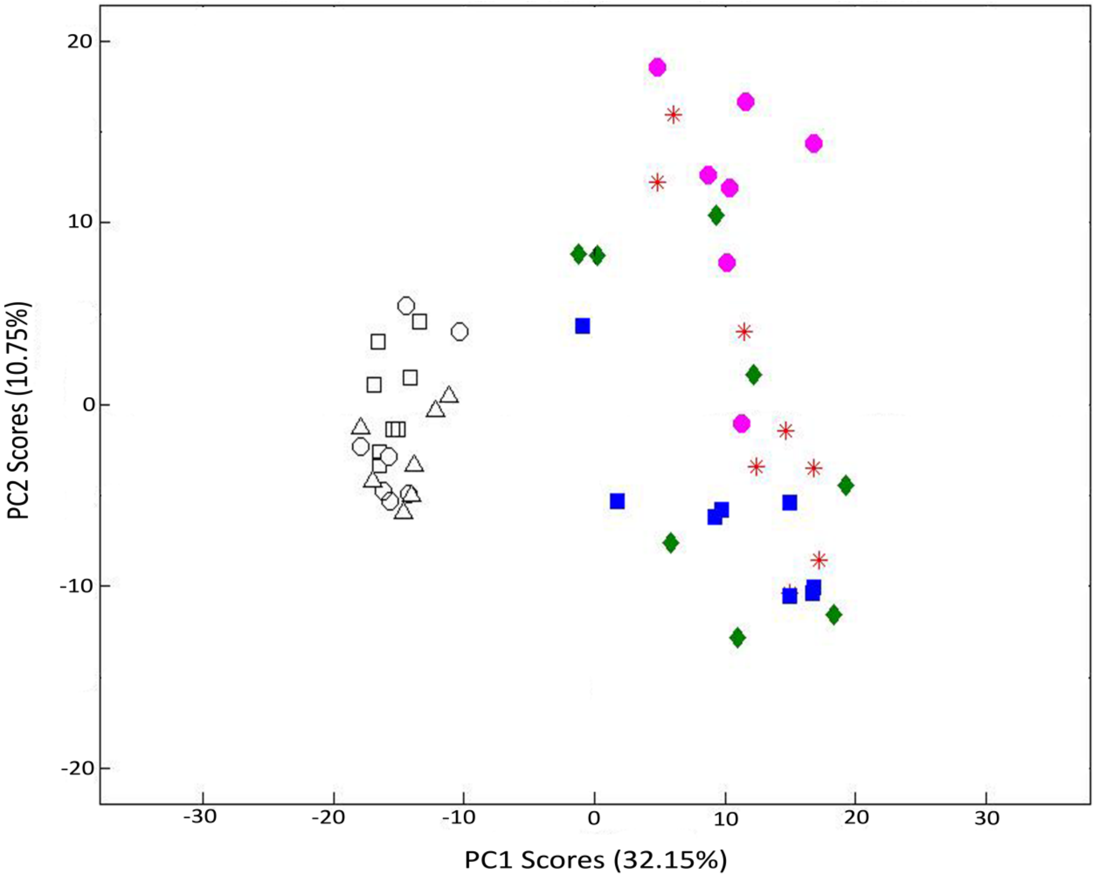

Figure S2. PCA scores plot from analysis of the FT-ICR mass spectra from *C. reinhardtii* exposed to supra-environmental concentrations of ceria NPs. Polar algal extracts were analysed in negative ion mode, each in triplicate: control (○), 10000µg/L bulk ceria (□), 1µg/L ionic Ce (△), 10,000µg/L ceria NPs (■), 2000µg/L ceria NPs (♦), 400µg/L ceria NPs (✳) and 80µg/L ceria NPs (●). ANOVA (with Tukeys post-hoc test) of the PC scores identified a significant difference between all control sample classes (unexposed, bulk and ionic) and all ceria NP-exposed samples along the PC1 axis (p-value: 1.48×10^{-20}), with no significant differences within these two groups.

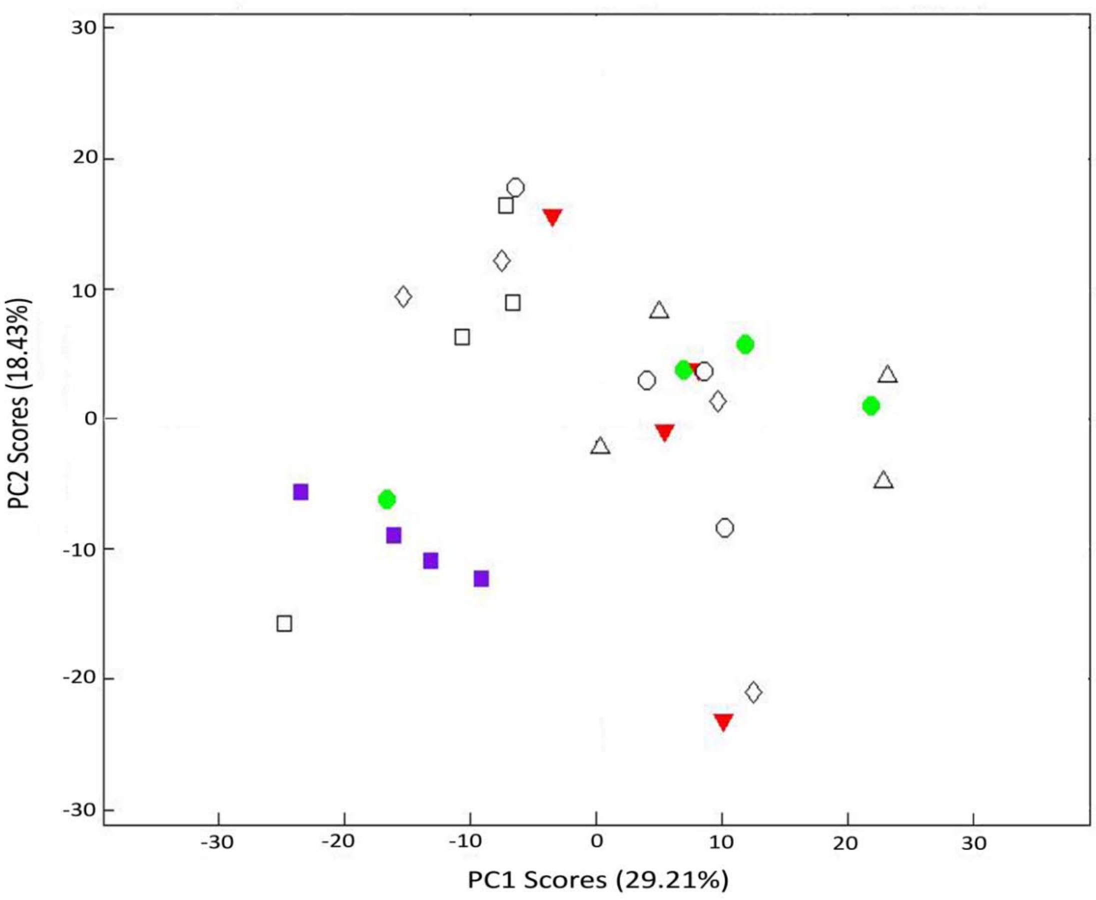

Figure S3. PCA scores plot from analysis of the FT-ICR mass spectra from *C. reinhardtii* exposed to predicted environmental concentrations of ceria NPs. Polar algal extracts were analysed in negative ion mode, each in triplicate: control (○), 10000µg/L bulk ceria (□), 1µg/L ionic Ce (△), 1.94mg/L free PVP (◊), 0.72µg/L ceria NPs (■), 0.144µg/L ceria NPs (▼) and 0.029µg/L ceria NPs (●). ANOVA of the PC scores did not identify any significant differences between sample classes.

TABLE S1. KEGG pathway enrichment analysis of the transcriptomic and metabolomic changes elicited in *C. reinhardtii* in response to 10,000µg/L ceria NPs.[a]

KEGG Pathways	Transcript Enrichment			Metabolite enrichment			Combined	
	Hits	q-value	Direction	Hits	q-value	Direction	Hits	Score
Tyrosine metabolism	4	1.64E-01	↘	2	**1.56E-05**	**↑**	6	2.55E-06
Pantothenate and CoA biosynthesis	1	7.59E-01	↓	2	**1.56E-05**	**↗**	3	1.18E-05
Valine, leucine and isoleucine biosynthesis	1	7.76E-01	↓	9	**1.56E-05**	**↗**	10	1.21E-05
Purine metabolism	9	7.87E-01	↘	3	**1.56E-05**	**↗**	12	1.22E-05
Photosynthesis	9	**1.37E-05**	**↓**	ND	ND	ND	9	1.37E-05
Pyruvate metabolism	3	6.39E-01	↓	3	**3.95E-05**	**↑**	6	2.52E-05
Pyrimidine metabolism	1	9.95E-01	↑	2	**3.31E-05**	**↓**	3	3.29E-05
Porphyrin and chlorophyll metabolism	5	2.31E-01	↘	2	**1.63E-04**	**↑**	7	3.77E-05
Lysine degradation	4	**7.76E-02**	**↗**	2	**5.23E-04**	–	6	4.06E-05
Fatty acid biosynthesis	4	**1.87E-02**	**↓**	2	**2.48E-03**	**↑**	6	4.63E-05

Glyoxylate and dicarboxylate metabolism	4	1.24E-01	↓	3	**6.87E-04**	**↓**	7	8.50E-05
Isoquinoline alkaloid biosynthesis	2	**2.79E-02**	–	1	**3.43E-03**	**↑**	3	9.59E-05
Glutathione metabolism	6	**2.36E-02**	**↘**	1	**4.58E-03**	**↑**	7	1.08E-04
Riboflavin metabolism	2	2.11E-01	↓	2	**6.87E-04**	–	4	1.45E-04
Carbon fixation in photosynthetic organisms	4	2.89E-01	↓	2	**6.87E-04**	**↓**	6	1.99E-04
Glycine, serine and threonine metabolism	1	8.78E-01	↑	5	**5.23E-04**	**↓**	6	4.59E-04
Glycerolipid metabolism	1	7.93E-01	↓	3	**9.03E-04**	**↑**	4	7.15E-04
Aminoacyl-tRNA biosynthesis	1	9.10E-01	↓	3	**9.58E-04**	**↘**	4	8.71E-04
Glycolysis or Gluconeogenesis	ND	ND	ND	3	**9.03E-04**	**↘**	3	9.03E-04
Fructose and mannose metabolism	2	5.68E-01	–	2	**1.77E-03**	**↑**	4	1.00E-03
Galactose metabolism	1	7.20E-01	↓	2	**1.77E-03**	**↑**	3	1.27E-03
Photosynthesis -	5	**1.43E-03**	**↓**	ND	ND	ND	5	1.43E-03

antenna proteins								
Pentose and glucuronate interconversions	1	4.89E-01	↓	2	**3.43E-03**	↑	3	1.68E-03
Arginine and proline metabolism	4	5.36E-01	↘	6	**3.43E-03**	↑	10	1.84E-03
Phenylalanine metabolism	5	**2.10E-03**	↘	ND	ND	ND	5	2.10E-03
Steroid biosynthesis	ND	ND	ND	3	**4.05E-03**	↓	3	4.05E-03
Biotin metabolism	4	**1.87E-02**	–	ND	ND	ND	4	1.87E-02
Oxidative phosphorylation	8	**4.76E-02**	↘	ND	ND	ND	8	4.76E-02
Ascorbate and aldarate metabolism	3	**4.94E-02**	↓	ND	ND	ND	3	4.94E-02
Tryptophan metabolism	3	**4.94E-02**	↘	ND	ND	ND	3	4.94E-02

[a] Transcriptomic changes are derived from Algal Functional Annotation Tool and metabolomic changes are derived from Met-PA. Hits show the number of pathway members in the Test Set (gene transcripts differentially expressed in algal cells following a 72-hour exposure to 10000µg/L ceria NPs, SAM, q<0.05). q-values denote false discovery rate corrected p-values for enrichment compared with a background of all identified transcripts or metabolites. Arrows indicate the direction of molecular perturbation with a consistent increase in concentration shown as ↑, a consistent decrease as ↓, a majority increase as ↗ and a majority decrease as ↘. Significant pathway enrichments with q<0.05 are shown in bold; ND denotes no enrichment detected. The combined score was generated by multiplying the q-values for both 'omics approaches and is used for the overall ranking of the pathways.

TABLE S2. Putative metabolite annotation of the significantly changing peaks detected in the mass spectra of the polar extracts of *C. reinhardtii* following exposure to 10,000μg/L ceria NPs.

Observed		Statistics		Identification				
m/z	Average intensity[a]	q-value[b]	Fold change[c]	Empirical formula	Ion form	Theoretical mass (Da)[d]	Mass error (ppm)[e]	Putative metabolite name(s)[f]
101.06080	30873.77	0.005	0.554219	C5H10O2	[M-H]-	101.0608	-0.04	['3-Methylbutanoic acid']
106.01937	12067.65	0.002	1.916562	0				0
107.01574	43308.76	0.000	2.126308	0				0
115.07649	105222.5	0.020	0.642291	0				0
116.07985	8818.179	0.007	0.633818	0				0
118.05102	12166.65	0.034	0.633111	C4H9NO3	[M-H]-	118.051	0.44	['L-Allothreonine', 'L-Homoserine', 'L-Threonine']
122.00956	23351.07	0.012	2.046954	HNO3	[M+Hac-H]-	122.0095	0.51	['Nitrate']
123.00959	37831.25	0.010	4.30716	0				0
124.00597	149721	0.012	4.530747	0				0

125.00121	11636.75	0.023	7.798644	C3H6O3	[M+Cl]-	125.0011	0.91	['(R)-Lactate', '(S)-Lactate', '3-Hydroxypropanoate', 'D-Glyceraldehyde', 'Glycerone']
125.00121	11636.75	0.023	7.798644	C4H8O2	[M+K-2H]-	125.001	1.39	['(R)-Acetoin', 'Butanoic acid']
125.06089	27196.78	0.000	0.328721	0				0
127.00049	9292.715	0.040	1.237452	0				0
127.00135	993526.4	0.014	1.305243	C3H6O4	[M+Na-2H]-	127.0013	0.56	['D-Glycerate']
127.01683	53567.11	0.045	3.803953	C3H8O3	[M+Cl]-	127.0167	0.66	['Glycerol']
127.01683	53567.11	0.045	3.803953	C4H10O2	[M+K-2H]-	127.0167	1.13	['(R,R)-Butane-2,3-diol', '(S,S)-Butane-2,3-diol']
128.00472	33995.99	0.012	1.397677	0				0
128.03540	181704.2	0.046	3.950371	C5H7NO3	[M-H]-	128.0353	0.64	['1-Pyrroline-4-hydroxy-2-carboxylate', '4-Oxoproline', '5-Oxoproline', 'L-1-Pyrroline-3-hydroxy-5-carboxylate']
128.04018	152351.1	0.037	4.618801	0				0
129.01389	18687.5	0.045	3.739633	C3H8O3	[M+(37Cl)]-	129.0138	0.72	['Glycerol']
129.01943	16694.17	0.007	2.159602	C3H2O2	[M+Hac-H]-	129.0193	0.75	['Propynoate']

129.01943	16694.17	0.007	2.159602	C5H6O4	[M-H]-	129.0193	0.75	['2,5-Dioxopentanoate', '2-Methylmaleate', '4,5-Dioxopentanoate', 'Itaconate', 'Mesaconate']
129.03655	470067.7	0.036	4.824628	0				0
130.05106	13411.74	0.002	3.143455	C5H9NO3	[M-H]-	130.051	0.71	['(S)-4-Amino-5-oxopentanoate', '5-Amino-2-oxopentanoic acid', '5-Aminolevulinate', 'L-Glutamate 5-semialdehyde', 'N-Acetyl-beta-alanine', 'cis-4-Hydroxy-D-proline', 'trans-4-Hydroxy-L-proline']
131.07147	34166.84	0.014	0.793074	C4H8O	[M+Hac-H]-	131.0714	0.77	['Butanal']
133.01435	45910.48	0.040	0.721393	C2H2O3	[M+Hac-H]-	133.0142	0.76	['Glyoxylate']
133.01435	45910.48	0.040	0.721393	C4H6O5	[M-H]-	133.0142	0.76	['(R)-Malate', '(S)-Malate', '3-Dehydro-L-threonate']
133.01568	51056.12	0.002	5.528595	0				0
133.03148	31051.46	0.025	3.696145	0				0
134.04733	83219.52	0.000	0.321791	C5H5N5	[M-H]-	134.0472	0.83	['Adenine']
134.05077	161904.5	0.002	1.885636	0				0

135.04527	51830.54	0.000	1.970527	C8H8O2	[M-H]-	135.0452	0.86	['3-Vinylcatechol', '4-Hydroxyacetophenone', '4-Hydroxyphenylacetaldehyde', 'Phenylacetic acid', 'Toluate', 'm-Methylbenzoate', 'o-Toluate']
135.04713	504412.9	0.002	2.020203	0				0
136.04863	4869.502	0.033	2.568085	0				0
136.05050	11362.58	0.007	2.116039	0				0
143.07152	41916.62	0.042	1.177413	0				0
143.99159	50679.44	0.027	1.921153	0				0
144.06676	13915.23	0.011	4.554482	C6H11NO3	[M-H]-	144.0666	0.99	['(S)-5-Amino-3-oxohexanoic acid', '2-Amino-5-oxohexanoate', '4-Acetamidobutanoate', '6-Amino-2-oxohexanoate', 'L-2-Aminoadipate 6-semialdehyde']
145.05078	16716.52	0.007	1.407145	C4H6O2	[M+Hac-H]-	145.0506	1.01	['Diacetyl']
145.05078	16716.52	0.007	1.407145	C6H10O4	[M-H]-	145.0506	1.01	['(R)-3-Hydroxy-3-methyl-2-oxopentanoate', '(R)-4-Dehydropantoate', '(S)-2-Aceto-2-

								hydroxybutanoate', '2-Dehydropantoate', '4-Hydroxy-2-oxohexanoic acid', 'Adipate']
145.08717	30236.98	0.026	1.223963	0				0
145.09841	20850.02	0.033	0.679907	C6H14N2O2	[M-H]-	145.0983	1.09	['(3S)-3,6-Diaminohexanoate', '(3S,5S)-3,5-Diaminohexanoate', '2,5-Diaminohexanoate', 'D-Lysine', 'L-Lysine']
147.04719	21792.38	0.041	3.724082	0				0
150.04231	337081.4	0.000	8.778464	C5H5N5O	[M-H]-	150.0421	1.18	['Guanine']
151.04567	19689.98	0.036	6.99551	0				0
158.98900	21554.73	0.025	1.894868	0				0
160.06632	103398.1	0.020	6.863768	0				0
161.06268	461675.7	0.023	7.638953	0				0
162.97779	152196	0.007	1.794965	0				0
169.01739	76278.74	0.002	2.447252	0				0
171.02750	46142.5	0.037	6.528302	C5H10O5	[M+Na-2H]-	171.0275	0.04	['D-Lyxose', 'D-Ribose', 'D-Ribulose', 'D-Xylose', 'D-Xylulose', 'L-Arabinose', 'L-Lyxose', 'L-Ribulose', 'L-Xylulose']
171.04181	143743.2	0.025	4.84874	0				0

171.10267	19974.7	0.007	2.075481	$C_9H_{16}O_3$	[M-H]-	171.1027	0.01	['9-Oxononanoic acid']
171.13905	94920.1	0.001	1.816465	$C_{10}H_{20}O_2$	[M-H]-	171.1391	-0.02	['Decanoic acid']
175.07241	23558.65	0.002	3.258927	0				0
180.06659	10135.61	0.030	1.545147	$C_9H_{11}NO_3$	[M-H]-	180.0666	-0.15	['3-Amino-3-(4-hydroxyphenyl)propanoate', 'L-Tyrosine']
181.07094	102350.4	0.001	6.90273	0				0
181.07174	496771.2	0.021	8.142082	$C_6H_{14}O_6$	[M-H]-	181.0718	-0.13	['D-Sorbitol', 'Galactitol', 'Mannitol']
194.09373	25572.91	0.002	0.475613	0				0
194.98878	32394.24	0.013	2.049982	0				0
195.06633	24089.82	0.024	1.530928	$C_{10}H_{12}O_4$	[M-H]-	195.0663	0.24	['5-Hydroxyconiferyl alcohol']
195.06633	24089.82	0.024	1.530928	$C_8H_8O_2$	[M+Hac-H]-	195.0663	0.24	['3-Vinylcatechol', '4-Hydroxyacetophenone', '4-Hydroxyphenylacetaldehyde', 'Phenylacetic acid', 'Toluate', 'm-Methylbenzoate', 'o-Toluate']
195.06817	10184.87	0.030	0.342329	0				0
195.08041	9003.352	0.012	0.385506	0				0
195.08091	11434.34	0.012	0.493433	0				0

195.08278	33344.7	0.007	0.488406	0				0
195.08328	41396.65	0.019	0.59062	0				0
195.08708	1.2E+08	0.020	0.696022	0				0
195.09144	29076.72	0.018	0.488304	0				0
195.09195	22527.32	0.012	0.46541	0				0
196.09065	5311906	0.007	0.722561	0				0
197.04298	28407.8	0.007	2.227069	C7H12O5	[M+Na-2H]-	197.0431	-0.83	['(2R,3S)-3-Isopropylmalate', '2-Propylmalate', '3-Propylmalate', 'alpha-Isopropylmalate']
197.09016	12825.03	0.043	0.636569	0				0
197.09168	793446.9	0.001	0.541202	0				0
197.09412	157673.7	0.001	0.61381	0				0
198.09505	57560.42	0.002	0.598494	0				0
199.05899	19204.86	0.009	2.336553	0				0
199.06535	237634.2	0.025	2.344363	0				0
200.06623	68526.14	0.028	2.349185	C10H13NO	[M+(37Cl)]-	200.0662	0.32	['(R)-2-Methylimino-1-phenylpropan-1-ol']
201.11328	39973.01	0.023	1.266359	0				0
202.10851	40477.23	0.017	4.019783	0				0

204.12417	194549	0.020	0.478965	C9H19NO4	[M-H]-	204.1241	0.18	['Pantothenol']
206.07183	26525.99	0.010	2.837502	0				0
206.10343	10356.26	0.040	2.222161	0				0
206.96764	31387.89	0.048	0.513623	C3H7O7P	[M+Na-2H]-	206.9676	0.14	['2-Phospho-D-glycerate', '3-Phospho-D-glycerate']
207.05105	18245.86	0.002	1.944437	C5H8O5	[M+Hac-H]-	207.051	0.1	['(R)-2-Methylmalate', '(S)-2-Methylmalate', '2-Dehydro-3-deoxy-D-xylonate', '2-Dehydro-3-deoxy-L-arabinonate', '2-Hydroxyglutarate', 'D-Xylonolactone', 'D-erythro-3-Methylmalate', 'D-threo-3-Methylmalate', 'L-Arabinono-1,4-lactone', 'L-threo-3-Methylmalate']
207.06392	10948.02	0.025	0.367141	0				0
207.06820	107658	0.009	2.879166	0				0
207.08744	330446.2	0.000	0.419149	C6H12O4	[M+Hac-H]-	207.0874	0.13	['(R)-2,3-Dihydroxy-3-methylpentanoate', '(R)-Mevalonate', '(R)-Pantoate']
208.07447	16500.64	0.019	3.265773	C8H15NO3	[M+Cl]-	208.0746	-0.6	['Swainsonine']
208.09080	29208.43	0.000	0.460788	0				0

209.00305	14327.23	0.012	1.840601	0				0
209.00436	658144.3	0.012	1.723801	0				0
209.03032	46674.11	0.022	0.383615	C4H6O6	[M+Hac-H]-	209.0303	0.13	['(R,R)-Tartaric acid', 'meso-Tartaric acid']
209.10310	148090.3	0.000	0.354921	0				0
210.00775	33866.26	0.019	1.683987	0				0
210.03844	80262.18	0.043	9.313115	C7H11NO5	[M+Na-2H]-	210.0384	0.23	['AminoDHQ', 'L-2-Amino-6-oxoheptanedioate', 'N-Acetyl-L-glutamate']
210.06325	1120700	0.000	9.656773	C5H5N5O	[M+Hac-H]-	210.0633	-0.06	['Guanine']
210.10644	13343.04	0.000	0.35914	0				0
210.96263	21812.29	0.025	1.337578	0				0
211.04914	44724.8	0.041	5.741316	C7H14N2O3	[M+K-2H]-	211.049	0.43	['N-Acetylornithine']
211.06666	74397.41	0.009	6.337529	C7H14N2O3	[M+(37Cl)]-	211.0669	-1.11	['N-Acetylornithine']
213.01216	14687.62	0.030	1.869251	0				0
213.05209	9498.671	0.046	0.276794	C6H6N2O3	[M+Hac-H]-	213.0517	1.85	['Imidazol-5-yl-pyruvate']
213.05353	410477.9	0.002	0.241493	0				0
214.05689	29305.62	0.003	0.289547	0				0
214.94951	133315.4	0.048	2.388955	0				0
214.99243	149122.6	0.031	6.534752	0				0

215.05060	112775.1	0.002	0.251586	0				0
215.12890	17366.19	0.036	1.324041	0				0
216.94658	34360.69	0.015	2.230875	0				0
216.99042	118752.1	0.036	6.527365	0				0
218.10342	16818.62	0.027	3.475418	$C_9H_{17}NO_5$	[M-H]-	218.1034	0.1	['Pantothenate']
218.10342	16818.62	0.027	3.475418	$C_7H_{13}NO_3$	[M+Hac-H]-	218.1034	0.1	['5-Acetamidopentanoate', 'Calystegin A3']
221.10308	52837.1	0.005	0.351009	0				0
230.13970	16640.41	0.043	1.490469	0				0
232.04512	101730.3	0.001	6.687574	0				0
232.08737	27714.42	0.043	4.114087	0				0
235.09351	71972.22	0.043	2.673723	0				0
236.91023	13568.8	0.009	2.715028	0				0
237.09789	91157.76	0.050	0.110461	0				0
237.13428	64291.55	0.001	0.288764	0				0
242.00705	222874.6	0.047	2.388989	$C_{10}H_7NO_5$	[M+Na-2H]-	242.0071	-0.18	['7,8-Dihydroxykynurenate']
243.02747	13930.42	0.042	0.436293	$C_6H_{13}O_8P$	[M-H]-	243.0275	-0.25	['L-Fucose 1-phosphate', 'L-Fuculose 1-phosphate', 'L-Rhamnulose 1-phosphate']

243.02747	13930.42	0.042	0.436293	C4H9O6P	[M+Hac-H]-	243.0275	-0.25	['L-3,4-Dihydroxybutan-2-one 4-phosphate']
243.02747	13930.42	0.042	0.436293	C11H10O5	[M+Na-2H]-	243.0275	-0.1	['2-Succinylbenzoate']
243.06564	41538.53	0.046	2.466848	0				0
246.07470	26007.7	0.013	0.692404	0				0
247.04377	289347.4	0.025	3.504037	0				0
247.11864	32203.92	0.031	0.764237	0				0
248.01902	53903.16	0.000	6.599916	0				0
250.16594	171950.7	0.002	1.890207	0				0
251.14995	224983	0.000	0.274976	0				0
251.16928	20770.07	0.007	1.782244	0				0
252.14519	68254.85	0.002	0.446779	0				0
252.15328	28899.13	0.005	0.353457	0				0
252.99412	10659.27	0.041	1.719025	0				0
253.03050	81187.8	0.050	2.914994	0				0
254.00599	36147.59	0.033	5.55626	0				0
254.12445	38329	0.005	0.46297	0				0
255.23101	127422.2	0.031	1.519548	0				0

258.13462	10598.41	0.027	2.462186	C10H17NO3	[M+Hac-H]-	258.1347	-0.3	['Ecgonine methyl ester']
259.13698	43988.62	0.007	2.028055	0				0
261.05910	51406.24	0.035	0.418581	0				0
261.13430	67006.42	0.000	0.398177	0				0
261.13741	52314.38	0.028	11.56825	C13H24N2O	[M+K-2H]-	261.1375	-0.23	['Anapheline', 'Cuscohygrine']
262.04858	11838.22	0.033	0.754668	C10H13NO5	[M+Cl]-	262.0488	-0.75	['L-Arogenate']
262.04858	11838.22	0.033	0.754668	C14H11NO3	[M+Na-2H]-	262.0486	0.07	['1,3-Dihydroxy-N-methylacridone']
262.95282	26036.05	0.034	0.561716	0				0
263.14992	17158.54	0.019	0.546253	0				0
264.10881	62573.94	0.040	4.086474	0				0
264.11358	167548.2	0.018	2.696031	0				0
264.14518	133340.5	0.002	0.268863	C9H19NO4	[M+Hac-H]-	264.1453	-0.31	['Pantothenol']
265.10994	586610.7	0.021	2.670175	0				0
265.11688	23703.76	0.034	4.961067	0				0
265.12920	57396.9	0.013	0.596789	0				0
266.00473	35571.79	0.011	0.562049	0				0
266.11328	76585.66	0.027	5.303706	0				0

266.16084	128937.5	0.000	0.38977	0				0
267.10848	31495.09	0.023	0.475203	0				0
267.16417	15700.57	0.007	0.450783	0				0
269.08780	21215.64	0.043	2.818885	C7H14O7	[M+Hac-H]-	269.0878	-0.03	['Sedoheptulose']
269.08780	21215.64	0.043	2.818885	C13H16N2O2	[M+(37Cl)]-	269.0876	0.63	['Melatonin']
270.00094	27572.49	0.031	4.033076	0				0
270.12073	69511.52	0.000	0.219278	0				0
276.94965	67873.11	0.044	0.585453	0				0
278.22059	21780.29	0.033	0.484564	0				0
281.12162	9869.658	0.026	1.895051	0				0
281.17337	17077.39	0.050	0.730643	0				0
282.93668	60618.49	0.025	0.536672	0				0
298.13941	35270.74	0.044	7.657525	0				0
298.91048	32697.21	0.034	0.571895	0				0
301.23827	31644.28	0.022	1.50498	0				0
306.98124	41272.54	0.026	1.328424	0				0
307.21249	25661.22	0.007	0.660474	0				0
312.96831	17810.28	0.018	2.154808	0				0

313.23831	23609.29	0.002	1.758984	C18H34O4	[M-H]-	313.2384	-0.39	['12,13-DHOME', '9,10-DHOME']
313.23831	23609.29	0.002	1.758984	C16H30O2	[M+Hac-H]-	313.2384	-0.39	['(9Z)-Hexadecenoic acid']
314.04816	91295.39	0.013	11.84962	0				0
315.25395	332203.4	0.027	1.754906	C16H32O2	[M+Hac-H]-	315.2541	-0.42	['Hexadecanoic acid']
316.25730	72575.73	0.035	1.687626	0				0
317.05465	24071.02	0.020	1.605501	0				0
317.14520	420316.9	0.003	2.142644	0				0
317.25033	48400.76	0.002	2.343127	0				0
318.14853	52635.76	0.007	2.050006	0				0
323.02844	98446	0.001	0.134838	C9H13N2O9P	[M-H]-	323.0286	-0.48	['3-UMP', 'Pseudouridine 5-phosphate', 'UMP']
325.16562	16123.04	0.000	1.955838	C15H22O4	[M+Hac-H]-	325.1657	-0.13	['Xanthoxic acid']
326.23356	47488.22	0.041	1.889902	0				0
327.21760	13919.77	0.041	1.3891	C18H32O5	[M-H]-	327.2177	-0.3	['2,3-Dinor-8-iso prostaglandin F1alpha']
329.04675	333960.8	0.022	5.708872	0				0
331.02016	25624.84	0.036	0.499861	0				0
331.15337	11675.17	0.048	0.268324	0				0
331.16084	5821712	0.012	0.289025	0				0

331.22377	19654.41	0.043	2.335481	0				0
332.16425	663745.9	0.011	0.278188	0				0
332.23609	66338.89	0.041	3.067825	0				0
333.02347	17989.18	0.002	0.694154	C6H11O10P	[M+Hac-H]-	333.0228	1.89	['1-Phospho-alpha-D-galacturonate', '3-Dehydro-L-gulonate 6-phosphate', '6-Phospho-2-dehydro-D-gluconate', 'D-Glucuronate 1-phosphate']
333.16521	107904.6	0.010	0.262135	0				0
333.23949	16444.08	0.044	2.65673	0				0
334.20418	34627.02	0.012	3.419776	0				0
334.98187	48520.54	0.012	0.622182	0				0
335.01254	18000.28	0.000	0.497865	0				0
335.24387	52501.21	0.001	0.445466	0				0
336.03020	71474.89	0.007	7.857722	0				0
336.97089	434801.7	0.024	0.488314	0				0
337.10345	21658.69	0.028	0.634258	0				0
337.97424	37909.81	0.024	0.505985	0				0
338.96903	63891.38	0.025	0.489913	0				0

339.02712	30498.23	0.021	0.787708	C15H12O7	[M+Cl]-	339.0277	-1.73	['Pentahydroxyflavanone', 'Taxifolin']
339.02712	30498.23	0.021	0.787708	C16H14O6	[M+K-2H]-	339.0276	-1.55	['Dihydrokalafungin']
340.2493	66525.71	0.046	1.995322	0				0
342.95783	384937.9	0.044	0.637668	0				0
343.06232	40358.9	0.025	0.334359	0				0
344.05168	8954.303	0.044	0.517629	0				0
344.95600	25848.01	0.044	0.662248	0				0
345.01052	37311.57	0.024	0.137237	C9H13N2O9P	[M+Na-2H]-	345.0105	-0.06	['3-UMP', 'Pseudouridine 5-phosphate', 'UMP']
345.06970	14658.73	0.009	0.63415	0				0
345.07793	23778.38	0.025	0.614163	0				0
346.29625	31508.81	0.030	0.63781	0				0
352.00416	42238.26	0.000	6.253932	0				0
356.99956	12848.51	0.017	0.445892	0				0
358.85986	10275.81	0.043	0.551457	0				0
359.22048	15893	0.036	0.484055	C20H34O4	[M+Na-2H]-	359.2204	0.28	['11,12-DHET', '14,15-DHET', '5,6-DHET', '8,9-DHET', 'Aphidicolin']
360.07151	18390.7	0.000	0.296749	0				0

362.05077	20108.6	0.043	0.21384	$C_{10}H_{14}N_5O_8P$	[M-H]-	362.0507	0.12	['GMP', 'Guanosine 3-phosphate', 'Precursor Z']
362.05077	20108.6	0.043	0.21384	$C_{11}H_{21}NO_6S_2$	[M+Cl]-	362.0504	0.93	['3-Methylthiopropyl-desulfoglucosinolate']
367.21280	4350.24	0.044	2.098926	$C_{20}H_{32}O_6$	[M-H]-	367.2126	0.51	['11-Dehydro-thromboxane B2', '6-Keto-prostaglandin E1', 'Prostaglandin G2']
372.30388	6548.387	0.011	0.249228	0				0
373.01061	62341.25	0.001	2.132947	0				0
374.06951	44513.22	0.001	11.34243	0				0
375.20256	14240.8	0.013	0.583005	0				0
376.21634	11998.6	0.007	3.418642	0				0
378.97657	23316.8	0.013	1.967506	0				0
378.98138	12508.15	0.040	0.551989	0				0
380.28067	8580.011	0.041	0.614527	0				0
380.91375	149444.7	0.029	0.57645	0				0
382.91187	20486.07	0.030	0.564546	0				0
383.19224	9437.492	0.001	0.50751	$C_{20}H_{30}N_2O_3$	[M+(37Cl)]-	383.1921	0.38	['13-(2-Methylcrotonoyl)oxylupanine']
387.00383	26549.33	0.018	0.744522	0				0
388.96335	10294.51	0.041	2.21757	0				0

389.00095	18494.72	0.025	0.754746	C10H13N2O11P	[M+Na-2H]-	389.0004	1.49	['Orotidine 5-phosphate']
389.06802	229368.4	0.021	5.691306	0				0
389.21814	47920.13	0.008	0.67408	0				0
391.04155	21919.98	0.043	0.431156	0				0
392.07058	17269.3	0.004	0.660111	0				0
392.99232	11725.5	0.036	4.092264	0				0
393.02939	7243.929	0.050	0.463244	0				0
394.96663	5123.92	0.042	1.790546	0				0
394.97136	33099.07	0.007	1.907879	0				0
395.01856	9389.987	0.040	0.340605	0				0
395.08979	71644.07	0.024	0.79668	C20H22O6	[M+K-2H]-	395.0902	-1.16	['Matairesinol']
396.03026	24616.43	0.032	6.617968	0				0
396.05140	85028.69	0.004	7.096663	0				0
396.88767	44300.63	0.022	0.414127	0				0
396.98296	29663.34	0.010	0.555085	0				0
399.02612	10204.56	0.035	0.64467	0				0
399.09969	11447.64	0.022	2.165422	0				0

400.21064	122029.4	0.024	0.355362	0	0
403.00006	1174850	0.026	0.789238	0	0
403.99680	4369.525	0.030	3.246265	0	0
404.00347	127158	0.041	0.803715	0	0
404.99818	85438.79	0.016	0.773985	0	0
405.00387	20616.95	0.011	0.681733	0	0
405.03176	45695.85	0.017	0.144539	0	0
406.00154	9153.281	0.036	0.75085	0	0
406.94931	21107.95	0.012	0.77953	0	0
407.02420	34013.66	0.025	5.287421	0	0
410.08090	10456.76	0.025	0.660721	0	0
412.02528	61712.16	0.000	5.521004	0	0
413.29089	36494.4	0.023	0.40733	0	0
415.00007	8541.158	0.019	0.584558	0	0
416.97952	6271.924	0.001	0.429897	0	0
417.03668	59464.16	0.046	3.30599	0	0
417.22850	10569.18	0.020	2.89085	0	0
417.32214	332910.6	0.044	0.781391	0	0

418.97400	399597.6	0.023	0.574542	0				0
419.33022	10613.98	0.043	0.755125	$C_{28}H_{46}O$	[M+Na-2H]-	419.3295	1.64	['24-Methylenecholesterol', '4alpha-Methylzymosterol', 'Campest-4-en-3-one', 'Episterol', 'Fecosterol']
419.97741	43435	0.027	0.576194	0				0
420.96513	10609.33	0.050	0.666701	0				0
420.97215	57853.43	0.020	0.545912	0				0
420.97769	6686.12	0.024	0.637563	0				0
422.22977	8619.516	0.007	2.141872	0				0
430.01096	20642.08	0.020	0.659557	0				0
436.94617	10299.27	0.043	0.387488	0				0
440.85139	22451.31	0.049	0.470746	0				0
440.93488	43480.3	0.031	0.515917	0				0
441.03916	23696.46	0.043	0.411719	0				0
442.93315	8267.073	0.011	0.432965	0				0
445.24430	10413.22	0.041	0.540845	$C_{20}H_{34}O_7$	[M+Hac-H]-	445.2443	-0.02	['Oleandolide']
445.25469	17190.69	0.032	1.335831	$C_{24}H_{40}O_5$	[M+(37Cl)]-	445.254	1.49	['Cholic acid']
446.14642	4508.743	0.028	1.818024	0				0

446.85994	6630.954	0.024	0.302032	0				0
446.93506	4342.773	0.036	0.673843	0				0
447.33275	7762.377	0.038	2.399131	0				0
451.09239	7009.633	0.018	0.602381	0				0
455.01357	95338.11	0.035	1.962844	0				0
455.09737	70691.46	0.013	1.730946	C17H21N4O9P	[M-H]-	455.0973	0.06	['FMN']
455.96808	20402.8	0.001	6.154062	0				0
456.01703	11786	0.036	2.135413	0				0
456.10076	13121.74	0.031	1.728465	0				0
457.00828	33531.7	0.044	0.434057	0				0
457.31713	7573.774	0.050	2.146374	0				0
461.02098	18029.07	0.013	0.345368	0				0
461.31204	4932.762	0.012	0.571876	0				0
462.16243	10244.3	0.041	1.672694	0				0
462.91683	178675.6	0.020	0.597486	0				0
464.91496	25587.43	0.031	0.660485	0				0
465.20477	8437.601	0.007	3.673081	0				0
467.30828	2286.352	0.034	2.761173	0				0

467.31436	100336.9	0.001	2.938404	C28H46O4	[M+Na-2H]-	467.3143	0.17	['3-Dehydroteasterone']
468.31763	23929.52	0.001	2.993613	0				0
470.98753	102075.1	0.012	1.542226	0				0
471.99111	12580.58	0.036	1.567841	0				0
472.90393	9042.702	0.046	0.391256	0				0
473.04494	20347.17	0.011	2.170725	0				0
477.07949	16095.65	0.027	1.852751	C17H21N4O9P	[M+Na-2H]-	477.0793	0.42	['FMN']
477.95016	13801.5	0.025	4.073854	0				0
478.05438	51793.25	0.011	9.214642	0				0
479.26913	12800.19	0.033	0.308484	0				0
483.27280	17228.21	0.048	0.427259	C27H42O6	[M+Na-2H]-	483.2728	-0.02	['3-Dehydroecdysone']
487.30580	36843.2	0.014	4.941723	0				0
490.86467	6192.843	0.029	0.437448	0				0
494.02849	32949.37	0.001	5.84974	0				0
494.88582	16112.09	0.043	0.472906	0				0

500.97064	4122.168	0.044	0.559497	0	0
500.97718	218491.7	0.025	0.628774	0	0
501.98050	25990.31	0.043	0.638596	0	0
506.96396	32383.23	0.041	0.784985	0	0
510.00237	18256.89	0.043	2.839915	0	0
512.01404	13813.01	0.020	0.656641	0	0
516.01022	34202.9	0.002	4.753122	0	0
516.95101	67361.46	0.036	0.423923	0	0
516.97205	19412.49	0.027	0.457413	0	0
518.94914	16997.17	0.044	0.419874	0	0
522.83353	14325.62	0.041	0.41742	0	0
522.93790	53976.83	0.013	0.547931	0	0
527.95779	50976.84	0.008	0.068359	0	0
529.46253	26172.26	0.017	0.491351	0	0
537.01664	63204.62	0.043	1.974318	0	0
537.10055	22497.61	0.011	1.941507	0	0
537.97128	20506.44	0.012	4.053712	0	0
538.82841	15268.5	0.045	0.424234	0	0

538.91170	13424.44	0.044	0.396541	0				0
539.07325	9539.12	0.026	0.448904	0				0
544.91185	2683.584	0.040	0.573179	0				0
544.91992	144393.8	0.011	0.582322	0				0
545.92328	15383.57	0.016	0.62287	0				0
546.91805	23881.46	0.043	0.691761	0				0
549.03685	7352.459	0.023	2.782517	0				0
552.99049	76596.34	0.049	1.435629	0				0
553.07450	7110.883	0.008	2.911447	0				0
553.94515	12636.18	0.031	4.78392	0				0
555.28442	110453	0.004	0.149613	0				0
556.07675	10407.29	0.031	0.641266	0				0
557.10821	46958.45	0.002	0.069674	0				0
558.06419	23231.02	0.008	0.188537	$C_{15}H_{23}N_5O_{14}P_2$	[M-H]-	558.0644	-0.38	['ADP-ribose', 'Phosphoribosyl-AMP']
558.95624	26757.04	0.043	1.519944	0				0
562.91299	10276.38	0.048	0.512478	0				0
564.34422	146251.7	0.038	0.615312	0				0
565.34736	49145.49	0.028	0.603372	0				0

576.88866	14082.87	0.046	0.440311	0	0

a) Average intensity across all samples.

b) From t-test between unexposed control and 10,000ug/L ceria NP exposed samples with a false discovery rate (FDR) of 5% to correct for multiple hypothesis testing.

c) Fold change in intensity from control to NP exposed group.

d) Calculated for the specified ion form of the empirical formula.

e) Error between the observed and theoretical masses, presented as parts per million of the theoretical mass.

f) Derived from the transformation mapping approach for metabolite identification, described in Weber and Viant (2010).

TABLE S3. Significantly differentially expressed gene transcripts of *C. reinhardtii* following exposure to 10,000μg/L ceria NPs relative to controls.

Probe	Gene ID (Augustus 9)	Putative Identity	Fold-change[a]	q-value[b]	Chromosome	Gene start (bp)	Gene end (bp)	KEGG ID
CUST_14053_PI425379931	Au9.Cre05.g235850	hypothetical protein CHLREDRAFT_151001	6.298	8.40E-03	chromosome_5	1237659	1241153	
CUST_2595_PI425379931	Au9.Cre02.g089400	hydroxyproline-rich glycoprotein	5.773	1.25E-02	chromosome_2	2025984	2030918	
CUST_11072_PI425379931	Au9.Cre06.g302050	Glycosyl transferase	5.679	2.75E-02	chromosome_6	6435637	6451284	K00706
CUST_13501_PI425379931	Au9.Cre05.g243600	glyoxal or galactose oxidase	4.999	2.75E-02	chromosome_5	2523771	2546350	
CUST_2674_PI425379931	Au9.Cre05.g243450	glyoxal or galactose oxidase	4.872	2.75E-02	chromosome_5	2496721	2504660	
CUST_10131_PI425379931	Au9.Cre13.g605200	Matrix metalloproteinase	4.147	3.54E-02	chromosome_13	6182735	6188609	
CUST_3362_PI425379931	Au9.Cre20.g758600	predicted protein	4.036	1.05E-02	scaffold_20	171591	174752	
CUST_14219_PI425379931	Au9.Cre02.g127250	hydroxyproline-rich glycoprotein, cell wall protein	3.826	8.40E-03	chromosome_2	6909281	6914671	
CUST_13377_PI425379931	Au9.Cre06.g292900	glycosyltransferase-like 1b	3.797	1.26E-02	chromosome_6	5157291	5163612	

CUST_3569_PI425379931	Au9.Cre17.g732350	glyoxal or galactose oxidase	3.725	3.89E-02	chromosome_17	4512061	4520282	
CUST_5561_PI425379931	Au9.Cre01.g036350	Plasma membrane-type proton ATPase	3.697	3.89E-02	chromosome_1	5055136	5067549	K05850
CUST_96_PI425379931	Au9.Cre01.g047150	predicted protein	3.622	1.94E-02	chromosome_1	6489928	6493130	
CUST_9049_PI425379931	Au9.Cre05.g235600	hypothetical protein CHLREDRAFT_151001	3.548	8.40E-03	chromosome_5	1207134	1210265	
CUST_2852_PI425379931	Au9.Cre06.g299900	hypothetical protein CHLREDRAFT_205652	3.496	2.83E-02	chromosome_6	6134122	6138691	
CUST_431_PI425379931	Au9.Cre08.g361400	tesmin/tso1-related	3.483	9.21E-03	chromosome_8	495624	505192	
CUST_13156_PI425379931	Au9.Cre03.g155750	lithostathine	3.451	2.75E-02	chromosome_3	1001702	1006243	
CUST_9609_PI425379931	Au9.Cre09.g393700	Matrix metalloproteinase	3.368	9.46E-03	chromosome_9	1215145	1220632	
CUST_1269_PI425379931	Au9.Cre19.g754150	predicted protein	3.327	6.85E-03	scaffold_19	361144	365912	
CUST_12973_PI425379931	Au9.Cre02.g117200	beta-galactosidase	3.176	2.75E-02	chromosome_2	5684579	5691266	K12308
CUST_10355_PI425379931	Au9.Cre06.g263700	predicted protein	3.04	3.68E-02	chromosome_6	1932276	1935573	
CUST_5289_PI425379931	Au9.Cre16.g657900	er-targeted preprotein translocase subunit	3.031	2.75E-02	chromosome_16	1314865	1317210	K09540
CUST_14634_PI425379931	Au9.Cre10.g441550	hypothetical protein CHLREDRAFT_144191	2.954	2.75E-02	chromosome_10	3024020	3029805	

CUST_8481_PI425379931	Au9.Cre09.g390300	Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	2.937	1.52E-02	chromosome_9	689304	702835	K14510
CUST_4080_PI425379931	Au9.Cre17.g732600	glyoxal or galactose oxidase	2.91	2.88E-02	chromosome_17	4560471	4574487	
CUST_1157_PI425379931	Au9.Cre01.g026500	pepsin-type aspartyl protease	2.904	3.66E-02	chromosome_1	3888839	3892804	
CUST_14359_PI425379931	Au9.Cre01.g046400	Membrane selenoprotein	2.893	2.88E-02	chromosome_1	6423308	6429972	
CUST_6563_PI425379931	Au9.Cre01.g046450	Membrane selenoprotein	2.832	3.80E-02	chromosome_1	6431298	6435508	
CUST_4754_PI425379931	Au9.Cre12.g487050	predicted protein	2.804	1.76E-02	chromosome_12	470518	474583	
CUST_12086_PI425379931	Au9.Cre06.g306000	glyoxal or galactose oxidase	2.804	2.11E-02	chromosome_6	6952881	6959606	
CUST_6740_PI425379931	Au9.Cre03.g170300	subtilisin/kexin-related serine protease	2.795	1.29E-02	chromosome_3	2826365	2832941	
CUST_11277_PI425379931	Au9.Cre01.g046500	Membrane selenoprotein	2.769	3.41E-02	chromosome_1	6436858	6441033	
CUST_12187_PI425379931	Au9.Cre09.g400950	major facilitator superfamily mfs_1	2.718	8.40E-03	chromosome_9	2341085	2348989	
CUST_9476_PI425379931	Au9.Cre13.g595800	hypothetical protein CHLREDRAFT_176850	2.716	3.56E-02	chromosome_13	4690748	4694410	
CUST_2807_PI425379931	Au9.Cre17.g717850	cell wall protein pherophorin-C8	2.711	1.05E-02	chromosome_17	2686130	2693029	
CUST_9544_PI425379931	Au9.Cre02.g122550	predicted protein	2.704	4.26E-02	chromosome_2	6355638	6359241	
CUST_8113_PI425379931	Au9.Cre01.g046350	Membrane selenoprotein	2.691	3.80E-02	chromosome_1	6416868	6422024	
CUST_5213_PI425379931	Au9.Cre03.g173100	glycoside hydrolase family 16	2.664	3.17E-02	chromosome_3	3138146	3144897	

CUST_9447_PI425379931	Au9.Cre02.g110650	glycosyl transferase family 8	2.644	4.83E-02	chromosome_2	4863914	4871374	
CUST_10731_PI425379931	Au9.Cre09.g398900	vegetative cell wall protein gp1	2.582	6.85E-03	chromosome_9	1995091	1997997	
CUST_7642_PI425379931	Au9.Cre02.g142650	predicted protein	2.56	6.85E-03	chromosome_2	9274420	9280446	
CUST_1113_PI425379931	Au9.Cre02.g124550	O-methyltransferase	2.527	1.09E-02	chromosome_2	6561602	6564087	
CUST_13989_PI425379931	Au9.Cre13.g569450	predicted protein	2.509	6.85E-03	chromosome_13	1091471	1096468	
CUST_9987_PI425379931	Au9.Cre16.g692350	serine-threonine protein kinase, plant-type	2.5	6.85E-03	chromosome_16	6039976	6050997	K13417
CUST_4067_PI425379931	Au9.Cre01.g053150	Glycerol-3-Phosphate Dehydrogenase/Dihydroxyacetone-3-Phosphate Reductase	2.493	2.23E-02	chromosome_1	7368409	7375573	K00006
CUST_13169_PI425379931	Au9.Cre02.g081700	predicted protein	2.467	4.34E-02	chromosome_2	1096096	1100288	
CUST_9799_PI425379931	Au9.Cre13.g598700	cysteine-rich secretory protein (crisp/scp/tpx1)-related	2.463	8.40E-03	chromosome_13	5026161	5031508	
CUST_1446_PI425379931	Au9.Cre06.g275050	Gamma-glutamyl hydrolase	2.451	4.26E-02	chromosome_6	3090461	3095393	K01307
CUST_8139_PI425379931	Au9.Cre14.g620250	predicted protein	2.445	3.80E-02	chromosome_14	1822549	1830691	
CUST_1860_PI425379931	Au9.Cre10.g455050	hypothetical protein CHLREDRAFT_168119	2.444	1.00E-02	chromosome_10	4946641	4955171	
CUST_7865_PI425379931	Au9.Cre17.g708450	Matrix metalloproteinase	2.442	2.72E-02	chromosome_17	1678666	1685730	

CUST_12299_PI425379931	Au9.Cre07.g343150	predicted protein	2.428	2.75E-02	chromosome_7	4166768	4176266	
CUST_11664_PI425379931	Au9.Cre18.g749150	Serine/threonine protein kinase	2.427	8.40E-03	scaffold_18	897371	902556	
CUST_433_PI425379931	Au9.Cre18.g749050	serine-threonine protein kinase	2.426	8.40E-03	scaffold_18	884203	889456	
CUST_308_PI425379931	Au9.Cre17.g713750	Serine/threonine protein kinase	2.405	2.72E-02	chromosome_17	2275865	2280125	K04373
CUST_1880_PI425379931	Au9.Cre18.g749100	serine-threonine protein kinase	2.392	8.40E-03	scaffold_18	889503	895616	
CUST_12511_PI425379931	Au9.Cre10.g429600	zinc finger dhhc domain containing protein	2.373	4.22E-03	chromosome_10	1577326	1586276	K05766
CUST_10098_PI425379931	Au9.Cre03.g197800	myosin i, high molecular weight form	2.368	1.09E-02	chromosome_3	5716230	5721323	K03165
CUST_14610_PI425379931	Au9.Cre18.g749200	serine-threonine protein kinase	2.351	9.46E-03	scaffold_18	905805	910181	
CUST_378_PI425379931	Au9.Cre06.g309450	carboxypeptidase d	2.334	1.09E-02	chromosome_6	7326129	7331732	K01294
CUST_6088_PI425379931	Au9.Cre12.g501600	predicted protein	2.329	2.29E-02	chromosome_12	2132945	2137701	
CUST_3018_PI425379931	Au9.Cre17.g728450		2.321	3.80E-02	chromosome_17	3936167	3954837	
CUST_8044_PI425379931	Au9.Cre04.g214650	Glycosyl transferase	2.321	9.46E-03	chromosome_4	513498	548581	K00706
CUST_13776_PI425379931	Au9.Cre11.g481600	hydroxyproline-rich glycoprotein, stress-induced	2.302	8.40E-03	chromosome_11	2467344	2470141	
CUST_9510_PI425379931	Au9.Cre03.g195900	predicted protein	2.271	8.40E-03	chromosome_3	5555407	5559238	
CUST_10548_PI425379931	Au9.Cre23.g767950	calcium/calmodulin-dependent	2.253	6.85E-03	scaffold_23	319317	322178	

		protein kinase-related						
CUST_282_PI425379931	Au9.Cre10.g431800	Arylsulfatase-like protein	2.227	4.26E-02	chromosome_10	1855836	1859625	K01130
CUST_10639_PI425379931	Au9.Cre03.g150250	predicted protein	2.224	8.40E-03	chromosome_3	320857	329682	
CUST_280_PI425379931	Au9.Cre17.g710350	glycosyltransferase-like 1b	2.213	1.51E-02	chromosome_17	1914267	1921398	
CUST_353_PI425379931	Au9.Cre09.g403150	predicted protein	2.213	2.09E-02	chromosome_9	2622823	2626877	
CUST_2155_PI425379931	Au9.Cre01.g054750	calcium/calmodulin-dependent protein kinase-related	2.209	6.85E-03	chromosome_1	7562853	7565904	K06641
CUST_4496_PI425379931	Au9.Cre13.g585050	expressed hypothetical protein	2.208	1.96E-02	chromosome_13	3145373	3150323	
CUST_10521_PI425379931	Au9.Cre12.g498650	Aurora-like kinase	2.193	3.93E-02	chromosome_12	1842933	1848546	K11481
CUST_7021_PI425379931	Au9.Cre06.g258800	hydroxyproline-rich glycoprotein component of the outer cell wall	2.192	3.17E-02	chromosome_6	1374349	1379615	
CUST_384_PI425379931	Au9.Cre13.g575200	serine/threonine protein phosphatase	2.189	8.40E-03	chromosome_13	1810455	1817072	K14501
CUST_13971_PI425379931	Au9.Cre18.g749000	serine-threonine protein kinase	2.185	2.72E-02	scaffold_18	878889	884154	
CUST_10099_PI425379931	Au9.Cre03.g174800	hypothetical protein	2.185	1.09E-02	chromosome_3	3338866	3344800	
CUST_2816_PI425379931	Au9.Cre06.g299950	predicted protein	2.181	3.80E-02	chromosome_6	6140156	6145845	
CUST_10897_PI425379931	Au9.Cre02.g077750	Flagellar Associated Protein	2.163	1.94E-02	chromosome_2	587531	593538	
CUST_9700_PI425379931	Au9.Cre13.g600900	glyoxal or galactose oxidase	2.155	4.26E-02	chromosome_13	5260019	5265086	

CUST_5278_PI425379931	Au9.Cre10.g446650	pentatricopeptide repeat-containing	2.153	1.29E-02	chromosome_10	3737180	3747527	K12854
CUST_11891_PI425379931	Au9.Cre03.g201650	predicted protein	2.149	8.40E-03	chromosome_3	6254327	6256808	
CUST_2543_PI425379931	Au9.Cre10.g421350	Matrix metalloproteinase	2.142	2.11E-02	chromosome_10	540508	546731	
CUST_12906_PI425379931	Au9.Cre10.g465500	cyclic nucleotide-binding protein	2.139	3.89E-02	chromosome_10	6352119	6355356	
CUST_1588_PI425379931	Au9.Cre04.g226050	periplasmic arylsulfatase	2.122	2.11E-02	chromosome_4	2327318	2333885	K01130
CUST_2858_PI425379931	Au9.Cre17.g733450	gag/pol/env polyprotein	2.118	1.52E-02	chromosome_17	4770865	4786616	
CUST_4419_PI425379931	Au9.Cre10.g446600	gag/pol/env polyprotein	2.103	1.52E-02	chromosome_10	3723086	3736827	K04228
CUST_8171_PI425379931	Au9.Cre05.g239700	hypothetical protein CHLREDRAFT_150908	2.1	2.11E-02	chromosome_5	1865642	1869547	
CUST_11126_PI425379931	Au9.Cre01.g014950	hypothetical protein CHLREDRAFT_193168	2.098	8.40E-03	chromosome_1	2383511	2388248	
CUST_13067_PI425379931	Au9.Cre50.g789900	gag/pol/env polyprotein	2.096	1.09E-02	scaffold_50	1792	15915	
CUST_11869_PI425379931	Au9.Cre01.g062000	predicted protein	2.092	2.11E-02	chromosome_1	8573660	8579621	
CUST_3023_PI425379931	Au9.Cre17.g731050	abc transporter family protein	2.08	1.35E-02	chromosome_17	4376729	4381385	K12608
CUST_1556_PI425379931	Au9.Cre03.g163800	predicted protein	2.073	8.40E-03	chromosome_3	2022867	2030948	
CUST_403_PI425379931	Au9.Cre07.g342700	predicted protein	2.068	2.11E-02	chromosome_7	4116697	4119140	
CUST_2885_PI425379931	Au9.Cre10.g458800	hypothetical protein CHLREDRAFT_187729	2.065	1.52E-02	chromosome_10	5460293	5464867	

CUST_14_PI425379931	Au9.Cre12.g529900	spindle pole body protein	2.06	1.76E-02	chromosome_12	5258519	5264020	
CUST_4850_PI425379931	Au9.Cre03.g202250	DNA polymerase delta, subunit C	2.06	1.09E-02	chromosome_3	6334116	6337499	K03504
CUST_3525_PI425379931	Au9.Cre08.g371350	hypothetical protein CHLREDRAFT_179239	2.058	1.00E-02	chromosome_8	1957423	1958926	
CUST_7973_PI425379931	Au9.Cre07.g340950	reticulon3-a3	2.05	8.40E-03	chromosome_7	3847629	3855007	
CUST_219_PI425379931	Au9.Cre17.g710850	solute carrier family member e3	2.048	3.80E-02	chromosome_17	1962277	1966331	
CUST_9279_PI425379931	Au9.Cre07.g330850	solute carrier family 35	2.045	9.46E-03	chromosome_7	2362977	2367452	
CUST_7779_PI425379931	Au9.Cre24.g769750	kelch-related proteins	2.043	2.83E-02	scaffold_24	142696	147130	
CUST_438_PI425379931	Au9.Cre19.g753800	3',5'-cyclic-nucleotide phosphodiesterase	2.04	1.52E-02	scaffold_19	318492	328090	
CUST_12092_PI425379931	Au9.Cre16.g648450	hypothetical protein CHLREDRAFT_185177	2.037	1.00E-02	chromosome_16	122796	134285	
CUST_11489_PI425379931	Au9.Cre14.g618550	predicted protein	2.037	1.96E-02	chromosome_14	1520289	1526088	
CUST_2799_PI425379931	Au9.Cre16.g693550	hydroxyproline-rich cell wall protein	2.035	1.09E-02	chromosome_16	6217711	6219581	
CUST_7893_PI425379931	Au9.Cre16.g676700	hypothetical protein CHLREDRAFT_191559	2.033	3.80E-02	chromosome_16	4050248	4055190	
CUST_14174_PI425379931	Au9.Cre01.g027900	Intraflagellar transport protein 74/72	2.027	2.29E-02	chromosome_1	4034222	4036285	
CUST_7208_PI425379931	Au9.Cre07.g356150	caax prenyl protease	2.024	8.40E-03	chromosome_7	5912860	5918171	K01047

CUST_6378_PI425379931	Au9.Cre17.g696700	cell wall protein pherophorin-C22	2.021	3.41E-02	chromosome_17	75402	77574	
CUST_2866_PI425379931	Au9.Cre13.g607000	aminoacyl-histidine dipeptidase	2.019	4.74E-02	chromosome_13	6431118	6437643	K01270
CUST_10532_PI425379931	Au9.Cre10.g436600	ribosome-associated gtpase	2.018	2.75E-02	chromosome_10	2493327	2496382	
CUST_14047_PI425379931	Au9.Cre07.g330750	hypothetical protein CHLREDRAFT_144348	2.001	2.75E-02	chromosome_7	2351481	2355512	
CUST_2439_PI425379931	Au9.Cre02.g090950	predicted protein	1.996	3.80E-02	chromosome_2	2245032	2259080	
CUST_10492_PI425379931	Au9.Cre01.g031050	Global transcription factor	1.995	8.07E-03	chromosome_1	4384037	4391942	
CUST_8183_PI425379931	Au9.Cre14.g629000	reticulon3-a3	1.992	4.59E-02	chromosome_14	3136014	3142649	
CUST_393_PI425379931	Au9.Cre14.g610100	predicted protein	1.992	2.11E-02	chromosome_14	335555	339423	
CUST_8174_PI425379931	Au9.Cre12.g536900	cobalamin synthesis protein p47k	1.991	2.72E-02	chromosome_12	6114176	6128387	
CUST_8207_PI425379931	Au9.Cre12.g549000	cell wall protein pherophorin-C4	1.984	2.75E-02	chromosome_12	7702572	7705412	
CUST_1938_PI425379931	Au9.Cre03.g156850	serine-threonine protein kinase, plant-type	1.981	2.75E-02	chromosome_3	1127149	1135912	
CUST_12225_PI425379931	Au9.Cre13.g591150	Histone H2A	1.975	6.85E-03	chromosome_13	4158442	4159526	K11251
CUST_11312_PI425379931	Au9.Cre04.g216900	hypothetical protein CHLREDRAFT_195076	1.97	2.45E-02	chromosome_4	907904	915825	
CUST_13038_PI425379931	Au9.Cre17.g704100	predicted protein	1.945	2.09E-02	chromosome_17	1120021	1123013	
CUST_5532_PI425379931	Au9.Cre12.g514550	Actin filament-coating protein	1.942	1.22E-02	chromosome_12	3555258	3563556	

		tropomyosin						
CUST_7404_PI425379931	Au9.Cre07.g319450	hypothetical protein CHLREDRAFT_142763	1.933	4.59E-02	chromosome_7	1002918	1008747	
CUST_1520_PI425379931	Au9.Cre17.g710300	hydroxyproline-rich stress-induced	1.927	3.54E-02	chromosome_17	1909427	1913558	
CUST_11554_PI425379931	Au9.Cre17.g717900	cell wall protein pherophorin-C1	1.915	1.52E-02	chromosome_17	2695040	2698180	
CUST_8318_PI425379931	Au9.Cre01.g010100	predicted protein	1.91	4.98E-02	chromosome_1	1665412	1667706	
CUST_13521_PI425379931	Au9.Cre12.g507350	hypothetical protein CHLREDRAFT_169699	1.907	2.29E-02	chromosome_12	2689328	2695428	
CUST_2039_PI425379931	Au9.Cre12.g513450	Eta tubulin; was TUH;Eta tubulin; was TUH	1.902	2.88E-02	chromosome_12	3422074	3426335	K07375
CUST_5095_PI425379931	Au9.Cre15.g642300	atp-dependent dna helicase pif1	1.884	1.05E-02	chromosome_15	1602196	1605831	
CUST_4422_PI425379931	Au9.Cre09.g409900	hydroxyproline-rich stress-induced	1.871	4.26E-02	chromosome_9	3638552	3642220	
CUST_11668_PI425379931	Au9.Cre01.g051950	pepsin-type aspartyl protease	1.869	2.75E-02	chromosome_1	7204009	7208514	
CUST_1233_PI425379931	Au9.Cre13.g565800	UDP-Glucose:protein transglucosylase	1.863	2.66E-02	chromosome_13	585110	587095	
CUST_2057_PI425379931	Au9.Cre02.g133950	Transient potential receptor channel	1.86	1.05E-02	chromosome_2	7829971	7849779	
CUST_5566_PI425379931	Au9.Cre01.g056850	DNA helicase PIF1/RRM3	1.859	1.29E-02	chromosome_1	7874938	7881995	
CUST_7871_PI425379931	Au9.Cre01.g000650	Copper amine oxidase	1.858	2.69E-02	chromosome_1	74656	81967	K00276

CUST_399_PI425379931	Au9.Cre12.g547450	guanine nucleotide exchange factor	1.857	1.52E-02	chromosome_12	7531165	7538015	K10848
CUST_390_PI425379931	Au9.Cre01.g016200	predicted protein	1.857	4.74E-02	chromosome_1	2538804	2544520	
CUST_4534_PI425379931	Au9.Cre09.g390700	exostosin-like glycosyltransferase	1.851	8.40E-03	chromosome_9	756508	766989	
CUST_5960_PI425379931	Au9.Cre02.g076200	aminopeptidase n	1.846	9.46E-03	chromosome_2	425257	435962	
CUST_8954_PI425379931	Au9.Cre12.g512100	putative DNA helicase	1.841	1.09E-02	chromosome_12	3248917	3255278	K03581
CUST_2735_PI425379931	Au9.Cre17.g711350	zinc finger protein 862	1.837	1.09E-02	chromosome_17	2013237	2017468	K14311
CUST_8932_PI425379931	Au9.Cre13.g564750	3',5'-cyclic-nucleotide phosphodiesterase	1.828	2.29E-02	chromosome_13	404017	417609	
CUST_3858_PI425379931	Au9.Cre03.g194350	predicted protein	1.825	1.09E-02	chromosome_3	5396768	5400523	
CUST_11754_PI425379931	Au9.Cre17.g701500	DnaJ-like protein	1.824	3.41E-02	chromosome_17	763264	766734	K09503
CUST_3445_PI425379931	Au9.Cre02.g135050	Flagellar Associated Protein	1.824	1.35E-02	chromosome_2	8083560	8090589	
CUST_13658_PI425379931	Au9.Cre16.g667700	hypothetical protein CHLREDRAFT_170874	1.823	1.94E-02	chromosome_16	2799240	2805011	
CUST_929_PI425379931	Au9.Cre13.g607800	hypothetical protein CHLREDRAFT_177753	1.82	2.89E-02	chromosome_13	6553639	6560074	
CUST_12326_PI425379931	Au9.Cre13.g601550	mapkk-related serine/threonine protein kinases	1.817	2.75E-02	chromosome_13	5329834	5335778	
CUST_2282_PI425379931	Au9.Cre01.g010150	ribosomal biogenesis gtpase	1.817	2.63E-02	chromosome_1	1668544	1673344	

CUST_12659_PI425379931	Au9.Cre06.g267250	MAP Kinase Phosphatase 2	1.815	1.09E-02	chromosome_6	2304624	2314249	K05766
CUST_13022_PI425379931	unknown		1.808	4.26E-02				
CUST_4039_PI425379931	Au9.Cre13.g592550	predicted protein	1.8	2.88E-02	chromosome_13	4331941	4342396	
CUST_3743_PI425379931	Au9.Cre17.g720750	trf4 poly(A) polymerase	1.799	8.40E-03	chromosome_17	3073904	3079955	K03514
CUST_4317_PI425379931	Au9.Cre10.g440850	glutathione peroxidase	1.798	4.34E-02	chromosome_10	2954695	2959142	K00432
CUST_13801_PI425379931	Au9.Cre12.g531200	multicopper oxidase	1.796	2.72E-02	chromosome_12	5380829	5390295	K14735
CUST_6406_PI425379931			1.796	4.98E-02				
CUST_8136_PI425379931	Au9.Cre10.g460700	calcium/calmodulin-dependent protein kinase-related	1.791	2.29E-02	chromosome_10	5698365	5701416	K13412
CUST_8230_PI425379931	Au9.Cre02.g082950	predicted protein	1.787	3.54E-02	chromosome_2	1223484	1228349	
CUST_7795_PI425379931	Au9.Cre02.g117250	beta-galactosidase	1.786	4.98E-02	chromosome_2	5691724	5699025	K12308
CUST_11888_PI425379931	Au9.Cre01.g003900	predicted protein	1.781	2.88E-02	chromosome_1	730625	732438	
CUST_14_PI425399726	Au9.Cre12.g513450	Eta tubulin; was TUH;Eta tubulin; was TUH	1.774	3.54E-02	chromosome_12	3422074	3426335	K07375
CUST_10528_PI425379931	Au9.Cre03.g190500	glycoside-hydrolase-like protein	1.772	8.40E-03	chromosome_3	4954965	4962646	K05546
CUST_3311_PI425379931	Au9.Cre03.g210250	map microtubule affinity-regulating kinase 3-like	1.763	4.56E-02	chromosome_3	7552266	7557537	
CUST_6820_PI425379931	Au9.Cre17.g741150	serine-threonine protein kinase,	1.761	2.11E-02	chromosome_17	6120926	6137531	

		plant-type						
CUST_12819_PI425379931	Au9.Cre03.g161100	importin alpha subunit-related	1.75	4.26E-02	chromosome_3	1698502	1702293	
CUST_3355_PI425379931	Au9.Cre16.g661800	unknown [Picea sitchensis]	1.744	2.29E-02	chromosome_16	1811503	1814356	
CUST_7232_PI425379931	Au9.Cre01.g004900	hypothetical protein CHLREDRAFT_132881	1.744	1.52E-02	chromosome_1	898457	900957	K01423
CUST_2753_PI425379931	Au9.Cre08.g380050	predicted protein	1.743	1.09E-02	chromosome_8	3319845	3321429	
CUST_3857_PI425379931	Au9.Cre17.g742500	hypothetical protein CHLREDRAFT_194227	1.74	2.45E-02	chromosome_17	6350617	6355925	
CUST_4748_PI425379931	Au9.Cre01.g036250	calcium/calmodulin-dependent protein kinase-related	1.74	1.52E-02	chromosome_1	5039034	5049979	K12761
CUST_4214_PI425379931	Au9.Cre13.g570750	Chitinase	1.739	1.00E-02	chromosome_13	1251324	1253090	
CUST_11415_PI425379931	Au9.Cre12.g542900	serine-threonine protein kinase	1.735	4.26E-02	chromosome_12	7035580	7047103	K04422
CUST_2931_PI425379931	Au9.Cre17.g703750	cell polarity protein	1.73	1.09E-02	chromosome_17	1053941	1073122	
CUST_1865_PI425379931	Au9.Cre07.g322400	hypothetical protein CHLREDRAFT_142813	1.727	4.83E-02	chromosome_7	1376377	1379860	
CUST_14234_PI425379931	Au9.Cre01.g030400		1.727	1.09E-02	chromosome_1	4296176	4297741	
CUST_8303_PI425379931	Au9.Cre06.g272250	hypothetical protein CHLREDRAFT_187032	1.726	3.56E-02	chromosome_6	2873205	2877607	
CUST_8074_PI425379931	Au9.Cre01.g061400	zinc finger protein 862	1.724	2.11E-02	chromosome_1	8483491	8487746	

CUST_14101_PI425379931	Au9.Cre12.g544650	predicted protein	1.723	1.52E-02	chromosome_12	7204432	7211220	
CUST_6776_PI425379931	Au9.Cre02.g146650	Tubulin tyrosine ligase	1.723	2.75E-02	chromosome_2	9828365	9837750	
CUST_6437_PI425379931	Au9.Cre13.g581300		1.72	8.40E-03	chromosome_13	2630395	2640390	
CUST_11336_PI425379931	Au9.Cre19.g754000	hypothetical protein SORBIDRAFT_03g019750	1.718	3.93E-02	scaffold_19	343842	353511	
CUST_3991_PI425379931	Au9.Cre13.g601450	Alpha/beta hydrolase	1.715	1.05E-02	chromosome_13	5322308	5326198	
CUST_3316_PI425379931	Au9.Cre05.g236400	hypothetical protein CHLREDRAFT_192771	1.715	2.69E-02	chromosome_5	1352184	1359583	
CUST_6019_PI425379931	Au9.Cre16.g676000	hypothetical protein CHLREDRAFT_187397	1.714	3.54E-02	chromosome_16	3950584	3956239	
CUST_14265_PI425379931	Au9.Cre03.g168500	hypothetical protein MICPUCDRAFT_70223 [Micromonas pusilla CCMP1545]	1.711	3.19E-02	chromosome_3	2635141	2637386	
CUST_4615_PI425379931	Au9.Cre03.g177400		1.707	2.72E-02	chromosome_3	3651037	3667477	K01768
CUST_11345_PI425379931	Au9.Cre17.g706400	hypothetical protein CHLREDRAFT_206015	1.695	1.52E-02	chromosome_17	1401584	1403931	
CUST_8152_PI425379931	Au9.Cre04.g225850	R-SNARE protein, VAMP72-family	1.693	4.34E-02	chromosome_4	2309940	2313038	K08515
CUST_6001_PI425379931	Au9.Cre06.g252600	hypothetical protein CHLREDRAFT_187283	1.686	4.10E-02	chromosome_6	463772	468840	

CUST_13574_PI425379931	Au9.Cre16.g649050	guanylate cyclase	1.683	2.72E-02	chromosome_16	202678	213804	K12319
CUST_10267_PI425379931	Au9.Cre01.g017550	leucine-rich repeat-containing protein	1.679	3.17E-02	chromosome_1	2695800	2700505	K13730
CUST_10660_PI425379931	Au9.Cre01.g028850	Rhodanese-related sulfurtransferase	1.678	4.83E-02	chromosome_1	4124889	4126945	
CUST_57_PI425379931	Au9.Cre02.g142300	molybdenum cofactor sulfurase	1.674	2.88E-02	chromosome_2	9217220	9222628	
CUST_9898_PI425379931	Au9.Cre26.g772850	predicted protein	1.673	4.26E-02	scaffold_26	124321	128625	
CUST_8641_PI425379931	Au9.Cre12.g553550	predicted protein	1.67	3.80E-02	chromosome_12	8297578	8301830	
CUST_6694_PI425379931	Au9.Cre06.g258550	predicted protein	1.67	1.76E-02	chromosome_6	1327893	1339998	
CUST_10186_PI425379931	Au9.Cre02.g089750	predicted protein	1.669	2.75E-02	chromosome_2	2075074	2081568	
CUST_1652_PI425379931	Au9.Cre17.g714850	hydroxyproline-rich cell wall protein	1.667	3.89E-02	chromosome_17	2358555	2360206	
CUST_1750_PI425379931	Au9.Cre13.g606600	cGMP-dependent protein kinase	1.663	4.98E-02	chromosome_13	6368859	6373329	K07376
CUST_6876_PI425379931	Au9.Cre03.g155250	predicted protein	1.661	3.54E-02	chromosome_3	945734	950815	
CUST_10037_PI425379931	Au9.Cre10.g431050	Speract/scavenger receptor, transmembrane glycoprotein	1.66	3.80E-02	chromosome_10	1768896	1780745	K13912
CUST_9267_PI425379931	Au9.Cre13.g603250	protein of clr family	1.657	3.54E-02	chromosome_13	5817272	5823988	
CUST_7827_PI425379931	Au9.Cre02.g088650	predicted protein	1.652	1.29E-02	chromosome_2	1908245	1917993	
CUST_13133_PI425379931	Au9.Cre02.g089700	predicted protein [Micromonas pusilla CCMP1545]	1.648	3.47E-02	chromosome_2	2066896	2074468	

CUST_12411_PI425379931	Au9.Cre14.g608750	hypothetical protein CHLREDRAFT_179445	1.644	3.41E-02	chromosome_14	152753	156744	
CUST_8807_PI425379931	Au9.Cre02.g114900	ankyrin repeat-containing	1.644	2.75E-02	chromosome_2	5407791	5413643	K12460
CUST_11045_PI425379931	Au9.Cre16.g691350	hypothetical protein CHLREDRAFT_193706	1.642	2.72E-02	chromosome_16	5914894	5919686	
CUST_8369_PI425379931	Au9.Cre12.g512900	predicted protein	1.64	2.83E-02	chromosome_12	3351995	3353426	
CUST_4152_PI425379931	Au9.Cre17.g700650	gpr1 fun34 yaah family protein	1.639	4.26E-02	chromosome_17	662744	665017	
CUST_9190_PI425379931	Au9.Cre22.g765600	nitrilase-related	1.636	2.89E-02	scaffold_22	413491	417287	
CUST_11963_PI425379931	Au9.Cre07.g348000	predicted protein	1.634	1.13E-02	chromosome_7	4862510	4864029	
CUST_12014_PI425379931	Au9.Cre12.g535450	predicted protein	1.63	2.75E-02	chromosome_12	5945782	5947999	
CUST_9767_PI425379931	Au9.Cre06.g303000	f-box protein	1.628	3.93E-02	chromosome_6	6556413	6563495	
CUST_14007_PI425379931	Au9.Cre01.g063400	predicted protein	1.627	3.66E-02	chromosome_1	8744103	8745320	
CUST_13672_PI425379931	Au9.Cre03.g175350	hypothetical protein CHLREDRAFT_9571	1.623	2.75E-02	chromosome_3	3407114	3411227	
CUST_14133_PI425379931	Au9.Cre19.g753200	predicted protein	1.621	2.29E-02	scaffold_19	203709	206581	
CUST_11311_PI425379931	Au9.Cre16.g657100	hypothetical protein CHLREDRAFT_185095	1.619	2.72E-02	chromosome_16	1240610	1247304	
CUST_13808_PI425379931	Au9.Cre03.g150050	predicted protein	1.619	3.47E-02	chromosome_3	299425	302902	

CUST_7384_PI425379931	Au9.Cre01.g067150	alpha-2-macroglobulin domain protein	1.615	4.74E-02	chromosome_1	9210052	9227288	
CUST_8606_PI425379931	Au9.Cre10.g446000	hypothetical protein CHLREDRAFT_93782	1.614	2.75E-02	chromosome_10	3670337	3676045	
CUST_4397_PI425379931	Au9.Cre08.g375000	dual specificity protein phosphatase	1.614	8.40E-03	chromosome_8	2642335	2658566	
CUST_5390_PI425379931	Au9.Cre10.g432550	voltage-gated K+ channel, alpha subunit	1.613	2.43E-02	chromosome_10	1964890	1971191	K04885
CUST_242_PI425379931	Au9.Cre12.g523050	Putative T-complex protein 1 component	1.609	7.71E-03	chromosome_12	4517175	4531298	K00889
CUST_9591_PI425379931	Au9.Cre12.g542450	mitochondrial transcription termination factor	1.602	2.75E-02	chromosome_12	6963796	6972808	K14326
CUST_6886_PI425379931	Au9.Cre03.g193200	collagen alpha chain	1.599	8.40E-03	chromosome_3	5289288	5291573	
CUST_14441_PI425379931	Au9.Cre06.g260500	WASP-interacting protein VRP1/WIP, contains WH2 domain	1.595	3.17E-02	chromosome_6	1565417	1574232	
CUST_14079_PI425379931	Au9.Cre13.g586200	o-linked n-acetylglucosamine transferase, ogt	1.593	2.45E-02	chromosome_13	3293436	3297169	
CUST_6307_PI425379931	Au9.Cre06.g307150	beta-amylase	1.59	1.82E-02	chromosome_6	7100928	7104803	K01177
CUST_8524_PI425379931	Au9.Cre06.g259600	subunit of GARP complex	1.59	2.75E-02	chromosome_6	1475015	1483867	
CUST_13962_PI425379931	Au9.Cre09.g401950	camp-dependent protein kinase	1.589	2.75E-02	chromosome_9	2480041	2490697	

		regulatory						
CUST_13391_PI425379931	Au9.Cre08.g383550	ring zinc finger protein	1.586	1.09E-02	chromosome_8	3778017	3785521	K11420
CUST_743_PI425379931	Au9.Cre03.g194300	Phytoene/squalene synthetase	1.582	3.80E-02	chromosome_3	5393152	5396617	K02291
CUST_5096_PI425379931	Au9.Cre12.g515200	Flagellar Associated Protein	1.581	2.88E-02	chromosome_12	3633655	3636495	
CUST_10762_PI425379931	Au9.Cre02.g115800	hypothetical protein CHLREDRAFT_181241	1.577	2.72E-02	chromosome_2	5529236	5531667	
CUST_4685_PI425379931	Au9.Cre09.g403800	Flagellar outer dynein arm heavy chain beta	1.575	2.43E-02	chromosome_9	2717292	2736929	K10413
CUST_11780_PI425379931	Au9.Cre24.g769850		1.574	4.26E-02	scaffold_24	149456	175867	
CUST_6425_PI425379931	Au9.Cre07.g339500	predicted protein	1.567	4.26E-02	chromosome_7	3682559	3684393	
CUST_3621_PI425379931	Au9.Cre12.g549150	predicted protein	1.565	2.11E-02	chromosome_12	7716393	7720924	
CUST_2124_PI425379931	Au9.Cre03.g192050	Iron permease, membrane protein	1.565	4.74E-02	chromosome_3	5148490	5152439	
CUST_4734_PI425379931	Au9.Cre17.g698000	mitochondrial F1F0 ATP synthase, beta subunit	1.563	4.86E-02	chromosome_17	263116	267695	K02133
CUST_3476_PI425379931	Au9.Cre06.g278500	tRNA (guanine-N1)-methyltransferase	1.562	3.80E-02	chromosome_6	3506215	3509791	
CUST_8226_PI425379931	Au9.Cre01.g036700	calcium/calmodulin-dependent protein kinase-related	1.552	1.96E-02	chromosome_1	5090678	5096310	K13412
CUST_6739_PI425379931	Au9.Cre17.g740100	hypothetical protein	1.55	2.09E-02	chromosome_17	5973400	5978574	

		CHLREDRAFT_194197						
CUST_11705_PI425379931	Au9.Cre03.g154500	sand family protein	1.55	3.80E-02	chromosome_3	864414	869475	
CUST_13007_PI425379931	Au9.Cre11.g482950	serine-threonine protein kinase, plant-type	1.548	2.75E-02	chromosome_11	2635286	2645805	
CUST_4621_PI425379931	Au9.Cre41.g786850	predicted protein	1.546	4.41E-02	scaffold_41	62668	68625	
CUST_13992_PI425379931	Au9.Cre04.g227450	phosphate phosphoenolpyruvate translocator-like protein	1.538	8.07E-03	chromosome_4	2539317	2545523	
CUST_6180_PI425379931	Au9.Cre16.g662850	eukaryotic initiation factor	1.537	3.89E-02	chromosome_16	1951851	1955462	
CUST_4838_PI425379931	Au9.Cre13.g588600	kinesin heavy chain	1.533	1.26E-02	chromosome_13	3693197	3704861	
CUST_5115_PI425379931	Au9.Cre16.g683500	ATP-dependent RNA helicase	1.532	2.27E-02	chromosome_16	4914143	4918618	K01509
CUST_2551_PI425379931	Au9.Cre06.g275350	lhy protein	1.53	2.75E-02	chromosome_6	3120756	3130084	K12133
CUST_8555_PI425379931			1.53	4.26E-02				
CUST_4046_PI425379931	Au9.Cre16.g662900	Signal Peptidase, 12 kDa subunit	1.523	2.88E-02	chromosome_16	1955984	1956995	
CUST_482_PI425379931	Au9.Cre12.g542700	Mitotic checkpoint protein MAD1	1.523	4.74E-02	chromosome_12	7006119	7013905	
CUST_7082_PI425379931	Au9.Cre13.g583100		1.521	3.89E-02	chromosome_13	2840151	2858423	K02527
CUST_13496_PI425379931	Au9.Cre03.g207500	predicted protein	1.52	8.40E-03	chromosome_3	7003315	7005880	
CUST_962_PI425379931	Au9.Cre13.g581100	predicted protein	1.519	1.05E-02	chromosome_13	2609951	2612813	
CUST_14430_PI425379931	Au9.Cre12.g493750	predicted protein	1.519	1.96E-02	chromosome_12	1333255	1343835	

CUST_11396_PI425379931	Au9.Cre02.g082100	predicted protein	1.519	2.69E-02	chromosome_2	1150758	1152734	
CUST_2065_PI425379931	Au9.Cre01.g017250	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.519	6.85E-03	chromosome_1	2672384	2674939	
CUST_1327_PI425379931	Au9.Cre12.g524100	mRNA cap-binding protein	1.517	2.75E-02	chromosome_12	4640893	4649099	K12882
CUST_13112_PI425379931	Au9.Cre32.g781200	predicted protein	1.516	2.75E-02	scaffold_32	68684	78577	
CUST_11037_PI425379931	Au9.Cre29.g778450	predicted protein	1.515	8.40E-03	scaffold_29	124406	128019	
CUST_2342_PI425379931	Au9.Cre18.g748400	ribosome binding protein 1	1.512	1.09E-02	scaffold_18	799819	809314	
CUST_5266_PI425379931	Au9.Cre06.g300900	polyadenylated-RNA export factor	1.512	3.47E-02	chromosome_6	6269334	6274936	K06063
CUST_8330_PI425379931	Au9.Cre07.g334300	Transient receptor potential ion channel protein	1.511	2.75E-02	chromosome_7	2996976	3013586	K06666
CUST_9195_PI425379931	Au9.Cre12.g535500	predicted protein	1.508	2.75E-02	chromosome_12	5949472	5954381	
CUST_8442_PI425379931	Au9.Cre06.g271150	Flagellar Associated Protein	1.507	3.68E-02	chromosome_6	2767004	2778025	
CUST_11577_PI425379931	Au9.Cre10.g432850	Flagellar Associated Protein	1.506	3.41E-02	chromosome_10	2001257	2003924	
CUST_4481_PI425379931	Au9.Cre64.g793100	presenilin protease	1.505	1.96E-02	scaffold_64	26038	32205	
CUST_5794_PI425379931	Au9.Cre02.g147650	mannose-6-phosphate isomerase	1.505	4.26E-02	chromosome_2	9932745	9936300	K01809
CUST_13745_PI425379931	Au9.Cre05.g240900	hydroxyproline-rich cell wall protein	1.504	4.98E-02	chromosome_5	2048651	2060058	
CUST_4459_PI425379931	Au9.Cre07.g317650	udp-glucose:sterol glucosyltransferase	1.503	4.26E-02	chromosome_7	751174	754200	

CUST_13025_PI425379931	Au9.Cre14.g613900	T-type cyclin	1.502	4.83E-02	chromosome_14	958721	962829	K05868
CUST_4363_PI425379931	Au9.Cre15.g646050	serine-threonine protein kinase	1.498	1.52E-02	chromosome_15	2752854	2764420	
CUST_12399_PI425379931	Au9.Cre07.g327300	Transcription factor Abd-B, contains HOX domain	1.498	4.41E-02	chromosome_7	1911852	1920027	
CUST_14257_PI425379931	Au9.Cre01.g033600	helicase ski2w	1.498	3.68E-02	chromosome_1	4673096	4679118	
CUST_13867_PI425379931	Au9.Cre12.g560000		1.496	1.94E-02	chromosome_12	9115640	9126695	
CUST_1928_PI425379931	Au9.Cre17.g718200	predicted protein	1.495	8.40E-03	chromosome_17	2736996	2738973	
CUST_13538_PI425379931	Au9.Cre01.g058000	nalp (nacht, leucine rich repeat and pyrin domain containing)-related	1.495	1.05E-02	chromosome_1	8077508	8098936	
CUST_7756_PI425379931	Au9.Cre17.g740850	hypothetical protein CHLREDRAFT_194202	1.487	1.52E-02	chromosome_17	6095773	6102445	
CUST_7368_PI425379931	Au9.Cre04.g211950	exostosin-like glycosyltransferase	1.487	3.80E-02	chromosome_4	54046	61891	K02367
CUST_10096_PI425379931	Au9.Cre16.g688250	hypothetical protein CHLREDRAFT_183364	1.486	2.75E-02	chromosome_16	5506405	5508186	
CUST_4609_PI425379931	Au9.Cre12.g549200	predicted protein	1.485	2.69E-02	chromosome_12	7720961	7727343	
CUST_4241_PI425379931	Au9.Cre17.g705200	predicted protein	1.484	1.05E-02	chromosome_17	1236167	1244159	
CUST_74_PI425379931	Au9.Cre16.g688150	hypothetical protein CHLREDRAFT_183364	1.482	2.75E-02	chromosome_16	5498889	5502745	
CUST_11755_PI425379931	Au9.Cre02.g109050	hypothetical protein	1.48	2.75E-02	chromosome_2	4684768	4691924	

		CHLREDRAFT_186812						
CUST_9883_PI425379931	Au9.Cre05.g239000	hypothetical protein CHLREDRAFT_176384	1.478	2.75E-02	chromosome_5	1757252	1772483	
CUST_9067_PI425379931	Au9.Cre13.g604600	predicted protein [Physcomitrella patens subsp. patens]	1.477	3.41E-02	chromosome_13	6092486	6100267	
CUST_14090_PI425379931	Au9.Cre02.g108350	myb transcription factor 1	1.473	4.56E-02	chromosome_2	4609342	4616129	K12823
CUST_4394_PI425379931	Au9.Cre24.g768800	sirtuin type partial	1.472	2.29E-02	scaffold_24	29456	36857	
CUST_2874_PI425379931	Au9.Cre13.g591800	predicted protein	1.472	3.80E-02	chromosome_13	4253323	4259221	
CUST_4196_PI425379931	Au9.Cre08.g361900	flagellar associated protein	1.472	4.05E-02	chromosome_8	546177	553211	
CUST_5248_PI425379931	Au9.Cre13.g576300	gamma-secretase accessory subunit	1.47	3.12E-02	chromosome_13	1930690	1933207	K06172
CUST_5680_PI425379931	Au9.Cre06.g310000	Epsilon4-Adaptin	1.47	2.11E-02	chromosome_6	7456500	7463841	K12400
CUST_2658_PI425379931	Au9.Cre02.g124500	protein of clr family	1.47	2.83E-02	chromosome_2	6553998	6560872	
CUST_7990_PI425379931	Au9.Cre12.g491000	predicted protein	1.469	3.80E-02	chromosome_12	950069	956220	
CUST_12263_PI425379931	Au9.Cre04.g223900	transcription factor ccaat displacement protein cdp1	1.468	2.75E-02	chromosome_4	1975643	1985678	
CUST_6564_PI425379931	Au9.Cre12.g533500		1.466	4.65E-02	chromosome_12	5687017	5705865	K01768
CUST_13032_PI425379931	Au9.Cre03.g159950	nucleolar protein 10	1.466	3.89E-02	chromosome_3	1545478	1552193	
CUST_8358_PI425379931	Au9.Cre06.g306200	hypothetical protein	1.463	6.85E-03	chromosome_6	7005390	7008426	

		CHLREDRAFT_144900						
CUST_7314_PI425379931	Au9.Cre02.g145500	Serine/threonine protein kinase	1.459	4.34E-02	chromosome_2	9669431	9675649	K04422
CUST_4542_PI425379931	Au9.Cre14.g630050	Calcium-responsive transcription coactivator	1.455	3.89E-02	chromosome_14	3298133	3304644	
CUST_1279_PI425379931	Au9.Cre03.g188000	hypothetical protein CHLREDRAFT_189210	1.455	4.26E-02	chromosome_3	4704365	4714693	
CUST_8480_PI425379931	Au9.Cre26.g773050	predicted protein	1.454	3.41E-02	scaffold_26	142906	144272	
CUST_9782_PI425379931	Au9.Cre16.g695150	ribosome binding protein 1	1.453	1.94E-02	chromosome_16	6458871	6465113	
CUST_729_PI425379931	Au9.Cre06.g287150	leucine-rich repeat-containing 50 protein	1.453	2.11E-02	chromosome_6	4407655	4420959	K01768
CUST_2388_PI425379931	Au9.Cre10.g449300	ribosome binding protein 1	1.452	2.75E-02	chromosome_10	4035434	4043729	
CUST_1170_PI425379931	Au9.Cre17.g721950	Predicted E3 ubiquitin ligase	1.447	3.89E-02	chromosome_17	3197930	3202959	K04556
CUST_10252_PI425379931	Au9.Cre01.g040650	predicted protein	1.443	4.26E-02	chromosome_1	5540386	5548521	
CUST_3866_PI425379931	Au9.Cre08.g375150	ankyrin repeat domain-containing protein	1.442	2.75E-02	chromosome_8	2672329	2680974	
CUST_169_PI425379931	Au9.Cre10.g449200	ankyrin repeat-containing	1.44	2.29E-02	chromosome_10	4008220	4023129	K08803
CUST_5638_PI425379931	Au9.Cre18.g749650	ClpB chaperone, Hsp100 family	1.436	4.56E-02	scaffold_18	969556	980002	
CUST_12_PI425379931	Au9.Cre01.g052250	Thioredoxin x	1.432	3.89E-02	chromosome_1	7229531	7231320	K00384

CUST_14613_PI425379931	Au9.Cre09.g394550	Ribose-phosphate pyrophosphokinase	1.429	2.75E-02	chromosome_9	1326185	1330003	K00948
CUST_2462_PI425379931	Au9.Cre09.g412650	hypothetical protein CHLREDRAFT_150019	1.428	3.89E-02	chromosome_9	4050971	4056156	
CUST_7980_PI425379931	Au9.Cre01.g050650	hypothetical protein CHLREDRAFT_195864	1.428	2.75E-02	chromosome_1	6960456	6969312	
CUST_7859_PI425379931	Au9.Cre15.g636250	predicted protein	1.427	2.75E-02	chromosome_15	436298	444556	
CUST_9655_PI425379931	Au9.Cre09.g399650	predicted protein	1.425	2.72E-02	chromosome_9	2084828	2088470	
CUST_11933_PI425379931	Au9.Cre07.g330700	Flagellar Associated Protein	1.425	3.89E-02	chromosome_7	2344849	2350473	
CUST_8937_PI425379931	Au9.Cre05.g236200	ctr1-like protein kinase	1.425	4.10E-02	chromosome_5	1309394	1325165	
CUST_5078_PI425379931	Au9.Cre29.g778350	predicted protein	1.424	2.45E-02	scaffold_29	112507	114755	
CUST_7204_PI425379931	Au9.Cre01.g000600	WD-40 repeat family protein	1.422	2.75E-02	chromosome_1	68193	73415	K01062
CUST_176_PI425379931	Au9.Cre12.g515250	hypothetical protein TcasGA2_TC005512	1.42	2.11E-02	chromosome_12	3636647	3642758	
CUST_6941_PI425379931	Au9.Cre06.g268800	Flagellar Associated Protein	1.416	2.11E-02	chromosome_6	2451568	2466025	
CUST_8204_PI425379931	Au9.Cre05.g240100	hypothetical protein CHLREDRAFT_150899	1.415	4.65E-02	chromosome_5	1919682	1928593	
CUST_2919_PI425379931	Au9.Cre07.g325750	Flagellar Associated Protein	1.413	3.80E-02	chromosome_7	1732123	1742939	K12196
CUST_3066_PI425379931	Au9.Cre08.g363600	drug metabolite transporter	1.408	8.40E-03	chromosome_8	881353	885314	

		superfamily						
CUST_6308_PI425379931	Au9.Cre14.g618950	predicted protein	1.406	2.72E-02	chromosome_14	1623085	1626852	
CUST_1077_PI425379931	Au9.Cre08.g382100	predicted protein	1.403	3.80E-02	chromosome_8	3561879	3571100	
CUST_8707_PI425379931	Au9.Cre01.g061100	NADH:ubiquinone oxidoreductase 18 kDa subunit	1.399	3.54E-02	chromosome_1	8452416	8454693	
CUST_13936_PI425379931	Au9.Cre16.g664200	3',5'-cyclic-nucleotide phosphodiesterase	1.397	4.83E-02	chromosome_16	2148295	2155963	K13755
CUST_6497_PI425379931	Au9.Cre12.g518550	Flagellar Associated Protein	1.395	4.98E-02	chromosome_12	4049633	4063568	
CUST_8531_PI425379931	Au9.Cre06.g309350	KDEL receptor-like protein	1.395	4.86E-02	chromosome_6	7318801	7321802	K10949
CUST_14373_PI425379931	Au9.Cre02.g091150	COP-II coat subunit	1.392	3.17E-02	chromosome_2	2273640	2282841	K14007
CUST_11847_PI425379931	Au9.Cre16.g649500	hypothetical protein CHLREDRAFT_193199	1.388	4.74E-02	chromosome_16	268387	271664	
CUST_4706_PI425379931	Au9.Cre17.g723150	endoplasmic reticulum oxidoreductin 1	1.374	3.89E-02	chromosome_17	3308159	3312896	K10976
CUST_12958_PI425379931	Au9.Cre07.g354650		1.374	4.26E-02	chromosome_7	5745748	5760452	
CUST_7353_PI425379931	Au9.Cre03.g151000	Dual-Specificity Protein Phosphatase 8	1.363	3.54E-02	chromosome_3	439405	444695	K07199
CUST_4043_PI425379931	Au9.Cre02.g145100	Flagellar Associated Protein, calcium-transporting ATPase	1.361	4.26E-02	chromosome_2	9605508	9616745	K05850

CUST_7443_PI425379931	Au9.Cre12.g488550	DNA methylase in the FkbM family	1.359	3.80E-02	chromosome_12	648989	654789	
CUST_1589_PI425379931	Au9.Cre12.g484250	Flagellar inner arm dynein 1 heavy chain alpha	1.359	3.54E-02	chromosome_12	113086	133222	K10413
CUST_11745_PI425379931	Au9.Cre01.g040850	predicted protein	1.359	4.83E-02	chromosome_1	5556413	5570101	
CUST_12143_PI425379931	Au9.Cre06.g278900	predicted protein	1.351	2.75E-02	chromosome_6	3536435	3541162	
CUST_4617_PI425379931	Au9.Cre06.g267550	Bardet-Biedl syndrome 5 protein	1.35	4.26E-02	chromosome_6	2344726	2348059	
CUST_11421_PI425379931	Au9.Cre12.g546650	Ubiquitin-conjugating enzyme E2	1.349	2.75E-02	chromosome_12	7423559	7426500	K10575
CUST_3588_PI425379931	Au9.Cre09.g416450	hypothetical protein CHLREDRAFT_192167	1.349	3.66E-02	chromosome_9	4586897	4589947	
CUST_9805_PI425379931	Au9.Cre16.g685600	hypothetical protein CHLREDRAFT_170787	1.344	2.72E-02	chromosome_16	5144659	5151138	
CUST_1434_PI425379931	Au9.Cre16.g672100	hypothetical protein CHLREDRAFT_174455	1.342	3.80E-02	chromosome_16	3374193	3383450	
CUST_13475_PI425379931	Au9.Cre01.g018150	protein-s isoprenylcysteine o-	1.341	4.26E-02	chromosome_1	2774980	2778331	
CUST_11248_PI425379931	Au9.Cre16.g654350	splicing factor-like protein	1.34	3.54E-02	chromosome_16	829237	833701	
CUST_3983_PI425379931	Au9.Cre20.g758500	Puf protein	1.334	3.47E-02	scaffold_20	153595	161965	
CUST_10699_PI425379931	Au9.Cre12.g537200	2-oxoglutarate dehydrogenase, E1 subunit	1.315	3.68E-02	chromosome_12	6166447	6178148	K00164
CUST_5513_PI425379931	Au9.Cre02.g081800	predicted protein	1.314	4.98E-02	chromosome_2	1105416	1118575	K01768

CUST_1780_PI425379931	Au9.Cre10.g434450	NADH:ubiquinone oxidoreductase 39 kDa subunit	1.284	4.83E-02	chromosome_10	2238872	2241969	K03953
CUST_6108_PI425379931	Au9.Cre26.g772450	Adenylate Kinase 1	1.273	3.41E-02	scaffold_26	78900	84197	
CUST_8251_PI425379931	Au9.Cre01.g010900	Glyceraldehyde-3-Phosphate Dehydrogenase	0.788	2.88E-02	chromosome_1	1847708	1850334	
CUST_6858_PI425379931	Au9.Cre08.g378050	NADH:ubiquinone oxidoreductase 16 kDa subunit	0.786	4.34E-02	chromosome_8	3053188	3055056	
CUST_12355_PI425379931	Au9.Cre01.g015750	nipsnap-related	0.784	3.54E-02	chromosome_1	2490484	2493613	
CUST_8075_PI425379931	Au9.Cre11.g472200	split hand foot malformation type 1	0.777	4.56E-02	chromosome_11	848137	849689	
CUST_13178_PI425379931	Au9.Cre10.g465300		0.77	4.65E-02	chromosome_10	6309277	6328456	K01768
CUST_13673_PI425379931	Au9.Cre10.g447500	kinesin motor domain containing protein	0.769	2.53E-02	chromosome_10	3830929	3836684	
CUST_8536_PI425379931	Au9.Cre07.g321100	xylulokinase	0.769	3.89E-02	chromosome_7	1184370	1189205	K00854
CUST_7882_PI425379931	Au9.Cre01.g072950	DnaJ-like protein	0.768	3.41E-02	chromosome_1	9951374	9954189	
CUST_7188_PI425379931	Au9.Cre12.g500100	predicted protein	0.765	3.04E-02	chromosome_12	1974576	1977937	
CUST_9533_PI425379931	Au9.Cre02.g088750	ATM/ATR-like kinase	0.761	3.93E-02	chromosome_2	1921922	1949144	
CUST_8730_PI425379931	Au9.Cre08.g379550	major facilitator superfamily protein	0.759	4.05E-02	chromosome_8	3239215	3245032	K12301
CUST_4768_PI425379931	Au9.Cre03.g186650	hypothetical protein CHLREDRAFT_189197	0.758	3.29E-02	chromosome_3	4563179	4565678	

CUST_1302_PI425379931	Au9.Cre09.g413650	hypothetical protein CHLREDRAFT_150040	0.757	1.59E-02	chromosome_9	4250333	4257398	
CUST_2704_PI425379931	Au9.Cre03.g168250	predicted protein	0.756	4.83E-02	chromosome_3	2609149	2612084	
CUST_10486_PI425379931	Au9.Cre05.g233050	Flagellar Associated Protein	0.755	1.83E-02	chromosome_5	645254	646405	
CUST_13901_PI425379931	Au9.Cre07.g326400	golgi membrane protein yip1	0.751	4.86E-02	chromosome_7	1805752	1808683	
CUST_8967_PI425379931	Au9.Cre17.g737000	hypothetical protein CHLREDRAFT_159618	0.75	2.69E-02	chromosome_17	5487192	5488864	
CUST_3285_PI425379931	Au9.Cre16.g679500	NADH:ubiquinone oxidoreductase 11 kDa subunit	0.75	3.12E-02	chromosome_16	4389787	4391753	K03946
CUST_5276_PI425379931	Au9.Cre13.g566850	SOUL heme-binding protein	0.749	3.68E-02	chromosome_13	732956	735360	
CUST_1084_PI425379931	Au9.Cre08.g374100	hypothetical protein ACLA_028940	0.748	4.98E-02	chromosome_8	2491753	2496174	
CUST_11544_PI425379931	Au9.Cre03.g185550	Sedoheptulose-1,7-bisphosphatase	0.745	3.12E-02	chromosome_3	4474617	4477233	K01100
CUST_222_PI425379931	Au9.Cre10.g448000	hypothetical protein CHLREDRAFT_187618	0.742	2.69E-02	chromosome_10	3888944	3891264	
CUST_11237_PI425379931	Au9.Cre04.g220500	hypothetical protein CHLREDRAFT_189397	0.742	2.66E-02	chromosome_4	1491271	1492379	
CUST_4869_PI425379931	Au9.Cre13.g597450	glutaredoxin-like protein	0.74	3.89E-02	chromosome_13	4888466	4892709	
CUST_5811_PI425379931	Au9.Cre12.g490450	predicted protein	0.74	1.09E-02	chromosome_12	889052	891167	
CUST_12001_PI425379931	Au9.Cre06.g280650	predicted protein	0.74	3.19E-02	chromosome_6	3747413	3749761	

CUST_11691_PI425379931	Au9.Cre25.g770800	ser thr protein kinase	0.739	3.04E-02	scaffold_25	9850	29175	
CUST_8794_PI425379931	Au9.Cre01.g013550	Amphiphysin	0.739	2.24E-02	chromosome_1	2241260	2245020	K10352
CUST_7127_PI425379931	Au9.Cre01.g042550	predicted protein	0.738	2.10E-02	chromosome_1	5862841	5868205	
CUST_5705_PI425379931	Au9.Cre15.g635600	Nascent polypeptide associated-complex, alpha subunit	0.737	2.72E-02	chromosome_15	290257	293388	
CUST_7701_PI425379931	Au9.Cre17.g724600	Pheophorbide a oxygenase; Rieske iron-sulfur cluster protein;Pheophorbide a oxygenase; Rieske iron-sulfur cluster protein;Pheophorbide a oxygenase; Rieske iron-sulfur cluster protein;Pheophorbide a oxygenase; Rieske iron-sulfur cluster protein	0.735	4.86E-02	chromosome_17	3454799	3459056	K13071
CUST_1010_PI425379931	Au9.Cre02.g078700	Jumonji protein	0.735	4.34E-02	chromosome_2	747271	753298	
CUST_244_PI425379931	Au9.Cre01.g066450	Small ubiquitin-like modifier	0.735	3.93E-02	chromosome_1	9065055	9066665	
CUST_2943_PI425379931	Au9.Cre74.g795150	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases (ISS)	0.733	4.34E-02	scaffold_74	1	6499	
CUST_2099_PI425379931	Au9.Cre01.g050900	glycosyl family 2	0.732	4.05E-02	chromosome_1	6996826	6999424	K00754

CUST_13015_PI425379931	Au9.Cre17.g725300	Splicing factor 3b, subunit 4	0.73	4.98E-02	chromosome_17	3550249	3554735	K12887
CUST_9077_PI425379931	Au9.Cre07.g329700	26S proteasome regulatory subunit	0.73	1.56E-02	chromosome_7	2209273	2214999	K03062
CUST_9453_PI425379931	Au9.Cre04.g228600	hypothetical protein CHLREDRAFT_189488	0.73	3.19E-02	chromosome_4	2780783	2784976	
CUST_579_PI425379931	Au9.Cre13.g582250	glycosyl hydrolase family 85 protein	0.729	3.56E-02	chromosome_13	2728617	2737323	K01227
CUST_5972_PI425379931	Au9.Cre03.g211000	Mitochondrial FAD carrier protein	0.729	3.89E-02	chromosome_3	7684988	7689375	
CUST_7835_PI425379931	Au9.Cre04.g216300	hypothetical protein CHLREDRAFT_185179	0.728	3.89E-02	chromosome_4	771800	774644	
CUST_1908_PI425379931	Au9.Cre01.g002000	hypothetical protein CHLREDRAFT_193344	0.727	8.07E-03	chromosome_1	310051	314190	
CUST_5855_PI425379931	Au9.Cre18.g751500	udp-sugar diphosphatase	0.726	3.29E-02	scaffold_18	1245967	1249703	
CUST_3576_PI425379931	Au9.Cre03.g189950	HSP70-HSP90 organizing protein	0.726	2.11E-02	chromosome_3	4882142	4887102	K09553
CUST_7520_PI425379931	Au9.Cre02.g138100	hypothetical protein CHLREDRAFT_192792	0.726	1.59E-02	chromosome_2	8610767	8613229	
CUST_14299_PI425379931	Au9.Cre10.g449900	predicted protein	0.724	3.68E-02	chromosome_10	4168847	4171741	
CUST_11138_PI425379931	Au9.Cre13.g598750	Phosphoglucomutase	0.723	3.89E-02	chromosome_13	5032040	5037797	
CUST_10600_PI425379931	Au9.Cre06.g281300	predicted protein	0.723	9.24E-03	chromosome_6	3806036	3807731	
CUST_5777_PI425379931	Au9.Cre03.g161000	Adenosine/AMP deaminase	0.723	1.85E-02	chromosome_3	1687332	1691953	K01488

CUST_9887_PI425379931	Au9.Cre12.g527850	Translin-like protein	0.722	3.66E-02	chromosome_12	5063495	5066955	
CUST_3488_PI425379931	Au9.Cre11.g481450	CF0 ATP synthase subunit II precursor	0.722	1.82E-02	chromosome_11	2450939	2452185	K02109
CUST_1158_PI425379931	Au9.Cre06.g300950	hypothetical protein CHLREDRAFT_188910	0.722	7.97E-03	chromosome_6	6277867	6279757	
CUST_867_PI425379931	Au9.Cre01.g037800	thioredoxin-like ATP binding protein 2	0.721	2.43E-02	chromosome_1	5212491	5214962	
CUST_12604_PI425379931	Au9.Cre06.g282250	acetyltransferase-related	0.72	1.73E-02	chromosome_6	3900123	3907354	
CUST_6413_PI425379931	Au9.Cre02.g088000	prohibitin	0.72	1.22E-02	chromosome_2	1827090	1831709	
CUST_11071_PI425379931	Au9.Cre16.g657600	hypothetical protein CHLREDRAFT_176937	0.718	4.74E-02	chromosome_16	1284225	1287382	
CUST_12235_PI425379931	Au9.Cre06.g302750	Serine/threonine kinase receptor-associated protein	0.718	2.63E-02	chromosome_6	6529833	6533710	K13137
CUST_7481_PI425379931	Au9.Cre16.g661250	hypothetical protein CHLREDRAFT_193085	0.717	4.59E-02	chromosome_16	1728503	1732699	K03406
CUST_12839_PI425379931	Au9.Cre03.g190400	hypothetical protein CHLREDRAFT_170664	0.717	1.91E-02	chromosome_3	4945316	4949040	
CUST_8214_PI425379931	Au9.Cre12.g548200	predicted protein	0.716	3.12E-02	chromosome_12	7630023	7635614	
CUST_12648_PI425379931	Au9.Cre03.g190300	hypothetical protein	0.716	1.46E-02	chromosome_3	4932629	4936406	

		CHLREDRAFT_170664							
CUST_12509_PI425379931	Au9.Cre03.g198300	pol-like protein	0.714	3.29E-02	chromosome_3	5796409	5800594		
CUST_2295_PI425379931	Au9.Cre02.g092150	peptidyl-prolyl cis-trans isomerase, FKBP-type	0.714	2.66E-02	chromosome_2	2391898	2396085	K13730	
CUST_10439_PI425379931	Au9.Cre17.g715500	tsa family	0.713	2.10E-02	chromosome_17	2416477	2419166		
CUST_9725_PI425379931	Au9.Cre12.g513750	Glutaredoxin, CPYC type	0.713	2.27E-02	chromosome_12	3449754	3451325	K00384	
CUST_11839_PI425379931	Au9.Cre01.g061700	Exportin	0.713	1.59E-02	chromosome_1	8526743	8535620		
CUST_12651_PI425379931	Au9.Cre03.g196450	Paf1 complex component	0.711	1.36E-02	chromosome_3	5595355	5599826		
CUST_8953_PI425379931	Au9.Cre08.g363450	hypothetical protein CHLREDRAFT_192211	0.71	2.89E-02	chromosome_8	871693	876350		
CUST_2545_PI425379931	Au9.Cre23.g766950	bax inhibitor-related	0.709	4.26E-02	scaffold_23	152184	154787		
CUST_13927_PI425379931	Au9.Cre06.g253350	glycine cleavage system, H-protein	0.709	4.44E-02	chromosome_6	612257	614003		
CUST_4218_PI425379931	Au9.Cre05.g232000	chaperone protein	0.709	4.34E-02	chromosome_5	448396	453871	K14002	
CUST_2854_PI425379931	Au9.Cre09.g392650	ring finger protein 32	0.708	2.65E-02	chromosome_9	1067714	1073207	K10601	
CUST_14149_PI425379931	Au9.Cre03.g171300	Glycolate oxidase	0.707	3.41E-02	chromosome_3	2939945	2943466	K11517	
CUST_2891_PI425379931	Au9.Cre06.g256450	Flagellar Associated Protein	0.706	4.74E-02	chromosome_6	1065275	1067726		
CUST_7986_PI425379931	Au9.Cre02.g115900	hypothetical protein CHLREDRAFT_181241	0.706	1.71E-02	chromosome_2	5536033	5538522		

CUST_5073_PI425379931	Au9.Cre54.g790800	pol-like protein	0.704	3.89E-02	scaffold_54	34116	50102	
CUST_13115_PI425379931	Au9.Cre10.g419950	mitogen activated protein kinase kinase kinase 9	0.704	3.68E-02	chromosome_10	300190	306946	
CUST_8870_PI425379931	Au9.Cre08.g377100	Adenylate Kinase 6	0.704	1.12E-02	chromosome_8	2891311	2895166	K00939
CUST_4185_PI425379931	Au9.Cre13.g601850	pol-like protein	0.703	7.79E-03	chromosome_13	5365288	5366259	
CUST_2176_PI425379931	Au9.Cre13.g570900	Peptide methionine-S-sulfoxide reductase	0.703	2.91E-02	chromosome_13	1259555	1262462	
CUST_9785_PI425379931	Au9.Cre11.g470000	reverse transcriptase	0.702	3.47E-02	chromosome_11	437245	449044	
CUST_6760_PI425379931	Au9.Cre03.g172100	peptide deformylase	0.702	4.22E-03	chromosome_3	3044966	3046887	K00604
CUST_3214_PI425379931	Au9.Cre02.g130800	low-co2-inducible protein	0.702	2.29E-02	chromosome_2	7356813	7362008	
CUST_9815_PI425379931	Au9.Cre17.g733700	predicted protein	0.701	4.26E-02	chromosome_17	4829639	4832304	
CUST_3971_PI425379931	Au9.Cre12.g521400	cobyrinic acid -diamide synthase	0.701	1.13E-02	chromosome_12	4315110	4320542	K02224
CUST_6396_PI425379931	Au9.Cre07.g341600	GrpE nucleotide release factor; GrpE nucleotide release factor;GrpE nucleotide release factor; GrpE nucleotide release factor;GrpE nucleotide release factor; GrpE nucleotide release factor;GrpE nucleotide release factor; GrpE	0.701	2.83E-02	chromosome_7	3970964	3974783	

		nucleotide release factor;GrpE						
CUST_13335_PI425379931	Au9.Cre12.g531700	amp deaminase	0.7	2.27E-02	chromosome_12	5431476	5439056	K01490
CUST_2314_PI425379931	Au9.Cre11.g472050	Ubiquinone/menaquinone biosynthesis methyltransferase	0.7	4.86E-02	chromosome_11	830818	836570	
CUST_9919_PI425379931	Au9.Cre08.g384950	hydroxymethylpyrimidine kinase (ISS)	0.7	2.91E-02	chromosome_8	4004056	4006481	K14153
CUST_13652_PI425379931	Au9.Cre16.g689000	hypothetical protein CHLREDRAFT_193656	0.699	4.26E-02	chromosome_16	5614363	5617818	
CUST_4910_PI425379931	Au9.Cre12.g542150	integral membrane protein	0.699	1.76E-02	chromosome_12	6944602	6946448	
CUST_3962_PI425379931	Au9.Cre08.g364200	predicted protein	0.699	3.89E-02	chromosome_8	991177	992002	
CUST_14583_PI425379931	Au9.Cre07.g340200	pgr5-like a	0.699	1.65E-02	chromosome_7	3766935	3769431	
CUST_1797_PI425379931	Au9.Cre13.g580050	AAA+-type ATPase	0.698	3.89E-02	chromosome_13	2492250	2499917	K01509
CUST_2271_PI425379931	Au9.Cre07.g339050	actin-depolymerizing factor 3	0.698	1.58E-02	chromosome_7	3617293	3621336	K05765
CUST_906_PI425379931	Au9.Cre03.g178450	Chaperonin 10	0.698	1.73E-02	chromosome_3	3800951	3802359	
CUST_7803_PI425379931	Au9.Cre02.g128300	Histone-lysine N-methyltransferase	0.698	6.32E-03	chromosome_2	7035925	7046116	

CUST_12947_PI425379931	Au9.Cre12.g507700	KEKE-like motif-containing transcription regulator (Rlr1)/suppressor of sin4	0.697	1.13E-02	chromosome_12	2740619	2755917	
CUST_11285_PI425379931	Au9.Cre37.g784800	pol-like protein	0.696	3.54E-02	scaffold_37	18096	23691	
CUST_13847_PI425379931	Au9.Cre13.g574000	chloride channel	0.696	7.88E-03	chromosome_13	1648194	1662652	K05011
CUST_9869_PI425379931	Au9.Cre01.g020300	Succinate dehydrogenase subunit D	0.696	2.18E-02	chromosome_1	3050519	3057897	K00237
CUST_14132_PI425379931	Au9.Cre03.g154850	ubiquinone biosynthesis protein	0.695	3.89E-02	chromosome_3	907158	910313	
CUST_4849_PI425379931	Au9.Cre16.g666600	reverse transcriptase	0.694	2.88E-02	chromosome_16	2441553	2451701	
CUST_171_PI425379931	Au9.Cre03.g189050	glycoprotein endo-alpha- -mannosidase-like protein	0.694	2.69E-02	chromosome_3	4796207	4801178	
CUST_9217_PI425379931	Au9.Cre02.g083700	signal transducer for phototaxis	0.694	3.41E-02	chromosome_2	1315913	1322258	
CUST_4133_PI425379931	Au9.Cre12.g516450	gamma carbonic anhydrase	0.693	0.00E+00	chromosome_12	3817752	3819397	K00680
CUST_9448_PI425379931	Au9.Cre07.g327400	NADH:ubiquinone oxidoreductase ND9 subunit	0.693	1.22E-02	chromosome_7	1928668	1930467	K03936
CUST_13598_PI425379931	Au9.Cre01.g065150	Histidinol phosphate aminotransferase	0.693	1.85E-02	chromosome_1	8935581	8940040	
CUST_3034_PI425379931	Au9.Cre16.g692900	hypothetical protein CHLREDRAFT_178046	0.692	1.65E-02	chromosome_16	6118210	6121675	
CUST_8669_PI425379931	Au9.Cre13.g563150	hypothetical protein	0.692	2.45E-02	chromosome_13	166407	170827	

		CHLREDRAFT_143294						
CUST_12626_PI425379931	Au9.Cre06.g259400	S-adenosyl-L-methionine-dependent methyltransferase	0.692	1.37E-02	chromosome_6	1443773	1447672	
CUST_5584_PI425379931	Au9.Cre07.g333200	pol-like protein	0.691	3.19E-02	chromosome_7	2730432	2733925	
CUST_7479_PI425379931	Au9.Cre06.g289150	CDF transporter, membrane protein	0.691	1.85E-02	chromosome_6	4668642	4675497	
CUST_2112_PI425379931	Au9.Cre01.g060600	alpha beta hydrolase fold protein	0.691	3.41E-02	chromosome_1	8401837	8405084	
CUST_5171_PI425379931	Au9.Cre16.g675800	hypothetical protein CHLREDRAFT_149171	0.69	2.83E-02	chromosome_16	3926970	3929088	
CUST_7457_PI425379931	Au9.Cre02.g093050	heat shock protein 70D	0.69	2.88E-02	chromosome_2	2483396	2484793	
CUST_12485_PI425379931	Au9.Cre10.g452000	cation transport protein chac-related	0.689	4.83E-02	chromosome_10	4488874	4491021	
CUST_6956_PI425379931	Au9.Cre06.g290850	predicted protein	0.689	2.23E-02	chromosome_6	4913384	4916103	
CUST_12165_PI425379931	Au9.Cre12.g560350	NimA-related protein kinase 2	0.688	3.25E-02	chromosome_12	9160194	9166337	K06228
CUST_2310_PI425379931	Au9.Cre07.g357550	predicted protein	0.688	1.85E-02	chromosome_7	6117546	6125185	
CUST_14484_PI425379931	Au9.Cre10.g446100	Thioredoxin y	0.687	1.22E-02	chromosome_10	3678225	3680227	K13989
CUST_9305_PI425379931	Au9.Cre07.g325100	ae007549_12 uncharacterized conserved membrane sana family	0.687	3.93E-02	chromosome_7	1642153	1644528	
CUST_12279_PI425379931	Au9.Cre03.g181050	predicted protein	0.687	1.85E-02	chromosome_3	4050787	4056606	

CUST_5611_PI425379931	Au9.Cre03.g177300	haloperoxidase-like protein	0.686	2.53E-02	chromosome_3	3640827	3643908	
CUST_2386_PI425379931	Au9.Cre51.g790250	pol-like protein	0.685	2.11E-02	scaffold_51	41536	45718	
CUST_1332_PI425379931	Au9.Cre22.g763250	Phosphoglycerate Kinase; phosphoglycerate kinase, chloroplast precursor, phosphoglycerate kinase;Phosphoglycerate Kinase; phosphoglycerate kinase, chloroplast precursor, phosphoglycerate kinase	0.685	2.66E-02	scaffold_22	125396	129780	
CUST_442_PI425379931	Au9.Cre02.g080250	fanciful k+ uptake-b family transporter	0.685	2.24E-02	chromosome_2	931195	934607	
CUST_8583_PI425379931	Au9.Cre15.g641900	phosphatidylethanolamine n-methyltransferase	0.684	9.80E-03	chromosome_15	1456608	1461756	K00570
CUST_7268_PI425379931	Au9.Cre07.g328400	rna binding protein	0.684	3.89E-02	chromosome_7	2054539	2058114	K14651
CUST_6839_PI425379931	Au9.Cre01.g027050	predicted protein	0.684	4.98E-02	chromosome_1	3947465	3949158	
CUST_10383_PI425379931	Au9.Cre10.g455400	RNA methylase	0.683	2.83E-02	chromosome_10	5001407	5004407	
CUST_5851_PI425379931	Au9.Cre09.g399550	rglg2 (ring domain ligase2) ubiquitin-protein ligase	0.683	3.89E-02	chromosome_9	2069794	2075768	K09561

CUST_2414_PI425379931	Au9.Cre06.g283800	predicted protein	0.683	1.85E-02	chromosome_6	4050712	4056998	
CUST_7609_PI425379931	Au9.Cre03.g206600	Acetohydroxyacid dehydratase	0.683	4.26E-02	chromosome_3	6915031	6922211	K01687
CUST_13709_PI425379931	Au9.Cre12.g554800	Phosphoribulokinase	0.682	2.72E-02	chromosome_12	8449153	8452598	K00855
CUST_1149_PI425379931	Au9.Cre07.g353950	xp-g/rad2 dna repair endonuclease family	0.682	4.59E-02	chromosome_7	5639642	5647547	K10746
CUST_12329_PI425379931	Au9.Cre06.g304500	zygote-specific protein	0.682	2.66E-02	chromosome_6	6770935	6774688	
CUST_6182_PI425379931	Au9.Cre16.g672350	brca1 associated ring	0.681	1.85E-02	chromosome_16	3419781	3426366	
CUST_13242_PI425379931	Au9.Cre01.g019300		0.68	2.88E-02	chromosome_1	2909903	2925888	K01768
CUST_5549_PI425379931	Au9.Cre06.g286250	mitochondrial substrate carrier protein	0.679	3.47E-02	chromosome_6	4326203	4329799	K13577
CUST_14224_PI425379931	Au9.Cre02.g079200	CCAAT-binding transcription factor subunit A	0.679	6.78E-03	chromosome_2	815470	817843	K08065
CUST_3617_PI425379931	Au9.Cre39.g785800	endonuclease-reverse transcriptase	0.678	4.98E-02	scaffold_39	959	5745	
CUST_4955_PI425379931	Au9.Cre12.g541850	acylphosphatase organ-common type isozyme variant 1	0.678	9.66E-03	chromosome_12	6915595	6917472	K01512
CUST_3928_PI425379931	Au9.Cre12.g501550	hypothetical protein CHLREDRAFT_182999	0.678	9.66E-03	chromosome_12	2131301	2132702	
CUST_2162_PI425379931	Au9.Cre03.g172750	hypothetical protein CHLREDRAFT_143922	0.678	3.25E-02	chromosome_3	3107857	3109605	

CUST_10187_PI425379931	Au9.Cre16.g670950	chloroplast cytochrome c	0.677	6.32E-03	chromosome_16	3229466	3231441	K08906
CUST_2393_PI425379931	Au9.Cre16.g666750	pol-like protein	0.677	3.93E-02	chromosome_16	2540897	2544851	
CUST_6061_PI425379931	Au9.Cre10.g450150	predicted protein	0.677	2.66E-02	chromosome_10	4215166	4218541	
CUST_12595_PI425379931	Au9.Cre02.g101550	Mg2+ transporter protein, CorA-like	0.677	1.65E-02	chromosome_2	3772680	3775745	
CUST_4693_PI425379931	Au9.Cre02.g094250	mitochondrial carrier protein related	0.677	2.53E-02	chromosome_2	2668656	2671988	K13354
CUST_3115_PI425379931	Au9.Cre01.g042950	salt tolerant protein	0.677	2.66E-02	chromosome_1	5906616	5909691	
CUST_12600_PI425379931	Au9.Cre51.g790300	reverse transcriptases	0.676	1.91E-02	scaffold_51	49550	56515	
CUST_6682_PI425379931	Au9.Cre21.g761450	endonuclease-reverse transcriptase	0.676	4.59E-02	scaffold_21	231135	233256	
CUST_12701_PI425379931	Au9.Cre01.g049600	F0-ATPase complex, subunit I	0.676	4.41E-02	chromosome_1	6774421	6776974	
CUST_6173_PI425379931	Au9.Cre24.g768650	predicted protein	0.675	2.66E-02	scaffold_24	9640	12745	
CUST_4616_PI425379931	Au9.Cre07.g326900	hypothetical protein CHLREDRAFT_188528	0.675	1.65E-02	chromosome_7	1866923	1869667	
CUST_3528_PI425379931	Au9.Cre06.g303150	Putative tyrosine kinase	0.675	4.75E-03	chromosome_6	6575716	6594382	K04422
CUST_3135_PI425379931	Au9.Cre02.g088850	6,7-dimethyl-8-ribityllumazine synthase	0.675	2.96E-02	chromosome_2	1952205	1953921	K00794
CUST_13854_PI425379931	Au9.Cre07.g351700	Predicted membrane protein	0.674	6.62E-03	chromosome_7	5320879	5323065	
CUST_14593_PI425379931	Au9.Cre07.g332450	nmt1 thi5 like domain protein	0.674	2.66E-02	chromosome_7	2570476	2573604	K02051
CUST_5976_PI425379931	Au9.Cre01.g005550	ARF-like GTPase	0.674	4.75E-03	chromosome_1	974404	975625	K07937

CUST_89_PI425379931	Au9.Cre17.g742850	Histone-lysine N-methyltransferase	0.673	3.96E-03	chromosome_17	6414331	6415896	
CUST_2817_PI425379931	Au9.Cre06.g261000	10 kDa photosystem II polypeptide	0.673	1.13E-02	chromosome_6	1638321	1639901	K03541
CUST_12110_PI425379931	Au9.Cre01.g021350	predicted protein	0.673	2.69E-02	chromosome_1	3169584	3172231	
CUST_13869_PI425379931	Au9.Cre12.g554750	ubiquitin-like protein	0.672	1.45E-02	chromosome_12	8445435	8447186	K03873
CUST_7401_PI425379931	Au9.Cre03.g196100	predicted protein	0.671	3.80E-02	chromosome_3	5570336	5573606	
CUST_5241_PI425379931	Au9.Cre13.g585300	monogalactosyldiacylglycerol synthase	0.67	4.86E-02	chromosome_13	3174588	3180639	
CUST_2227_PI425379931	Au9.Cre16.g684650	nickel chaperone for hydrogenase or urease	0.669	1.13E-02	chromosome_16	5045135	5049396	K12605
CUST_14435_PI425379931	Au9.Cre12.g548550	predicted protein	0.669	2.89E-02	chromosome_12	7667463	7670894	
CUST_5778_PI425379931	Au9.Cre04.g222450	hypothetical protein CHLREDRAFT_181482	0.669	2.27E-02	chromosome_4	1745372	1746510	
CUST_11638_PI425379931	Au9.Cre01.g073100	Serine/threonine protein kinase/TGF-beta stimulated factor	0.669	3.55E-02	chromosome_1	9967078	9973204	
CUST_11001_PI425379931	Au9.Cre12.g561650	pol-like protein	0.668	5.74E-03	chromosome_12	9326443	9328764	
CUST_12783_PI425379931	Au9.Cre10.g452650	mitochondrial inner membrane translocase	0.668	1.03E-02	chromosome_10	4573302	4577656	
CUST_12993_PI425379931	Au9.Cre01.g045550	triose phosphate translocator	0.668	2.63E-02	chromosome_1	6236240	6241092	
CUST_6047_PI425379931	Au9.Cre12.g555100	predicted protein	0.667	1.13E-02	chromosome_12	8496657	8499702	

CUST_11825_PI425379931	Au9.Cre10.g457000	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	0.667	4.34E-02	chromosome_10	5221944	5226727	K10598
CUST_4014_PI425379931	Au9.Cre13.g596300	B-box zinc finger protein	0.666	5.74E-03	chromosome_13	4746141	4749429	
CUST_3619_PI425379931	Au9.Cre12.g490550	predicted protein	0.666	3.89E-02	chromosome_12	895560	898003	
CUST_1716_PI425379931	Au9.Cre17.g707700	Manganese transport protein	0.665	3.29E-02	chromosome_17	1593560	1598394	K12347
CUST_1897_PI425379931	Au9.Cre13.g601950	hypothetical protein CHLREDRAFT_180886	0.665	3.19E-02	chromosome_13	5373382	5375817	
CUST_9953_PI425379931	Au9.Cre01.g007600	predicted protein	0.665	3.55E-02	chromosome_1	1294029	1299289	
CUST_6397_PI425379931	Au9.Cre09.g409500	chloroplast nucleoid dna-binding protein	0.664	1.13E-02	chromosome_9	3588265	3592870	K14525
CUST_9477_PI425379931	Au9.Cre05.g233550	serine-threonine protein kinase	0.663	1.73E-02	chromosome_5	727225	740896	
CUST_9876_PI425379931	Au9.Cre01.g054100	leucine-rich repeat-containing protein	0.663	3.19E-02	chromosome_1	7493487	7499722	K13730
CUST_13104_PI425379931	Au9.Cre01.g001750	Chloroplast trigger factor	0.663	2.27E-02	chromosome_1	287370	294187	
CUST_9411_PI425379931	Au9.Cre34.g783750	hypothetical protein CHLREDRAFT_180858	0.662	3.29E-02	scaffold_34	140140	144315	
CUST_3203_PI425379931	Au9.Cre13.g597850	predicted protein	0.662	3.55E-02	chromosome_13	4936709	4940714	
CUST_170_PI425379931	Au9.Cre07.g313850	wd40 repeat protein	0.662	2.91E-02	chromosome_7	243532	255526	K03362
CUST_5044_PI425379931	Au9.Cre03.g159350	wd40 repeat protein	0.662	3.89E-02	chromosome_3	1475434	1487911	K03130

CUST_3078_PI425379931	Au9.Cre17.g708300	26S proteasome regulatory subunit	0.661	0.00E+00	chromosome_17	1661387	1664132	K03031
CUST_12537_PI425379931	Au9.Cre16.g667500	voltage-activated ion	0.661	4.75E-03	chromosome_16	2680100	2686091	
CUST_5624_PI425379931	Au9.Cre06.g300700	nad-dependent epimerase dehydratase	0.661	3.55E-02	chromosome_6	6242459	6245142	
CUST_12158_PI425379931	Au9.Cre12.g547550	predicted protein	0.66	1.73E-02	chromosome_12	7539705	7545656	
CUST_9751_PI425379931	Au9.Cre12.g498950	hypothetical protein CHLREDRAFT_194644	0.66	0.00E+00	chromosome_12	1872859	1875671	
CUST_11818_PI425379931	Au9.Cre12.g486500	iron ion binding acting on paired with incorporation or reduction of molecular 2-oxoglutarate as one and incorporation of one atom each of oxygen into both donors	0.659	4.05E-02	chromosome_12	411119	414793	
CUST_13713_PI425379931	Au9.Cre11.g475850	DnaJ-like Zinc-finger protein	0.659	2.45E-02	chromosome_11	1439454	1441843	K12603
CUST_10775_PI425379931	Au9.Cre01.g006650	pol-like protein	0.659	5.74E-03	chromosome_1	1133293	1136934	
CUST_13837_PI425379931	Au9.Cre07.g321600	hypothetical protein CHLREDRAFT_142802	0.657	3.89E-02	chromosome_7	1241750	1243825	
CUST_6209_PI425379931	Au9.Cre02.g112950	hypothetical protein CHLREDRAFT_166632	0.656	1.04E-02	chromosome_2	5179387	5181710	
CUST_483_PI425379931	Au9.Cre19.g752000	dead box protein	0.655	1.13E-02	scaffold_19	52786	60047	

CUST_11804_PI425379931	Au9.Cre17.g741850	Heterogeneous Nuclear Ribonucleoprotein	0.655	1.13E-02	chromosome_17	6265730	6267802	
CUST_2530_PI425379931	Au9.Cre10.g419050	mitochondrial F1F0 ATP synthase, alpha subunit	0.655	7.40E-03	chromosome_10	193560	200139	K02111
CUST_4421_PI425379931	Au9.Cre06.g278200	rhythm of chloroplast 66	0.655	3.66E-02	chromosome_6	3477479	3487350	K12130
CUST_10285_PI425379931	Au9.Cre01.g037200	predicted protein	0.655	5.18E-03	chromosome_1	5150074	5151312	
CUST_5857_PI425379931	Au9.Cre01.g020750	predicted protein	0.655	2.43E-02	chromosome_1	3085376	3088537	K03348
CUST_11753_PI425379931	Au9.Cre10.g446200	hypothetical protein CHLREDRAFT_187586	0.654	4.26E-02	chromosome_10	3683451	3685577	
CUST_10998_PI425379931	Au9.Cre09.g416300	hypothetical protein CHLREDRAFT_192178	0.654	1.12E-02	chromosome_9	4549299	4555938	
CUST_1298_PI425379931	Au9.Cre01.g016450	mynd finger family expressed	0.654	9.80E-03	chromosome_1	2580455	2587140	
CUST_3471_PI425379931	Au9.Cre10.g421250	Component of the Exocyst Complex	0.653	4.98E-02	chromosome_10	526909	534500	K07195
CUST_8508_PI425379931	Au9.Cre09.g414050	rvb1-like protein	0.653	1.28E-02	chromosome_9	4303296	4307588	K04499
CUST_3924_PI425379931	Au9.Cre19.g751650	Dihydroorotase dehydrogenase	0.652	0.00E+00	scaffold_19	21650	25585	
CUST_12039_PI425379931	Au9.Cre06.g259450	predicted protein	0.651	2.89E-02	chromosome_6	1447961	1450346	
CUST_2215_PI425379931	Au9.Cre01.g014000	predicted protein	0.651	1.96E-02	chromosome_1	2291239	2293242	
CUST_12928_PI425379931	Au9.Cre12.g555550	gelsolin precursor	0.65	3.19E-02	chromosome_12	8526887	8536052	K05768

CUST_9612_PI425379931	Au9.Cre10.g444550	signal peptide peptidase	0.649	0.00E+00	chromosome_10	3378948	3385970	K03313
CUST_11498_PI425379931	Au9.Cre10.g435800	chloroplast stem-loop-binding protein	0.649	2.66E-02	chromosome_10	2402951	2409343	K01784
CUST_4068_PI425379931	Au9.Cre10.g445150	polymyositis/scleroderma autoantigen-related	0.648	1.22E-02	chromosome_10	3466428	3472194	
CUST_10815_PI425379931	Au9.Cre06.g293150	putative phosphomutase	0.648	3.29E-02	chromosome_6	5229916	5234068	
CUST_6058_PI425379931	Au9.Cre02.g093650	rieske (2fe-2s) domain protein	0.648	2.66E-02	chromosome_2	2599455	2601108	
CUST_7308_PI425379931	Au9.Cre01.g049700	kinesin-like protein	0.648	2.29E-02	chromosome_1	6785682	6788786	
CUST_1198_PI425379931	Au9.Cre17.g720400	heavy metal transporting ATPase	0.647	2.66E-02	chromosome_17	3013946	3020397	K01547
CUST_8149_PI425379931	Au9.Cre10.g419500	predicted protein	0.647	3.19E-02	chromosome_10	262111	266496	
CUST_7244_PI425379931	Au9.Cre07.g325050	exostosin-like glycosyltransferase	0.647	3.41E-02	chromosome_7	1634429	1642134	K02367
CUST_6421_PI425379931	Au9.Cre17.g700100	macrophage migration inhibitory factor	0.646	6.62E-03	chromosome_17	606842	608673	K07253
CUST_5050_PI425379931	Au9.Cre16.g682800	rna-binding protein	0.646	1.45E-02	chromosome_16	4853720	4857263	
CUST_12870_PI425379931	Au9.Cre07.g331500	Inactive subunit of chloroplast ClpP complex	0.646	2.29E-02	chromosome_7	2466271	2473689	
CUST_12756_PI425379931	Au9.Cre02.g076300	Uroporphyrinogen decarboxylase	0.646	4.00E-03	chromosome_2	442913	445864	K01599
CUST_10631_PI425379931	Au9.Cre17.g722000	Solute carrier protein	0.645	2.66E-02	chromosome_17	3203234	3207342	

CUST_9522_PI425379931	Au9.Cre12.g544150	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	0.645	3.29E-02	chromosome_12	7157729	7160337	K05864
CUST_6987_PI425379931	Au9.Cre07.g317200	hypothetical protein CHLREDRAFT_187479	0.645	2.06E-02	chromosome_7	679465	684180	
CUST_10436_PI425379931	Au9.Cre12.g517250	hypothetical protein CHLREDRAFT_176330	0.644	3.66E-02	chromosome_12	3894874	3897546	
CUST_6062_PI425379931	Au9.Cre12.g507000		0.644	3.89E-02	chromosome_12	2634496	2655408	
CUST_9951_PI425379931	Au9.Cre12.g545650	predicted protein	0.643	4.34E-02	chromosome_12	7325002	7329827	
CUST_12457_PI425379931	Au9.Cre06.g252100	294687m protein	0.642	1.73E-02	chromosome_6	403014	413049	K00507
CUST_9653_PI425379931	Au9.Cre14.g631850	orphan 2	0.641	6.59E-03	chromosome_14	3608424	3611325	K13248
CUST_14609_PI425379931	Au9.Cre02.g114600	2-cys peroxiredoxin	0.641	3.55E-02	chromosome_2	5383656	5385624	K13279
CUST_3761_PI425379931	Au9.Cre16.g696000	utp--glucose-1-phosphate uridylyltransferase family protein	0.64	1.85E-02	chromosome_16	6579093	6587813	K00972
CUST_7984_PI425379931	Au9.Cre01.g028350	DegP-type protease	0.64	4.59E-02	chromosome_1	4063835	4069052	K08372
CUST_14345_PI425379931	Au9.Cre12.g555250	NADH:ubiquinone oxidoreductase B14 subunit	0.639	0.00E+00	chromosome_12	8510946	8512919	K03950
CUST_10607_PI425379931	Au9.Cre10.g421500	predicted protein	0.639	0.00E+00	chromosome_10	561116	564667	
CUST_960_PI425379931	Au9.Cre03.g189350	hypothetical protein CHLREDRAFT_156911	0.639	1.13E-02	chromosome_3	4829076	4831275	

CUST_13174_PI425379931	Au9.Cre16.g659900	hypothetical protein CHLREDRAFT_193064	0.638	4.98E-02	chromosome_16	1560533	1563585	
CUST_6011_PI425379931	Au9.Cre10.g419250	predicted protein	0.638	2.66E-02	chromosome_10	229119	231178	
CUST_12243_PI425379931	Au9.Cre07.g312300	antibiotic biosynthesis monooxygenase	0.638	0.00E+00	chromosome_7	43680	45391	
CUST_14070_PI425379931	Au9.Cre13.g581150	gcn5-related n-acetyltransferase	0.636	9.73E-03	chromosome_13	2614265	2617585	
CUST_10733_PI425379931	Au9.Cre12.g540100	predicted protein	0.636	1.91E-02	chromosome_12	6717558	6721029	
CUST_3106_PI425379931	Au9.Cre10.g457700	calcium calmodulin-dependent protein kinase id	0.636	0.00E+00	chromosome_10	5310500	5314354	K05869
CUST_2659_PI425379931	Au9.Cre10.g419000	myeloid leukemia factor	0.636	1.71E-02	chromosome_10	188700	192238	
CUST_13875_PI425379931	Au9.Cre06.g261650	prefoldin chaperone 1	0.636	1.13E-02	chromosome_6	1706427	1707875	
CUST_7705_PI425379931	Au9.Cre05.g248000	hypothetical protein CHLREDRAFT_167685	0.635	1.00E-02	chromosome_5	3261831	3268567	
CUST_6015_PI425379931	Au9.Cre02.g097900	aspartate aminotransferase	0.634	4.00E-03	chromosome_2	3221301	3227506	K00813
CUST_892_PI425379931	Au9.Cre12.g546150	cytochrome b6f complex PetM subunit	0.633	1.59E-02	chromosome_12	7387491	7388347	
CUST_7490_PI425379931	Au9.Cre06.g300800	Plastid ribosomal protein L27	0.633	1.46E-02	chromosome_6	6257309	6259059	K02899
CUST_2479_PI425379931	Au9.Cre02.g099250	predicted protein	0.632	2.18E-02	chromosome_2	3436676	3437867	
CUST_4161_PI425379931	Au9.Cre20.g757850	predicted protein	0.631	3.25E-02	scaffold_20	53126	56026	

CUST_7718_PI425379931	Au9.Cre19.g752300	heparan sulfate sulfotransferase	0.631	4.00E-03	scaffold_19	93695	96075	
CUST_12780_PI425379931	Au9.Cre06.g248800	protein kinase	0.631	2.18E-02	chromosome_6	23321	25731	
CUST_4095_PI425379931	Au9.Cre01.g031100	predicted protein	0.631	1.13E-02	chromosome_1	4393118	4396913	
CUST_13130_PI425379931	Au9.Cre17.g724700	Pheophorbide a oxygenase; Rieske iron-sulfur cluster protein;Pheophorbide a oxygenase; Rieske iron-sulfur cluster protein;Pheophorbide a oxygenase; Rieske iron-sulfur cluster protein;Pheophorbide a oxygenase; Rieske iron-sulfur cluster protein	0.63	1.91E-02	chromosome_17	3463081	3467504	K13071
CUST_6661_PI425379931	Au9.Cre10.g450900	predicted protein	0.63	2.83E-02	chromosome_10	4296802	4300643	
CUST_1417_PI425379931	Au9.Cre06.g294000	dienelactone hydrolase	0.63	7.40E-03	chromosome_6	5337284	5340609	K01061
CUST_11509_PI425379931	Au9.Cre12.g499950	serine esterase family protein	0.629	1.58E-02	chromosome_12	1962516	1966517	
CUST_6528_PI425379931	Au9.Cre05.g234750	predicted protein	0.629	1.25E-02	chromosome_5	943336	945240	
CUST_7139_PI425379931	Au9.Cre01.g055550	cytochrome c oxidase assembly protein	0.629	2.24E-02	chromosome_1	7662030	7665589	K02258
CUST_7840_PI425379931	Au9.Cre13.g584000	predicted protein	0.628	1.56E-02	chromosome_13	2971917	2976299	
CUST_4540_PI425379931	Au9.Cre08.g372450	Oxygen evolving enhancer protein 3	0.628	1.08E-02	chromosome_8	2108627	2110421	

CUST_6905_PI425379931	Au9.Cre06.g309600	hypothetical protein CHLREDRAFT_188815	0.627	1.28E-02	chromosome_6	7345890	7350208	
CUST_4495_PI425379931	Au9.Cre03.g189700	hypothetical protein CHLREDRAFT_183306	0.627	2.43E-02	chromosome_3	4867407	4870449	
CUST_6981_PI425379931	Au9.Cre02.g113100	brain protein 44-like protein	0.627	5.99E-03	chromosome_2	5188566	5190699	K11086
CUST_12593_PI425379931	Au9.Cre12.g551050	predicted protein	0.626	3.41E-02	chromosome_12	7922735	7927293	
CUST_7309_PI425379931	Au9.Cre04.g218700	Putative organellar translation initiation factor	0.626	0.00E+00	chromosome_4	1180492	1181871	
CUST_123_PI425379931	Au9.Cre29.g777950	S-adenosyl-L-methionine-dependent methyltransferase	0.625	1.91E-02	scaffold_29	58631	61159	
CUST_61_PI425379931	Au9.Cre14.g611200	mitochondrial transcription termination mterf	0.625	0.00E+00	chromosome_14	467631	470414	
CUST_8286_PI425379931	Au9.Cre13.g591300		0.625	2.89E-02	chromosome_13	4167987	4194696	
CUST_1692_PI425379931	Au9.Cre12.g512700	Transcription initiation factor IIE, beta subunit	0.625	1.13E-02	chromosome_12	3324899	3327753	K03137
CUST_14471_PI425379931	Au9.Cre17.g718450	Matrix metalloproteinase	0.624	1.59E-02	chromosome_17	2753556	2761859	
CUST_6615_PI425379931	Au9.Cre13.g602650	predicted protein	0.624	7.97E-03	chromosome_13	5731690	5735248	
CUST_2683_PI425379931	Au9.Cre13.g592950	j1a crystallin	0.624	2.45E-02	chromosome_13	4389855	4397772	
CUST_9399_PI425379931	Au9.Cre13.g562750	predicted protein	0.624	3.55E-02	chromosome_13	127371	132985	

CUST_1136_PI425379931	Au9.Cre08.g384850	short-chain dehydrogenase reductase sdr	0.624	0.00E+00	chromosome_8	3984116	3999401	
CUST_11116_PI425379931	Au9.Cre13.g567050	reverse transcriptase	0.623	3.12E-02	chromosome_13	759979	764417	K14401
CUST_10580_PI425379931	Au9.Cre09.g411150	hypothetical protein CHLREDRAFT_192098	0.623	3.12E-02	chromosome_9	3809422	3816787	
CUST_3312_PI425379931	Au9.Cre13.g570850	predicted protein	0.622	1.73E-02	chromosome_13	1256315	1259203	
CUST_10788_PI425379931	Au9.Cre06.g272300	hypothetical protein CHLREDRAFT_167070	0.622	5.34E-03	chromosome_6	2877776	2882001	
CUST_13859_PI425379931	Au9.Cre05.g241050	s-antigen	0.622	4.41E-02	chromosome_5	2066029	2068504	
CUST_5173_PI425379931	Au9.Cre03.g187450	Ribose-5-phosphate isomerase	0.622	2.66E-02	chromosome_3	4648022	4649461	K01807
CUST_12244_PI425379931	Au9.Cre13.g568850	iron-sulfur cluster assembly scaffold protein	0.621	3.19E-02	chromosome_13	1042030	1043126	K00566
CUST_8446_PI425379931	Au9.Cre02.g092600	Coproporphyrinogen III oxidase	0.62	2.45E-02	chromosome_2	2434062	2436694	K00228
CUST_4738_PI425379931	Au9.Cre19.g751900	ef hand family protein	0.619	1.83E-02	scaffold_19	43620	48885	
CUST_7864_PI425379931	Au9.Cre12.g561100	hypothetical protein CHLREDRAFT_180470	0.619	2.10E-02	chromosome_12	9249254	9253092	
CUST_11928_PI425379931	Au9.Cre07.g321300	ribonuclease p	0.619	2.53E-02	chromosome_7	1204501	1207143	
CUST_10706_PI425379931	Au9.Cre06.g289450	suppression of tumorigenicity 5 (st5)	0.619	1.13E-02	chromosome_6	4710968	4722369	
CUST_11850_PI425379931	Au9.Cre05.g247400	Protein with rhodanese-like domain	0.619	1.49E-02	chromosome_5	3156075	3157905	

CUST_3623_PI425379931	Au9.Cre13.g577850	peptidyl-prolyl cis-trans isomerase, FKBP-type	0.618	8.40E-03	chromosome_13	2135193	2138435	
CUST_628_PI425379931	Au9.Cre03.g208950	endonuclease-reverse transcriptase	0.618	1.96E-02	chromosome_3	7298810	7303105	
CUST_10213_PI425379931	Au9.Cre01.g039700	predicted protein	0.617	1.91E-02	chromosome_1	5424896	5432263	
CUST_5133_PI425379931	Au9.Cre16.g688550	glutathione-S-transferase	0.616	3.55E-02	chromosome_16	5542673	5544808	K01830
CUST_12658_PI425379931	Au9.Cre14.g621650	malonyl-CoA:acyl-carrier-protein transacylase	0.616	1.25E-02	chromosome_14	1998411	2002849	K00645
CUST_10944_PI425379931	Au9.Cre09.g398350	ubiquitination factor e4	0.616	1.46E-02	chromosome_9	1876556	1884718	K10597
CUST_3147_PI425379931	Au9.Cre01.g019250	sugar nucleotide epimerase	0.616	4.98E-02	chromosome_1	2906655	2909847	K10046
CUST_1278_PI425379931	Au9.Cre05.g236500	ceramidase	0.615	1.71E-02	chromosome_5	1364534	1389634	
CUST_4824_PI425379931	Au9.Cre13.g589700	subunit of ESCRT-III complex	0.613	6.46E-03	chromosome_13	3845659	3848591	K12195
CUST_6349_PI425379931	Au9.Cre12.g510050	Copper target 1 protein	0.613	2.23E-02	chromosome_12	3029425	3032251	K04035
CUST_2171_PI425379931	Au9.Cre08.g366950	hypothetical protein CHLREDRAFT_192240	0.613	4.05E-02	chromosome_8	1421251	1427433	
CUST_3274_PI425379931	Au9.Cre15.g646250	nitrogen metabolic regulation protein nmr-related	0.612	0.00E+00	chromosome_15	2792636	2796146	
CUST_7632_PI425379931	Au9.Cre12.g549800	Casein kinase II, alpha subunit	0.612	1.13E-02	chromosome_12	7775816	7780861	K03097
CUST_2003_PI425379931	Au9.Cre09.g405800	inosine-5-monophosphate dehydrogenase related	0.611	1.51E-02	chromosome_9	3007806	3011805	K00088

CUST_7272_PI425379931	Au9.Cre20.g758650	predicted protein	0.61	3.68E-02	scaffold_20	176300	180305	
CUST_4514_PI425379931	Au9.Cre08.g380300	peptide methionine sulfoxide reductase	0.61	1.13E-02	chromosome_8	3355726	3358758	
CUST_2110_PI425379931	Au9.Cre06.g289700	Component of TRAPP complex	0.61	1.76E-02	chromosome_6	4742440	4745465	K13345
CUST_14521_PI425379931	Au9.Cre03.g186900	hypothetical protein CHLREDRAFT_170601	0.61	1.37E-02	chromosome_3	4596007	4597076	K12456
CUST_2152_PI425379931	Au9.Cre23.g766050	cytochrome c oxidase assembly protein	0.609	6.62E-03	scaffold_23	45623	46839	
CUST_522_PI425379931	Au9.Cre13.g582500	14 kda phosphohistidine phosphatase	0.608	3.19E-02	chromosome_13	2772784	2774485	
CUST_3479_PI425379931	Au9.Cre10.g456450	hypothetical protein CHLREDRAFT_187697	0.608	1.85E-02	chromosome_10	5134732	5137015	
CUST_7791_PI425379931	Au9.Cre21.g762250	hypothetical protein CHLREDRAFT_154955	0.607	3.41E-02	scaffold_21	496949	498830	
CUST_10969_PI425379931	Au9.Cre13.g605900		0.607	1.13E-02	chromosome_13	6278140	6291462	
CUST_11363_PI425379931	Au9.Cre17.g730350	predicted protein	0.606	2.66E-02	chromosome_17	4225041	4229173	
CUST_12440_PI425379931	Au9.Cre09.g415200	exostosin-like glycosyltransferase	0.606	8.07E-03	chromosome_9	4431512	4438907	
CUST_5452_PI425379931	Au9.Cre08.g379850	serine-threonine protein kinase	0.606	1.08E-02	chromosome_8	3286813	3296664	K08016
CUST_3725_PI425379931	Au9.Cre01.g051800	aspartate aminotransferase	0.606	0.00E+00	chromosome_1	7190010	7194364	K00812

CUST_9817_PI425379931	Au9.Cre01.g045400	predicted protein	0.606	3.68E-02	chromosome_1	6214348	6218439	
CUST_7162_PI425379931	Au9.Cre17.g725800	hypothetical protein CHLREDRAFT_184858	0.605	2.96E-02	chromosome_17	3604395	3605489	
CUST_14011_PI425379931	Au9.Cre12.g549950	sft2 domain containing 2	0.605	2.63E-02	chromosome_12	7792737	7795826	
CUST_10030_PI425379931	Au9.Cre01.g043100	predicted protein	0.605	3.41E-02	chromosome_1	5919250	5921388	K08773
CUST_6243_PI425379931	Au9.Cre07.g355650	Ammonium transporter	0.604	4.30E-03	chromosome_7	5860391	5868381	
CUST_10259_PI425379931	Au9.Cre05.g241800	MaoC-like dehydratase	0.604	2.29E-02	chromosome_5	2213266	2219337	
CUST_10583_PI425379931	Au9.Cre22.g763750	Similar to AtTic21/PIC1; was also designated Tic21	0.602	2.66E-02	scaffold_22	181128	184635	
CUST_5540_PI425379931	Au9.Cre13.g589350	flagellar/basal body protein	0.602	4.34E-02	chromosome_13	3797981	3802889	K10798
CUST_7128_PI425379931	Au9.Cre16.g651350	hypothetical protein CHLREDRAFT_177124	0.601	7.73E-03	chromosome_16	462920	471967	
CUST_5991_PI425379931	Au9.Cre12.g511500	predicted protein	0.601	8.40E-03	chromosome_12	3186811	3188826	
CUST_6099_PI425379931	Au9.Cre01.g026650	molybdopterin binding domain protein	0.601	0.00E+00	chromosome_1	3900095	3903406	K00953
CUST_10036_PI425379931	Au9.Cre12.g526050	Holocytochrome-c synthase	0.6	1.85E-02	chromosome_12	4857766	4861178	
CUST_3973_PI425379931	Au9.Cre06.g261150	biotin synthase	0.6	1.03E-02	chromosome_6	1659321	1665729	K01012
CUST_5217_PI425379931	Au9.Cre17.g701800	predicted protein	0.599	2.96E-02	chromosome_17	789995	795807	

CUST_3414_PI425379931	Au9.Cre07.g330250	Subunit H of photosystem I	0.599	2.43E-02	chromosome_7	2299558	2301177	K02695
CUST_11199_PI425379931	Au9.Cre17.g713300	light regulation of gametogenesis6 protein	0.598	2.83E-02	chromosome_17	2208695	2219826	
CUST_12040_PI425379931	Au9.Cre17.g703000	predicted protein	0.598	2.11E-02	chromosome_17	945724	950919	
CUST_3497_PI425379931	Au9.Cre10.g444050	MaoC-like dehydratase	0.598	1.71E-02	chromosome_10	3328719	3336857	
CUST_8706_PI425379931	Au9.Cre02.g112000	amino acid transporter	0.598	1.13E-02	chromosome_2	5057375	5061430	
CUST_14077_PI425379931	Au9.Cre12.g559500	lecithin-cholesterol acyltransferase-related	0.597	4.86E-02	chromosome_12	9043396	9047377	
CUST_9098_PI425379931	Au9.Cre08.g369450	ERD4-related membrane protein	0.597	1.37E-02	chromosome_8	1700575	1703504	
CUST_13840_PI425379931	Au9.Cre07.g339800	mitogen activated protein kinase kinase kinase 5	0.597	1.85E-02	chromosome_7	3714563	3718198	
CUST_6404_PI425379931	Au9.Cre02.g145050	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplast precursor	0.597	1.91E-02	chromosome_2	9599687	9602934	K00919
CUST_6904_PI425379931	Au9.Cre26.g773100	pap fibrillin family protein	0.596	7.73E-03	scaffold_26	144386	151880	
CUST_10881_PI425379931	Au9.Cre13.g592250	predicted protein	0.596	1.45E-02	chromosome_13	4308732	4311010	
CUST_6969_PI425379931	Au9.Cre17.g739550		0.595	3.89E-02	chromosome_17	5859944	5878424	
CUST_2886_PI425379931	Au9.Cre12.g522600	Cytochrome c	0.595	4.41E-02	chromosome_12	4462110	4463322	

CUST_3809_PI425379931	Au9.Cre13.g594350	hypothetical protein CHLREDRAFT_151387	0.593	0.00E+00	chromosome_13	4540160	4544124	
CUST_9698_PI425379931	Au9.Cre16.g662050	ERD4-related membrane protein	0.592	1.65E-02	chromosome_16	1856053	1857962	
CUST_6727_PI425379931	Au9.Cre16.g660000	transmembrane protein htp-1 related	0.592	1.56E-02	chromosome_16	1568658	1571497	
CUST_3383_PI425379931	Au9.Cre08.g365850	cartenoid oxygenase	0.592	1.26E-02	chromosome_8	1252873	1256403	
CUST_14468_PI425379931	Au9.Cre07.g351550	cct motif family protein	0.592	1.13E-02	chromosome_7	5305531	5313336	
CUST_11914_PI425379931	Au9.Cre01.g056450	synaptojanin 2 binding protein	0.592	1.49E-02	chromosome_1	7837188	7839139	
CUST_253_PI425379931	Au9.Cre12.g561750	hypothetical protein CHLREDRAFT_181247	0.591	7.21E-03	chromosome_12	9341788	9345792	
CUST_6654_PI425379931	Au9.Cre08.g367150	major facilitator superfamily mfs_1	0.591	4.34E-02	chromosome_8	1441457	1447780	K13950
CUST_12295_PI425379931	Au9.Cre04.g214000	scavenger receptor cysteine-rich partial	0.591	2.88E-02	chromosome_4	401596	413151	K13912
CUST_13595_PI425379931	Au9.Cre03.g173350	ankyrin repeat-containing	0.591	4.16E-02	chromosome_3	3160003	3164319	K11420
CUST_3681_PI425379931	Au9.Cre02.g124050	ERD4-related membrane protein	0.591	1.49E-02	chromosome_2	6510830	6513913	
CUST_3014_PI425379931	Au9.Cre02.g083550	fad monooxygenase	0.591	2.66E-02	chromosome_2	1300833	1306269	
CUST_7046_PI425379931	Au9.Cre01.g071500	guanylate cyclase	0.59	3.89E-02	chromosome_1	9763152	9774883	
CUST_6386_PI425379931	Au9.Cre01.g016500	Dihydrolipoamide dehydrogenase	0.59	1.04E-02	chromosome_1	2587381	2593530	

CUST_10360_PI425379931	Au9.Cre45.g788600	predicted protein	0.589	3.19E-02	scaffold_45	77644	78705	
CUST_12543_PI425379931	Au9.Cre02.g119900	Papain-type cysteine protease	0.589	4.83E-02	chromosome_2	6019560	6023185	K08568
CUST_11654_PI425379931	Au9.Cre02.g144150	eag-like k	0.588	2.88E-02	chromosome_2	9484494	9489215	
CUST_11822_PI425379931	Au9.Cre01.g006200	predicted protein	0.587	2.18E-02	chromosome_1	1055813	1057054	
CUST_5076_PI425379931	Au9.Cre06.g276800	Histone H4	0.586	3.04E-02	chromosome_6	3249453	3250338	K11254
CUST_4595_PI425379931	Au9.Cre75.g795400	low molecular weight protein tyrosine phosphatase	0.585	1.22E-02	scaffold_75	2036	5767	
CUST_10430_PI425379931	Au9.Cre16.g672950	Low CO2 inducible gene	0.585	0.00E+00	chromosome_16	3486205	3487938	
CUST_13568_PI425379931	Au9.Cre06.g308950	reticulon/nogo	0.585	1.37E-02	chromosome_6	7276001	7278932	K00861
CUST_10533_PI425379931	Au9.Cre05.g246300	hypothetical protein CHLREDRAFT_167657	0.585	2.29E-02	chromosome_5	3011614	3016685	
CUST_11934_PI425379931	Au9.Cre04.g215900	tumor necrosis factor receptor related	0.585	1.91E-02	chromosome_4	711609	717125	
CUST_5165_PI425379931	Au9.Cre17.g743050	pol-like protein	0.584	1.00E-02	chromosome_17	6455831	6459356	
CUST_7914_PI425379931	Au9.Cre17.g726600	MaoC-like dehydratase	0.584	1.49E-02	chromosome_17	3670063	3677814	
CUST_11634_PI425379931	Au9.Cre07.g334500	photosystem i subunit o	0.584	2.18E-02	chromosome_7	3035497	3038625	
CUST_352_PI425379931	Au9.Cre08.g375800	predicted protein	0.583	6.32E-03	chromosome_8	2742755	2755901	
CUST_10266_PI425379931	Au9.Cre06.g273050	transcriptional regulator-like protein	0.583	7.97E-03	chromosome_6	2934609	2937995	

CUST_10745_PI425379931	Au9.Cre52.g790500	pol-like protein	0.582	1.46E-02	scaffold_52	24766	28067	
CUST_290_PI425379931	Au9.Cre17.g715250	Acetyl-CoA biotin carboxyl carrier	0.582	9.80E-03	chromosome_17	2391327	2394327	K02160
CUST_9232_PI425379931	Au9.Cre12.g561000	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	0.581	1.76E-02	chromosome_12	9234549	9237206	K05864
CUST_10798_PI425379931	Au9.Cre10.g458750	predicted protein	0.581	4.00E-03	chromosome_10	5458677	5460143	
CUST_14314_PI425379931	Au9.Cre02.g137100	MaoC-like dehydratase	0.581	1.22E-02	chromosome_2	8370748	8375299	
CUST_4879_PI425379931	Au9.Cre11.g473400	hypothetical protein CHLREDRAFT_178998	0.579	3.19E-02	chromosome_11	999110	1004241	
CUST_945_PI425379931	Au9.Cre04.g212700	squamosa promoter binding protein	0.579	2.72E-02	chromosome_4	152766	166064	
CUST_10385_PI425379931	Au9.Cre08.g373050	Acetyl-CoA carboxylase	0.577	0.00E+00	chromosome_8	2214546	2229831	
CUST_11241_PI425379931	Au9.Cre06.g273900	histone h2a	0.577	8.40E-03	chromosome_6	3005186	3005947	K11251
CUST_5315_PI425379931	Au9.Cre01.g035250	predicted protein [Micromonas sp. RCC299]	0.577	9.24E-03	chromosome_1	4912723	4916638	
CUST_10658_PI425379931	Au9.Cre08.g384100	predicted protein	0.576	4.74E-02	chromosome_8	3852306	3854935	
CUST_8028_PI425379931	Au9.Cre06.g285250	chloropyll a-b binding protein of LHCII type I, chloroplast precursor	0.576	3.12E-02	chromosome_6	4214720	4216568	
CUST_9506_PI425379931	Au9.Cre01.g038500	cytochrome P450	0.576	1.22E-02	chromosome_1	5302516	5306907	K00517
CUST_2577_PI425379931	Au9.Cre14.g621550	Thioredoxin m	0.575	6.78E-03	chromosome_14	1986954	1988066	

CUST_1131_PI425379931	Au9.Cre14.g616500	predicted protein	0.574	4.86E-02	chromosome_14	1258849	1260984	
CUST_13640_PI425379931	Au9.Cre12.g496700	thioredoxin-like protein	0.574	3.41E-02	chromosome_12	1656273	1658166	
CUST_5005_PI425379931	Au9.Cre02.g076250	chloroplast elongation factor G	0.574	2.24E-02	chromosome_2	436382	441503	K14536
CUST_8649_PI425379931	Au9.Cre07.g321950	manganese transport protein	0.573	4.15E-03	chromosome_7	1270880	1278795	K12347
CUST_2129_PI425379931	Au9.Cre08.g361700	hypothetical protein CHLREDRAFT_192195	0.572	2.18E-02	chromosome_8	531462	534953	
CUST_2030_PI425379931	Au9.Cre01.g022700	predicted protein	0.57	1.22E-02	chromosome_1	3337740	3345813	
CUST_5734_PI425379931	Au9.Cre02.g137300	reverse transcriptases	0.569	1.13E-02	chromosome_2	8441582	8448157	
CUST_111_PI425379931	Au9.Cre18.g751050	predicted protein	0.568	0.00E+00	scaffold_18	1189612	1193467	
CUST_2449_PI425379931	Au9.Cre06.g272650	light-harvesting protein of photosystem I	0.568	2.69E-02	chromosome_6	2906970	2909263	K08911
CUST_3461_PI425379931	Au9.Cre05.g245500	Flagellar Associated Protein	0.568	7.73E-03	chromosome_5	2870608	2882904	K12460
CUST_4923_PI425379931	Au9.Cre01.g053850	ring finger and wd repeat domain 2	0.568	3.12E-02	chromosome_1	7468361	7473552	K10143
CUST_585_PI425379931	Au9.Cre10.g433950	hypothetical protein CHLREDRAFT_155007	0.567	7.40E-03	chromosome_10	2181051	2183008	
CUST_2625_PI425379931	Au9.Cre07.g339150	Chaperonin 60B2	0.567	2.27E-02	chromosome_7	3650489	3657567	K04077
CUST_13162_PI425379931	Au9.Cre06.g249300	Actin-related protein	0.567	4.75E-03	chromosome_6	61026	63399	K05692
CUST_10244_PI425379931	Au9.Cre66.g793500	hypothetical protein	0.566	0.00E+00	scaffold_66	11906	14491	

		CHLREDRAFT_180952						
CUST_12360_PI425379931	Au9.Cre12.g559800	glutathione S-transferase	0.566	8.40E-03	chromosome_12	9101943	9104876	K00799
CUST_14589_PI425379931	Au9.Cre01.g030550	ubiquitin-associated uba/ubx domain-containing	0.566	0.00E+00	chromosome_1	4316122	4321527	K14011
CUST_5242_PI425379931	Au9.Cre16.g650500	hypothetical protein CHLREDRAFT_120756	0.565	4.30E-03	chromosome_16	361125	365251	
CUST_5034_PI425379931	Au9.Cre16.g647950	hypothetical protein CHLREDRAFT_177206	0.565	1.58E-02	chromosome_16	64206	68557	
CUST_14012_PI425379931	Au9.Cre02.g114450	hypothetical protein CHLREDRAFT_186741	0.564	0.00E+00	chromosome_2	5365507	5368257	
CUST_7432_PI425379931	Au9.Cre14.g630950	rhodanese domain protein	0.562	9.98E-03	chromosome_14	3456971	3459121	K01069
CUST_6649_PI425379931	Au9.Cre14.g629050	plastocyanin-like protein	0.562	4.05E-02	chromosome_14	3144155	3147765	
CUST_1617_PI425379931	Au9.Cre08.g370500	aig2 family protein	0.562	5.64E-03	chromosome_8	1849788	1854812	
CUST_5466_PI425379931	Au9.Cre08.g369600	MATE efflux family protein	0.562	4.30E-03	chromosome_8	1711781	1718121	
CUST_12053_PI425379931	Au9.Cre34.g783550	predicted protein	0.56	4.75E-03	scaffold_34	83416	87589	
CUST_6879_PI425379931	Au9.Cre09.g416750	T-complex protein 1, beta subunit	0.56	6.32E-03	chromosome_9	4621851	4626389	K04077
CUST_6418_PI425379931	Au9.Cre03.g208050	FABZ; 3R-hydroxymyristoyl ACP dehydrase	0.56	6.32E-03	chromosome_3	7067607	7069747	K02372
CUST_10864_PI425379931	Au9.Cre03.g182150	predicted protein	0.56	5.69E-03	chromosome_3	4139796	4142105	

CUST_12571_PI425379931	Au9.Cre16.g675450	short-chain dehydrogenase reductase superfamily protein	0.559	4.30E-03	chromosome_16	3876466	3879665	K00059
CUST_5645_PI425379931	Au9.Cre03.g203600	glycerophosphoryl diester phosphodiesterase family protein	0.559	1.85E-02	chromosome_3	6548603	6552111	K01126
CUST_789_PI425379931	Au9.Cre17.g713200	chloroplast oxoglutarate-malate translocator	0.556	0.00E+00	chromosome_17	2201731	2205794	K09477
CUST_1747_PI425379931	Au9.Cre16.g655100	thyroid hormone receptor interactor 4	0.556	4.59E-02	chromosome_16	974179	977180	
CUST_11853_PI425379931	Au9.Cre10.g420400	predicted protein	0.556	5.74E-03	chromosome_10	337200	349471	K14289
CUST_3862_PI425379931	Au9.Cre10.g422200	copper-translocating P-type ATPase	0.554	9.80E-03	chromosome_10	660710	668515	K01541
CUST_6033_PI425379931	Au9.Cre06.g263500	zinc finger and btb domain containing 8 opposite strand	0.554	3.96E-03	chromosome_6	1905175	1907807	
CUST_6251_PI425379931	Au9.Cre16.g652750	Flavin-containing monooxygenase	0.553	4.05E-02	chromosome_16	665767	676282	K00485
CUST_13922_PI425379931	Au9.Cre08.g358900	hypoxanthine-guanine phosphoribosyltransferase	0.553	1.13E-02	chromosome_8	107490	110995	K00760
CUST_12877_PI425379931	Au9.Cre03.g164300	predicted protein	0.553	1.49E-02	chromosome_3	2078252	2080460	
CUST_8720_PI425379931	Au9.Cre17.g713350	oxoglutarate:malate antiporter	0.552	0.00E+00	chromosome_17	2219831	2224233	K09477
CUST_3234_PI425379931	Au9.Cre16.g665750	Pseudouridine synthase	0.552	7.40E-03	chromosome_16	2326900	2329928	K11131
CUST_13477_PI425379931	Au9.Cre07.g328100	hypothetical protein	0.552	1.22E-02	chromosome_7	2022695	2025136	

		CHLREDRAFT_182976						
CUST_7380_PI425379931	Au9.Cre17.g711500	predicted protein	0.55	1.76E-02	chromosome_17	2042231	2048652	
CUST_10810_PI425379931	Au9.Cre16.g691400	predicted protein	0.55	4.30E-03	chromosome_16	5921657	5928821	
CUST_12801_PI425379931	Au9.Cre13.g569600	Predicted cell growth/differentiation regulator, contains RA domain	0.55	2.72E-02	chromosome_13	1117883	1124880	
CUST_13766_PI425379931	Au9.Cre03.g198850	thylakoid lumen protein	0.549	0.00E+00	chromosome_3	5917725	5921290	
CUST_2382_PI425379931	Au9.Cre58.g791500	speract scavenger transmembrane glycoprotein	0.547	3.29E-02	scaffold_58	13970	14475	
CUST_5872_PI425379931	Au9.Cre16.g672650	mitochondrial substrate carrier protein	0.546	1.13E-02	chromosome_16	3450992	3454183	K13577
CUST_4403_PI425379931	Au9.Cre16.g659450	alpha-1,4-N-acetylglucosaminyltransferase	0.546	4.12E-03	chromosome_16	1512801	1516493	K01988
CUST_8462_PI425379931	Au9.Cre13.g584800	predicted protein	0.546	1.37E-02	chromosome_13	3106862	3112795	
CUST_4469_PI425379931	Au9.Cre13.g581000	endoplasmic reticulum-resident kdel protein	0.545	8.29E-03	chromosome_13	2597831	2602642	K13667
CUST_6338_PI425379931	Au9.Cre02.g121050	predicted protein	0.545	4.75E-03	chromosome_2	6201835	6204472	
CUST_5220_PI425379931	Au9.Cre44.g788150	hypothetical protein CHLREDRAFT_194403	0.544	5.18E-03	scaffold_44	63532	73515	
CUST_3475_PI425379931	Au9.Cre08.g367900	hypothetical protein	0.544	0.00E+00	chromosome_8	1524092	1531427	

		CHLREDRAFT_184737						
CUST_2492_PI425379931	Au9.Cre12.g527200	hypothetical protein CHLREDRAFT_184905	0.543	2.24E-02	chromosome_12	5014600	5016891	
CUST_6013_PI425379931	Au9.Cre07.g330050	hypothetical protein CHLREDRAFT_169483	0.543	1.91E-02	chromosome_7	2279173	2282362	
CUST_12146_PI425379931	Au9.Cre08.g383600	Scavenger receptor cysteine rich (SRCR) protein	0.542	4.34E-02	chromosome_8	3785637	3795081	
CUST_841_PI425379931	Au9.Cre05.g235100	pol-like protein	0.542	0.00E+00	chromosome_5	1036049	1047240	
CUST_14064_PI425379931	Au9.Cre12.g538750	Sm protein LSm1	0.541	0.00E+00	chromosome_12	6418919	6420323	K12620
CUST_3503_PI425379931	Au9.Cre12.g508300	predicted protein	0.541	1.05E-02	chromosome_12	2856510	2859201	
CUST_4563_PI425379931	Au9.Cre02.g099050		0.541	1.94E-02	chromosome_2	3366406	3400337	
CUST_5780_PI425379931	Au9.Cre12.g550850	Oxygen-evolving enhancer protein 2 of photosystem II	0.538	2.18E-02	chromosome_12	7897719	7899791	K02717
CUST_10235_PI425379931	Au9.Cre12.g520900	hypothetical protein CHLREDRAFT_150799	0.534	1.46E-02	chromosome_12	4274300	4276814	
CUST_758_PI425379931	Au9.Cre12.g551300	periplasmic L-amino acid oxidase, catalytic subunit	0.533	0.00E+00	chromosome_12	7947598	7953621	
CUST_11318_PI425379931	Au9.Cre06.g262100	glutathione reductase	0.531	0.00E+00	chromosome_6	1741327	1747591	K00383
CUST_4583_PI425379931	Au9.Cre14.g628500	nad-dependent epimerase	0.527	2.66E-02	chromosome_14	3024396	3026996	

		dehydratase						
CUST_5728_PI425379931	Au9.Cre14.g621500	predicted protein	0.526	3.41E-02	chromosome_14	1983951	1986702	
CUST_12215_PI425379931	Au9.Cre12.g542300	glycerate kinase	0.525	4.00E-03	chromosome_12	6953771	6957585	K00865
CUST_14541_PI425379931	Au9.Cre05.g235050	reverse transcriptases	0.525	8.29E-03	chromosome_5	1012463	1035038	
CUST_7855_PI425379931	Au9.Cre17.g742950	pol-like protein	0.524	0.00E+00	chromosome_17	6433131	6438396	
CUST_1540_PI425379931	Au9.Cre17.g741950	Bardet-Biedl syndrome protein 1	0.524	4.75E-03	chromosome_17	6278390	6282341	
CUST_14551_PI425379931	Au9.Cre03.g208450	pol-like protein	0.524	6.75E-03	chromosome_3	7147393	7150998	
CUST_1005_PI425379931	Au9.Cre02.g110900	hypothetical protein CHLREDRAFT_186787	0.524	0.00E+00	chromosome_2	4905668	4909813	
CUST_11052_PI425379931	Au9.Cre05.g246900	blue-copper- protein	0.523	2.66E-02	chromosome_5	3087124	3091271	
CUST_4612_PI425379931	Au9.Cre16.g687900	light-harvesting protein of photosystem I	0.522	2.23E-02	chromosome_16	5478659	5481474	K08911
CUST_12579_PI425379931	Au9.Cre04.g215450	kelch-related proteins	0.522	6.32E-03	chromosome_4	654648	657035	
CUST_2539_PI425379931	Au9.Cre01.g031500	multi-copper oxidase	0.522	3.19E-02	chromosome_1	4424429	4431271	K00423
CUST_1485_PI425379931	Au9.Cre03.g151450	predicted protein	0.521	3.68E-02	chromosome_3	502316	505841	
CUST_11523_PI425379931	Au9.Cre02.g080900	Peroxiredoxin type II	0.52	5.34E-03	chromosome_2	1018282	1020848	K11187
CUST_7921_PI425379931	Au9.Cre10.g421700	glycerol-3-phosphate dehydrogenase	0.519	1.76E-02	chromosome_10	589661	599140	K00006

CUST_14080_PI425379931	Au9.Cre13.g592600	pol-like protein	0.517	7.40E-03	chromosome_13	4344665	4348370	
CUST_9106_PI425379931	Au9.Cre11.g476750	Ferredoxin-NADP reductase	0.516	5.74E-03	chromosome_11	1594720	1598363	K02641
CUST_6104_PI425379931	Au9.Cre11.g468950	Ubiquinol:cytochrome c oxidoreductase 7 kDa subunit	0.516	0.00E+00	chromosome_11	292596	293513	K00419
CUST_6147_PI425379931	Au9.Cre10.g440150	hypothetical protein CHLREDRAFT_182903	0.516	0.00E+00	chromosome_10	2870566	2872513	
CUST_900_PI425379931			0.516	2.24E-02				
CUST_8281_PI425379931	Au9.Cre13.g573250	Rhodanese-related sulfurtransferase	0.514	7.73E-03	chromosome_13	1571992	1574347	
CUST_233_PI425379931	Au9.Cre02.g077950	rwd domain containing 3	0.514	9.24E-03	chromosome_2	617471	627832	
CUST_2632_PI425379931	Au9.Cre14.g628350	peptidase subunit of mitochondrial ATP-dependent protease hslUV	0.513	4.59E-03	chromosome_14	3013710	3016751	
CUST_3226_PI425379931	Au9.Cre03.g188400	Respiratory burst oxidase	0.513	3.04E-02	chromosome_3	4740745	4745844	K13447
CUST_10755_PI425379931	Au9.Cre01.g038750	chromosome 7 open reading frame 62	0.513	2.24E-02	chromosome_1	5330795	5334037	
CUST_752_PI425379931	Au9.Cre01.g006750	polyprotein-like	0.513	6.09E-03	chromosome_1	1157297	1163772	K10592
CUST_2476_PI425379931	Au9.Cre16.g660650	hypothetical protein pK2044_00930 [Klebsiella pneumoniae NTUH-K2044]	0.512	5.34E-03	chromosome_16	1650262	1656673	
CUST_6105_PI425379931	Au9.Cre12.g539450	pol-like protein	0.512	1.83E-02	chromosome_12	6572079	6577193	

CUST_4102_PI425379931	Au9.Cre02.g121750	tim-barrel nifr3 family	0.512	3.12E-02	chromosome_2	6274715	6277686	
CUST_3039_PI425379931	Au9.Cre02.g082500	photosystem I reaction center subunit N	0.512	0.00E+00	chromosome_2	1184182	1186249	K02701
CUST_1752_PI425379931	Au9.Cre03.g193950	ferredoxin-thioredoxin reductase	0.511	0.00E+00	chromosome_3	5353543	5355050	
CUST_9736_PI425379931	Au9.Cre17.g721350	glutathione s-transferase	0.509	2.66E-02	chromosome_17	3123963	3128955	K00799
CUST_7095_PI425379931	Au9.Cre03.g155350	pyridoxamine 5 -phosphate oxidase family protein	0.509	1.09E-02	chromosome_3	956665	961695	
CUST_8096_PI425379931	Au9.Cre13.g573200	predicted protein	0.508	4.59E-02	chromosome_13	1567875	1571846	
CUST_1388_PI425379931	Au9.Cre20.g761100	pol-like protein	0.507	1.91E-02	scaffold_20	572936	576221	
CUST_11589_PI425379931	Au9.Cre17.g733250	peptidyl-prolyl cis-trans isomerase, FKBP-type	0.507	1.65E-02	chromosome_17	4736083	4739704	
CUST_9021_PI425379931	Au9.Cre12.g553150	allophanate hydrolase	0.507	3.12E-02	chromosome_12	8249951	8250562	
CUST_9969_PI425379931	Au9.Cre03.g208650	pol-like protein	0.507	0.00E+00	chromosome_3	7227320	7231915	
CUST_13858_PI425379931	Au9.Cre02.g082750	4.1 kDa photosystem II subunit	0.506	2.89E-02	chromosome_2	1208647	1209571	
CUST_11042_PI425379931	Au9.Cre10.g443500	hypothetical protein CHLREDRAFT_188331	0.505	0.00E+00	chromosome_10	3261803	3264759	
CUST_1923_PI425379931	Au9.Cre13.g578700	predicted protein	0.504	0.00E+00	chromosome_13	2255685	2257146	
CUST_7134_PI425379931	Au9.Cre12.g496000	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	0.504	0.00E+00	chromosome_12	1566196	1569316	K09565

CUST_10124_PI425379931	Au9.Cre02.g107000	cyclin dependent kinase	0.502	2.83E-02	chromosome_2	4422666	4427701	K04563
CUST_5200_PI425379931	Au9.Cre07.g333800	pol-like protein	0.501	0.00E+00	chromosome_7	2929765	2931570	
CUST_13824_PI425379931	Au9.Cre06.g265750	glycosyltransferase-like isoform cra_a	0.501	1.36E-02	chromosome_6	2139123	2143131	
CUST_11878_PI425379931	Au9.Cre02.g087700	ascorbate peroxidase	0.501	0.00E+00	chromosome_2	1773933	1777822	K00434
CUST_9446_PI425379931	Au9.Cre03.g156050	ribosome recycling factor	0.5	7.73E-03	chromosome_3	1043818	1046909	
CUST_181_PI425379931	Au9.Cre51.g790150	pol-like protein	0.499	0.00E+00	scaffold_51	27926	32567	
CUST_3105_PI425379931	Au9.Cre22.g763350	hypoxia-inducible factor 1 alpha inhibitor-related	0.499	2.96E-02	scaffold_22	132230	137475	
CUST_7076_PI425379931	Au9.Cre03.g210350	hypothetical protein CHLREDRAFT_193444	0.499	4.75E-03	chromosome_3	7563381	7565147	
CUST_13820_PI425379931	Au9.Cre06.g278100	pol-like protein	0.498	1.58E-02	chromosome_6	3452555	3455580	
CUST_1231_PI425379931	Au9.Cre16.g689300	Serine/Threonine protein kinase	0.497	2.11E-02	chromosome_16	5656971	5661328	K02644
CUST_11837_PI425379931	Au9.Cre14.g631600	nadp oxidoreductase coenzyme f420-dependent	0.497	2.27E-02	chromosome_14	3587530	3590545	
CUST_4413_PI425379931	Au9.Cre01.g043950	serine-threonine protein kinase	0.496	6.32E-03	chromosome_1	6010070	6015155	
CUST_6152_PI425379931	Au9.Cre10.g419650	predicted protein	0.493	0.00E+00	chromosome_10	276934	278599	
CUST_6354_PI425379931	Au9.Cre08.g372150	hypothetical protein CHLREDRAFT_179255	0.493	4.41E-02	chromosome_8	2077746	2080857	

CUST_2580_PI425379931	Au9.Cre06.g284250	chlorophyll a-b binding protein of LHCII	0.492	9.24E-03	chromosome_6	4101494	4103651	
CUST_11670_PI425379931	Au9.Cre02.g086100	predicted protein	0.491	1.85E-02	chromosome_2	1590172	1592064	
CUST_5372_PI425379931	Au9.Cre37.g785000	pol-like protein	0.489	0.00E+00	scaffold_37	118236	121737	
CUST_2712_PI425379931	Au9.Cre06.g278000	pol-like protein	0.489	1.83E-02	chromosome_6	3425035	3427960	
CUST_7002_PI425379931	Au9.Cre03.g154750	predicted protein	0.489	1.39E-02	chromosome_3	895914	898935	
CUST_12089_PI425379931	Au9.Cre12.g489300	notch-like protein	0.488	3.56E-02	chromosome_12	746884	754442	
CUST_8394_PI425379931	Au9.Cre10.g446500	hypothetical protein CHLREDRAFT_155961	0.488	6.32E-03	chromosome_10	3718054	3721085	
CUST_9043_PI425379931	Au9.Cre04.g220050	tak1	0.487	2.43E-02	chromosome_4	1411080	1422441	K04427
CUST_2977_PI425379931	Au9.Cre17.g743100	pol-like protein	0.486	4.15E-03	chromosome_17	6473691	6477056	
CUST_1121_PI425379931	Au9.Cre12.g547350	guanylate cyclase	0.486	1.85E-02	chromosome_12	7504865	7527665	
CUST_4679_PI425379931	Au9.Cre16.g648950	hypothetical protein CHLREDRAFT_193213	0.485	1.91E-02	chromosome_16	185424	189274	
CUST_7563_PI425379931	Au9.Cre05.g244800	transcriptional repressor	0.485	7.79E-03	chromosome_5	2737166	2746995	
CUST_1942_PI425379931	Au9.Cre12.g539300	heat shock protein 70d	0.483	0.00E+00	chromosome_12	6540184	6543155	
CUST_1286_PI425379931	Au9.Cre22.g764150	hypothetical protein	0.482	2.72E-02	scaffold_22	230107	232858	
CUST_7892_PI425379931	Au9.Cre10.g435500	Elongation factor Ts-like protein	0.482	1.13E-02	chromosome_10	2372714	2375412	

CUST_5478_PI425379931	unknown		0.481	4.75E-03				
CUST_10087_PI425379931	Au9.Cre01.g016900	predicted protein	0.481	0.00E+00	chromosome_1	2638858	2640709	
CUST_8586_PI425379931	Au9.Cre03.g185750	ubiquitination factor e4	0.48	0.00E+00	chromosome_3	4489065	4492226	K09561
CUST_14155_PI425379931	Au9.Cre03.g184250	Calmodulin	0.478	2.53E-02	chromosome_3	4340377	4343434	
CUST_6959_PI425379931	Au9.Cre22.g763650	predicted protein	0.477	3.12E-02	scaffold_22	168056	173407	
CUST_546_PI425379931	Au9.Cre30.g779150	pol-like protein	0.475	0.00E+00	scaffold_30	33670	40205	
CUST_8892_PI425379931	Au9.Cre07.g333750	pol-like protein	0.474	4.16E-02	chromosome_7	2880201	2892812	
CUST_3612_PI425379931	Au9.Cre10.g446350	oxygen-evolving enhancer	0.473	1.85E-02	chromosome_10	3704995	3707907	
CUST_12602_PI425379931	Au9.Cre03.g200250	mutase family protein	0.472	0.00E+00	chromosome_3	6073984	6078549	K03417
CUST_9910_PI425379931	Au9.Cre03.g158450	predicted protein	0.472	4.34E-02	chromosome_3	1359457	1371072	
CUST_6371_PI425379931	Au9.Cre03.g177700	transcription factor regulating nitrogen metabolism	0.47	0.00E+00	chromosome_3	3705187	3712021	
CUST_2234_PI425379931	Au9.Cre01.g065350	hypothetical protein CHLREDRAFT_149836	0.47	1.13E-02	chromosome_1	8957478	8967473	
CUST_14035_PI425379931	Au9.Cre12.g537900	predicted protein	0.467	1.85E-02	chromosome_12	6338874	6342935	K03846
CUST_3278_PI425379931	Au9.Cre25.g771250	hypothetical protein CHLREDRAFT_177541	0.466	3.29E-02	scaffold_25	96496	101057	
CUST_172_PI425379931	Au9.Cre13.g602200	pol-like protein	0.466	2.83E-02	chromosome_13	5549562	5551723	

CUST_1182_PI425379931	Au9.Cre04.g218550	predicted protein	0.466	3.41E-02	chromosome_4	1166316	1169827	
CUST_3120_PI425379931	Au9.Cre03.g153600	predicted protein	0.466	1.46E-02	chromosome_3	763465	769260	
CUST_13749_PI425379931	Au9.Cre02.g097200	Scavenger receptor cysteine rich (SRCR) protein	0.466	7.88E-03	chromosome_2	3135328	3150135	
CUST_7682_PI425379931	Au9.Cre05.g239050	S-adenosyl-L-methionine-dependent methyltransferase	0.464	7.88E-03	chromosome_5	1772636	1782011	K00599
CUST_5198_PI425379931	Au9.Cre10.g425900	light-harvesting protein of photosystem I	0.463	3.89E-02	chromosome_10	1160709	1163206	K08910
CUST_1331_PI425379931	Au9.Cre08.g360650	hypothetical protein CHLREDRAFT_194775	0.463	0.00E+00	chromosome_8	390207	391704	
CUST_3683_PI425379931	Au9.Cre07.g330800	hypothetical protein CHLREDRAFT_144346	0.463	1.13E-02	chromosome_7	2358363	2362954	
CUST_9695_PI425379931	Au9.Cre12.g497300	Rhodanese-like Ca-sensing receptor	0.461	0.00E+00	chromosome_12	1707290	1710715	
CUST_9407_PI425379931	Au9.Cre11.g470100	pol-like protein	0.461	3.41E-02	chromosome_11	466455	467286	
CUST_4949_PI425379931	Au9.Cre10.g451850	katanin p60 atpase-containing	0.461	1.37E-02	chromosome_10	4474499	4479133	K12196
CUST_12234_PI425379931	Au9.Cre02.g137450	pol-like protein	0.461	2.53E-02	chromosome_2	8518341	8528316	
CUST_7821_PI425379931	Au9.Cre09.g395900	serine-threonine protein kinase, plant-type	0.46	0.00E+00	chromosome_9	1490613	1495915	
CUST_662_PI425379931	Au9.Cre08.g373350	pol-like protein	0.46	2.66E-02	chromosome_8	2296640	2298075	

CUST_4106_PI425379931	Au9.Cre14.g622300	reverse transcriptase	0.458	2.63E-02	chromosome_14	2142809	2157504	
CUST_1289_PI425379931	Au9.Cre47.g789200	pol-like protein	0.457	3.56E-02	scaffold_47	1	2997	
CUST_3356_PI425379931	Au9.Cre05.g243300	carbonic anhydrase	0.457	4.22E-03	chromosome_5	2467647	2468772	
CUST_2199_PI425379931	Au9.Cre14.g622500	pol-like protein	0.456	3.19E-02	chromosome_14	2193639	2194464	
CUST_2777_PI425379931	Au9.Cre14.g622450	reverse transcriptases	0.456	6.32E-03	chromosome_14	2183235	2193006	K14401
CUST_8196_PI425379931	Au9.Cre01.g024600	predicted protein	0.456	0.00E+00	chromosome_1	3633042	3634083	
CUST_10729_PI425379931	Au9.Cre17.g719350	flagellar associated protein	0.455	4.10E-02	chromosome_17	2856126	2864885	
CUST_1818_PI425379931	Au9.Cre06.g310600	hypothetical protein CHLREDRAFT_169965	0.453	8.40E-03	chromosome_6	7517138	7521099	
CUST_7552_PI425379931	Au9.Cre47.g789250	reverse transcriptases	0.452	2.06E-02	scaffold_47	5320	27235	
CUST_395_PI425379931	Au9.Cre30.g779400	pol-like protein	0.452	0.00E+00	scaffold_30	152466	157997	
CUST_14455_PI425379931	Au9.Cre03.g192150	predicted protein	0.452	2.53E-02	chromosome_3	5157445	5159065	
CUST_10956_PI425379931	Au9.Cre14.g622350	pol-like protein	0.451	0.00E+00	chromosome_14	2158555	2162076	
CUST_11737_PI425379931	Au9.Cre16.g671250	monovalent cation:proton antiporter-1 family	0.45	1.59E-02	chromosome_16	3261502	3271019	K05742
CUST_5761_PI425379931	Au9.Cre12.g539550	pol-like protein	0.45	3.41E-02	chromosome_12	6624254	6627095	
CUST_4159_PI425379931	Au9.Cre12.g504650	Histone H3; Histone H3;Histone H3; Histone H3	0.45	4.30E-03	chromosome_12	2448006	2449053	K11253

CUST_11465_PI425379931	Au9.Cre06.g281600	low-CO2-inducible protein	0.45	2.11E-02	chromosome_6	3840388	3845932	
CUST_3690_PI425379931	Au9.Cre16.g682200	hypothetical protein CHLREDRAFT_189273	0.449	4.59E-03	chromosome_16	4747689	4749870	
CUST_12899_PI425379931	Au9.Cre11.g477350	hypothetical protein CHLREDRAFT_151152	0.447	1.49E-02	chromosome_11	1679374	1684015	
CUST_2923_PI425379931	Au9.Cre12.g544600	predicted protein	0.446	2.69E-02	chromosome_12	7199002	7203373	
CUST_11386_PI425379931	Au9.Cre36.g784450	predicted protein	0.443	1.76E-02	scaffold_36	106406	109747	
CUST_4866_PI425379931	Au9.Cre30.g779500	pol-like protein	0.443	3.12E-02	scaffold_30	236554	237710	
CUST_5958_PI425379931	Au9.Cre10.g428950	thij/pfpi	0.442	3.93E-02	chromosome_10	1480486	1485172	K01423
CUST_9505_PI425379931	Au9.Cre06.g271200	NADH oxidase	0.441	4.59E-03	chromosome_6	2782063	2789311	K00356
CUST_5045_PI425379931	Au9.Cre09.g399600	predicted protein	0.44	1.73E-02	chromosome_9	2084058	2084502	
CUST_5858_PI425379931	Au9.Cre06.g295450	Hydroxypyruvate reductase	0.44	6.46E-03	chromosome_6	5562721	5568069	K00015
CUST_1991_PI425379931	Au9.Cre01.g067900	4-diphosphocytidyl-2C-methyl-D-erythritol synthase, chloroplast precursor	0.439	2.11E-02	chromosome_1	9303376	9304946	
CUST_12684_PI425379931	Au9.Cre10.g466850	peptidyl-prolyl cis-trans isomerase, FKBP-type	0.438	1.28E-02	chromosome_10	6527735	6530338	
CUST_1128_PI425379931	Au9.Cre18.g747750	gamma hydroxybutyrate dehydrogenase	0.437	1.73E-02	scaffold_18	683913	687280	

CUST_649_PI425379931	Au9.Cre03.g211450	hnh endonuclease	0.437	0.00E+00	chromosome_3	7751790	7758713	
CUST_916_PI425379931	Au9.Cre51.g790050	pol-like protein	0.436	1.13E-02	scaffold_51	54	2197	
CUST_11245_PI425379931	Au9.Cre02.g138350	predicted protein	0.436	2.45E-02	chromosome_2	8639904	8642016	
CUST_13718_PI425379931	Au9.Cre16.g691800	flavoprotein	0.435	0.00E+00	chromosome_16	5966693	5976578	K00492
CUST_2518_PI425379931	Au9.Cre06.g283050	light-harvesting protein of photosystem I	0.432	1.35E-02	chromosome_6	3977925	3980018	
CUST_14407_PI425379931	Au9.Cre07.g332250	R1 Protein, alpha-glucan water dikinase	0.429	9.73E-03	chromosome_7	2542476	2546157	
CUST_6550_PI425379931	Au9.Cre01.g013000	dna polymerase type-x family member	0.429	1.49E-02	chromosome_1	2183177	2190822	
CUST_6791_PI425379931	Au9.Cre13.g605500	hypothetical protein CHLREDRAFT_177705	0.427	7.21E-03	chromosome_13	6231021	6234699	
CUST_10773_PI425379931	Au9.Cre03.g151950	zygote-specific protein	0.426	0.00E+00	chromosome_3	540726	541665	
CUST_4293_PI425379931	Au9.Cre10.g436050	superoxide dismutase [Fe]	0.424	0.00E+00	chromosome_10	2439589	2440792	K04564
CUST_12025_PI425379931	Au9.Cre17.g696750		0.423	1.91E-02	chromosome_17	81150	91425	K14491
CUST_5035_PI425379931	Au9.Cre12.g545900	Mitogen Activated Protein Kinase Kinase Kinase 9	0.422	3.93E-02	chromosome_12	7359012	7361753	
CUST_13228_PI425379931	Au9.Cre12.g510400	predicted protein	0.422	6.32E-03	chromosome_12	3099250	3101737	
CUST_11905_PI425379931	Au9.Cre11.g467850	taz protein (tafazzin)	0.422	1.26E-02	chromosome_11	71345	76056	

CUST_8859_PI425379931	Au9.Cre02.g130450	predicted protein	0.422	2.72E-02	chromosome_2	7308696	7311818	
CUST_12873_PI425379931	Au9.Cre24.g769600	na+ h+ antiporter	0.421	2.88E-02	scaffold_24	109526	115117	
CUST_8063_PI425379931	Au9.Cre24.g769400	apospory-associated protein c-related	0.421	1.13E-02	scaffold_24	88986	93717	
CUST_1517_PI425379931	Au9.Cre16.g666650	pol-related	0.421	1.91E-02	chromosome_16	2515636	2521971	
CUST_4575_PI425379931	Au9.Cre16.g666900	pol-like protein	0.42	1.13E-02	chromosome_16	2570960	2572561	
CUST_1495_PI425379931	Au9.Cre13.g566000	Formate-tetrahydrofolate ligase	0.417	0.00E+00	chromosome_13	607997	618347	K00288
CUST_11254_PI425379931	Au9.Cre09.g402200	predicted protein	0.417	0.00E+00	chromosome_9	2519998	2521907	
CUST_5056_PI425379931	Au9.Cre07.g312700	pol-like protein	0.414	7.40E-03	chromosome_7	82530	87825	
CUST_7476_PI425379931	Au9.Cre03.g158800	s-formylglutathione hydrolase	0.414	0.00E+00	chromosome_3	1411873	1414864	K01070
CUST_3679_PI425379931	Au9.Cre12.g555350	ER retention protein	0.413	5.30E-03	chromosome_12	8516750	8518539	
CUST_4806_PI425379931	Au9.Cre07.g341400	MaoC-like dehydratase	0.413	8.40E-03	chromosome_7	3938433	3950759	
CUST_4112_PI425379931	Au9.Cre06.g263550	R53.5-related protein	0.413	0.00E+00	chromosome_6	1907913	1909951	
CUST_7077_PI425379931	Au9.Cre01.g050550	predicted protein	0.413	0.00E+00	chromosome_1	6938305	6939505	
CUST_1820_PI425379931	Au9.Cre11.g469950	MaoC-like dehydratase	0.412	6.46E-03	chromosome_11	411455	421021	
CUST_5003_PI425379931	Au9.Cre17.g743000	reverse transcriptases	0.411	2.63E-02	chromosome_17	6444217	6452308	
CUST_1304_PI425379931	Au9.Cre03.g208400	reverse transcriptases	0.408	1.13E-02	chromosome_3	7132659	7140570	

CUST_4521_PI425379931	Au9.Cre03.g164000	predicted protein	0.408	0.00E+00	chromosome_3	2051634	2055049	
CUST_2481_PI425379931	Au9.Cre09.g417000	hypothetical protein CHLREDRAFT_175511	0.407	3.41E-02	chromosome_9	4654064	4656132	
CUST_12969_PI425379931	Au9.Cre11.g468050	predicted protein	0.406	0.00E+00	chromosome_11	96924	101523	
CUST_9747_PI425379931	Au9.Cre09.g399250	ketoacid isomerase-like protein	0.406	2.18E-02	chromosome_9	2032983	2035597	
CUST_1263_PI425379931	Au9.Cre30.g779300	pol-like protein	0.404	0.00E+00	scaffold_30	101196	115207	
CUST_9202_PI425379931	Au9.Cre03.g150950	glycosyl transferase	0.404	6.62E-03	chromosome_3	437398	439261	K00721
CUST_4526_PI425379931	Au9.Cre06.g303300	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	0.402	0.00E+00	chromosome_6	6619153	6623098	
CUST_6165_PI425379931	Au9.Cre53.g790600	pol-like protein	0.401	0.00E+00	scaffold_53	476	3925	
CUST_1169_PI425379931	Au9.Cre01.g038900	phospholipase-related	0.401	1.13E-02	chromosome_1	5345110	5348123	K01054
CUST_10572_PI425379931	Au9.Cre05.g240850	Hydroxymethylpyrimidine phosphate synthase; Hydroxymethylpyrimidine phosphate synthase	0.4	0.00E+00	chromosome_5	2039096	2047535	K03147
CUST_6327_PI425379931	Au9.Cre02.g093250	pol-like protein	0.4	9.24E-03	chromosome_2	2539756	2541301	
CUST_2847_PI425379931	Au9.Cre16.g685500	kelch repeat domain	0.395	0.00E+00	chromosome_16	5134629	5137850	
CUST_7623_PI425379931	Au9.Cre13.g598900	light-harvesting protein of photosystem I	0.394	1.13E-02	chromosome_13	5048702	5051040	

CUST_7818_PI425379931	Au9.Cre07.g356300	ubiquitin-like protein	0.393	1.13E-02	chromosome_7	5939252	5940669	
CUST_3797_PI425379931	Au9.Cre06.g299700	SOUL heme-binding protein	0.393	0.00E+00	chromosome_6	6115091	6117345	
CUST_235_PI425379931	Au9.Cre05.g233900	L-ascorbate peroxidase	0.393	0.00E+00	chromosome_5	798281	801706	K00434
CUST_13606_PI425379931	Au9.Cre10.g423050	gag/pol/env polyprotein	0.392	7.40E-03	chromosome_10	778846	782592	K04228
CUST_14111_PI425379931	Au9.Cre04.g216250	Flagellar Associated Protein	0.392	7.79E-03	chromosome_4	767586	768807	
CUST_7130_PI425379931	Au9.Cre12.g513700	dead box atp-dependent rna helicase	0.391	0.00E+00	chromosome_12	3440910	3449635	
CUST_14057_PI425379931	Au9.Cre51.g790200	pol-like protein	0.39	0.00E+00	scaffold_51	36970	39055	
CUST_6547_PI425379931	Au9.Cre07.g334750	protein phosphatase 2c	0.389	2.66E-02	chromosome_7	3064056	3071717	
CUST_8178_PI425379931	Au9.Cre40.g786150	pol-like protein	0.386	0.00E+00	scaffold_40	26980	31115	
CUST_11886_PI425379931	Au9.Cre02.g110800	drug transporter-related	0.386	9.24E-03	chromosome_2	4888084	4897695	
CUST_4714_PI425379931	Au9.Cre04.g222850	hypothetical protein CHLREDRAFT_94488	0.385	8.29E-03	chromosome_4	1811612	1813286	
CUST_14199_PI425379931	Au9.Cre12.g539250	hypothetical protein CHLREDRAFT_180456	0.384	4.59E-03	chromosome_12	6535894	6538515	
CUST_4951_PI425379931	Au9.Cre01.g017700	MaoC-like dehydratase	0.384	7.21E-03	chromosome_1	2720121	2729419	
CUST_4757_PI425379931	Au9.Cre26.g774100	atp-binding cassette protein c4-like	0.381	4.30E-03	scaffold_26	310787	317272	
CUST_14031_PI425379931	Au9.Cre02.g137250	pol-like protein	0.381	6.09E-03	chromosome_2	8422148	8423419	

CUST_14604_PI425379931	Au9.Cre01.g003950		0.378	1.83E-02	chromosome_1	733795	752444	
CUST_1654_PI425379931	Au9.Cre55.g790850	pol-like protein	0.375	3.93E-03	scaffold_55	22120	23265	
CUST_2982_PI425379931	Au9.Cre03.g151650	S-adenosyl-L-methionine-dependent methyltransferase	0.374	3.56E-02	chromosome_3	521746	525589	
CUST_73_PI425379931	Au9.Cre16.g666700	pol-like protein	0.372	5.55E-03	chromosome_16	2539742	2540883	
CUST_4166_PI425379931	Au9.Cre40.g786250	pol-like protein	0.37	7.21E-03	scaffold_40	81326	83607	
CUST_1960_PI425379931	Au9.Cre12.g536300	predicted protein	0.368	0.00E+00	chromosome_12	6042656	6050437	
CUST_11772_PI425379931	Au9.Cre09.g405450	hypothetical protein	0.368	0.00E+00	chromosome_9	2978547	2980611	
CUST_13142_PI425379931	Au9.Cre13.g602100	pol-like protein	0.364	5.18E-03	chromosome_13	5499622	5503417	
CUST_2584_PI425379931	Au9.Cre12.g494850	Adenylate Kinase 3	0.364	6.09E-03	chromosome_12	1443798	1446667	K00939
CUST_1335_PI425379931	Au9.Cre14.g617450	heat shock protein 22E	0.363	1.28E-02	chromosome_14	1395808	1397277	
CUST_9659_PI425379931	Au9.Cre52.g790450	pol-like protein	0.36	0.00E+00	scaffold_52	17390	19275	
CUST_1770_PI425379931	Au9.Cre02.g137150	pol-like protein	0.36	4.30E-03	chromosome_2	8384148	8385409	
CUST_6054_PI425379931	Au9.Cre04.g228650	mgatp-energized glutathione s-conjugate	0.359	0.00E+00	chromosome_4	2788797	2812072	K05667
CUST_12679_PI425379931	Au9.Cre10.g452050	light-harvesting protein of photosystem I	0.357	6.46E-03	chromosome_10	4491980	4495280	K08908
CUST_2400_PI425379931	Au9.Cre06.g283950	chloropyll a-b binding protein of	0.356	9.24E-03	chromosome_6	4071795	4073491	K08912

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CUST_893_PI425379931	Au9.Cre29.g777900	methyltransferase family	0.353	1.05E-02	scaffold_29	53466	57277	
CUST_7411_PI425379931	Au9.Cre13.g594200	hypothetical protein CHLREDRAFT_151390	0.352	1.37E-02	chromosome_13	4530080	4532030	
CUST_1932_PI425379931	Au9.Cre01.g062500	predicted protein	0.35	0.00E+00	chromosome_1	8630590	8632381	
CUST_13194_PI425379931	Au9.Cre14.g625350	integral membrane protein	0.347	5.55E-03	chromosome_14	2555159	2561648	
CUST_11585_PI425379931	Au9.Cre08.g360100	allophanate hydrolase	0.347	5.34E-03	chromosome_8	283650	289781	K01457
CUST_6228_PI425379931	Au9.Cre01.g062700	pol-like protein	0.347	6.09E-03	chromosome_1	8660510	8662241	
CUST_6719_PI425379931	Au9.Cre07.g348350	predicted protein	0.346	1.65E-02	chromosome_7	4906089	4910029	
CUST_3411_PI425379931	Au9.Cre14.g613800	hypothetical protein CHLREDRAFT_152091	0.344	1.83E-02	chromosome_14	937561	942310	
CUST_3026_PI425379931	Au9.Cre17.g742900	reverse transcriptase	0.343	0.00E+00	chromosome_17	6416817	6432678	K14401
CUST_10153_PI425379931	Au9.Cre08.g359350	biotin carboxylase, acetyl-CoA carboxylase component	0.341	0.00E+00	chromosome_8	157589	166955	K01961
CUST_7007_PI425379931	Au9.Cre25.g771750	reverse transcriptases	0.339	5.10E-03	scaffold_25	301804	307399	
CUST_13960_PI425379931	Au9.Cre51.g790350	pol-like protein	0.338	0.00E+00	scaffold_51	59446	62951	
CUST_7697_PI425379931	Au9.Cre12.g539500	pol-like protein	0.338	0.00E+00	chromosome_12	6613678	6621033	
CUST_6993_PI425379931	Au9.Cre02.g117150	AAA+-type ATPase	0.338	0.00E+00	chromosome_2	5674217	5680078	K00413

CUST_7042_PI425379931	Au9.Cre30.g779250	reverse transcriptases	0.337	0.00E+00	scaffold_30	77600	93665	
CUST_2961_PI425379931	Au9.Cre12.g493050	predicted protein	0.336	4.15E-03	chromosome_12	1237066	1242769	
CUST_1855_PI425379931	Au9.Cre02.g141750	tubulin polymerization promoting protein	0.336	7.40E-03	chromosome_2	9151084	9154269	
CUST_560_PI425379931	Au9.Cre13.g597250	hypothetical protein CHLREDRAFT_151338	0.334	4.30E-03	chromosome_13	4866406	4872285	
CUST_10335_PI425379931	Au9.Cre03.g168950	predicted protein	0.334	4.59E-03	chromosome_3	2693550	2694908	
CUST_12182_PI425379931	Au9.Cre16.g666850	reverse transcriptases	0.33	0.00E+00	chromosome_16	2559862	2565553	
CUST_10962_PI425379931	Au9.Cre01.g069500	predicted protein; DNA Repair Enzyme;predicted protein; DNA Repair Enzyme	0.328	5.34E-03	chromosome_1	9494272	9494747	
CUST_6452_PI425379931	Au9.Cre01.g062100	predicted protein	0.328	4.75E-03	chromosome_1	8589674	8592559	
CUST_9251_PI425379931	Au9.Cre01.g033800	dead box atp-dependent rna helicase	0.328	8.07E-03	chromosome_1	4702069	4705460	
CUST_11144_PI425379931	Au9.Cre02.g093000	heat shock protein 70d	0.324	0.00E+00	chromosome_2	2480020	2481435	
CUST_7684_PI425379931	Au9.Cre14.g625250	lactosylceramide 4-alpha-galactosyltransferase (alpha- 1,4-galactosyltransferase)	0.322	1.59E-02	chromosome_14	2535669	2540201	
CUST_9766_PI425379931	Au9.Cre02.g097800	ABC transporter	0.319	1.73E-02	chromosome_2	3208392	3215493	K05666

CUST_6610_PI425379931	Au9.Cre18.g747850	fibrillin 2	0.312	5.10E-03	scaffold_18	697989	700592	
CUST_11004_PI425379931	Au9.Cre13.g572750	Copper amine oxidase, amiloride-sensitive	0.31	4.16E-02	chromosome_13	1494443	1502684	K11182
CUST_6968_PI425379931	Au9.Cre18.g745750		0.309	4.30E-03	scaffold_18	361782	388626	
CUST_10722_PI425379931	Au9.Cre03.g148700	predicted protein	0.309	8.07E-03	chromosome_3	129652	132185	
CUST_2563_PI425379931	Au9.Cre01.g060950	N-acetyl-gamma-glutamyl-phosphate reductase	0.308	1.26E-02	chromosome_1	8435584	8441177	
CUST_12376_PI425379931	Au9.Cre12.g554100	predicted protein	0.305	2.29E-02	chromosome_12	8388735	8397670	
CUST_12075_PI425379931	Au9.Cre17.g727300	NADH:flavin oxidoreductase	0.301	6.04E-03	chromosome_17	3739694	3743659	K10680
CUST_10059_PI425379931	Au9.Cre16.g648300	major facilitator superfamily	0.299	1.00E-02	chromosome_16	103204	109365	K12301
CUST_2075_PI425379931	Au9.Cre10.g432950	predicted protein	0.294	0.00E+00	chromosome_10	2009810	2013802	
CUST_1922_PI425379931	Au9.Cre12.g504600	Histone H4	0.291	0.00E+00	chromosome_12	2447167	2447805	K11254
CUST_338_PI425379931	Au9.Cre05.g234900	pol-like protein	0.29	0.00E+00	chromosome_5	971469	974854	
CUST_9410_PI425379931	Au9.Cre03.g162800	low-CO2-inducible membrane protein	0.251	1.83E-02	chromosome_3	1912556	1915165	
CUST_217_PI425379931	Au9.Cre08.g365900	stress-related chlorophyll a/b binding protein 1	0.25	9.80E-03	chromosome_8	1257470	1259618	K08907
CUST_14577_PI425379931	Au9.Cre37.g784750	heat shock protein 70D	0.249	0.00E+00	scaffold_37	14323	16445	

CUST_2423_PI425379931	Au9.Cre12.g537000	predicted protein	0.247	7.21E-03	chromosome_12	6136367	6139268	
CUST_13597_PI425379931	Au9.Cre01.g000150	Zinc-nutrition responsive permease transporter	0.242	9.46E-03	chromosome_1	25206	29917	
CUST_10411_PI425379931	Au9.Cre12.g506750	cell wall protein pherophorin-c4	0.241	2.83E-02	chromosome_12	2606280	2612075	
CUST_2806_PI425379931	Au9.Cre12.g530600	glutamine synthetase	0.238	4.98E-02	chromosome_12	5319964	5322778	K01915
CUST_2027_PI425379931	Au9.Cre10.g463500	mapkk-related serine/threonine protein kinases	0.236	1.13E-02	chromosome_10	6086696	6094614	
CUST_6973_PI425379931	Au9.Cre17.g707550		0.214	4.34E-02	chromosome_17	1570470	1580906	
CUST_6270_PI425379931	Au9.Cre01.g012050	Formate/nitrite transporter	0.207	0.00E+00	chromosome_1	2014474	2018767	K00122
CUST_9724_PI425379931	Au9.Cre07.g355150	zinc-nutrition responsive transporter	0.188	0.00E+00	chromosome_7	5797046	5800997	
CUST_11710_PI425379931	Au9.Cre14.g620650	cell wall protein pherophorin-C13	0.181	0.00E+00	chromosome_14	1862034	1865728	
CUST_14340_PI425379931	Au9.Cre16.g658400	Apoferredoxin	0.164	8.07E-03	chromosome_16	1387335	1388912	K02639
CUST_13661_PI425379931	Au9.Cre16.g673250	squamosa promoter binding protein	0.139	3.12E-02	chromosome_16	3522344	3532692	
CUST_11046_PI425379931	Au9.Cre08.g360050	urea carboxylase	0.0977	1.13E-02	chromosome_8	273181	283469	K01941
CUST_1662_PI425379931	Au9.Cre14.g615350	truncated hemoglobin	0.0688	0.00E+00	chromosome_14	1124848	1127027	K03406

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[a] Fold-change indicates expression in NP exposed *C. reinhardtii* normalised to expression in control samples.

[b] q-value shows multiple testing corrected probability values determined by SAM within MeV.

TABLE S4. Composition of the Bolds Basal Medium (BBM) growth media for *C. reinhardtii*.[α]

Stock solution no.	Name	Formula	Weight (g)	Distilled water (mL)	Volume required for 1L BBM (ml)
1	di-potassium hydrogen orthophosphate	K_2HPO_4	1.875	250	10
2	Potassium di-hydrogen orthophosphate	KH_2PO_4	4.375	250	10
3	Magnesium sulphate	$MgSO_4.7H_2O$	1.875	250	10
4	Sodium nitrate	$NaNO_3$	6.250	250	10
5	Calcium chloride	$CaCl_2.2H_2O$	0.625	250	10
6	Sodium chloride	NaCl	0.625	250	10
7	Ferrous sulphate	$FeSO_47H_2O$	0.498	100	1
	Sulphuric acid conc. (wt per mL = 1.84g)	H_2SO_4	0.1mL		
8	Boric acid	H_3BO_3	1.142	100	1
9	Zinc sulphate	$ZnSO_4.7H_2O$	0.353	25	0.1
10	Manganese chloride	$MnCl_2.4H_2O$	0.058	25	0.1
11	Cupric sulphate	$CuSO_4.5H_2O$	0.063	25	0.1
12	Cobaltous nitrate	$Co(NO_3)_2.6H_2O$	0.020	25	0.1
13	Sodium molybdate	$Na_2MoO_4.2H_2O$	0.048	25	0.1

[α] Each stock solution was made individually using distilled water and autoclaved. The volumes given in the final column of the table were made up to 1L final volume using distilled water. The pH of the final media was in the range of 6.7 ± 0.3 and autoclaved prior to use.